A generic framework for individual-based modelling and physical-biological interaction

The increased availability of high-resolution ocean data globally has enabled more detailed analyses of physical-biological interactions and their consequences to the ecosystem. We present IBMlib, which is a versatile, portable and computationally effective framework for conducting Lagrangian simulations in the marine environment. The purpose of the framework is to handle complex individual-level biological models of organisms, combined with realistic 3D oceanographic model of physics and biogeochemistry describing the environment of the organisms without assumptions about spatial or temporal scales. The open-source framework features a minimal robust interface to facilitate the coupling between individual-level biological models and oceanographic models, and we provide application examples including forward/backward simulations, habitat connectivity calculations, assessing ocean conditions, comparison of physical circulation models, model ensemble runs and recently posterior Eulerian simulations using the IBMlib framework. We present the code design ideas behind the longevity of the code, our implementation experiences, as well as code performance benchmarking. The framework may contribute substantially to progresses in representing, understanding, predicting and eventually managing marine ecosystems.
Effect of fish length and nutritional condition on the fecundity of distressed Atlantic cod Gadus morhua from the Baltic Sea: Potential fecundity of Baltic G. Morhua

General information
State: Accepted/In press
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Swedish University of Agricultural Sciences, Institute of Marine Research, Swedish University of Agricultural Sciences, GEOMAR Helmholtz Center for Ocean Research Kiel, University of Hamburg
Authors: Mion, M. (Ekstern), Thorsen, A. (Ekstern), Vitale, F. (Ekstern), Dierking, J. (Ekstern), Herrmann, J. P. (Ekstern), Huwer, B. (Intern), von Dewitz, B. (Ekstern), Casini, M. (Ekstern)
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Scopus rating (2016): CiteScore 1.57 SJR 0.741 SNIP 0.882
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.951 SNIP 0.935 CiteScore 1.64
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.944 SNIP 0.934 CiteScore 1.76
Web of Science (2014): Indexed yes
First genetic quantification of sex- and stage-specific feeding in the ubiquitous copepod Acartia tonsa

Marine copepods provide the major food-web link between primary producers and higher trophic levels, and their feeding ecology is of acute interest in light of global change impacts on food-web functioning. Recently, quantitative polymerase chain reaction (qPCR) protocols have been developed, which can complement classic diet quantification methods, such as stable isotope or fatty acid analyses tools. Here, we present first results of feeding experiments assessing sex- and stage-specific food intake by the ubiquitous calanoid copepod Acartia tonsa by 18S targeted qPCR and microscopic grazing assessment. In triplicated mixed-diet feeding treatments, three suitable A. tonsa diets, the cryptophyte Rhodomonas balthica, the haptophyte Isochrysis galbana, and the diatom Thalassiosira weissflogii, were offered in equal biomass proportions under constant conditions. Prey uptake substantially varied between different algal species, as did the extent of sex- and stage-specificity of prey uptake. Male adult copepods had higher R. balthica gut contents than females, and nauplii contained more of this prey source than copepodites or adult copepods in mixed treatments. A trend towards higher amounts of ingested T. weissflogii in adult females than in males and in naupliii than in other stages was
detected. Genetic gut content quantifications indicated low feeding on I. galbana, and no consistent sex- or stage-specific differences of I. galbana content in A. tonsa. Our results highlight diet-specific feeding differences between Acartia life stages and sexes, which can have implications on food-web dynamics and specific nutrient transfer to higher trophic levels in copepod populations of varying age composition under changing environmental parameters, such as rising temperatures and increasing ocean acidification.

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Technical University of Denmark, GEOMAR Helmholtz Center for Ocean Research Kiel
Authors: Ismar, S. M. (Ekstern), Kottmann, J. S. (Intern), Sommer, U. (Ekstern)
Publication date: 2018
Main Research Area: Technical/natural sciences

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Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.41 SJR 1.198 SNIP 0.993
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.315 SNIP 0.932 CiteScore 2.21
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.204 SNIP 1.041 CiteScore 2.32
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.272 SNIP 1.064 CiteScore 2.4
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.306 SNIP 1.107 CiteScore 2.43
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.145 SNIP 1.073 CiteScore 2.22
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.235 SNIP 1.069
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.178 SNIP 1.052
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.236 SNIP 1.022
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.348 SNIP 1.21
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.195 SNIP 1.09
Flabellum alabastrum deep sea cup coral meadows from West Greenland: Density, catchability and habitat suitability modelling

**General information**
State: Accepted/In press
Organisations: Arctic Section, National Institute of Aquatic Resources, Section for Marine Living Resources, Natural History Museum of Denmark, Aarhus University
Authors: Jørgensbye, H. (Intern), Tendal, O. S. (Ekstern), Wegeberg, S. (Ekstern), Mosegaard, H. (Intern)
Publication date: 2018
Main Research Area: Technical/natural sciences

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Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.76 SJR 1.45 SNIP 1.119
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.369 SNIP 1.174 CiteScore 2.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.557 SNIP 1.279 CiteScore 2.67
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.077 SNIP 1.314 CiteScore 3.11
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.024 SNIP 1.165 CiteScore 2.81
Integrated ecological-economic fisheries models - evaluation, review and challenges for implementation

Marine ecosystems evolve under many interconnected and area-specific pressures. In order to fulfill society's intensifying and diversifying needs whilst ensuring ecologically sustainable development, more effective marine spatial planning and broader-scope management of marine resources is necessary. Integrated ecological–socioeconomic fisheries models (IESFM) of marine systems are needed to evaluate impacts and sustainability of potential management actions and understand, and anticipate ecological, economic, and social dynamics at a range of scales from local to national and regional. To make these models most effective, it is important to determine how model characteristics and methods of communicating results influence the model implementation, the nature of the advice that can be provided and the impact on decisions taken by managers. This paper presents a global review and comparative evaluation of 35 IESFM’s applied to marine fisheries and marine ecosystem resources to identify the characteristics that determine their usefulness, effectiveness and implementation. The focus is on fully integrated models that allow for feedbacks between ecological and human processes though not all the models reviewed achieve that

General information

State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Oceans and Arctic, National Oceanographic and Atmospheric Administration, Christian-Albrechts-Universität zu Kiel, CSIRO, University of Washington, Plymouth Marine Laboratory, IFREMER, Thünen Institute of Sea Fisheries, New Economics Foundation, University of British Columbia, University of Vigo, AZTI-Tecnalia, Université Bretagne Loire, Institut de Ciències del Mar-CSIC, Wageningen University, National Marine Fisheries Research Institute, Scottish Pelagic Fishermen’s Association, AZTI Technalia, University of Southern Denmark, Swiss Federal Institute of Aquatic Science and Technology, Wageningen IMARES, Commonwealth Scientific and Industrial Research Organisation, University of Copenhagen, Swedish Agency for Marine and Water Management, Stockholm University, Lund University
No increase in marine microplastic concentration over the last three decades - A case study from the Baltic Sea

Microplastic is considered a potential threat to marine life as it is ingested by a wide variety of species. Most studies on microplastic ingestion are short-term investigations and little is currently known about how this potential threat has developed over the last decades where global plastic production has increased exponentially. Here we present the first long-term study on microplastic in the marine environment, covering three decades from 1987 to 2015, based on a unique sample set originally collected and conserved for food web studies. We investigated the microplastic concentration in plankton samples and in digestive tracts of two economically and ecologically important planktivorous forage fish species, Atlantic herring (Clupea harengus) and European sprat (Sprattus sprattus), in the Baltic Sea, an ecosystem which is under high anthropogenic pressure and has undergone considerable changes over the past decades. Surprisingly, neither the concentration of microplastic in the plankton samples nor in the digestive tracts changed significantly over the investigated time period. Average microplastic concentration in the plankton samples was 0.21±0.15 particles m⁻³. Of 814 fish examined, 20% contained plastic particles, of which 95% were characterized as microplastic.
Population genetics of pike

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Wennerström, L. (Ekstern), Bekkevold, D. (Intern), Laikre, L. (Ekstern)
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Main Research Area: Technical/natural sciences
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Status for laksen og dens forvaltning i Danmark 2017

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine Living Resources
Authors: Koed, A. (Intern), Sivebæk, F. (Intern), Eg Nielsen, E. (Intern)
Publication date: 2018
Temperature induced variation in gene expression of thyroid hormone receptors and deiodinases of European eel (Anguilla anguilla) larvae

Thyroid hormones (THs) are key regulators of growth, development, and metabolism in vertebrates and influence early life development of fish. TH is produced in the thyroid gland (or thyroid follicles) mainly as T4 (thyroxine), which is metabolized to T3 (3,5,3'-triiodothyronine) and T2 (3,5-diodothyronine) by deiodinase (DIO) enzymes in peripheral tissues. The action of these hormones is mostly exerted by binding to a specific nuclear thyroid hormone receptor (THR). In this study, we i) cloned and characterized thr sequences, ii) investigated the expression pattern of the different subtypes of thrs and dios, and iii) studied how temperature affects the expression of those genes in artificially produced early life history stages of European eel (Anguilla anguilla), reared in different thermal regimes (16, 18, 20 and 22°C) from hatch until first-feeding.

We identified 2 subtypes of thr (thrα and thrβ) with 2 isoforms each (thrαA, thrαB, thrβA, thrβB) and 3 subtypes of deiodinases (dio1, dio2, dio3). All thr genes identified showed high similarity to the closely related Japanese eel (Anguilla japonica). We found that all genes investigated in this study were affected by larval age (in real time or at specific developmental stages), temperature, and/or their interaction. More specifically, the warmer the temperature the earlier the expression response of a specific target gene. In real time, the expression profiles appeared very similar and only shifted with temperature. In developmental time, gene expression of all genes differed across selected developmental stages, such as at hatch, during teeth formation or at first-feeding. Thus, we demonstrate that the expression of thrs and dios show sensitivity to temperature and are involved in and during early life development of European eel.
What we once knew – Mapping of marine sediments on the Greenland west coast: Comparing fishers’ ecological knowledge with historical and recent sources

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Organisations: Arctic Section, National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University
Authors: Jørgensbye, H. (Intern), Wegeberg, S. (Ekstern)
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.63
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.18
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.46
ISI indexed (2013): ISI indexed yes
A Hidden Markov Movement Model for rapidly identifying behavioral states from animal tracks

1. Electronic telemetry is frequently used to document animal movement through time. Methods that can identify underlying behaviors driving specific movement patterns can help us understand how and why animals use available space, thereby aiding conservation and management efforts. For aquatic animal tracking data with significant measurement error, a Bayesian state-space model called the first-Difference Correlated Random Walk with Switching (DCRWS) has often been used for this purpose. However, for aquatic animals, highly accurate tracking data of animal movement are now becoming more common. 2. We developed a new Hidden Markov Model (HMM) for identifying behavioral states from animal tracks with negligible error, which we called the Hidden Markov Movement Model (HMMM). We implemented as the basis for the HMMM the process equation of the DCRWS, but we used the method of maximum likelihood and the R package TMB for rapid model fitting. 3. We compared the HMMM to a modified version of the DCRWS for highly accurate tracks, the DCRWSnome, and to a common HMM for animal tracks fitted with the R package moveHMM. We show that the HMMM is both accurate and suitable for multiple species by fitting it to real tracks from a grey seal, lake trout, and blue shark, as well as to simulated data. 4. The HMMM is a fast and reliable tool for making meaningful inference from animal movement data that is ideally suited for ecologists who want to use the popular DCRWS implementation for highly accurate tracking data. It additionally provides a groundwork for development of more complex modelling of animal movement with TMB. To facilitate its uptake, we make it available through the R package swim.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Dalhousie University, Michigan State University
Analysis of marine protected areas – in the Danish part of the North Sea and the Central Baltic around Bornholm: Part 1: The coherence of the present network of MPAs

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Oceans and Arctic, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Monitoring and Data, DHI Denmark, Geological Survey of Denmark and Greenland, Aarhus University, University of Copenhagen
Number of pages: 105
Publication date: 2017

Publication information
Publisher: National Institute of Aquatic Resources, Technical University of Denmark
ISBN (Electronic): 978-87-7481-245-6
Original language: English
Analysis of marine protected areas – in the Danish part of the North Sea and the Central Baltic around Bornholm: Part 2: Ecological and economic value, human pressures, and MPA selection

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Oceans and Arctic, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Monitoring and Data, DHI Denmark, Geological Survey of Denmark and Greenland, Aarhus University, University of Copenhagen
Number of pages: 120
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Original language: English

A spatiotemporal model for snow crab (Chionoecetes opilio) stock size in the southern Gulf of St. Lawrence
We develop a high-resolution spatiotemporal model of stock size and harvest rates for snow crab (Chionoecetes opilio) in the southern Gulf of St. Lawrence, which supports an economically important fishery off the east coast of Canada. It is a spatial and weekly model during 1997–2014 that utilizes within-season depletion based on catch per unit of effort (CPUE; kg·pot⁻¹) and also biomass values from a survey designed specifically for this stock. The model is formulated in a state-space framework. The main contribution of the model is to provide a better understanding of fishery-dependent factors that affect CPUE. There is strong evidence of density dependence in the relationship with CPUE and stock biomass, in addition to a general increase in CPUE catchability over time that may be related to changes in gear soak time and spatial variation in catchability. We also find that a natural mortality rate of 0.4 provides a better fit to survey results. Model results suggest that there is no evidence of effort saturation in the fishery
A stochastic surplus production model in continuous time

Surplus production modelling has a long history as a method for managing data-limited fish stocks. Recent advancements have cast surplus production models as state-space models that separate random variability of stock dynamics from error in observed indices of biomass. We present a stochastic surplus production model in continuous time (SPiCT), which in addition to stock dynamics also models the dynamics of the fisheries. This enables error in the catch process to be reflected in the uncertainty of estimated model parameters and management quantities. Benefits of the continuous-time state-space model formulation include the ability to provide estimates of exploitable biomass and fishing mortality at any point in time from data sampled at arbitrary and possibly irregular intervals. We show in a simulation that the ability to analyse subannual data can increase the effective sample size and improve estimation of reference points relative to discrete-time analysis of aggregated annual data. Finally, subannual data from five North Sea stocks are analysed with particular focus on using residual analysis to diagnose model insufficiencies and identify necessary model extensions such as robust estimation and incorporation of seasonality. We argue that including all known sources of uncertainty, propagation of that uncertainty to reference points and checking of model assumptions using residuals are critical prerequisites to rigorous fish stock management based on surplus production models.
Billedmosaik til kortlægning af udbredelse af jomfruhummer

General information
State: Published
Organisations: National Institute of Aquatic Resources, Arctic Section, Section for Marine Living Resources, Section for Maritime Service
Authors: Lundgren, B. (Intern), Stage, B. (Intern), Pedersen, E. M. (Intern), Lisbjerg, D. (Intern)
Publication date: 2017
Event: Poster session presented at Dansk Havforskermøde, Helsingør, Denmark.
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Publication: Research › Poster – Annual report year: 2017

Changes in food web function and diversity due to non-indigenous species

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Oceans and Arctic, Abo Academy University, University of Erlangen-Nuremberg
Authors: Lehtiniemi, M. (Ekstern), Bonsdorff, E. (Ekstern), Funk, S. (Ekstern), Herlevi, H. (Ekstern), Huwer, B. (Intern), Jaspers, C. (Intern)
Number of pages: 127
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Changes in reproductive life history and resource allocation impacting population dynamics of Baltic cod

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Monitoring and Data, Section for Ecosystem based Marine Management, Institute Management
Authors: Tomkiewicz, J. (Intern), Huwer, B. (Intern), Cordón, C. T. F. (Intern), Storr-Paulsen, M. (Intern), Eero, M. (Intern), Köster, F. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2017

Choosing the observational likelihood in state-space stock assessment models

Data used in stock assessment models result from combinations of biological, ecological, fishery, and sampling processes. Since different types of errors propagate through these processes it can be difficult to identify a particular family of distributions for modelling errors on observations a priori. By implementing several observational likelihoods, modelling both numbers- and proportions-at-age, in an age based state-space stock assessment model, we compare the model fit for each choice of likelihood along with the implications for spawning stock biomass and average fishing mortality. We propose using AIC intervals based on fitting the full observational model for comparing different observational likelihoods. Using data from four stocks, we show that the model fit is improved by modelling the correlation of observations within years. However, the best choice of observational likelihood differs for different stocks, and the choice is important for the short-term conclusions drawn from the assessment model; in particular, the choice can influence total allowable catch advise based on reference points.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Albertsen, C. M. (Intern), Nielsen, A. (Intern), Thygesen, U. H. (Intern)
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Main Research Area: Technical/natural sciences
Publication information
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.56 SJR 1.322 SNIP 1.163
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.256 SNIP 1.051 CiteScore 2.22
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Connecting single-stock assessment models through correlated survival

Fisheries management is mainly conducted via single-stock assessment models assuming that fish stocks do not interact, except through assumed natural mortalities. Currently, the main alternative is complex ecosystem models which require extensive data, are difficult to calibrate, and have long run times. We propose a simple alternative. In three case studies each with two stocks, we improve the single-stock models, as measured by Akaike information criterion, by adding correlation in the cohort survival. To limit the number of parameters, the correlations are parameterized through the corresponding partial correlations. We consider six models where the partial correlation matrix between stocks follows a band structure ranging from independent assessments to complex correlation structures. Further, a simulation study illustrates the importance of handling correlated data sufficiently by investigating the coverage of confidence intervals for estimated...
fishing mortality. The results presented will allow managers to evaluate stock statuses based on a more accurate
evaluation of model output uncertainty. The methods are directly implementable for stocks with an analytical assessment
and do not require any new data sources.

**General information**
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Albertsen, C. M. (Intern), Nielsen, A. (Intern), Thygesen, U. H. (Intern)
Pages: 235-244
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BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.63
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.18
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.46
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.35
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.32
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Consequences of eye fluke infection on anti-predator behaviours in invasive round gobies in Kalmar Sound

Larvae of the eye fluke, Diplostomum, emerge from snails and infect fish by penetrating skin or gills, then move to the lens where they may impair the vision of the fish. For the fluke to reproduce, a bird must eat the infected fish, and it has been suggested that they therefore actively manipulate the fish’s behaviour to increase the risk of predation. We found that round gobies Neogobius melanostomus, a species that was recently introduced to the Kalmar Sound of the Baltic Sea, had an eye fluke prevalence of 90–100%. We investigated how the infection related to behavioural variation in round gobies. Our results showed that the more intense the parasite-induced cataract, the weaker the host’s response was to simulated avian attack. The eye flukes did not impair other potentially important anti-predator behaviours, such as shelter use, boldness and the preference for shade. Our results are in accordance with the suggestion that parasites induce changes in host behaviour that will facilitate transfer to their final host.

General information
State: Published
Organisations: Section for Marine Living Resources, Linnaeus University
Authors: Flink, H. (Ekstern), Behrens, J. W. (Intern), Svensson, P. A. (Ekstern)
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Journal: Parasitology Research
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.2 SJR 0.882 SNIP 0.958
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.956 SNIP 0.994 CiteScore 2.07
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.982 SNIP 1.207 CiteScore 2.26
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.078 SNIP 1.155 CiteScore 2.4
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.167 SNIP 1.313 CiteScore 2.8
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.996 SNIP 1.057 CiteScore 2.3
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.863 SNIP 0.92
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.747 SNIP 0.93
BFI (2008): BFI-level 1
Dynamiske brugerstyrede havkort til værdiløft af dansk industrifiskeri (GUDP-VIND)

General information
Early engagement of stakeholders with individual-based modelling can inform research for improving invasive species management: the round goby as a case study

Individual-based models (IBMs) incorporating realistic representations of key range-front processes such as dispersal can be used as tools to investigate the dynamics of invasive species. Managers can apply insights from these models to take effective action to prevent further spread and prioritize measures preventing establishment of invasive species. We highlight here how early-stage IBMs (constructed under constraints of time and data availability) can also play an important role in defining key research priorities for providing key information on the biology of an invasive species in order that subsequent models can provide robust insight into potential management interventions. The round goby, Neogobius melanostomus, is currently spreading through the Baltic Sea, with major negative effects being reported in the wake of its invasion. Together with stakeholders, we parameterize an IBM to investigate the goby's potential spread pattern throughout the Gulf of Gdansk and the Baltic Sea. Model parameters were assigned by integrating information obtained through stakeholder interaction, from scientific literature, or estimated using an inverse modeling approach when not available. IBMs can provide valuable direction to research on invasive species even when there is limited data and/or time available to parameterize/fit them to the degree to which we might aspire in an ideal world. Co-development of models with stakeholders can be used to recognize important invasion patterns, in addition to identifying and estimating unknown environmental parameters, thereby guiding the direction of future research. Well-parameterized and validated models are not required in the earlier stages of the modeling cycle where their main utility is as a tool for thought.
Effectiveness of fully documented fisheries to estimate discards in a participatory research scheme

A key challenge for fisheries science and management is the access to reliable and verifiable catch data. In science, the challenge is to collect reliable, precise and traceable data to provide sound advice. In management, the challenge is that catch documentation is necessary to enforce regulations. Currently, catch inspection at sea, self-reporting through e-log and on-board observers are the primary methods to document catches at sea. However, at-sea control and on-board observers are costly and have limited coverage, while self-reporting is susceptible to fraud and provides limited coverage. New cost-effective methods are currently emerging involving Remote Electronic Monitoring (REM) and on-board cameras. Previous studies have tested REM with promising results. However, evaluation of the potential biases of REM is needed before full benefits can be obtained. We deployed REM with on-board cameras on 14 fishing vessels and were able to inspect 56% of 1523 hauls made in the 6 month trial period, using an estimated 582 man-hours of video audit. The results showed an overall good agreement between the fishers self-reported discards and the video inspectors discard estimates. However, there was large variation in precision between individual vessels and species. Additionally, trial setup and process errors were shown to have a large effect on the precision of the video inspectors discard estimates. Nevertheless, despite challenges, REM was evaluated to have the potential to streamline monitoring and scientific documentation in a medium-size fishing fleet

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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.21 SJR 1.12 SNIP 1.136
Effects of acoustic telemetry transmitters on gill ventilation rate and haematocrit levels of round goby Neogobius melanostomus
Erfaringsopsamling med kirurgisk implantering af akustiske transmitters i sortmundet kutling (Neogobius melanostomus)

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources
Authors: Christoffersen, M. (Intern), Sokolova, M. (Intern), Svendsen, J. C. (Intern), Deurs, M. V. (Intern), Behrens, J. (Intern)
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Event: Abstract from Dansk Havforskermøde, Helsingør, Denmark.
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Erfaringsopsamling med kirurgisk implantering af akustiske transmitters i sortmundet kutling

General information
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Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Marine Ecology and Oceanography
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Event: Abstract from Dansk Havforskermøde, Helsingør, Denmark.
Main Research Area: Technical/natural sciences

Estimating uncertainty of data limited stock assessments
Many methods exist to assess the fishing status of data-limited stocks; however, little is known about the accuracy or the uncertainty of such assessments. Here we evaluate a new size-based data-limited stock assessment method by applying it to well-assessed, data-rich fish stocks treated as data-limited. Particular emphasis is put on providing uncertainty estimates of the data-limited assessment. We assess four cod stocks in the North-East Atlantic and compare our estimates of stock status (F/Fmsy) with the official assessments. The estimated stock status of all four cod stocks followed the established stock assessments remarkably well and the official assessments fell well within the uncertainty bounds. The estimation of spawning stock biomass followed the same trends as the official assessment, but not the same levels. We conclude that the data-limited assessment method can be used for stock assessment and that the uncertainty estimates are reliable. Further work is needed to quantify the spawning biomass of the stock.

General information
State: Published
Organisations: Centre for Ocean Life, National Institute of Aquatic Resources, Section for Marine Living Resources, Centre for Ecological and Evolutionary Synthesis, Faroe Marine Research Institute
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Pages: 69-77
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Evaluating dispersal potential of an invasive fish by the use of aerobic scope and osmoregulation capacity

Non-indigenous species (NIS) can impact marine biodiversity and ecosystem structure and function. Once introduced into a new region, secondary dispersal is limited by the physiology of the organism in relation to the ambient environment and by complex interactions between a suite of ecological factors such as presence of predators, competitors, and parasites. Early prediction of dispersal potential and future 'area of impact' is challenging, but also a great asset in taking appropriate management actions. Aerobic scope (AS) in fish has been linked to various fitness-related parameters, and may be
valuable in determining dispersal potential of aquatic invasive species in novel environments. Round goby, Neogobius melanostomus, one of the most wide-ranging invasive fish species in Europe and North America, currently thrives in brackish and fresh water, but its ability to survive in high salinity waters is unknown to date. We show that AS in round goby is reduced by 30% and blood plasma osmolality increased (indicating reduced capacity for osmoregulation) at salinities approaching oceanic conditions, following slow ramping (5 PSU per week) and subsequent long-term acclimation to salinities ranging between 0 and 30 PSU (8 days at final treatment salinities before blood plasma osmolality measurements, 12-20 additional days before respirometry). Survival was also reduced at the highest salinities yet a significant proportion (61%) of the fish survived at 30 PSU. Reduced physiological performance at the highest salinities may affect growth and competitive ability under oceanic conditions, but to what extent reduced AS and osmoregulatory capacity will slow the current 30 km year-1 rate of advance of the species through the steep salinity gradient from the brackish Baltic Sea and into the oceanic North Sea remains speculative. An unintended natural experiment is in progress to test whether the rate of advance slows down. At the current rate of advance the species will reach the oceanic North Sea by 2018/2019, therefore time for taking preventative action is short.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, University of Copenhagen
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Publication date: 2017
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Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94
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Web of Science (2013): Indexed yes
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Scopus rating (2012): SJR 1.945 SNIP 1.142 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
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Scopus rating (2010): SJR 2.631 SNIP 1.161
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.473 SNIP 0.985
Extracting DNA from 'jaws': High yield and quality from archived tiger shark (Galeocerdo cuvier) skeletal material

Archived specimens are highly valuable sources of DNA for retrospective genetic/genomic analysis. However, often limited effort has been made to evaluate and optimize extraction methods, which may be crucial for downstream applications. Here, we assessed and optimized the usefulness of abundant archived skeletal material from sharks as a source of DNA for temporal genomic studies. Six different methods for DNA extraction, encompassing two different commercial kits and three different protocols, were applied to material, so-called bio-swarf, from contemporary and archived jaws and vertebrae of tiger sharks (Galeocerdo cuvier). Protocols were compared for DNA yield and quality using a qPCR approach. For jaw swarf, all methods provided relatively high DNA yield and quality, while large differences in yield between protocols were observed for vertebrae. Similar results were obtained from samples of white shark (Carcharodon carcharias). Application of the optimized methods to 38 museum and private angler trophy specimens dating back to 1912 yielded sufficient DNA for downstream genomic analysis for 68% of the samples. No clear relationships between age of samples, DNA quality and quantity were observed, likely reflecting different preparation and storage methods for the trophies. Trial sequencing of DNA capture genomic libraries using 20 000 baits revealed that a significant proportion of captured sequences were derived from tiger sharks. This study demonstrates that archived shark jaws and vertebrae are potential high-yield sources of DNA for genomic-scale analysis. It also highlights that even for similar tissue types, a careful evaluation of extraction protocols can vastly improve DNA yield.
Female nutrition and assisted reproduction in European eel: influences on oogenesis and egg quality

The European eel (Anguilla anguilla) has an enigmatic life-cycle. One of its most unique features is the 5000 to 6000 km separating the growth areas in Europe and North Africa from the spawning grounds in the Sargasso Sea. Even more enigmatic is the fact that naturally matured eels have never been caught and thus, spawning in the wild has never been observed. Because sexual maturation is blocked until the silvering phase and start of spawning migration, eels do not mature spontaneously in captivity and gonad development is induced by the application of exogenous hormones. In female eels, induction of egg production involves a long-term hormonal treatment of salmon or carp pituitary extracts (SPE or CPE) followed by the induction of oocyte maturation and ovulation which includes a SPE primer and a maturation-inducing hormone (MIH), generally 17α, 20β-dihydroxy-4-pregnen-3-one (DHP). Recent progress in techniques for induction of maturation and fertilization of the eggs has enabled the production of many viable eggs and yolk-sac larvae that are able of exogenous feeding. The present studies have contributed to this progress by addressing some of the challenges commonly associated with the induction of female maturation and egg quality. The main objectives of this PhD study were to improve female response to hormonal treatments and resulting egg quality. These challenges were addressed by working with both cultured and wild female eels, testing different broodstock diets and hormonal treatments, and identifying possible factors associated with egg quality. The results showed that dietary fatty acid composition has a significant influence on ovarian development in response to hormonal treatments. During oocyte maturation and ovulation, the expression of hormone receptors at the time SPE and DHP were administrated differed between high and low egg quality groups. It appears that a mismatch between hormone receptor expression and the administration of SPE and DHP may be determinant for acquisition of oocyte developmental competence. Moreover, lipid
analysis of eggs obtained from wild-caught female eels showed that the level of most fatty acids were similar between high and low quality eggs. Additionally, levels of essential fatty acids were considerable different from those reported elsewhere for cultured European female eel. Experiments part of this PhD project resulted in a high number of high quality eggs which enabled us to determine the relation between oocyte stage at the time oocyte maturation and ovulation are induced, and egg quality for the first time. As a result, we presented improved guidelines to induce oocyte maturation and ovulation, based on a lipid droplet-based oocyte maturation scale, which may result in an increase in production of viable European eel eggs. Overall, this PhD project contributed to the development of assisted reproduction procedures by providing new and valuable knowledge about the factors influencing the maturational response of European female eels to hormonal treatments and resulting egg quality.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management
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Flabellum alabastrum, en Vestgrønlandsk bægerkoral

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Københavns Universitet
Authors: Jørgensbye, H. (Intern), Tendal, O. S. (Forskerdatabase)
Publication date: 2017
Event: Poster session presented at Dansk Havforskermøde, Helsingør, Denmark.
Main Research Area: Technical/natural sciences
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Food for thought: pretty good multispecies yield
MSY principles for marine fisheries management reflect a focus on obtaining continued high catches to provide food and livelihoods for humanity, while not compromising ecosystems. However, maintaining healthy stocks to provide the maximum sustainable yield on a single-species basis does not ensure that broader ecosystem, economic, and social objectives are addressed. We investigate how the principles of a “pretty good yield” range of fishing mortalities assumed to provide >95% of the average yield for a single stock can be expanded to a pretty good multispecies yield (PGMY) space and further to pretty good multidimensional yield to accommodate situations where the yield from a stock affects the ecosystem, economic and social benefits, or sustainability. We demonstrate in a European example that PGMY is a practical concept. As PGMY provides a safe operating space for management that adheres to the principles of MSY, it allows the consideration of other aspects to be included in operational management advice in both data-rich and data-limited situations. PGMY furthermore provides a way to integrate advice across stocks, avoiding clearly infeasible management combinations, and thereby hopefully increasing confidence in scientific advice.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, CSIRO Oceans and Atmosphere, National Oceanographic and Atmospheric Administration, Ministry for Primary Industries, AZTI-Tecnalia, University of Washington, University of New Brunswick, Marine Institute
Authors: Rindorf, A. (Intern), Dichmont, C. M. (Ekstern), Levin, P. (Ekstern), Mace, P. (Ekstern), Pascoe, S. (Ekstern), Preliezdo, R. (Ekstern), Punt, A. (Ekstern), Reid, D. G. (Ekstern), Stephenson, R. (Ekstern), Ulrich, C. (Intern), Vinther, M. (Intern), Worsøe Clausen, L. (Intern)
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Forskningsskibet Dana er netop vendt hjem fra Østersøen

General information
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Organisations: National Institute of Aquatic Resources, Section for Monitoring and Data, Section for Marine Living Resources
Authors: Storr-Paulsen, M. (Intern), Huwer, B. (Intern)
Pages: 14-16
Genetic diversity and connectivity within *Mytilus* spp. in the subarctic and Arctic

Climate changes in the Arctic are predicted to alter distributions of marine species. However, such changes are difficult to quantify because information on present species distribution and the genetic variation within species is lacking or poorly examined. Blue mussels, *Mytilus* spp., are ecosystem engineers in the coastal zone globally. To improve knowledge of distribution and genetic structure of the *Mytilus edulis* complex in the Arctic, we analyzed 81 SNPs in 534 *Mytilus* spp. individuals sampled at 13 sites to provide baseline data for distribution and genetic variation of *Mytilus mussels* in the European Arctic. *Mytilus edulis* was the most abundant species found with a clear genetic split between populations in Greenland and the Eastern Atlantic. Surprisingly, analyses revealed the presence of *Mytilus trossulus* in high Arctic NW Greenland (77°N) and *Mytilus galloprovincialis* or their hybrids in SW Greenland, Svalbard, and the Pechora Sea. Furthermore, a high degree of hybridization and introgression between species was observed. Our study highlights the importance of distinguishing between congener species, which can display local adaptation and suggests that information on dispersal routes and barriers is essential for accurate predictions of regional susceptibility to range expansions or invasions of boreal species in the Arctic.
Genome architecture enables local adaptation of Atlantic cod despite high connectivity

Adaptation to local conditions is a fundamental process in evolution; however, mechanisms maintaining local adaptation despite high gene flow are still poorly understood. Marine ecosystems provide a wide array of diverse habitats that frequently promote ecological adaptation even in species characterized by strong levels of gene flow. As one example, populations of the marine fish Atlantic cod (Gadus morhua) are highly connected due to immense dispersal capabilities but nevertheless show local adaptation in several key traits. By combining population genomic analyses based on 12K single-nucleotide polymorphisms with larval dispersal patterns inferred using a biophysical ocean model, we show that Atlantic cod individuals residing in sheltered estuarine habitats of Scandinavian fjords mainly belong to offshore oceanic populations with considerable connectivity between these diverse ecosystems. Nevertheless, we also find evidence for discrete fjord populations that are genetically differentiated from offshore populations, indicative of local adaptation, the degree of which appears to be influenced by connectivity. Analyses of the genomic architecture reveal a significant overrepresentation of a large ~5 Mb chromosomal rearrangement in fjord cod, previously proposed to comprise genes critical for the survival at low salinities. This suggests that despite considerable connectivity with offshore populations, local adaptation to fjord environments may be enabled by suppression of recombination in the rearranged region. Our study provides new insights into the potential of local adaptation in high gene flow species within fine geographical scales and highlights the importance of genome architecture in analyses of ecological adaptation. This article is protected by copyright. All rights reserved.

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State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Oslo, University of Gothenburg, National Research Council of Italy, Swedish Institute for the Marine Environment
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Main Research Area: Technical/natural sciences
Geostatistical modelling of the spatial life history of post-larval deepwater hake Merluccius paradoxus in the Benguela Current Large Marine Ecosystem

Optimal and sustainable management of fish resources cannot be ensured without a thorough understanding of the migration patterns and population (demographic stock) structure. Recent studies suggest that these aspects of the economically and ecologically important deepwater hake Merluccius paradoxus are not reflected in the current assessment and management practices for the Benguela Current Large Marine Ecosystem. In this study, we compiled data from multiple demersal trawl surveys from the entire distribution area and applied state-of-the-art geostatistical population modelling (GeoPop) to estimate growth rate, mortality, and spatial and temporal distribution patterns of M. paradoxus. The data and the model enabled us to follow temporal and spatial changes in the distribution and infer movements from the recruitment/nursery areas, through the juvenile phase and the adults’ migration to the spawning areas outside/upstream of the nursery areas. The results indicated one primary recruitment/nursery area on the west coast of South Africa and a secondary less-productive recruitment/nursery area on the south coast near Port Elizabeth. Juveniles initially migrated away from the main recruitment area, followed by natal homing by larger individuals. This pattern was highly consistent through the time-series of the study. This perception of a, primarily, panmictic population that performs transboundary migrations between Namibia and South Africa corresponds largely to the hypothesis and data plots given in recent studies. We recommend that fisheries assessment, advice and management take into consideration these aspects of the distribution and population (stock) structure of M. paradoxus.

General information
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Organisations: National Institute of Aquatic Resources, Section for Oceans and Arctic, Department of Applied Mathematics and Computer Science, Section for Marine Living Resources, Department for Agriculture, Forestry and Fisheries, Ministry of Fisheries and Marine Resources
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BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.36 SJR 0.661 SNIP 0.8
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.696 SNIP 0.732 CiteScore 1.19
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.568 SNIP 0.879 CiteScore 1.15
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.71 SNIP 0.749 CiteScore 1.25
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.529 SNIP 0.488 CiteScore 1.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
glmmTMB balances speed and flexibility among packages for Zero-inflated Generalized Linear Mixed Modeling

Count data can be analyzed using generalized linear mixed models when observations are correlated in ways that require random effects. However, count data are often zero-inflated, containing more zeros than would be expected from the typical error distributions. We present a new package, glmmTMB, and compare it to other R packages that fit zero-inflated mixed models. The glmmTMB package fits many types of GLMMs and extensions, including models with continuously distributed responses, but here we focus on count responses. glmmTMB is faster than glmmADMB, MCMCglmm, and brms, and more flexible than INLA and mgcv for zero-inflated modeling. One unique feature of glmmTMB (among packages that fit zero-inflated mixed models) is its ability to estimate the Conway-Maxwell-Poisson distribution parameterized by the mean. Overall, its most appealing features for new users may be the combination of speed, flexibility, and its interface's similarity to lme4.

General information
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Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, University of Zurich, International Council for the Exploration of the Sea, University of Bergen, Swiss Federal Institute of Technology, McMaster University
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Pages: 378-400
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If you can’t beat them, eat them: using acoustic telemetry to develop an economically viable fishery for the highly invasive round goby (Neogobius melanostomus)

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Freshwater Fisheries Ecology
Authors: Christoffersen, M. (Intern), Svendsen, J. C. (Intern), Behrens, J. (Intern), Jepsen, N. (Intern), van Deurs, M. (Intern)
Publication date: 2017
Event: Abstract from ICES Annual Science Conference 2017, Fort Lauderdale, United States.
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Impacts of climate change on pelagic fisheries

General information
State: Published
Organisations: National Institute of Aquatic Resources, Centre for Ocean Life, Section for Marine Living Resources
Authors: Muhling, B. (Ekstern), Lindegren, M. (Intern), Worsøe Clausen, L. (Intern), Hobday, A. (Ekstern)
Number of pages: 1,048
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Chapter: 23
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Book chapter – Annual report year: 2017

Inclusion of ecological, economic, social, and institutional considerations when setting targets and limits for multispecies fisheries: Introduction to the Symposium: ‘Targets and Limits for Long Term Fisheries Management’ Quo Vadimus

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Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, NOAA, Saint Mary's University, Aalborg University, AZTI Technalia, IMARES, Thünen Institute of Baltic Sea Fisheries, Ministry for Primary Industries, Hellenic Centre for Marine Research, Galway - Mayo Institute of Technology, Imperial College London, University of Washington, Marine Institute, University of St Andrews, IFREMER, University of Kiel
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Is the osmorespiratory compromise limiting invasive species?

The round goby (Neogobius melanostomus) is a benthic fish native to the brackish waters of the Black and Caspian Seas; however, it has invaded several brackish and freshwater areas in North America and northern Europe. Notably, there are no records of N. melanostomus in high salinity marine habitats and the physiological mechanisms potentially constraining the invasion into this environment are largely unknown. The gills play major roles in gas exchange and ionic regulation and it has been hypothesized that an osmorespiratory compromise impacts performance of each process. The tradeoff of the large gill exchange capacity ideal for gas exchange is greater passive ion fluxes. High ionic waters would result in greater passive ion uptake that would require greater active ion excretion. This osmoregulatory disturbance may interfere with fish invasion by disrupting the regular activity of the gills, thus modifying the usual physiological mechanisms. To
examine if the osmorespiratory compromise could constrain the invasion of *N. melanostomus* into high salinity environments, this study compared Na+/K+ ATPase activity of metabolic phenotypes exposed to 0, 15 and 30 ppt water. Additionally, we examined variation in two important MO2 measures, standard metabolic rate (SMR) and maximum metabolic rate (MMR) when *N. melanostomus* is exposed to increasing water salinities. Fish with an initially higher MMR (at the control salinity - 0ppt) are likely to be more challenged by environmental stressors than fish with a lower MMR. Our results will enable a better understanding of the physiological mechanisms that may constrain invasive species in the aquatic environment.

**General information**
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management, University of Porto, University of West Georgia
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Publication date: 2017
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2017

**Lessons learned from practical approaches to reconcile mismatches between biological population structure and stock units of marine fish**
Recent advances in the application of stock identification methods have revealed inconsistencies between the spatial structure of biological populations and the definition of stock units used in assessment and management. From a fisheries management perspective, stocks are typically assumed to be discrete units with homogeneous vital rates that can be exploited independently of each other. However, the unit stock assumption is often violated leading to spatial mismatches that can bias stock assessment and impede sustainable fisheries management. The primary ecological concern is the potential for overexploitation of unique spawning components, which can lead to loss of productivity and reduced biodiversity along with destabilization of local and regional stock dynamics. Furthermore, ignoring complex population structure and stock connectivity can lead to misperception of the magnitude of fish productivity, which can translate to suboptimal utilization of the resource. We describe approaches that are currently being applied to improve the assessment and management process for marine fish in situations where complex spatial structure has led to an observed mismatch between the scale of biological populations and spatially-defined stock units. The approaches include: (i) status quo management, (ii) “weakest link” management, (iii) spatial and temporal closures, (iv) stock composition analysis, and (v) alteration of stock boundaries. We highlight case studies in the North Atlantic that illustrate each approach and synthesize the lessons learned from these real-world applications. Alignment of biological and management units requires continual monitoring through the application of stock identification methods in conjunction with responsive management to preserve biocomplexity and the natural stability and resilience of fish species.

**General information**
State: Published
Authors: Kerr, L. A. (Ekstern), Hintzen, N. T. (Ekstern), Cadrin, S. X. (Ekstern), Worsøe Clausen, L. (Intern), Dickey-Collas, M. (Intern), Goethel, D. R. (Ekstern), Hatfield, E. M. C. (Ekstern), Kritzer, J. P. (Ekstern), Nash, R. D. (Ekstern)
Pages: 1708-1722
Publication date: 2017
Main Research Area: Technical/natural sciences
Low genetic and phenotypic divergence in a contact zone between freshwater and marine sticklebacks: gene flow constrains adaptation

Background: Distinct hybrid zones and phenotypic and genomic divergence is often observed between marine and freshwater threespine sticklebacks (Gasterosteus aculeatus). Nevertheless, cases also exist where marine-freshwater divergence is diffuse despite seemingly similar environmental settings. In order to assess what characterizes these highly different outcomes, we focused on the latter kind of system in the Odder River, Denmark. Here, a previous study based on RAD (Restriction site Associated DNA) resequencing found non-significant genomewide differentiation between marine and freshwater sticklebacks. In the present study, we analyzed samples on a finer geographical scale. We assessed if the system should be regarded as panmictic, or if fine-scale genetic structure and local selection was present but dominated by strong migration. We also asked if specific population components, that is the two sexes and different lateral plate morphs, contributed disproportionately more to dispersal.

Results: We assessed variation at 96 SNPs and the Eda gene that affects lateral plate number, conducted molecular sex identification, and analyzed morphological traits. Genetic differentiation estimated by FST was non-significant throughout the system. Nevertheless, spatial autocorrelation analysis suggested fine scale genetic structure with a genetic patch size of 770 m. There was no evidence for sex-biased dispersal, but full-plated individuals showed higher dispersal than low- and partial-plated individuals. The system was dominated by full-plated morphs characteristic of marine sticklebacks, but in the upstream part of the river body shape and frequency of low-plated morphs changed in the direction expected for freshwater sticklebacks. Five markers including Eda were under possible diversifying selection. However, only subtle clinal patterns were observed for traits and markers. Conclusions: We suggest that gene flow from marine sticklebacks overwhelms adaptation to freshwater conditions, but the short genetic patch size means that the effect of gene flow on the most upstream region must be indirect and occurs over generations. The occurrence of both weak unimodal and strong bimodal hybrid zones within the same species is striking. We suggest environmental and demographic factors that could determine these outcomes, but also highlight the possibility that long-term population history and the presence or absence of genomic incompatibilities could be a contributing factor.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University, Universite Laval
Authors: Pedersen, S. H. (Ekstern), Ferchaud, A. (Ekstern), Bertelsen, M. S. (Ekstern), Bekkevold, D. (Intern), Hansen, M. M. (Ekstern)
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BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.94 SNIP 1.197 CiteScore 3.52
ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): SJR 1.94 SNIP 1.137 CiteScore 3.43
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.203 SNIP 1.223 CiteScore 3.73
Mærkningsmetode for små fisk: Et casestudie med kysttobis (Ammodytes tobianus)

General information
State: Published
Organisations: Section for Marine Ecology and Oceanography, National Institute of Aquatic Resources, Section for Marine Living Resources, Den Blå Planet
Authors: Jørgensen, M. G. P. (Intern), Deurs, M. V. (Intern), Butts, I. (Intern), Jørgensen, K. (Ekstern), Behrens, J. (Intern)
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Mapping sediments in the Greenlandic EEZ

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Organisations: Arctic Section, National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Jørgensbye, H. (Intern)
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Micro-and macro-plastics in marine species from Nordic waters

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Norwegian Institute for Water Research
Authors: Bråte, I. L. N. (Ekstern), Huwer, B. (Intern), Thomas, K. V. (Ekstern), Eidsvoll, D. P. (Ekstern), Halsband, C. (Ekstern), Almroth, B. C. (Ekstern), Lusher, A. (Ekstern)
Number of pages: 101
Newton step methods for AD of an objective defined using implicit functions

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Washington
Authors: Bell, B. M. (Ekstern), Kristensen, K. (Intern)
Pages: 1-17
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.952 SNIP 1.288 CiteScore 1.54
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.833 SNIP 1.708 CiteScore 1.69
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.719 SNIP 1.447 CiteScore 1.28
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.923 SNIP 1.377 CiteScore 1.16
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.848 SNIP 1.08 CiteScore 0.88
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.794 SNIP 1.201
No increase in marine microplastic concentration over the last three decades – A case study from the Baltic Sea

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Oceans and Arctic, University of Copenhagen, Technical University of Denmark, GEOMAR - Helmholtz Centre for Ocean Research Kiel
Authors: Beer, S. (Ekstern), Garm, A. (Ekstern), Huwer, B. (Intern), Dierking, J. (Ekstern), Nielsen, T. G. (Intern)
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Non-parallel divergence across Danish freshwater and marine three-spined stickleback Gasterosteus aculeatus populations
This work investigated whether multiple freshwater populations of three-spined stickleback Gasteros-teus aculeatus in different freshwater catchments in the Jutland Peninsula, Denmark, derived from the same marine populations show repeated adaptive responses. A total of 327 G. aculeatus collected at 13 sampling locations were screened for genetic variation using a combination of 70 genes putatively under selection and 26 neutral genes along with a marker linked to the ectodysplasin gene (eda), which is strongly correlated with plate armour morphs in the species. A highly significant genetic differentiation was found that was higher among different freshwater samples than between marine–freshwater samples. Tests for selection between marine and freshwater populations showed a very low degree of parallelism and no single nucleotide polymorphism was detected as outlier in all freshwater–marine pairwise comparisons, including the eda. This suggests that G. aculeatus is not necessarily the prime example of parallel local adaptation suggested in much of the literature and that important exceptions exist (i.e. the Jutland Peninsula). While marine populations in the results described here showed a high phenotype–genotype correlation at eda, a low association was found for most of the freshwater populations. The most extreme case was found in the freshwater Lake Hald where all low-plated phenotypes were either homozygotes for the allele supposed to be associated with completely plated morphs or heterozygotes, but none were homozygotes for the putative low-plated allele. Re-examination of data from seven G. aculeatus studies agrees in showing a high but partial association between phenotype–genotype at eda in G. aculeatus freshwater populations and that mismatches occur everywhere in the European regions studied (higher in some areas, i.e. Denmark). This is independent of the eda marker used.

General information
Overview of coralline red algal crusts and rhodolith beds (Corallinales, Rhodophyta) and their possible ecological importance in Greenland

Coralline red algae are a globally distributed and abundant group of shallow marine benthic calcifiers. They can form important ecosystems that provide a three-dimensional habitat to a large variety of marine organisms. While the study of coralline red algae has traditionally been focused on warm-water habitats, numerous recent reports have now described widespread coralline red algal ecosystems from high-latitude regions, particularly in the Northern Hemisphere. In fact, it is becoming increasingly evident that coralline red algae are likely the dominant marine calcifying organisms on the seafloor of the Arctic and subarctic photic zone. This article gives a first overview of the distribution of coralline red algal crusts and rhodolith (free-living coralline red algal nodules) grounds in Greenland and the first report of rhodoliths in East Greenland. Museum data and recent sampling information have been compiled to develop a distribution map of coralline genera and rhodolith communities. The depth range of coralline red algae in Greenland has been extended by 27 m, from 50 to 77 m depth. In addition, rhodoliths of the normally crust-forming species Clathromorphum compactum are described for the first time from a sheltered Greenland fjord. Based on the data compiled here, it becomes clear that rhodolith communities are a widespread feature of the Greenland shallow shelf areas. Gaining a better understanding of the distribution of these hitherto poorly understood high-latitude ecosystems is essential due to their function as spawning areas and nursery grounds for commercially important fish and invertebrates.

General information
State: Published
Organisations: Section for Marine Living Resources, National Institute of Aquatic Resources, Arctic Section, University of Toronto
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Scopus rating (2016): CiteScore 1.72 SJR 0.866 SNIP 0.761
Web of Science (2016): Indexed yes
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Scopus rating (2015): SJR 0.985 SNIP 0.751 CiteScore 1.62
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Pike (Esox lucius L.) on the edge: consistent individual movement patterns in transitional waters of the western Baltic

Pike in the western Baltic Sea live on the edge of their salinity tolerance. Under physiologically challenging conditions, organism may respond by moving to environmentally more benign areas during critical periods, such as during spawning. We hypothesised that pike in a brackish lagoon (8–10 ppt salinity) would perform spawning- and feeding-related movements between areas with different salinity regimes. Twenty-two pike were caught prior to spawning, tagged with acoustic transmitters, and their movements were tracked for 18 months. Pike showed two main patterns of movements that were consistent within individuals across two years. Whereas some individuals stayed in the lagoon year-round, most pike left the lagoon for longer periods after spawning and returned to the lagoon prior to following year’s spawning season. We found no evidence that probability of moving out of the lagoon co-varied with either length or condition factor. Despite the fact that the lagoon’s salinity is close to the reported upper limit for pike egg development, results indicated that all pike spawned in the lagoon. Correspondingly, genetic data showed that all fish belonged to the same reproductive population unit. Movement patterns thus appear to reflect individual variation in home-range and/or resource optimisation following ideal free principles.

General information
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PIT-tagging method for small fishes: A case study using sandeel (Ammodytes tobianus)

Passive integrated transponder (PIT) tags are commonly used to assess fish movement for use in fisheries management. Here, we investigated physiological and behavioral effects of tagging on sandeels (Ammodytes tobianus) using PIT tags constituting 2.1 ± 0.9% of their body weight. Swimming stamina (RSS), calculated as time spent swimming against the current relative to total swimming time, and tail beat frequency were compared between tagged and untagged fish as was blood hematocrit levels at 7, 14, and 42 d post-tagging. Survival and tag retention were also documented at 14, 42, and 84 d (via x-rays and dissections). RSS was not different between tagged and untagged fish with means (± SD) of 60 ± 9% and 61 ± 12%. Tail beat frequency was not different between tagged and untagged fish at 2.8 ± 0.3 and 3.0 ± 0.4 beats s⁻¹ for tagged and untagged fish, respectively. Likewise, hematocrit was not affected by tagging and levels were between 21–26% for both groups. Survival rates were high and did not differ between groups (96% for tagged and 99% untagged fish). Tag retention was 100%. X-rays and dissections did not reveal any signs of tag movement at 14–84 d, and there was no difference between relative positions of the tags. None of the tags were encapsulated in the body cavity after 14 d, whereas 40 and 56% of the tags were encapsulated in a thin tissue membrane between the intestine and kidney after 42 and 84 d, respectively. After 14 d all incisions had healed with only minor or no signs of the tag insertion site. Collectively, these data provide substantial evidence for the possibility of conducting large-scale tagging studies on this species in the field.

General information
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Organisations: Section for Marine Ecology and Oceanography, National Institute of Aquatic Resources, Section for Marine Living Resources, Auburn University, National Aquarium of Denmark
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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.105 SNIP 1.312 CiteScore 2.17
Web of Science (2014): Indexed yes
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ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): SJR 0.93 SNIP 1.177 CiteScore 1.78
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BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.154 SNIP 1.135 CiteScore 1.7
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Population structure and connectivity of tiger sharks (Galeocerdo cuvier) across the Indo-Pacific Ocean basin

Population genetic structure using nine polymorphic nuclear microsatellite loci was assessed for the tiger shark (Galeocerdo cuvier) at seven locations across the Indo-Pacific, and one location in the southern Atlantic. Genetic analyses revealed considerable genetic structuring (FST > 0.14, p<0.001) between all Indo-Pacific locations and Brazil. By contrast, no significant genetic differences were observed between locations from within the Pacific or Indian Oceans, identifying an apparent large, single Indo-Pacific population. A lack of differentiation between tiger sharks sampled in Hawaii and other Indo-Pacific locations identified herein is in contrast to an earlier global tiger shark nDNA study. The results of our power analysis provide evidence to suggest that the larger sample sizes used here negated any weak population subdivision observed previously. These results further highlight the need for crossjurisdictional efforts to manage the sustainable exploitation of large migratory sharks like G. cuvier.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Queensland, Queensland Department of Primary Industries
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Positioning of aquatic animals based on time-of-arrival and random walk models using YAPS (Yet Another Positioning Solver)

Aquatic positional telemetry offers vast opportunities to study in vivo behaviour of wild animals, but there is room for improvement in the data quality provided by current procedures for estimating positions. Here we present a novel positioning method called YAPS (Yet Another Positioning Solver), involving Maximum Likelihood analysis of a state-space model applied directly to time of arrival (TOA) data in combination with a movement model. YAPS avoids the sequential positioning-filtering-approach applied in alternative tools by using all available data in a single model, and offers better accuracy and error control. Feasibility and performance of YAPS was rigorously tested in a simulation study and by applying YAPS to data from an acoustic transmitter towed in a receiver array. Performance was compared to an alternative positioning model and proprietary software. The simulation study and field test revealed that YAPS performance was better and more consistent than alternatives. We conclude that YAPS outperformed the compared alternative methods, and that YAPS constitute a vast improvement to currently available positioning software in acoustic telemetry. Additionally, in contrast to vendor-supplied solutions, YAPS is transparent, flexible and can easily be adapted and extended for further improvements or to meet study specific requirements such as three-dimensional positioning.
Forage fish occupy a central position in marine food-webs worldwide by mediating the transfer of energy and organic matter from lower to higher trophic levels. The lesser sandeel (Ammodytes marinus) is one of the ecologically and economically most important forage fish species in the North-east Atlantic, acting as a key prey for predatory fish and seabirds, as well as supporting a large commercial fishery. In this case study, we investigate the underlying factors affecting recruitment and how these in turn affect productivity of the North Sea sandeel using long-term data and modelling. Our results demonstrate how sandeel productivity in the central North Sea (Dogger Bank) depends on a combination of external and internal regulatory factors, including fishing and climate effects, as well as density dependence and food availability of the preferred zooplankton prey (Calanus finmarchicus and Temora longicornis). Furthermore, our model scenarios suggest that while fishing largely contributed to the abrupt stock decline during the late 1990s and the following period of low biomass, a complete recovery of the stock to the highly productive levels of the early 1980s would only be possible through changes in the surrounding ecosystem, involving lower temperatures and improved feeding conditions. To that end, we stress the need for ecosystem-based management accounting for multiple internal and external factors occurring within the broader context of the ecosystem in which forage fish species, such as sandeel, play an important and integral part.

Productivity and recovery of forage fish under climate change and fishing: North Sea sandeel as a case study

Forage fish occupy a central position in marine food-webs worldwide by mediating the transfer of energy and organic matter from lower to higher trophic levels. The lesser sandeel (Ammodytes marinus) is one of the ecologically and economically most important forage fish species in the North-east Atlantic, acting as a key prey for predatory fish and seabirds, as well as supporting a large commercial fishery. In this case study, we investigate the underlying factors affecting recruitment and how these in turn affect productivity of the North Sea sandeel using long-term data and modelling. Our results demonstrate how sandeel productivity in the central North Sea (Dogger Bank) depends on a combination of external and internal regulatory factors, including fishing and climate effects, as well as density dependence and food availability of the preferred zooplankton prey (Calanus finmarchicus and Temora longicornis). Furthermore, our model scenarios suggest that while fishing largely contributed to the abrupt stock decline during the late 1990s and the following period of low biomass, a complete recovery of the stock to the highly productive levels of the early 1980s would only be possible through changes in the surrounding ecosystem, involving lower temperatures and improved feeding conditions. To that end, we stress the need for ecosystem-based management accounting for multiple internal and external factors occurring within the broader context of the ecosystem in which forage fish species, such as sandeel, play an important and integral part.
Remote electronic monitoring and the landing obligation – some insights into fishers’ and fishery inspectors’ opinions

The European fisheries management is currently undergoing a fundamental change in the handling of catches of commercial fisheries with the implementation of the 2013 Common Fisheries Policy. One of the main objectives of the policy is to end the practice of discarding in the EU by 2019. However, for such changes to be successful, it is vital to ensure stakeholders acceptance, and it is prudent to consider possible means to verify compliance with the new regulation. Remote Electronic Monitoring (REM) with Closed-Circuit Television (CCTV) has been tested in a variety of fisheries worldwide for different purposes and is currently considered as one possible tool to ensure compliance with a European ban on discards. This study focuses on Danish fishery inspectors and on fishers with REM experience, whose opinions are less well known. Their views on the landing obligation and on the use of REM were investigated using interviews and questionnaires, and contrasted to some fishers without REM experience. 80% of fishery inspectors and 58% of REM-experienced fishers expressed positive views on REM. 9 out of 10 interviewed fishers without REM experience were against REM. Participation in a REM trial has not led to antipathy towards REM. Fishery inspectors saw on-board observers, at-sea control and REM as the three best solutions to control the landing obligation but shared the general belief that the landing obligation cannot be enforced properly and will be difficult for fishers to comply with. The strengths and weaknesses of REM in this context are discussed.

General information

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Organisations: Section for Marine Living Resources, National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Monitoring and Data, Aalborg University, Ministry of Food, Agriculture and Fisheries
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Pages: 98-106
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Main Research Area: Technical/natural sciences
Responsible genetic approach to stock restoration, sea ranching and stock enhancement of marine fishes and invertebrates

The origins of agriculture date to about 9000 years, but commercial culture and supplementation of marine populations reach back only a few centuries. Hence, wild populations still play a major role in seafood production. Closed culture, stock restorations, sea ranching and stock enhancements of marine fishes and invertebrates have been implemented with various outcomes. A review of the literature indicates that considerable effort has been directed toward culture technologies to maximize production, but scant attention has been given to genetic risks to wild populations. Genetic risks from stock enhancements can be substantial, because of inattention to brood-stock sizes, and because hybridization between hatchery-reared and wild individuals can lower the fitness or lead to the extinction of a natural population. In many cases, small brood-stock sizes have led to the loss of genetic diversity. In some cases, hatchery-reared individuals appear to have replaced, rather than supplemented, wild populations. Here, we outline a responsible approach to managing genetic resources that includes six steps: (1) assess the costs and benefits of a stock restoration or enhancement, (2) set goals and genetic benchmarks, (3) use appropriate brood stock and limit domestication, (4) design release strategies that maximize the effectiveness of supplementation efforts, (5) track individuals after release and (6) minimize genetic impacts on wild populations. Stock supplementation is often viewed as an immediate solution to a stock decline, but should be undertaken as a last resort because of the high cost of implementation and the substantial ecological and genetic risks to wild populations.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Alaska Fairbanks, Alaska Department of Fish and Game
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Pages: 615-649
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Main Research Area: Technical/natural sciences

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Web of Science (2017): Indexed Yes
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.449 SNIP 1.453 CiteScore 2.57
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.071 SNIP 1.496 CiteScore 2.46
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.091 SNIP 1.578 CiteScore 2.3
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.241 SNIP 1.591 CiteScore 2.8
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.374 SNIP 1.803 CiteScore 2.84
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.478 SNIP 1.403
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.13 SNIP 1.325
BFI (2008): BFI-level 1
Shifts in North Sea forage fish productivity and potential fisheries yield

1. Forage fish populations support large scale fisheries and are key components of marine ecosystems across the world, linking secondary production to higher trophic levels. While climate-induced changes in the North Sea zooplankton community are described and documented in literature, the associated bottom-up effects and consequences for fisheries remain largely unidentified.

2. We investigated the temporal development in forage fish productivity and the associated influence on fisheries yield of herring, sprat, Norway pout and sandeel in the North Sea. Using principal component analysis, we analysed 40 years of recruitment success and growth proxies to reveal changes in productivity and patterns of synchronicity across stocks (i.e. functional complementarity). The relationship between forage fish production and Calanus finmarchicus (an indicator of climate change) was also analysed. We used a population model to demonstrate how observed shifts in productivity affected total forage fish biomass and fisheries yield.

3. The productivity of North Sea forage fish changed around 1993 from a higher average productivity to lower average productivity. During the higher productivity period, stocks displayed a covariance structure indicative of functional complementarity. Calanus finmarchicus was positively correlated to forage fish recruitment, however, for growth, the direction of the response differed between species and time periods. Maximum sustainable yield (MSY) and the associated fishing mortality (Fmsy) decreased by 33%–68% and 26%–64%, respectively, between the higher and lower productivity periods.

4. Synthesis and applications. The results demonstrate that fisheries reference points for short-lived planktivorous species are highly dynamic and respond rapidly to changes in system productivity. Furthermore, from an ecosystem-based fisheries management perspective, a link between functional complementarity and productivity, indicates that ecosystem resilience may decline with productivity. Based on this, we advise that system productivity, perhaps monitored as forage fish growth, becomes an integral part of management reference points; in both single species and ecosystem contexts. However, to retain social license of biological advice when fish catch opportunities are reduced, it is crucial that shifts in productivity are thoroughly documented and made apparent to managers and stakeholders.
Sortmundet kutling: Invasionen fra Sortehavet fortsætter

**General information**
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management
Authors: Ramkær, K. (Ekstern), van Deurs, M. (Intern), Christoffersen, M. (Intern)
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Main Research Area: Technical/natural sciences

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ISI indexed (2012): ISI indexed no
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Sortmundet kutling - Vi spiser os til løsningen

**General information**
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Krebs, M. L. (Ekstern), Behrens, J. (Intern)
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Original language: Danish
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Spatial distribution, origin and source and sink areas of marine litter in the water column of the North Sea

**General information**
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Institute of Marine Research, Swedish University of Agricultural Sciences, Marine Scotland, Johann Heinrich von Thünen-Institute, IFREMER, Wageningen IMARES
Authors: Huwer, B. (Intern), Kloppmann, M. (Ekstern), Loots, C. (Ekstern), van Damme, C. J. G. (Ekstern), Nash, R. (Ekstern), Bland, B. (Ekstern), Ritchie, L. (Ekstern)
Number of pages: 1
Publication date: 2017

**Host publication information**
Title of host publication: Book of Abstracts Sustain 2017
Article number: A-3
Main Research Area: Technical/natural sciences
Conference: Sustain 2017, Kgs. Lyngby, Denmark, 06/12/2017 - 06/12/2017
Electronic versions:
SustainAbstracts2017c.compressed_7.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2017
Spatiotemporal modelling of marine movement data using Template Model Builder (TMB)

Tracking of marine animals has increased exponentially in the past decade, and the resulting data could lead to an in-depth understanding of the causes and consequences of movement in the ocean. However, most common marine tracking systems are associated with large measurement errors. Accounting for these errors requires the use of hierarchical models, which are often difficult to fit to data. Using 3 case studies, we demonstrate that Template Model Builder (TMB), a new R package, is an accurate, efficient and flexible framework for modelling movement data. First, to demonstrate that TMB is as accurate but 30 times faster than bSam, a popular R package used to apply state-space models to Argos data, we modelled polar bear Ursus maritimus Argos data and compared the locations estimated by the models to GPS locations of these same bears. Second, to demonstrate how TMB’s gain in efficiency and frequentist framework facilitate model comparison, we developed models with different error structures and compared them to find the most effective model for light-based geolocations of rhinoceros auklets Cerorhinca monocerata. Finally, to maximize efficiency through TMB’s use of the Laplace approximation of the marginal likelihood, we modelled behavioural changes with continuous rather than discrete states. This new model directly accounts for the irregular sampling intervals characteristic of Fastloc-GPS data of grey seals Halichoerus grypus. Using real and simulated data, we show that TMB is a fast and powerful tool for modelling marine movement data. We discuss how TMB’s potential reaches beyond marine movement studies.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Dalhousie University, Macquarie University, University of Alberta, Bedford Institute of Oceanography
Authors: Auger-Méthé, M. (Ekstern), Albertsen, C. M. (Intern), Jonsen, I. D. (Ekstern), Derocher, A. E. (Ekstern), Lidgard, D. C. (Ekstern), Studholme, K. R. (Ekstern), Bowen, W. D. (Ekstern), Crossin, G. T. (Ekstern), Flemming, J. M. (Ekstern)
Pages: 237-249
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Marine Ecology Progress Series
Volume: 565
ISSN (Print): 1616-1599
Ratings:
Web of Science (2018): Indexed yes
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 2.4
Web of Science (2016): Indexed yes
Scopus rating (2015): CiteScore 2.56
Web of Science (2015): Indexed yes
Scopus rating (2014): CiteScore 2.75
Web of Science (2014): Indexed yes
Scopus rating (2013): CiteScore 2.79
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
Scopus rating (2012): CiteScore 2.9
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
Scopus rating (2011): CiteScore 2.85
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
Web of Science (2010): Indexed yes
Web of Science (2009): Indexed yes
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Stress and recovery from trawl capture of Norway lobster (Nephrops norvegicus) and potential for live storage

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Aquaculture, Section for Ecosystem based Marine Management, Section for Marine Living Resources, STMI
Authors: Skov, P. V. (Intern), Methling, C. (Intern), Larsen, B. K. (Intern), Unmack, C. P. (Ekstern), Karlsen, J. D. (Intern), Behrens, J. (Intern)
Publication date: 2017
Event: Abstract from Dansk Havforskermøde, Helsingør, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2017

Tagging method for small fishes: A case study using lesser sandeel (Ammodytes tobianus)

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, Den Blå Planet
Authors: Jørgensen, M. G. P. (Intern), Deurs, M. V. (Intern), Butts, I. (Intern), Jørgensen, K. (Ekstern), Behrens, J. (Intern)
Publication date: 2017
Event: Abstract from Dansk Havforskermøde, Helsingør, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2017

Take it with a grain of salt; salinity tolerance of round goby Neogobius melanostomus

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Tartu
Authors: Behrens, J. (Intern), van Deurs, M. (Intern), Ojaveer, H. (Ekstern), Christensen, E. A. F. (Intern)
Publication date: 2017
Event: Poster session presented at CeMEB 18th Assembly, Tjärnö, Sweden.
Main Research Area: Technical/natural sciences
Publication: Research › Poster – Annual report year: 2017

Temperature effects on gene expression and morphological development of European eel, Anguilla anguilla larvae

Temperature is important for optimization of rearing conditions in aquaculture, especially during the critical early life history stages of fish. Here, we experimentally investigated the impact of temperature (16, 18, 20, 22 and 24°C) on thermally induced phenotypic variability, from larval hatch to first-feeding, and the linked expression of targeted genes [heat shock proteins (hsp), growth hormone (gh) and insulin-like growth factors (igf)] associated to larval performance of European eel, Anguilla anguilla. Temperature effects on larval morphology and gene expression were investigated throughout early larval development (in real time from 0 to 18 days post hatch) and at specific developmental stages (hatch, jaw/teeth formation, and first-feeding). Results showed that hatch success, yolk utilization efficiency, survival, deformities, yolk utilization, and growth rates were all significantly affected by temperature. In real time, increasing temperature from 16 to 22°C accelerated larval development, while larval gene expression patterns (hsp70, hsp90, gh and igf-1) were delayed at cold temperatures (16°C) or accelerated at warm temperatures (20-22°C). All targeted genes (hsp70, hsp90, gh, igf-1, igf-2a, igf-2b) were differentially expressed during larval development. Moreover, expression of gh was highest at 16°C during the jaw/teeth formation, and the first-feeding developmental stages, while expression of hsp90 was highest at 22°C, suggesting thermal stress. Furthermore, 24°C was shown to be deleterious (resulting in 100% mortality), while 16°C and 22°C (~50 and 90% deformities respectively) represent the lower and upper thermal tolerance limits. In conclusion, the high survival, lowest incidence of deformities at hatch, high yolk utilization efficiency, high gh and low hsp expression,
suggest 18°C as the optimal temperature for offspring of European eel. Furthermore, our results suggest that the still enigmatic early life history stages of European eel may inhabit the deeper layer of the Sargasso Sea and indicate vulnerability of this critically endangered species to increasing ocean temperature.

General information
State: Published
Organisations: Section for Marine Ecology and Oceanography, National Institute of Aquatic Resources, Section for Marine Living Resources, IFREMER, GEOMAR - Helmholtz Centre for Ocean Research Kiel
Authors: Politis, S. N. (Intern), Mazurais, D. (Ekstern), Servili, A. (Ekstern), Zambonino-Infante, J. (Ekstern), Miest, J. J. (Ekstern), Sørensen, S. R. (Intern), Tomkiewicz, J. (Intern), Butts, I. A. E. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Volume: 12
Issue number: 8
Article number: e0182726
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.945 SNIP 1.142 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.631 SNIP 1.161
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.473 SNIP 0.985
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.323 SNIP 0.96
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.289 SNIP 0.525
Web of Science (2006): Indexed yes
Original language: English
Electronic versions:
The development of tools for tracing and evaluating the genetic impact of fish from aquaculture

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Padua
Authors: Bargelloni, L. (Ekstern), Nielsen, E. E. (Intern)
Pages: 87
Publication date: 2017
Conference: 12th International Symposium on Genetics in Aquaculture, Santiago de Compostella, Spain, 21/06/2015 - 21/06/2015
Main Research Area: Technical/natural sciences

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Journal: Aquaculture
Volume: 472
ISSN (Print): 0044-8486
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.75 SJR 1.101 SNIP 1.524
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.103 SNIP 1.254 CiteScore 2.12
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.002 SNIP 1.34 CiteScore 2.16
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.136 SNIP 1.3 CiteScore 2.18
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.212 SNIP 1.487 CiteScore 2.32
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.294 SNIP 1.542 CiteScore 2.39
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.151 SNIP 1.394
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.941 SNIP 1.263
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.909 SNIP 1.173
The invasive comb jelly *Mnemiopsis leidyi* in Europe and in the Baltic Sea: Invasion history, distribution, phenology and ecosystem impacts

**General information**

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Oceans and Arctic
Authors: Huwer, B. (Intern), Jaspers, C. (Intern)
Number of pages: 1
Publication date: 2017

**Host publication information**

Title of host publication: Book of Abstracts Sustain 2017
Article number: A-11
Main Research Area: Technical/natural sciences
Conference: Sustain 2017, Kgs. Lyngby, Denmark, 06/12/2017 - 06/12/2017
Electronic versions:
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2017

The parasitic nematode *Contracaecum osculatum* (liver worm) in Baltic cod: Spatial differences in prevalence and intensity of infection

**General information**

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Copenhagen
Authors: Sokolova, M. (Intern), Huwer, B. (Intern), Buchmann, K. (Ekstern), Behrens, J. (Intern)
Publication date: 2017

**Event**: Abstract from Joint spring symposium 2017, Danish Society for Parasitology and Danish Society for Tropical Medicine & International Health, Host-Parasite Communication, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2017

The role of egg cannibalism for the Calanus succession in the Disko Bay, Western Greenland

The present study is the first to describe egg cannibalism in the key Arctic copepod species Calanus finmarchicus, Calanus glacialis, and Calanus hyperboreus. Initially, a series of staining experiments evaluated the
application of Neutral Red for staining Calanus eggs. The method was effective and applied in subsequent feeding
experiments, where adult females were incubated in bottles with their own eggs. The results showed that all Calanus spp.
ingested C. finmarchicus and C. glacialis eggs. However, consumers showed a slight preference for C. finmarchicus eggs
when incubated with those of both species. The addition of phytoplankton even at high concentrations did not decrease
clearance rates for eggs, suggesting that the presence of alternative food does not afford eggs any protection from
cannibalism. To evaluate the potential impact of egg cannibalism on the succession of the three species, we calculated
and compared field egg mortality rates with
potential egg clearance rates for the Calanus complex based on rates from the experiments. Our results show that in
Disko Bay cannibalism by Calanus spp., even at its highest level just before the spring bloom, could only account for about
10% of observed in situ egg mortality, and much less for most of the season

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Marine Ecology
and Oceanography, Aarhus University
Authors: Frank-Gopolos, T. (Intern), Friis Møller, E. (Ekstern), Nielsen, T. G. (Intern)
Pages: 865–883
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Limnology and Oceanography
Volume: 62
Issue number: 3
ISSN (Print): 0024-3590
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.5 SJR 1.712 SNIP 1.225
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.472 SNIP 1.422 CiteScore 3.93
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.112 SNIP 1.584 CiteScore 3.73
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.256 SNIP 1.587 CiteScore 3.98
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.456 SNIP 1.5 CiteScore 3.81
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.374 SNIP 1.445 CiteScore 3.59
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.38 SNIP 1.425
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.329 SNIP 1.682
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.381 SNIP 1.615
Using accelerometry to quantify prey attack and handling behaviours in piscivorous pike Esox lucius

Accelerometer technology was used to evaluate behaviours in the teleost ambush predator pike Esox lucius foraging on crucian carp Carassius carassius. Automated rule-based estimates of prey-size determined handling time were obtained and are compared with video-recorded behaviours. Solutions to tag attachment and the limitations imposed by battery-time and data-logging capacities are evaluated.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Lund University, Institute of Fisheries of the National Academy of Agrarian Sciences of Ukraine
Authors: Deurs, M. V. (Intern), Andersson, A. (Ekstern), Vinterstare, J. (Ekstern), Didenko, A. (Ekstern), Persson, A. (Ekstern), Brönmark, C. (Ekstern), Nilsson, P. (Ekstern)
Pages: 2462-2469
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Biology
Volume: 90
Issue number: 6
ISSN (Print): 0022-1112
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.57 SJR 0.741 SNIP 0.882
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.951 SNIP 0.935 CiteScore 1.64
Validation of ecological state space models using the Laplace approximation

Many statistical models in ecology follow the state space paradigm. For such models, the important step of model validation rarely receives as much attention as estimation or hypothesis testing, perhaps due to lack of available algorithms and software. Model validation is often based on a naive adaptation of Pearson residuals, i.e. the difference between observations and posterior means, even if this approach is flawed. Here, we consider validation of state space models through one-step prediction errors, and discuss principles and practicalities arising when the model has been fitted with a tool for estimation in general mixed effects models. Implementing one-step predictions in the R package Template Model Builder, we demonstrate that it is possible to perform model validation with little effort, even if the ecological model is multivariate, has non-linear dynamics, and whether observations are continuous or discrete. With both simulated data,
and a real data set related to geolocation of seals, we demonstrate both the potential and the limitations of the techniques. Our results fill a need for convenient methods for validating a state space model, or alternatively, rejecting it while indicating useful directions in which the model could be improved.

**General information**

**State:** Published

**Organisations:** National Institute of Aquatic Resources, Section for Marine Living Resources, Department of Applied Mathematics and Computer Science

**Authors:** Thygesen, U. H. (Intern), Albertsen, C. M. (Intern), Berg, C. W. (Intern), Kristensen, K. (Intern), Nielsen, A. (Intern)

**Pages:** 317-339

**Publication date:** 2017

**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** Environmental and Ecological Statistics

**Volume:** 24

**Issue number:** 2

**Ratings:**

- Web of Science (2018): Indexed yes
- Web of Science (2017): Indexed yes
- Scopus rating (2016): CiteScore 0.82 SNIP 0.569 SJR 0.437
- Scopus rating (2015): CiteScore 0.73 SNIP 0.594 SJR 0.454
- Scopus rating (2014): CiteScore 1.1 SNIP 0.856 SJR 0.768
- Scopus rating (2013): CiteScore 1.03 SNIP 0.853 SJR 0.49
- Scopus rating (2012): CiteScore 1.18 SNIP 1.115 SJR 0.404
- Scopus rating (2011): CiteScore 1.29 SNIP 1.065 SJR 0.729
- Scopus rating (2010): SNIP 1.122 SJR 0.756
- Scopus rating (2009): SNIP 0.537 SJR 0.448
- Scopus rating (2008): SNIP 0.784 SJR 0.547
- Scopus rating (2007): SNIP 0.754 SJR 0.498
- Scopus rating (2006): SNIP 1.094 SJR 0.68
- Scopus rating (2005): SNIP 1.007 SJR 0.92
- Scopus rating (2004): SNIP 0.772 SJR 0.481
- Scopus rating (2003): SNIP 0.375 SJR 0.242
- Scopus rating (2002): SNIP 1.086 SJR 0.71
- Scopus rating (2001): SNIP 0.898 SJR 0.8
- Scopus rating (2000): SNIP 0.916 SJR 0.605
- Scopus rating (1999): SNIP 0.924 SJR 0.688

**Original language:** English

**Life Sciences, Ecology, Statistics, general, Mathematical and Computational Biology, Evolutionary Biology, SC3, Maximum likelihood estimation, Model validation, Residual analysis, Statistical ecology, State space methods, Time series analysis**

**DOIs:**

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**Source:** FindIt

**Source-ID:** 2358107098

**Publication:** Research - peer-review → Journal article – Annual report year: 2017

**When in life does density dependence occur in fish populations?**


**General information**

**State:** Published

**Organisations:** National Institute of Aquatic Resources, Centre for Ocean Life, Section for Marine Living Resources, Section for Marine Ecology and Oceanography

**Authors:** Andersen, K. H. (Intern), Jacobsen, N. S. (Intern), Jansen, T. (Intern), Beyer, J. E. (Intern)

**Pages:** 656-667

**Publication date:** 2017

**Main Research Area:** Technical/natural sciences
Will salinity hinder the ongoing northward dispersal of the invasive round goby into the oceanic North Sea?
Accounting for correlated observations in an age-based state-space stock assessment model

Fish stock assessment models often rely on size- or age-specific observations that are assumed to be statistically independent of each other. In reality, these observations are not raw observations, but rather they are estimates from a catch-standardization model or similar summary statistics based on observations from many fishing hauls and subsamples of the size and age composition of the data. Although aggregation mitigates the strong intra-haul correlation between sizes/ages that is usually found in haul-by-haul data, violations of the independence assumption can have a large impact on the results and specifically on reported confidence bounds. A state-space assessment model that allows for correlations between age groups within years in the observation model for catches and surveys is presented and applied to data on several North Sea fish stocks using various correlation structures. In all cases the independence assumption is rejected. Less fluctuating estimates of the fishing mortality is obtained due to a reduced process error. The improved model does not suffer from correlated residuals unlike the independent model, and the variance of forecasts is decreased.

Publication information
Journal: ICES Journal of Marine Science
Volume: 73
Issue number: 7
ISSN (Print): 1054-3139
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.63
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.18
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.46
ISI indexed (2013): ISI indexed yes
A comprehensive survey on selective breeding programs and seed market in the European aquaculture fish industry

The use of selective breeding is still relatively limited in aquaculture species. Information on such activities is sparse, hindering an overall evaluation of their success. Here, we report on the results of an online survey of the major aquaculture breeding companies operating in Europe. Six main reared fish species were targeted. A total of 31 respondents contributed to the survey, representing 75% of European breeding organizations. Family-based breeding schemes were predominant, but individual selection was more frequently applied in marine species. Artificial fertilization is the preferred means of reproduction; however, mass spawning is often used as a fallback method. The most frequently selected trait is growth performance, but the number of selected traits has been increasing over the years through the addition of traits such as disease resistance or product quality. The use of molecular tools is now common in all programs, mainly for pedigree traceability. An increasing number of programs use either genomic or marker-assisted selection.

Results related to the seed production market confirmed that for Atlantic salmon there are a few dominant players at the European level, with 30–50% market share. Only part of the European fish aquaculture industry today fully exploits selective breeding to the best advantage. A larger impact assessment still needs to be made by the remainder, particularly on the market share of fish seed (eggs, larvae or juveniles) and its consequences for hatchery stability.

General information

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Padova, Wageningen University & Research, European Commission - Joint Research Center
Authors: Chavanne, H. (Ekstern), Janssen, K. (Ekstern), Hofherr, J. (Ekstern), Contini, F. (Ekstern), Haffray, P. (Ekstern), Komen, H. (Ekstern), Eg Nielsen, E. (Intern), Bargelloni, L. (Ekstern)
Pages: 1287-1307
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information

Journal: Aquaculture International
A diffusion approximation based on renewal processes with applications to strongly biased run–tumble motion

We consider organisms which use a renewal strategy such as run–tumble when moving in space, for example to perform chemotaxis in chemical gradients. We derive a diffusion approximation for the motion, applying a central limit theorem due
to Anscombe for renewal-reward processes; this theorem has not previously been applied in this context. Our results extend previous work, which has established the mean drift but not the diffusivity. For a classical model of tumble rates applied to chemotaxis, we find that the resulting chemotactic drift saturates to the swimming velocity of the organism when the chemical gradients grow increasingly steep. The dispersal becomes anisotropic in steep gradients, with larger dispersal across the gradient than along the gradient. In contrast to one-dimensional settings, strong bias increases dispersal. We next include Brownian rotation in the model and find that, in limit of high chemotactic sensitivity, the chemotactic drift is 64 % of the swimming velocity, independent of the magnitude of the Brownian rotation. We finally derive characteristic timescales of the motion that can be used to assess whether the diffusion limit is justified in a given situation. The proposed technique for obtaining diffusion approximations is conceptually and computationally simple, and applicable also when statistics of the motion is obtained empirically or through Monte Carlo simulation of the motion.
An important step towards accurate estimation of diet composition and consumption rates for the harbor porpoise (Phocoena phocoena)

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, University of Veterinary Medicine Hannover
Authors: Ross, S. D. (Intern), Andreasen, H. (Intern), Andersen, N. G. (Intern)
Pages: 1491–1500
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Marine Mammal Science
Volume: 32
Issue number: 4
ISSN (Print): 0824-0469
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.87 SJR 1.008 SNIP 0.978
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.055 SNIP 0.972 CiteScore 1.73
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.987 SNIP 1.093 CiteScore 1.83
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.193 SNIP 1.206 CiteScore 1.78
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.029 SNIP 1.106 CiteScore 1.9
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.891 SNIP 1.002 CiteScore 1.59
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Challenging ICES age estimation protocols: lessons learned from the eastern Baltic cod stock

Over the recent decades, the International Council for the Exploration of the Sea (ICES) has set guidelines for best practise quality control of age estimation procedures. The applicability of these guidelines is assessed by reviewing the ageing issues of eastern Baltic cod (EBC) as a case study. Since the implementation of an age-based assessment of EBC in the beginning of the 1970s, the assessment has been hampered by the quality of the age composition data, in recent years to a degree that age-based assessment is no longer used. The reason for the age reading problems is the low visual contrast between growth zones in the otoliths which seems to be the result of complex interactions of the hydrography in the Baltic Sea with the cod’s biology and behaviour. Over the last 40 years, various expert groups have struggled to document and improve the agreement of age estimation between national otolith readers, standardize methods and age estimations through repeated exchanges and reference collections as well as an internationally agreed manual. Despite these initiatives the precision of the age estimations based on traditional ageing did not improve, with significant bias persisting between and within readers. Additionally, a wide range of alternative methods for deriving the age information necessary for stock assessment and for validation of the true age have been tested. However, these methods did not produce unbiased age estimates over the entire size and age range of the EBC
stock. An age-validation is urgently needed. Deviations from the ICES guidelines identified are as follows: (i) the lack of rigorous quality control, particularly the auditing of national trends in age precision over the years using a reference collection and (ii) the implementation of an age error matrix in the stock assessment.

**General information**

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, National Marine Fisheries Research Institute, Institute of Food Safety, Animal Health and Environment, Thünen Institute of Baltic Sea Fisheries, Swedish University of Agricultural Sciences

Authors: Hüsey, K. (Intern), Radtke, K. (Ekstern), Plikshs, M. (Ekstern), Oeberst, R. (Ekstern), Baranova, T. (Ekstern), Krumme, U. (Ekstern), Sjöberg, R. (Ekstern), Walther, Y. (Ekstern), Mosegaard, H. (Intern)

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Volume: 73
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ISSN (Print): 1054-3139
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.63
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.18
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.46
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.35
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.32
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Conserved structure and expression of hsp70 paralogs in teleost fishes

The cytosolic 70 KDa heat shock proteins (Hsp70s) are widely used as biomarkers of environmental stress in ecological and toxicological studies in fish. Here we analyze teleost genome sequences to show that two genes encoding inducible hsp70s (hsp70-1 and hsp70-2) are likely present in all teleost fish. Phylogenetic and synteny analyses indicate that hsp70-1 and hsp70-2 are distinct paralogs that originated prior to the diversification of the teleosts. The promoters of both genes contain a TATA box and conserved heat shock elements (HSEs), but unlike mammalian HSP70s, both genes contain an intron in the 5′ UTR. The hsp70-2 gene has undergone tandem duplication in several species. In addition, many other teleost genome assemblies have multiple copies of hsp70-2 present on separate, small, genomic scaffolds. To verify that these represent poorly assembled tandem duplicates, we cloned the genomic region surrounding hsp70-2 in Fundulus heteroclitus and showed that the hsp70-2 gene copies that are on separate scaffolds in the genome assembly are arranged as tandem duplicates. Real-time quantitative PCR of F. heteroclitus genomic DNA indicates that four copies of the hsp70-2 gene are likely present in the F. heteroclitus genome. Comparison of expression patterns in F. heteroclitus and Gasterosteus aculeatus demonstrates that hsp70-2 has a higher fold increase than hsp70-1 following heat shock in gill but not in muscle tissue, revealing a conserved difference in expression patterns between isoforms and tissues. These data indicate that ecological and toxicological studies using hsp70 as a biomarker in teleosts should take this complexity into account.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of British Columbia
Authors: Metzger, D. C. (Ekstern), Hansen, J. H. (Intern), Schulte, P. M. (Ekstern)
Pages: 10-20
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Comparative Biochemistry and Physiology. Part D: Genomics and Proteomics
Volume: 18
ISSN (Print): 1744-117X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.921 SNIP 0.834 CiteScore 2.73
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.023 SNIP 0.83 CiteScore 2.44
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.931 SNIP 0.841 CiteScore 2.4
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.814 SNIP 0.737 CiteScore 2.32
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.756 SNIP 0.88 CiteScore 2.52
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Dynamic optimal foraging theory explains vertical migrations of bigeye tuna

Bigeye tuna are known for remarkable daytime vertical migrations between deep water, where food is abundant but the water is cold, and the surface, where water is warm but food is relatively scarce. Here we investigate if these dive patterns can be explained by dynamic optimal foraging theory, where the tuna maximizes its energy harvest rate. We assume that foraging efficiency increases with body temperature, so that the vertical migrations are thermoregulatory. The tuna’s state is characterized by its mean body temperature and depth, and we solve the optimization problem numerically using dynamic programming. With little calibration of model parameters, our results are consistent with observed data on vertical movement: we find that small tuna should display constant-depth strategies while large tuna should display vertical migrations. The analysis supports the hypothesis that the tuna behaves such as to maximize its energy gains. The model therefore provides insight into the processes underlying observed behavioral patterns and allows generating predictions of foraging behavior in unobserved environments.
Dynamics of a physiologically structured population in a time-varying environment

Physiologically structured population models have become a valuable tool to model the dynamics of populations. In a stationary environment such models can exhibit equilibrium solutions as well as periodic solutions. However, for many organisms the environment is not stationary, but varies more or less regularly. In order to understand the interaction between an external environmental forcing and the internal dynamics in a population, we examine the response of a physiologically structured population model to a periodic variation in the food resource. We explore the addition of forcing in two cases: (A) where the population dynamics is in equilibrium in a stationary environment, and (B) where the population dynamics exhibits a periodic solution in a stationary environment. When forcing is applied in case A, the solutions are mainly periodic. In case B the forcing signal interacts with the oscillations of the unforced system, and both periodic and irregular (quasi-periodic or chaotic) solutions occur. In both cases the periodic solutions include one and multiple period cycles, and each cycle can have several reproduction pulses.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Dynamical Systems, National Institute of Aquatic Resources, Centre for Ocean Life, Section for Marine Living Resources
Authors: Heilmann, I. L. T. (Intern), Starke, J. (Intern), Andersen, K. H. (Intern), Thygesen, U. H. (Intern), Sørensen, M. P. (Intern)
Pages: 54-61
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Ecological Complexity
Volume: 28
ISSN (Print): 1476-945X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.11 SJR 0.799 SNIP 1.039
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.921 SNIP 1.073 CiteScore 2.01
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.876 SNIP 1.5 CiteScore 2.53
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.073 SNIP 1.632 CiteScore 3.29
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.001 SNIP 1.342 CiteScore 2.64
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.002 SNIP 0.976 CiteScore 1.91
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.922 SNIP 1.28
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.899 SNIP 0.902
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.694 SNIP 0.947
Evaluating genetic traceability methods for captive-bred marine fish and their applications in fisheries management and wildlife forensics

Growing demands for marine fish products is leading to increased pressure on already depleted wild populations and a rise in aquaculture production. Consequently, more captive-bred fish are released into the wild through accidental escape or deliberate releases. The increased mixing of captive-bred and wild fish may affect the ecological and/or genetic integrity of wild fish populations. Unambiguous identification tools for captive-bred fish will be highly valuable to manage risks (fisheries management) and tracing of escapees and seafood products (wildlife forensics). Using single nucleotide polymorphism (SNP) data from captive-bred and wild populations of Atlantic cod Gadus morhua L. and sole Solea solea L., we explored the efficiency of population and parentage assignment techniques for the identification and tracing of captive-bred fish. Simulated and empirical data were used to correct for stochastic genetic effects. Overall, parentage assignment performed well when a large effective population size characterized the broodstock and escapees originated from early generations of captive breeding. Consequently, parentage assignments are particularly useful from a fisheries management perspective to monitor the effects of deliberate releases of captive-bred fish on wild populations. Population assignment proved to be more efficient after several generations of captive breeding, which makes it a useful method in forensic applications for well-established aquaculture species. We suggest the implementation of a case-by-case strategy when choosing the best method.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Freshwater Fisheries Ecology
Authors: Bekkevold, D. (Intern), Eg Nielsen, E. (Intern), Sivebæk, F. (Intern)
Publication date: 2016

Publication information
Source/Publisher: Fiskepleje.dk
Main Research Area: Technical/natural sciences
Publication: Communication › Internet publication – Annual report year: 2016

Er det genetik der bestemmer, hvor længe laks opholder sig i havet?

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Freshwater Fisheries Ecology
Authors: Bekkevold, D. (Intern), Eg Nielsen, E. (Intern), Sivebæk, F. (Intern)
Publication date: 2016

Publication information
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Main Research Area: Technical/natural sciences
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Evaluating genetic traceability methods for captive-bred marine fish and their applications in fisheries management and wildlife forensics

Growing demands for marine fish products is leading to increased pressure on already depleted wild populations and a rise in aquaculture production. Consequently, more captive-bred fish are released into the wild through accidental escape or deliberate releases. The increased mixing of captive-bred and wild fish may affect the ecological and/or genetic integrity of wild fish populations. Unambiguous identification tools for captive-bred fish will be highly valuable to manage risks (fisheries management) and tracing of escapees and seafood products (wildlife forensics). Using single nucleotide polymorphism (SNP) data from captive-bred and wild populations of Atlantic cod Gadus morhua L. and sole Solea solea L., we explored the efficiency of population and parentage assignment techniques for the identification and tracing of captive-bred fish. Simulated and empirical data were used to correct for stochastic genetic effects. Overall, parentage assignment performed well when a large effective population size characterized the broodstock and escapees originated from early generations of captive breeding. Consequently, parentage assignments are particularly useful from a fisheries management perspective to monitor the effects of deliberate releases of captive-bred fish on wild populations. Population assignment proved to be more efficient after several generations of captive breeding, which makes it a useful method in forensic applications for well-established aquaculture species. We suggest the implementation of a case-by-case strategy when choosing the best method.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, KU Leuven, University of Bologna, Royal Zoological Society of Scotland, University of East Anglia, University of Padua, Wageningen University & Research, European Commission - Joint Research Center, Bangor University, Queen’s University Belfast
Authors: Bylemans, J. (Ekstern), Maes, G. E. (Ekstern), Diopere, E. (Ekstern), Cariani, A. (Ekstern), Senn, H. (Ekstern), Taylor, M. I. (Ekstern), Helyar, S. (Ekstern), Bargelloni, L. (Ekstern), Bonaldo, A. (Ekstern), Carvalho, G. (Ekstern), Guarnerio, I. (Ekstern), Komen, H. (Ekstern), Martinsohn, J. T. (Ekstern), Eg Nielsen, E. (Intern), Tinti, F. (Ekstern), Volckaert, F. A. M. (Ekstern), Ogden, R. (Ekstern)
Pages: 131-145
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Aquaculture Environment Interactions
Volume: 8
ISSN (Print): 1869-215X
Ratings:
Evaluation of otolith shape as a tool for stock discrimination in marine fishes using Baltic Sea cod as a case study

In the Western Baltic Sea two genetically distinct cod stocks "Eastern Baltic cod" and "Western Baltic cod" occur with considerable mixing of stocks. In this study we evaluated the applicability of otolith shape analysis for classification of individuals caught in the mixed stock cod fishery, using SNP (single nucleotide polymorphism) based genetic assignment of otolith shape baselines. We further developed a management aimed approach for mixed stock assignment by robust stochastic baseline selection and posterior bias correction by individual reassignment of the least likely classifications into the alternate stock. Classification criteria selected by Monte Carlo runs of Linear Discriminant Analysis were captured by otolith area and 20 Elliptic Fourier Descriptors of primarily low frequency harmonics. Classification success was considerably lower when using a baseline of spawning individuals only, compared to the better spatial coverage of a combined baseline also including genotyped individuals from the mixed stock area. Furthermore, the inclusion of genotyped individuals balanced the baseline size composition and to a large extent removed a strong size related bias in classification success. These results demonstrate the interplay of environmental, ontogenetic and genetic influences on otolith shape, which complicates the application of otolith shape for stock discrimination in mixed-stock scenarios. Rigorous genetic validation and further studies on the temporal dynamics of shape formation are necessary.
Explaining the catch efficiency of different cod pots using underwater video to observe cod entry and exit behaviour

Cod pots are considered seal-safe fishing gear and are proposed as a solution to mitigate the ongoing seal-fisheries conflict in the Baltic Sea. This study examined various factors which could affect the entry and exit behaviour of cod in relation to cod pots. Statistical modelling was used to determine which of these factors most affected the pots' catch per unit effort (CPUE). Two fishing trials were conducted off the coast of Bornholm, Denmark, using six pot types with different design features, equipped with underwater camera systems to record the behaviour of the cod in relation to the pots. Four pot types were floating pots with one entrance and two were bottom standing with three entrances. Different pot types showed significantly different CPUEs and the pot type was an explanatory factor for entry and exit rates for both trials. In trial 1 artificial light was used for filming and results showed an increase in entry rates during the night time, suggesting that lights attract fish to the pot when the dark surroundings make the effect of the light more noticeable. Exit rates in trial 1 increased with an increasing number of fish in the pot while they decreased with soak time. In trial 2, when no artificial light was used, a saturation effect was found in that the probability of cod entering the pot lessened as the number of cod already in the pot increased. However, the exit rates in trial 2 also decreased with increasing number of fish in the pot. The study offers greater depth to the understanding of CPUE results by examining fish behaviour around the pots and not just the raw catch data. This in turn contributes to the ongoing search for the most favourable pot designs.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management, Swedish University of Agricultural Sciences
Authors: Hedgärde, M. (Ekstern), Berg, C. W. (Intern), Kindt-Larsen, L. (Intern), Lunneryd, S. G. (Ekstern), Königson, S. (Ekstern)
Pages: 67-90
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Ocean Technology
Volume: 11
Issue number: 4
ISSN (Print): 1718-3200
Ratings:
Scopus rating (2016): CiteScore 0.13 SNIP 0.445 SJR 0.121
Scopus rating (2015): CiteScore 0.22 SNIP 0.604 SJR 0.153
Scopus rating (2014): CiteScore 0.13 SNIP 0.479 SJR 0.126
Scopus rating (2013): CiteScore 0.11 SNIP 0.408 SJR 0.117
Scopus rating (2012): CiteScore 0.07 SNIP 0.076 SJR 0.112
Scopus rating (2011): CiteScore 0.09 SNIP 0.246 SJR 0.105
Scopus rating (2010): SNIP 0.278 SJR 0.108
Original language: English
Attraction, Behaviour, Cod, CPUE, Pot, Saturation
Electronic versions:
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Links:
http://www.thejot.net/?page_id=837&show_article_preview=824
Links:
http://www.scopus.com/inward/record.url?scp=85030121587&partnerID=8YFLogxK (Link to publication in Scopus)
Source: Scopus
Source-ID: 85030121587
First-year survival of North East Atlantic mackerel (Scomber scombrus) from 1998 to 2012 appears to be driven by availability of Calanus, a preferred copepod prey

Mackerel (Scomber scombrus) is one of the ecologically and economically most important fish species in the Atlantic. Its recruitment has, for unknown reasons, been exceptional from 1998 to 2012. The majority (75%) of the survivors in the first winter were found north of an oceanographic division at approximately 52°N, despite the fact that mackerel spawns over a wide range of latitudes. Multivariate time series modelling of survivor abundance in the north revealed a significant correlation with the abundance of copepodites (stage I–IV) of Calanus sp. in the spawning season (April to June). The copepodites were a mix of C. helgolandicus (dominating) and C. finmarchicus. The growth of mackerel larvae is known to be positively related to the availability of nauplii and copepodites of preferred prey species, namely, large calanoid copepod species such as Calanus. The statistical relationship between mackerel survivors and abundance of Calanus, therefore, most likely, reflected a causal relationship: high availability of Calanus probably reduced starvation, stage-specific predation and cannibalism (owing to prey switching). The effects of other abundant, but less preferred zooplankton taxa, (Acartia sp., Branchiopoda spp. and Echinodermata spp. larvae), as well as stock size, temperature and wind-induced turbulence were not found to be significant. However, stock size was retained in the final model because of a significant interaction with Calanus in oceanic areas west of the North European continental shelf. This was suggested to be a consequence of a density driven expansion of the spawning area that increased the overlap between early life stages of mackerel and food (Calanus) in new areas.

General information
State: Published
Organisations: Section for Marine Living Resources, National Institute of Aquatic Resources, Greenland Institute of Natural Resources
Authors: Jansen, T. (Intern)
Pages: 457-469
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Fisheries Oceanography
Volume: 25
Issue number: 4
ISSN (Print): 1054-6006
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.19
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.4
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.61
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.61
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 2.21
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 2.42
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
Fish stock assessment under data limitations developing a new method based on a size-structured theoretical ecology framework

Fish stock assessment is an integral part of every fisheries management system. Modern assessment methods require data about the fishery and the stock, such as catches, survey estimates, aging information and life history parameters, all of which is difficult and expensive to gather. However, the majority of global fish catches comes from species that lack an official assessment due to lack of data. That is true especially for small scale fisheries and fisheries in developing countries. New methods are in need that require little amount of easily attainable data and provide scientific advice for fish stocks that are not assessed. The goal of the thesis is to develop a new data-limited stock assessment method that is: rooted in theoretical ecology, requires only information about the size composition of the catch or surveys (i.e. aging is not required), and does not require time-series. The method provides estimates of fishing mortality and the FMSY reference point, it is tested and validated, and is implemented as software package making it easy to use by stakeholders of different levels.

The basis of the method is a size-based theoretical ecology framework that describes exploited fish stocks. The model parameters correspond to Beverton-Holt life history invariants, which reduces the number of parameters and allows data-limited assessments to borrow information from data-rich stocks. The mathematical formulation of the single species population dynamics is used in a maximum-likelihood optimisation framework to estimate model parameters. The data-limited method estimates at the same time the fishing mortality rate and the biological reference point FMSY.

Minimum data requirements consist of a single size frequency distribution from the commercial catch or a scientific survey. If the total catch is known, important quantities about the stock (e.g. biomass of spawners, recruitment) can be quantified. The method is tested using simulated data and validated using a subset of available data from data-rich fish stocks. The implementation of the method as a software package in the R programming language is publicly available.
**Genetic structure of West Greenland populations of lumpfish Cyclopterus lumpus**

In this study, 11 microsatellite markers were used to determine the structure of West Greenlandic lumpfish Cyclopterus lumpus populations across six spawning locations spanning >1500 km and compared with neighbouring populations in Canada and Iceland. To evaluate whether data allow for identification of origin of C. lumpus in Greenlandic waters, genetic assignment analysis was performed for 86 C. lumpus sampled on a feeding migration. Significant structuring with isolation by distance was observed in the West Greenland samples and two major subpopulations, north and south, were suggested. Based on FST values, closer relationships were observed between Greenland and Canada, than Greenland and Iceland. Surprisingly, the North Greenland population showed more similarities with Canadian samples, than did the geographically closer south-west Greenland population. Origin could be assigned for a high proportion of non-spawning fish and demonstrated a marked east-west spatial separation of fish of Greenlandic and Icelandic genotypes.

**General information**

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Greenland Institute of Natural Resources, Greenland Institute of Natural Resources
Authors: Mayoral, E. G. (Intern), Olsen, M. (Ekstern), Hedeholm, R. (Ekstern), Post, S. L. (Intern), Eg Nielsen, E. (Intern), Bekkevold, D. (Intern)
Pages: 2625-2642
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Fish Biology
Volume: 89
Issue number: 6
ISSN (Print): 0022-1112
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 1.57 SJR 0.741 SNIP 0.882
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 0.951 SNIP 0.935 CiteScore 1.64
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 0.944 SNIP 0.934 CiteScore 1.76
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 1.049 SNIP 1.118 CiteScore 1.98
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.93 SNIP 1.035 CiteScore 1.88
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 0.895 SNIP 0.946 CiteScore 1.66
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 0.774 SNIP 0.834
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 0.773 SNIP 0.891
- Web of Science (2009): Indexed yes
Historical DNA documents long distance natal homing in marine fish

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Greenland Climate Research Centre, Stanford University, Greenland Institute of Natural Resources, Aarhus University
Pages: 2727-2734
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology
Volume: 25
Issue number: 12
ISSN (Print): 0962-1083
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.9 SJR 3.508 SNIP 1.651
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.862 SNIP 1.606 CiteScore 5.73
BFI (2014): BFI-level 2
Identification of high-risk areas for harbour porpoise Phocoena phocoena bycatch using remote electronic monitoring and satellite telemetry data

The bycatch of harbour porpoise Phocoena phocoena is an issue of major concern for fisheries management and for porpoise conservation. We used high-resolution spatial and temporal data on porpoise abundance and fishing effort from the Danish Skagerrak Sea to identify areas with potentially higher and lower risk of porpoise bycatch. From May 2010 to April 2011, 4 commercial gillnet vessels were equipped with remote electronic monitoring (REM) systems. The REM system recorded time, GPS position and closed-circuit television (CCTV) footage of all gillnet hauls. REM data were used for identifying areas with potentially higher and lower risk of porpoise bycatch.
to identify fishing grounds, quantify fishing effort and document harbour porpoise bycatch. Movement data from 66 harbour porpoises equipped with satellite transmitters from 1997 to 2012 were used to model population density. A simple model was constructed to investigate the relationship between the response (number of individuals caught) and porpoise density and fishing effort described by net soak time, net string length and target species. Results showed that a model including both porpoise density and fishing effort data predicted bycatch better than models containing only one factor. We therefore conclude that porpoise telemetry or REM data allow for identification of areas of potential high and low bycatch risk, and better predictions are obtained when combining the 2 sources of data. The final model can thus be used as a tool to identify areas of bycatch risk

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Monitoring and Data, Aarhus University, University of St Andrews
Authors: Kindt-Larsen, L. (Intern), Berg, C. W. (Intern), Tougaard, J. (Ekstern), Sørensen, T. K. (Intern), Geitner, K. (Intern), Northridge, S. (Ekstern), Sveegaard, S. (Ekstern), Larsen, F. (Intern)
Pages: 261-271
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Marine Ecology - Progress Series
Volume: 555
ISSN (Print): 0171-8630
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
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Scopus rating (2016): CiteScore 2.4
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BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56
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Scopus rating (2014): CiteScore 2.75
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ISI indexed (2013): ISI indexed yes
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BFI (2011): BFI-level 2
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Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
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BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
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Identifying blue whiting (Micromesistius poutassou) stock structure in the Northeast Atlantic by otolith shape analysis

Information on stock identification and spatial stock structure provide a basis for understanding fish population dynamics and improving fisheries management. In this study, otolith shape analysis was used to study the stock structure of blue whiting (Micromesistius poutassou) in the northeast Atlantic using 1693 samples from mature fish collected between 37°N and 75°N and 20°W and 25°E. The results indicated two stocks located north and south of ICES Divisions VIa and VIb (54°5N to 60°5N, 4°W to 11°W). The central area corresponds to the spawning area west of Scotland. Sampling year effects and misclassification in the linear discriminant analysis suggested exchanges between the northern and southern stocks. The results corroborate previous studies indicating a structuring of the blue whiting stock into two stocks, with some degree of mixing in the central overlap area.
Implementing a generic method for bias correction in statistical models using random effects, with spatial and population
dynamics examples

Statistical models play an important role in fisheries science when reconciling ecological theory with available data for wild populations or experimental studies. Ecological models increasingly include both fixed and random effects, and are often estimated using maximum likelihood techniques. Quantities of biological or management interest (“derived quantities”) are then often calculated as nonlinear functions of fixed and random effect estimates. However, the conventional “plug-in” estimator for a derived quantity in a maximum likelihood mixed-effects model will be biased whenever the estimator is calculated as a nonlinear function of random effects. We therefore describe and evaluate a new “epsilon” estimator as a generic bias-correction estimator for derived quantities. We use simulated data to compare the epsilon-method with an existing bias-correction algorithm for estimating recruitment in four configurations of an age-structured population dynamics model. This simulation experiment shows that the epsilon-method and the existing bias-correction method perform equally well in data-rich contexts, but the epsilon-method is slightly less biased in data-poor contexts. We then apply the epsilon-method to a spatial regression model when estimating an index of population abundance, and compare results with an alternative bias-correction algorithm that involves Markov-chain Monte Carlo sampling. This example shows that the epsilon-method leads to a biologically significant difference in estimates of average abundance relative to the conventional plug-in estimator, and also gives essentially identical estimates to a sample-based bias-correction estimator. The epsilon-method has been implemented by us as a generic option in the open-source Template Model Builder software, and could be adapted within other mixed-effects modeling tools such as Automatic Differentiation Model Builder.
Builder for random effects. It therefore has potential to improve estimation performance for mixed-effects models throughout fisheries science. Published by Elsevier B.V.

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Scopus rating (2011): SJR 1.154 SNIP 1.135 CiteScore 1.7
ISI indexed (2011): ISI indexed yes
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Scopus rating (2010): SJR 1.041 SNIP 1.1
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.985 SNIP 1.065
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.938 SNIP 1.142
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.022 SNIP 1.075
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.025 SNIP 1.274
Web of Science (2006): Indexed yes
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Inference in dynamic models of fitness optimization based on observed animal behaviour

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Thygesen, U. H. (Intern), Patterson, T. (Intern)
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Influence of twin and multi-rig trawl systems on CPUE in the Danish Norway lobster (Nephrops norvegicus) fishery
One of the most effective ways to alter catch and length compositions in trawls is to adjust the meshsize or add selective devices such as sorting grids and selective netting panels. These changes are often introduced into the fishery in a top-down manner whereby fishermen are forced to comply with specific legislation. However, fishermen have also introduced gear modifications that have contributed to improving species selectivity in trawls. One of the simplest and most effective modifications that came from industry was the development and introduction of twin and multi-rig trawls. Here we analyse catch rates of four target species, Norway lobster (Nephrops norvegicus), cod (Gadus morhua), plaice (Pleuronectes platessa) and haddock (Melanogrammus aeglefinus), to try and understand how the use of multi-rig trawls have altered catch rates within the Danish demersal trawl fishery over the last 16 years (1997–2012). Results showed that catch rates of Nephrops in multi-rig trawls were significantly higher (1.89–2.03) than those in single trawls. For cod, haddock and plaice there was no significant effect of gear type. The results are discussed in relation to the Common Fisheries Policy reform and the increasing importance of industry introduced gear modifications

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Kæmpeøksen fra Storå er ambassadør for en bestand i fremgang

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State: Published
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Authors: Sivebæk, F. (Intern), Eg Nielsen, E. (Intern)
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Laksen i Storå skal fremover klare sig uden udsætninger

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Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Institute Management, Section for Marine Living Resources
Authors: Sivebæk, F. (Intern), Koed, A. (Intern), Eg Nielsen, E. (Intern), Jepsen, N. (Intern), Aarestrup, K. (Intern)
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Learning from ‘apparent consensus’ in TAC disputes: Exploring knowledge overlaps in LEK and genetic categorization of Atlantic cod
The rapid development of genetic science has improved the methods for fisheries stock assessments with increasing implications for management. One key accomplishment has been the identification of different sub-populations of Atlantic cod. Recognizing that local coastal fishers in the North Atlantic have often held a local knowledge about local cod populations, this study examines the extent to which genetic analysis corroborates this local knowledge and vice versa. In Nuuk, capital of Greenland situated by the Nuuk fjord system, local fishers say that they and generations before them have been observing both inshore and offshore cod in the Nuuk fjord system. Fisher interviews were conducted in order to
understand the construction as well as the content of this specific local ecological knowledge. Furthermore, fishers were invited to assign cod from their catches into categories based on their knowledge of inshore and offshore cod. These cod were subsequently analyzed and assigned to population using genetic methodologies. The comparison between visual and genetic assignment was not able to confirm any convincing consensus between fishers' understanding of offshore and inshore cod and the corresponding genetic categories. However, an examination of existing inshore and off-shore catch surveys confirmed the relevance of the morphological characteristics (liver condition and shape) of ecologically defined inshore and off-shore cod that provided the basis for fishers' categorizations. This opens a discussion of the fishers' way of knowing about inshore and offshore cod respectively and if and how the content of their knowledge could be made relevant in relation to scientific advice procedures.
Marine ecosystem connectivity mediated by migrant–resident interactions and the concomitant cross-system flux of lipids

General information
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.686 SNIP 0.939 CiteScore 2.66
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.37 SNIP 0.886 CiteScore 2.37
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.876 SNIP 0.725 CiteScore 1.66
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.58 SNIP 0.518
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
Web of Science (2011): Indexed yes
Migration, distribution and population (stock) structure of shallow-water hake (Merluccius capensis) in the Benguela Current Large Marine Ecosystem inferred using a geostatistical population model

Shallow-water hake (Merluccius capensis) is of considerable ecological and economic importance in the Benguela Current Large Marine Ecosystem in South Africa and Namibia. Optimal management of the resource is currently constrained by the limited understanding of migration patterns and population (stock) structure. We combined data from multiple demersal trawl surveys from the entire distribution area to estimate growth rate, mortality and spatial and temporal patterns of M. capensis. Analyses were conducted using the geostatistical model GeoPop. The complexity of the model and the amount of data required a new level of soft- and hardware performance. This was achieved by utilizing Template Model Builder and high-end computational hardware (Amazon Elastic Compute Cloud, EC2). The data and the model enabled us to follow the distribution and infer movements of M. capensis from the recruitment/nursery areas, through the juvenile phase and the adults’ migration to the spawning areas outside/upstream of the nursery areas. This revealed some previously unknown migration patterns and indicated natal homing and the existence of three primary population components in the region, namely the Walvis (central and northern Namibia), the Orange (Southern Namibia-Northern SA) and the Agulhas (Southern part of SA) components. Our results also indicated substantial regional differences in mortality. We recommend that fisheries assessment, advice and management take consideration of these aspects of the distribution and population (stock) structure of M. capensis in the Benguela Current Large Marine Ecosystem.

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BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.067 SNIP 1.133 CiteScore 2.01
Web of Science (2015): Indexed yes
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Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.037 SNIP 1.173 CiteScore 1.85
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Myfish : Maximising yield of fisheries while balancing ecosystem, economic and social concerns: Legacy booklet

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Ocean warming expands habitat of a rich natural resource and benefits a national economy

Geographic redistribution of living natural resources changes access and thereby harvesting opportunities between countries. Internationally shared fish resources can be sensitive to shifts in the marine environment and this may have great impact on the economies of countries and regions that rely most heavily on fisheries to provide employment and food supply. Here we present a climate change-related biotic expansion of a rich natural resource with substantial economic consequences, namely the appearance of northeast Atlantic mackerel (Scomber scombrus) in Greenlandic waters. In recent years, the summer temperature has reached record highs in the Irminger Current, and this development has expanded the available and realized mackerel habitat in time and space. Observations in the Irminger Current in east Greenland in 2011 of this temperature-sensitive epipelagic fish were the first records so far northwest in the Atlantic. This change in migration pattern was followed by a rapid development of a large-scale fishery of substantial importance for the national economy of Greenland (23% of Greenland’s export value of all goods in 2014). A pelagic trawl survey was conducted in mid-summer 2014 and the results showed that the bulk of similar to 1 million Mg (=t) of mackerel in the Irminger Current in southeast Greenland were located in the relatively warm (>8.5 degrees C) surface layer. Mackerel was also observed in southwest Greenland. Finally, 15 CMIP5 Earth System Model projections of future marine climate were used to evaluate the epipelagic environment in Greenland. These projections for moderate and high CO2 emission scenarios (representative concentration pathways [RCP] 4.5 and 8.5) suggest how the available mackerel habitat may expand further in space and time. Overall, our results indicate that, if the stock remains large, productive, and continues its current migration pattern, then climate change has provided Greenland with a new unique opportunity for commercial exploitation. However, positive cases like this should not be cherry-picked and misused as arguments against timely and effective mitigation of climate change.
Scopus rating (2013): SJR 2.676 SNIP 1.863 CiteScore 4.77
ISI indexed (2013): ISI indexed yes
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Scopus rating (2011): SJR 3.286 SNIP 1.975 CiteScore 4.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
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Scopus rating (2010): SJR 2.784 SNIP 1.675
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.664 SNIP 1.759
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.869 SNIP 1.749
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.805 SNIP 1.876
Scopus rating (2006): SJR 3.065 SNIP 2.06
Scopus rating (2005): SJR 2.819 SNIP 1.966
Scopus rating (2004): SJR 2.65 SNIP 1.832
Scopus rating (2003): SJR 2.808 SNIP 2.089
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**Ontogeny and growth of early life stages of captive-bred European eel**
Captive breeding of European eel, Anguilla anguilla is challenged by the complex hormonal control of Anguillid eel reproduction and the distinctive ontogeny of the leptocephalus larvae that are unique to the Elopomorph superorder. Recent experimental research has succeeded in the production of viable eggs and larvae of European eel, providing the basis for studies on early life stages of this species in captivity. In this study, we describe and illustrate morphological characteristics of eggs, embryos, and larvae from fertilization to termination of the yolk sac stage and provide a comparison with additional commercially important eel species. Furthermore, we model growth during the critical first phase in larval ontogeny, i.e. the yolk sac stage, and test for maternal effects. The eggs of A. anguilla typically have numerous oil droplets that coalesce into a single large oil droplet, while the zygote forms a large perivitelline space, reaching an egg diameter of 1.45 ± 0.12 mm at 3.0 to 3.5 h post fertilization. Embryonic development from fertilization to larval hatch lasted ~46–48 h at 20 °C with the larvae emerging in a relatively undeveloped stage with a protuberant yolk sac. During the period of yolk and oil absorption, the larvae undertook significant changes in head and body morphology. At the completion of yolk sac absorption, the largely transparent larvae had a set of protruding teeth, pigmented eyes and tail, and a simple alimentary tract. Larvae appeared capable of feeding at ~12 days post hatch at 20 °C, and were able to survive another ~10 days without feeding. Larval length approached and asymptotic maximum of 6.8mma round day 10 in non-fed larvae. Larval batches from different maternal origins varied in yolk sac size and the extent of yolk sac resources influenced larval size at the end of the yolk sac stage. The ontogenetic description presented here fills
a gap in knowledge about the yet undiscovered early life stages of native European eel, which can provide a framework of reference for the development of hatchery technology. Such progress is urgently needed for a self-sustained aquaculture of this high-value and critically endangered species. Statement of relevance: European eel is a high-value species in aquaculture, however, production is presently hampered by reliance on wild caught fry. Captive production of glass eels will reopen markets in Europe and Asia, benefiting European eel producers. The results presented here document recent progress within assisted reproduction and larval culture of this species in aquaculture and aid establishing hatchery technology of this species.

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, Billund Aquakulturservice A/S, Danish Aquaculture Organisation
Authors: Sørensen, S. R. (Intern), Tomkiewicz, J. (Intern), Munk, P. (Intern), Butts, I. A. (Intern), Nielsen, A. (Intern), Lauesen, P. (Ekstern), Graver, C. (Ekstern)
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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.002 SNIP 1.34 CiteScore 2.16
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.136 SNIP 1.3 CiteScore 2.18
ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): SJR 1.212 SNIP 1.487 CiteScore 2.32
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Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.294 SNIP 1.542 CiteScore 2.39
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.151 SNIP 1.394
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.941 SNIP 1.263
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.909 SNIP 1.173
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.019 SNIP 1.318
Outlier loci detect intraspecific biodiversity amongst spring and autumn spawning herring across local scales

Herring, Clupea harengus, is one of the ecologically and commercially most important species in European northern seas, where two distinct ecotypes have been described based on spawning time; spring and autumn. To date, it is unknown if these spring and autumn spawning herring constitute genetically distinct units. We assessed levels of genetic divergence between spring and autumn spawning herring in the Baltic Sea using two types of DNA markers, microsatellites and Single Nucleotide Polymorphisms, and compared the results with data for autumn spawning North Sea herring. Temporally replicated analyses reveal clear genetic differences between ecotypes and hence support reproductive isolation. Loci showing non-neutral behaviour, so-called outlier loci, show convergence between autumn spawning herring from demographically disjoint populations, potentially reflecting selective processes associated with autumn spawning ecotypes. The abundance and exploitation of the two ecotypes have varied strongly over space and time in the Baltic Sea, where autumn spawners have faced strong depression for decades. The results therefore have practical implications by highlighting the need for specific management of these co-occurring ecotypes to meet requirements for sustainable exploitation and ensure optimal livelihood for coastal communities.

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Estonian University of Life Sciences, University of Tartu, Queen's University Belfast
Authors: Bekkevold, D. (Intern), Gross, R. (Ekstern), Arula, T. (Ekstern), Helyar, S. J. (Ekstern), Ojaveer, H. (Ekstern)
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Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
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Patterns and mechanisms of dispersal in a keystone seagrass species

*Z. noltei* shows low genetic connectivity (from 10 s to 100 s of km) in the Black Sea. Physical modelling of dispersal well agree with estimates of genetic connectivity. Physical and genetic connectivity show possible but rare long distance dispersal. Seeds get dispersed locally while shoots have higher dispersal potential. Physical and genetic measures estimate potential and realized connectivity.

General information

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Sinop University, Stazione Zoologica Anton Dohrn, National Institute for Marine Research and Development Grigore Antipa, Alexandru Ioan Cuza University, Institute of Oceanology, The A.O. Kovalevsky Institute of Marine Biological Researches,
Authors: Jahnke, M. (Ekstern), Christensen, A. (Intern), Micu, D. (Ekstern), Milchakova, N. (Ekstern), Sezgin, M. (Ekstern), Todorova, V. (Ekstern), Strungaru, S. (Ekstern), Procaccini, G. (Ekstern)
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Quantifying changes in abundance, biomass and spatial distribution of Northeast Atlantic (NEA) mackerel (Scomber scombrus) in the Nordic Seas from 2007 to 2014

The Northeast Atlantic (NEA) mackerel (Scomber scombrus) is a widely distributed pelagic fish species that plays a key role in the marine ecosystem. In recent years, there has been a large fishery targeting mackerel in the NEA. At the same time as the geographic range of the mackerel fishery has expanded and the spatial distribution of the stock been defectively determined, the stock assessment has been considered to be highly uncertain by
ICES. Limited tuning data, with only a triennial egg survey, have created challenges for the assessment and management of NEA mackerel, and ICES has repeatedly stated the need for an annual age-disaggregated abundance index of this stock. These were the motivations for establishment of an international pelagic trawl survey in 2007, the International Ecosystem Summer Surveys in the Nordic Seas (IESSNS). The estimated total biomass indices for NEA mackerel based on coordinated and standardized swept-area surface trawling in July–August from IESSNS increased from 1.96 million t [relative standard error (RSE) ¼ 30.35%] in 2007 to 8.77 million t (RSE ¼ 7.95%) in 2014. Simultaneously, the mackerel stock expanded its geographic range during the feeding season from 1.3 million km² in 2007 to at least 2.9 million km² in 2014, mainly towards western and northern regions of the Nordic seas. Estimates of abundance indices by age group were fairly precise (RSE 20%) for ages 3–12, while the precision was poorer for ages 1 and 2 and for age groups 13 and older (RSE > 50%). Furthermore, evaluation of the performance of the estimated abundance indices by age for this time-series, based on internal consistency and catch curves, suggest that the abundance indices of ages 3–12 track the temporal variation in abundance reasonably, and thus is applicable for stock assessments.

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State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Institute of Marine Research, Marine Research Institute, Faroe Marine Research Institute, Norwegian Computing Center, Marine Producers Norge A/S
Authors: Nøttestad, L. (Ekstern), Utne, K. R. (Ekstern), Óskarsson, G. .. (Ekstern), Jonsson, S. (Ekstern), Jacobsen, J. A. (Ekstern), Tangen, Ø. (Ekstern), Anthonypillai, V. (Ekstern), Aanes, S. (Ekstern), Vølstad, J. H. (Ekstern), Bernasconi, M. (Ekstern), Debes, H. (Ekstern), Smith, L. (Ekstern), Sveinbjörnsson, S. (Ekstern), Holst, J. C. (Ekstern), Jansen, T. (Intern), Slotte, A. (Ekstern)
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.63
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.18
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.46
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.35
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.32
Recombination patterns reveal information about centromere location on linkage maps

Linkage mapping is often used to identify genes associated with phenotypic traits and for aiding genome assemblies. Still, many emerging maps do not locate centromeres – an essential component of the genomic landscape. Here, we demonstrate that for genomes with strong chiasma interference, approximate centromere placement is possible by phasing the same data used to generate linkage maps. Assuming one obligate crossover per chromosome arm, information about centromere location can be revealed by tracking the accumulated recombination frequency along linkage groups, similar to half-tetrad analyses. We validate the method on a linkage map for sockeye salmon (Oncorhynchus nerka) with known centromeric regions. Further tests suggest that the method will work well in other salmonids and other eukaryotes. However, the method performed weakly when applied to a male linkage map (rainbow trout; O. mykiss) characterized by low and unevenly distributed recombination – a general feature of male meiosis in many species. Further, a high frequency of double crossovers along chromosome arms in barley reduced resolution for locating centromeric regions on most linkage groups. Despite these limitations, our method should work well for high-density maps in species with strong recombination interference and will enrich many existing and future mapping resources.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Washington
Authors: Limborg, M. T. (Intern), McKinney, G. J. (Ekstern), Seeb, L. W. (Ekstern), Seeb, J. E. (Ekstern)
Pages: 655-661
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Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology Resources
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ISSN (Print): 1755-098X
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 6.06 SJR 2.864 SNIP 2.176
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.305 SNIP 1.564 CiteScore 4.47
Web of Science (2015): Indexed yes
 centromeres, genomic architecture, genotyping by sequencing, linkage mapping, recombination

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Original language: English

Same-Risk-Area Assessment Model (SRAAM) User’s manual

General information
State: Published
Organisations: National Institute of Aquatic Resources, Arctic Section, Section for Marine Living Resources
Authors: Hansen, F. T. (Intern), Christensen, A. (Intern)
Number of pages: 42
Publication date: 2016

Publication information
Publisher: National Institute of Aquatic Resources, DTU Aqua. Technical University of Denmark
ISBN (Electronic): 978-87-7481-234-0
Original language: English

Series: DTU Aqua report
Number: 318-2016
Sorting duplicated loci disentangles complexities of polyploid genomes masked by genotyping by sequencing

Many plants and animals of polyploid origin are currently enjoying a genomics explosion enabled by modern sequencing and genotyping technologies. However, routine filtering of duplicated loci in most studies using genotyping by sequencing introduces an unacceptable, but often overlooked, bias when detecting selection. Retained duplicates from ancient whole-genome duplications (WGDs) may be found throughout genomes, whereas retained duplicates from recent WGDs are concentrated at distal ends of some chromosome arms. Additionally, segmental duplicates can be found at distal ends or nearly anywhere in a genome. Evidence shows that these duplications facilitate adaptation through one of two pathways: neo-functionalization or increased gene expression. Filtering duplicates removes distal ends of some chromosomes, and distal ends are especially known to harbour adaptively important genes. Thus, filtering of duplicated loci impoverishes the interpretation of genomic data as signals from contiguous duplicated genes are ignored. We review existing strategies to genotype and map duplicated loci; we focus in detail on an overlooked strategy of using gynogenetic haploids (1N) as a part of new genotyping by sequencing studies. We provide guidelines on how to use this haploid strategy for studies on polyploid-origin vertebrates including how it can be used to screen duplicated loci in natural populations. We conclude by discussing areas of research that will benefit from better inclusion of polyploid loci; we particularly stress the sometimes overlooked fact that basing genomic studies on dense maps provides value added in the form of locating and annotating outlier loci or colocating outliers into islands of divergence.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Washington, University of Copenhagen
Authors: Limborg, M. (Intern), Seeb, L. W. (Ekstern), Seeb, J. E. (Ekstern)
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Journal: Molecular Ecology
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Ratings:
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.9 SJR 3.508 SNIP 1.651
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.862 SNIP 1.606 CiteScore 5.73
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.068 SNIP 1.705 CiteScore 5.36
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Web of Science (2012): Indexed yes
Spatio-temporal trends in stock mixing of eastern and western Baltic cod in the Arkona Basin and the implications for recruitment

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Ecosystem based Marine Management, Section for Marine Living Resources, GEOMAR - Helmholtz Centre for Ocean Research Kiel
Authors: Hüssy, K. (Intern), Hinrichsen, H. (Ekstern), Eero, M. (Intern), Mosegaard, H. (Intern), Hansen, J. H. (Intern), Lehmann, A. (Ekstern), Lundgaard, L. S. (Intern)
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ISSN (Print): 1054-3139
Ratings:
State-space models' dirty little secrets: even simple linear Gaussian models can have estimation problems

State-space models (SSMs) are increasingly used in ecology to model time-series such as animal movement paths and population dynamics. This type of hierarchical model is often structured to account for two levels of variability: biological stochasticity and measurement error. SSMs are flexible. They can model linear and nonlinear processes using a variety of statistical distributions.

Recent ecological SSMs are often complex, with a large number of parameters to estimate. Through a simulation study, we show that even simple linear Gaussian SSMs can suffer from parameter- and state-estimation problems. We demonstrate that these problems occur primarily when measurement error
is larger than biological stochasticity, the condition that often drives ecologists to use SSMs. Using an animal movement
example, we show how these estimation problems can affect ecological inference. Biased parameter estimates of a SSM
describing the movement of polar bears (Ursus maritimus) result in overestimating their energy expenditure. We suggest
potential solutions, but show that it often remains difficult to estimate parameters. While SSMs are powerful tools, they can
give misleading results and we urge ecologists to assess whether the parameters can be estimated accurately before
drawing ecological conclusions from their results.

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State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Alberta,
Macquarie University, Dalhousie University
Authors: Auger-Méthé, M. (Ekstern), Field, C. (Ekstern), Albertsen, C. M. (Intern), Derocher, A. E. (Ekstern), Lewis, M. A.
(Ekstern), Jonsen, I. D. (Ekstern), Flemming, J. M. (Ekstern)
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Scopus rating (2016): CiteScore 4.63 SJR 1.625 SNIP 1.401
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.057 SNIP 1.684 CiteScore 5.3
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.103 SNIP 1.544 CiteScore 4.75
Web of Science (2014): Indexed yes
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Scopus rating (2013): SJR 1.886 SNIP 1.51 CiteScore 4.06
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Web of Science (2013): Indexed yes
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Scopus rating (2012): SJR 1.458 SNIP 0.896 CiteScore 2.44
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Web of Science (2012): Indexed yes
ISI indexed (2011): ISI indexed no
Original language: English
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Status på laksebestandene i danske vandløb

General information
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Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine
Living Resources
Authors: Sivebæk, F. (Intern), Eg Nielsen, E. (Intern)
Publication date: 2016
Steps toward nation-wide monitoring of non-indigenous species in Danish marine waters under the Marine Strategy Framework Directive

This report is the outcome of MONIS 2 – or in full, “Monitoring of Non-Indigenous Species in Danish Marine Water, phase 2” – and includes three deliverable: (1) a national Target Species List including 50 species, (2) a draft Technical Guidance Report, and (3) in silico designed and tested primers and probes for 48 of the 50 species on the Target Species List. The list is based on discussions at a workshop and subsequent scoring and ranking of relevant species. The draft Technical Guidance report is anchored in existing Standard Operating Procedures (i.e. protocols for sampling, storage and analysis) and adapted to the requirements of the Danish NOVANA programme. In addition, the report includes suggestions for next steps to take to implement and improve monitoring and assessment activities in regard to non-indigenous species in Danish marine water.

Testing the effect of soak time on catch damage in a coastal gillnetter and the consequences on processed fish quality

This study aims at testing how to improve catch quality aboard a coastal gillnetter by looking at an easily controllable parameter known to have an effect on the degree of fish damage, soak time, and investigating if the registered damages on whole fish have an effect on processed products such as fillets. Plaice (Pleuronectes platessa) was captured with commercial gillnets soaked for 12 and 24 hours. Damages were assessed using semi-quantitative indices of individual fish condition gathered in a Catch-damage-index for onboard fish and a Processed fish-damage-index for whole, skinned and filleted plaice processed at a land-based factory. Cumulative link mixed modelling allowed the estimation of the size of effects. Damage in fish was significantly more likely for longer soak times but effects were comparable to those of fish length and between-sets, making a change in soak time not so substantial for improving plaice quality in coastal gillnetting. Damage in fish was significantly more likely for whole than filleted fish, but there was substantial heterogeneity among fish. Severe damage in whole fish may not matter in filleted fish whereas some damage may only be visible at the fillet level.
The diet of whiting Merlangius merlangus in the western Baltic Sea

The diet of whiting Merlangius merlangus in the western Baltic Sea was investigated and compared to the diet in the southern North Sea. Clupeids were important prey in both areas, but especially in the western Baltic Sea where they
constituted up to 90% of the diet of larger individuals. Gobies, brown shrimps and polychaetes were the main prey of juveniles in the western Baltic Sea, while a wider range of species were consumed in the North Sea. The shift to piscivory occurred at smaller sizes in the western Baltic Sea and the fish prey consumed was proportionately larger than in the southern North Sea. Estimates of prey abundance and food intake of M. merlangus are required to evaluate its predatory significance in the western Baltic Sea, but its diet suggests that it could be just as significant a fish predator here as in the southern North Sea.
The influence of feeding behaviour on growth of Atlantic cod (Gadus morhua, Linnaeus, 1758) in the North Sea

The objective of this study was to resolve key mechanisms driving individual growth patterns of Atlantic cod (Gadus morhua). Growth dynamics were analysed by linking growth patterns with stomach content composition and environmental temperature. Samples were collected in August/September of the years 2009, 2010 and 2011 in the north-eastern part of the central North Sea. Prey selection was assessed by identification of individual prey items in the stomach content to species. Ten feeding groups were identified consisting of individuals with one prey type dominating their stomach contents (≥75% by mass), of which six were used for growth analyses: “Sandeel”, “Clupeids”, “Norway pout”, “Flatfishes”, “Crustaceans” and “Brittle stars”. For each group, growth patterns were estimated based on measures of otolith growth increments. The stomach contents showed that cod as a species are opportunistic in their prey selection, but at the same time indicated that the total, broad feeding niche width of the population is dominated by individual diet specialization and that many individuals temporally show a preference for a particular prey type. The contribution of invertebrates and particularly crustaceans decreased with increasing cod size, whereas that of fish and predominantly herring increased. Prey type had a significant effect on growth, while temperature had no effect. Slowest growth was observed in the cod group preying on sandeel, while cod preying on Norway pout showed the fastest growth. No significant difference was observed between groups preying on brittle stars, crustaceans, flatfishes and herring. Growth in the year before capture did however not differ between any of these groups. Across sampling years, growth chronology patterns were similar but not significantly influenced by temperature.

General information

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Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources
Authors: Hüssy, K. (Intern), Andersen, N. G. (Intern), Pedersen, E. M. (Intern)
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Publication information

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BFI (2017): BFI-level 1
TMB: Automatic differentiation and laplace approximation

TMB is an open source R package that enables quick implementation of complex nonlinear random effects (latent variable) models in a manner similar to the established AD Model Builder package (ADMB, http://admb-project.org; Fournier et al. 2011). In addition, it offers easy access to parallel computations. The user defines the joint likelihood for the data and the random effects as a C++ template function, while all the other operations are done in R; e.g., reading in the data. The package evaluates and maximizes the Laplace approximation of the marginal likelihood where the random effects are automatically integrated out. This approximation, and its derivatives, are obtained using automatic differentiation (up to order three) of the joint likelihood. The computations are designed to be fast for problems with many random effects (approximate to 10^6) and parameters (approximate to 10^3). Computation times using ADMB and TMB are compared on a suite of examples ranging from simple models to large spatial models where the random effects are a Gaussian random field. Speedups ranging from 1.5 to about 100 are obtained with increasing gains for large problems.
Oceans are exposed to anthropogenic climate change shifting marine systems toward potential instabilities. The physical, biological and social implications of such shifts can be assessed within individual scientific disciplines, but can only be fully understood by combining knowledge and expertise across disciplines. For climate change related problems these research directions have been well-established since the publication of the first IPCC report in 1990, however it is not well-documented to what extent these directions are reflected in published research. Focusing on the Nordic region, we evaluated the development of climate change related marine science by quantifying trends in number of publications, disciplinarity, and scientific focus of 1362 research articles published between 1990 and 2011. Our analysis showed a faster increase in publications within climate change related marine science than in general marine science indicating a growing prioritisation of research with a climate change focus. The composition of scientific disciplines producing climate change related publications, which initially was dominated by physical sciences, shifted toward a distribution with almost even representation of physical and biological sciences with social sciences constituting a minor constant proportion. These trends suggest that the predominantly model-based directions of the IPCC have favoured the more quantitatively oriented natural sciences rather than the qualitative traditions of social sciences. In addition, despite being an often declared prerequisite to successful climate science, we found surprisingly limited progress in implementing
interdisciplinary research indicating that further initiatives nurturing scientific interactions are required
Scopus rating (2004): SJR 1.727 SNIP 1.619
Scopus rating (2003): SJR 1.71 SNIP 1.337
Scopus rating (2002): SJR 1.544 SNIP 1.325
Scopus rating (2001): SJR 1.631 SNIP 1.351
Scopus rating (2000): SJR 1.81 SNIP 1.323
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.466 SNIP 1.431
Original language: English
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Source: PublicationPreSubmission
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Undgå indavi, hvis du udsætter ørreder i naturen

General information
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Authors: Sivebæk, F. (Intern), Eg Nielsen, E. (Intern)
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Publication: Communication › Internet publication – Annual report year: 2016

Validation of state-space models using Template Model Builder

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management
Publication date: 2016
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2016

Variability and connectivity of plaice populations from the Eastern North Sea to the Baltic Sea, part II. Biological evidence of population mixing
A multi-disciplinary study was conducted to clarify stock identity and connectivity patterns in the populations of European plaice (Pleuronectes platessa) in the Skagerrak-Kattegat transition area between the Eastern North Sea and the Baltic Sea. Five independent biological studies were carried out in parallel. Genetic markers suggested the existence of different genetic populations in the transition area. Growth backcalculation with otoliths resulted in significant although limited differences in growth rates between North Sea and Skagerrak, indicating weak differentiation or important mixing. Hydrogeographical drift modelling suggested that some North Sea juveniles could settle along the coast line of the Skagerrak and the Kattegat. Tagging data suggested that both juveniles and adult fish from the North Sea perform feeding migrations into Skagerrak in summer/autumn. Finally, survey data suggested that Skagerrak also belongs to the area distribution of North Sea plaice. The outcomes of the individual studies were then combined into an overall synthesis. The existence of some resident components was evidenced, but it was also demonstrated that North Sea plaice migrate for feeding into Skagerrak and might constitute a large share of the catches in this area. The mixing of different populations within a management area has implications for stock assessment and management. Choice must be made to either lump or split the populations, and the feasibility and constraints of both options are discussed. The outcomes of this work have directly influenced the management decisions in 2015.

General information
What's on a tuna’s mind? Confronting dynamic optimization models of behavior with tracking data

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Thygesen, U. H. (Intern)
Publication date: 2016
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2016

Accounting for correlated observations in an age-based state-space stock assessment model

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Berg, C. W. (Intern), Nielsen, A. (Intern)
Number of pages: 2
Publication date: 2015
Event: Abstract from ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2015

A conceptual framework for understanding the implications of and potential solutions for mismatches in scale of biological population structure and stock units

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Publication date: 2015
Event: Main Research Area: Technical/natural sciences
Electronic versions:
Bibliographical note
ICES CM 2015/E:07
Publication: Research › Conference abstract for conference – Annual report year: 2015
Aggregation and attachment responses of blue mussels, Mytilus edulis—impact of substrate composition, time scale and source of mussel seed

Survival after transplantation of mussel seeds is crucial for the production output of blue mussels (Mytilus edulis L.) in bottom cultures. Hence, an understanding of the interactions between bed formation, habitat structure and performance of mussel seed of different origins can contribute to an optimization of the production. The effect of substrate composition and timing of formation of a mussel bed in relation to aggregation and attachment of mussels were investigated with mussel seeds obtained from two different sources: mussel seed dredged from a natural mussel bed and mussel seed collected from a suspended long line culture. The mussels were applied to experimental units of complex and smooth substrate on the sea bed. Data on aggregation (day 0, day 1 and day 2), attachment strength (day 2 and 30), loss (day 2 and 30) and growth (day 0–30) of mussels were collected during the experiment. The results showed that complex substrate indeed had a stabilizing effect on the mussel structure resulting in less aggregation and increased attachment strength. The 3D matrix forming a mussel bed was achieved faster on complex substrate, and led to reduced mortality of transplanted mussels. Despite significantly lower specific growth rates on the complex substrate, the total biomass of mussels was significantly higher on complex substrate compared to on smooth substrate due to the higher survival of mussels. Furthermore, suspended mussels aggregated more and faster and had a stronger and more rapid attachment as compared to bottom mussels. Consequently, it was concluded that when transplanting mussels, seeding with substrate increases surface complexity on the seabed and increases survival of the mussels.
A holistic ecosystem approach for marine management and conservation: Opportunities through the application of genetic and genomic approaches

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Martinsohn, J. T. (Ekstern), Volckaert, F. (Ekstern), Bekkevold, D. (Intern)
Number of pages: 2
Publication date: 2015
Event: Paper presented at ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
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Publication: Research - peer-review › Journal article – Annual report year: 2014
A model of extracellular enzymes in free-living microbes: Which strategy pays off?

An initial modeling approach was applied to analyze how a single, nonmotile, free-living, heterotrophic bacterial cell may optimize the deployment of its extracellular enzymes. Free-living cells live in a dilute and complex substrate field, and to gain enough substrate, their extracellular enzymes must be utilized efficiently. The model revealed that surface-attached and free enzymes generate unique enzyme and substrate fields, and each deployment strategy has distinctive advantages. For a solitary cell, surface-attached enzymes are suggested to be the most cost-efficient strategy. This strategy entails potential substrates being reduced to very low concentrations. Free enzymes, on the other hand, generate a radically different substrate field, which suggests significant benefits for the strategy if free cells engage in social foraging or experience high substrate concentrations. Swimming has a slight positive effect for the attached-enzyme strategy, while the effect is negative for the free-enzyme strategy. The results of this study suggest that specific dissolved organic compounds in the ocean likely persist below a threshold concentration impervious to biological utilization. This could help explain the persistence and apparent refractory state of oceanic dissolved organic matter (DOM). Microbial extracellular enzyme strategies, therefore, have important implications for larger-scale processes, such as shaping the role of DOM in ocean carbon sequestration.
An effective algorithm for approximating adaptive behavior in seasonal environments

Behavior affects most aspects of ecological processes and rates, and yet modeling frameworks which efficiently predict and incorporate behavioral responses into ecosystem models remain elusive. Behavioral algorithms based on life-time optimization, adaptive dynamics or game theory are unsuited for large global models because of their high computational demand. We compare an easily integrated, computationally efficient behavioral algorithm known as Gilliam's rule against the solution from a life-history optimization. The approximation takes into account only the current conditions to optimize behavior; the so-called "myopic approximation", "short sighted", or "static optimization". We explore the performance of the myopic approximation with diel vertical migration (DVM) as an example of a daily routine, a behavior with seasonal dependence that trades off predation risk with foraging opportunities in aquatic environments. The myopic approximation proves to be a robust replacement for the life-history optimization, deviating only up to 25% in regions of strong seasonality. The myopic approximation has additional advantages in that it can readily accommodate density dependence and inter-annual variations, aspects that can only be accessed in dynamic programming approaches with escalating computational costs. Furthermore, the explanatory power of the myopic approximation is notably higher than when behavior is not implemented, highlighting the importance for adaptive DVM behavior in ecological models where techniques such as dynamic programming are simply too computational demanding to be implemented.

General information

State: Published
Organisations: National Institute of Aquatic Resources, Centre for Ocean Life, Department of Applied Mathematics and Computer Science, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, University of Bergen
Authors: Sainmont, J. (Intern), Andersen, K. H. (Intern), Thygesen, U. H. (Intern), Visser, A. W. (Intern), Fiksen, Ø. (Ekstern)
An integrated end-to-end modeling framework for testing ecosystem-wide effects of human-induced pressures in the Baltic Sea

We present an integrated end-to-end modeling framework that enables whole-of ecosystem climate, eutrophication, and spatial management scenario exploration in the Baltic Sea. The framework is built around the Baltic implementation of the spatially-explicit end-to-end ATLANTIS model, linked to the high-resolution coupled physical-biological model HBM-ERGOM and the fisheries bio-economic FishRent model. We investigate ecosystem-wide responses to changes in human-induced pressures by simulating several eutrophication scenarios that are relevant to existing Baltic Sea management plans (e.g. EU BSAP, EU CFP). We further present the structure and calibration of the Baltic ATLANTIS model and the operational linkage to the other models. Using the results of eutrophication scenarios, and focusing on the relative changes in fish and fishery production, we discuss the robustness of the model linking with respect to the underlying assumptions, strengths and weaknesses of individual models. Furthermore, we describe how to possibly expand the framework to account for spatial impacts and economic consequences, for instance by linking to the individual-vessel based DISPLACE modeling approach. We conclude that the proposed model integration and management scenario evaluation scheme lays the foundations for developing a robust framework for management strategy evaluation that is of strategic importance to stakeholders from around the Baltic Sea.

Archived DNA reveals fisheries and climate induced collapse of a major fishery

Fishing and climate change impact the demography of marine fishes, but it is generally ignored that many species are made up of genetically distinct locally adapted populations that may show idiosyncratic responses to environmental and anthropogenic pressures. Here, we track 80 years of Atlantic cod (Gadus morhua) population dynamics in West Greenland using DNA from archived otoliths in combination with fish population and niche based modeling. We document how the interacting effects of climate change and high fishing pressure lead to dramatic spatiotemporal changes in the proportions and abundance of different genetic populations, and eventually drove the cod fishery to a collapse in the early 1970s. Our results highlight the relevance of fisheries management at the level of genetic populations under future scenarios of climate change.
Arctic warming will promote Atlantic-Pacific fish interchange

Throughout much of the Quaternary Period, inhospitable environmental conditions above the Arctic Circle have been a formidable barrier separating most marine organisms in the North Atlantic from those in the North Pacific. Rapid warming has begun to lift this barrier, potentially facilitating the interchange of marine biota between the two seas. Here, we forecast the potential northward progression of 515 fish species following climate change, and report the rate of potential species interchange between the Atlantic and the Pacific via the Northwest Passage and the Northeast Passage. For this, we projected niche-based models under climate change scenarios and simulated the spread of species through the passages when climatic conditions became suitable. Results reveal a complex range of responses during this century, and accelerated interchange after 2050. By 2100 up to 41 species could enter the Pacific and 44 species could enter the Atlantic, via one or both passages. Consistent with historical and recent biodiversity interchanges, this exchange of fish species may trigger changes for biodiversity and food webs in the North Atlantic and North Pacific, with ecological and economic consequences to ecosystems that at present contribute 39% to global marine fish landings.

General information

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Lausanne, Université de Bordeaux, Greenland Climate Research Centre, Aarhus University, DHI Denmark, University of Copenhagen, Danish Meteorological Institute
Authors: Wisz, M. (Intern), Broennimann, O. (Ekstern), Grønkjær, P. (Ekstern), Møller, P. R. (Ekstern), Olsen, S. M. (Ekstern), Swingedouw, D. (Ekstern), Hedeholm, R. (Ekstern), Eg Nielsen, E. (Intern), Guisan, A. (Ekstern), Pellissier, L. (Ekstern)
Pages: 261-265
Behavior-dependent senescence in pelagic copepods

General information
State: Published
Organisations: National Institute of Aquatic Resources, Centre for Ocean Life, Section for Marine Living Resources
Authors: Kiørboe, T. (Intern), Ceballos, S. (Intern), Thygesen, U. H. (Intern)
Pages: 651-653
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Volume: 96
Issue number: 4
ISSN (Print): 0012-9623
Ratings:
Web of Science (2018): Indexed yes
Original language: English
Electronic versions:
Publishers_version.pdf
DOIs:
10.1890/0012-9623-96.4.651
Source: FindIt
Source-ID: 2286900282
Publication: Research - peer-review › Journal article – Annual report year: 2016
Beyond ocean connectivity: embracing advances on early life stages and adult connectivity to assessment and management challenges

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Centre for Ocean Life
Authors: Deurs, M. V. (Intern), Lindegren, M. (Intern), Persson, A. (Ekstern), Jacobsen, C. (Ekstern), Nilsson, A. (Ekstern)
Publication date: 2015
Event: Abstract from ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Publisher's version

Biogeographic changes in fish diversity driven by changes in climate and exploitation

General information
State: Published
Organisations: National Institute of Aquatic Resources, Centre for Ocean Life, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, University of Copenhagen
Authors: Bryndum, K. M. (Intern), Christensen, A. (Intern), She, J. (Ekstern), Richardson, K. (Ekstern), MacKenzie, B. (Intern)
Number of pages: 2
Publication date: 2015
Event: Abstract from ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Publisher's version

Choosing the observational likelihood in state-space stock assessment models
By implementing different observational likelihoods in a state-space age-based stock assessment model, we are able to compare the goodness-of-fit and effects on estimated fishing mortality for different model choices. Model fit is improved by estimating suitable correlations between agegroups. We show by simulations that modelling catch as numbers-at-age is more suitable than proportions if the uncertainty of age-classifications is small

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Department of Applied Mathematics and Computer Science
Authors: Albertsen, C. M. (Intern), Nielsen, A. (Intern), Thygesen, U. H. (Intern)
Publication date: 2015
Event: Abstract from ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Publisher's version

Connectivity, growth and survival in a spatially structured fish population, which is currently managed as seven separate stock units

General information
State: Published
Density dependent growth changes through juvenile and early adult life of North East Atlantic Mackerel (Scomber scombrus)

Density dependence of somatic growth has an important, but overlooked, impact on fisheries management advice. We therefore examined how growth relates to abundance in a case where growth has been observed to vary substantially in recent years, namely North East Atlantic mackerel, one of the most widespread and commercially important fish stocks in the North Atlantic. Growth of juvenile and early adult North East Atlantic mackerel was found to be decreasing since the late 1990s. Modelling showed that growth was related to density. Mean growth rate during the first year was tightly correlated with the density of juveniles and especially with juveniles from the previous cohort. This putative effect of juvenile density could be tracked in the length-at-age up to adult mackerel at commercially targeted sizes. However, as the mackerel grew towards adulthood, the effects of the same cohort became dominant. The effect of adult density was minor, but increasing with age. The ontogenetic progression in density dependent regulation of growth appeared to reflect the spatial dynamics (migration patterns) in the feeding season. This is the first time growth patterns quantified in the adult mackerel population have been linked to density related processes occurring within the nursery areas during the first year. These aspects of mackerel production have a substantial and direct impact on the management plan evaluations used when fisheries scientists provide advice for fisheries management.
Derfor bliver storlaks længere tid i havet

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine Living Resources
Authors: Sivebæk, F. (Intern), Eg Nielsen, E. (Intern)
Publication date: 2015

Publication information
Source/Publisher: Fiskepleje.dk
Main Research Area: Technical/natural sciences
Links:
http://www.fiskepleje.dk/Nyheder/2015/11/Storlaks-og-genetik?id=5eeb019b-bf72-454f-85a4-10fc5cde950f&utm_source=newsletter&utm_media=mail&utm_campaign=Nyhedsbrev%2023%20november%202015

DOI: 10.1016/j.fishres.2015.04.011
Effect of spatial differences in growth on distribution of seasonally co-occurring herring Clupea harengus stocks

The mechanisms most likely to determine the distribution of the two major herring Clupea harengus stocks in their common early summer feeding ground in the eastern North Sea, Skagerrak and Kattegat were investigated through analysis of acoustic survey data from six consecutive years. No change was detected in biomass of North Sea autumn spawning C. harengus (NSAS) over time, whereas the biomass of western Baltic spring spawning C. harengus (WBSS) declined severely. Analyses of centre of abundance by stock showed no change in NSAS distribution, whereas the WBSS changed to a more western distribution over time. Contrary to previous perception of the juvenile migration, NSAS were found to leave the study area at the age between 1 and 2 years and WBSS 1 year olds were encountered in the Skagerrak. The estimated parameters of von Bertalanffy growth equations showed marked differences between areas with fish in the eastern part of the area having the lowest size at age at all ages. Further, their growth conditions appeared to deteriorate progressively over the period studied. Both NSAS and WBSS showed the highest condition in the North Sea and Skagerrak while condition was substantially lower in age Kattegat. The westward movement of spring spawners over time suggests that growth rate and possibly density of conspecifics influence the migration pattern and distribution of C. harengus in the area. In contrast, there was no evidence to suggest that distribution was constant over time within stocks or that distribution reflected size-dependent limitations on migration distance.
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.57 SJR 0.741 SNIP 0.882
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.951 SNIP 0.935 CiteScore 1.64
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.944 SNIP 0.934 CiteScore 1.76
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.049 SNIP 1.118 CiteScore 1.98
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.93 SNIP 1.035 CiteScore 1.88
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.895 SNIP 0.946 CiteScore 1.66
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.774 SNIP 0.834
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.773 SNIP 0.891
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.883 SNIP 0.968
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.996 SNIP 1.06
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.897 SNIP 1.051
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.827 SNIP 0.898
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.945 SNIP 1.148
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.937 SNIP 1.096
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.949 SNIP 1.056
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.874 SNIP 1.1
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.751 SNIP 0.993
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.025 SNIP 1.176

Original language: English
Electronic versions:
Effects of copepod size on fish growth: A model based on data for North Sea sandeel

In productive marine off-shore ecosystems, the flow of energy from zooplankton to large predators is channeled through a few species of short-lived, highly abundant schooling planktivorous fish. There are indications that these species respond to qualitative and phenological changes in the zooplankton. If so, the climate-induced alterations of the local copepod communities that we see in temperate and arctic regions may influence the energy flux in marine food chains. In order to investigate how different processes contribute to the relationship between copepod size and fish growth, we merged 2 mechanistic models from relevant data: (1) a model of the bioenergetics and stomach filling/evacuation dynamics, and (2) a Holling type II functional response model that encompasses visual range from basic principles. The model predicts that going from a situation where large Calanus copepods (2 mm) dominate the prey field of lesser sandeel Ammodytes marinus in the central North Sea to a situation where only relatively small (1 mm) and less energy-rich copepods are available roughly halves the energy intake of sandeels even if prey biomass concentration remains constant. Visual constraint on foraging was the most important factor, followed by handling time limitation and prey energy content. These limitations became stronger with increasing fish length, showing that copepod size and energy content have a strong effect on the specific growth potential of these fish.
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes

Original language: English
Electronic versions:
Publishers version
DOIs:
10.3354/meps11092
Links:
Publication: Research - peer-review › Journal article – Annual report year: 2015

Estimering af zooplankton dødelighed i en 3D økosystemmodel ved at anvende en rumlig- og tidlig varierende fiskeprædation

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Aarhus University, Danish Meteorological Institute
Authors: Maar, M. (Ekstern), Rindorf, A. (Intern), Møller, E. F. (Ekstern), Christensen, A. (Intern), Madsen, K. S. (Ekstern), Deurs, M. V. (Intern)
Publication date: 2015
Event: Abstract from 18. Danske Havforskermøde, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2015

Fast fitting of non-Gaussian state-space models to animal movement data via Template Model Builder
State-space models (SSM) are often used for analyzing complex ecological processes that are not observed directly, such as marine animal movement. When outliers are present in the measurements, special care is needed in the analysis to obtain reliable location and process estimates. Here we recommend using the Laplace approximation combined with automatic differentiation (as implemented in the novel R package Template Model Builder; TMB) for the fast fitting of continuous-time multivariate non-Gaussian SSMs. Through Argos satellite tracking data, we demonstrate that the use of continuous-time t-distributed measurement errors for error-prone data is more robust to outliers and improves the location estimation compared to using discretized-time t-distributed errors (implemented with a Gibbs sampler) or using continuous-time Gaussian errors (as with the Kalman filter). Using TMB, we are able to estimate additional parameters compared to previous methods, all without requiring a substantial increase in computational time. The model implementation is made available through the R package argosTrack.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Dalhousie University, University of Windsor
Authors: Albertsen, C. M. (Intern), Whoriskey, K. (Ekstern), Yurkowski, D. (Ekstern), Nielsen, A. (Intern), Flemming, J. M. (Ekstern)
Pages: 2598-2604
Publication date: 2015
Main Research Area: Technical/natural sciences
Fishing for food: simple changes in codend design improves the quality of fish products

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources
Authors: Karlsen, J. D. (Intern), Krag, L. A. (Intern), Albertsen, C. M. (Intern), Frandsen, R. (Intern)
Publication date: 2015
Main Research Area: Technical/natural sciences

From fishing to fish processing: Separation of fish from crustaceans in the Norway lobster-directed multispecies trawl fishery improves seafood quality

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources
Authors: Karlsen, J. D. (Intern), Krag, L. A. (Intern), Albertsen, C. M. (Intern), Frandsen, R. (Intern)
Publication date: 2015
Event: Abstract from ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
From regionally predictable to locally complex population structure in a freshwater top predator: River systems are not always the unit of connectivity in Northern Pike Esox lucius

Contemporary genetic diversity is the product of both historical and contemporary forces, such as climatic and geological processes affecting range distribution and continuously moulded by evolutionary forces selection, gene flow and genetic drift. Predatory freshwater fishes, such as Northern Pike Esox lucius, commonly exhibit small population sizes, and several local populations are considered endangered. Pike inhabit diverse habitat types, including lakes, rivers and brackish marine waters, thus spanning from small isolated patches to large open marine systems. However, pike population structure from local to regional scales is relatively poorly described, in spite of its significance to developing conservation measures. We analysed microsatellite variation in a total of 1185 North European pike from 46 samples collected across both local and regional scales, as well as over time, to address two overarching questions: Is pike population structure associated with local and/or regional connectivity patterns, and which factors likely have the main influence on the contemporary distribution of genetic diversity? To answer
this, we combined estimators of population diversity and structure to assess evidence of whether populations within (i) habitats, (ii) drainage systems and (iii) geographical regions are closer related than among these ranges, and whether patterns are temporally stable. Contrasting previous predictions that genetic drift obscures signals of postglacial colonisation history, we identified clear regional differences in population genetic signatures, suggesting a major effect of drainage divides on colonisation history and connectivity. However, several populations deviated from the general pattern, showing that local processes may be complex and need to be examined case-by-case.
Fully documented fisheries - is remote electronic monitoring the future tool in fisheries control?

**General information**
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management, Section for Monitoring and Data, Ministry of Food, Agriculture and Fisheries
Authors: Schreiber Plet-Hansen, K. (Intern), Ulrich, C. (Intern), Olesen, H. J. (Intern), Mortensen, L. O. (Intern), Bergsson, H. (Ekstern)
Publication date: 2015
Event: Poster session presented at ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:

**Bibliographical note**
ICES CM 2015/L:36
Publication: Research › Poster – Annual report year: 2015

Gene-associated markers can assign origin in a weakly structured fish, Atlantic herring
Regulations on the exploitation of populations of commercially important fish species and the ensuing consumer interest in sustainable products have increased the need to accurately identify the population of origin of fish and fish products. Although genomics-based tools have proven highly useful, there are relatively few examples in marine fish displaying accurate origin assignment. We synthesize data for 156 single-nucleotide polymorphisms typed in 1039 herring, Clupea harengus L., spanning the Northeast Atlantic to develop a tool that allows assignment of individual herring to their regional origin. We show the method's suitability to address specific biological questions, as well as management applications. We analyse temporally replicated collections from two areas, the Skagerrak (n = 81, 84, 66) and the western Baltic (n = 52, 52). Both areas harbour heavily fished mixed-origin stocks, complicating management issues. We report novel genetic evidence that herring from the Baltic Sea contribute to catches in the North Sea, and find support that western Baltic feeding aggregations mainly constitute herring from the western Baltic with contributions from the Eastern Baltic. Our study describes a general approach and outlines a database allowing individual assignment and traceability of herring across a large part of its East Atlantic distribution

**General information**
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Matis Ltd., Bangor University
Authors: Bekkevold, D. (Intern), Helyar, S. J. (Ekstern), Limborg, M. T. (Intern), Eg Nielsen, E. (Intern), Hansen, J. H. (Intern), Worsøe Clausen, L. (Intern), Carvalho, G. R. (Ekstern)
Pages: 1790-1801
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
GOFORIT: IntelliGent Oceanographically – based short-term fishery FORecasting applications

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources
High-precision, low-cost animal positioning in passive acoustic telemetry

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Canterbury
Authors: Cagua, F. (Ekstern), Pedersen, M. W. (Intern), Roy, R. (Ekstern)
Publication date: 2015
Event: Abstract from Annual Conference. Australian Society for Fish Biology (ASFB), Sydney, Australia.
Main Research Area: Technical/natural sciences

Impacts of the local environment on recruitment – a comparative study of North Sea and Baltic Sea fish stocks

General information
State: Published
Organisations: National Institute of Aquatic Resources, Centre for Ocean Life, Section for Ecosystem based Marine Management, Section for Marine Living Resources
Authors: Pécuchet, L. (Intern), Nielsen, J. R. (Intern), Christensen, A. (Intern)
Publication date: 2015
Event: Abstract from 18. Danske Havforskermøde, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences

Impacts of the local environment on recruitment: a comparative study of North Sea and Baltic Sea fish stocks

While the impact of environmental forcing on recruitment variability in marine populations remains largely elusive, studies spanning large spatial areas and many stocks are able to identify patterns common to different regions and species. In this study, we investigate the effects of the environment on the residuals of a Ricker stock-recruitment (SR) model, used as a proxy of prerecruits’ survival, of 18 assessed stocks in the Baltic and North Seas. A probabilistic principal components (PCs) analysis permits the identification of groups of stocks with shared variability in the prerecruits’ survival, most notably a group of pelagics in the Baltic Sea and a group composed of gadoids and herring in the North Sea. The first two PCs generally grouped the stocks according to their localizations: the North Sea, the Kattegat-Western Baltic, and the Baltic
Sea. This suggests the importance of the local environmental variability on the recruitment strength. Hence, the prerecruits' survival variability is studied according to geographically disaggregated and potentially impacting abiotic or biotic variables. Time series (1990-2009) of nine environmental variables consistent with the spawning locations and season for each stock were extracted from a physical-biogeochemical model to evaluate their ability to explain the survival of prerecruits. Environmental variables explained >70% of the survival variability for eight stocks. The variables water current, salinity, temperature, and biomass of other fish stocks are regularly significant in the models. This study shows the importance of the local environment on the dynamics of SR. The results provide evidence of the necessity of including environmental variables in stock assessment for a realistic and efficient management of fisheries.
Improving the performance of a grid used in Norway lobster fisheries

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, SINTEF
Pages: 525-528
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Applied Ichthyology
Volume: 31
Issue number: 3
ISSN (Print): 0175-8659
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.94
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.84
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.06
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 0.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 0.99
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.04
Interrelations between senescence, life-history traits, and behavior in planktonic copepods

General information
State: Published
Organisations: National Institute of Aquatic Resources, Centre for Ocean Life, Department of Applied Mathematics and Computer Science, Section for Marine Living Resources, Spanish Institute of Oceanography
Authors: Kiørboe, T. (Intern), Ceballos, S. (Intern), Thygesen, U. H. (Intern)
Pages: 2225-2235
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Ecology
Volume: 96
Issue number: 8
ISSN (Print): 0012-9658
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.8 SJR 3.255 SNIP 1.76
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.934 SNIP 1.931 CiteScore 5.24
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.694 SNIP 1.987 CiteScore 5.09
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.679 SNIP 2.071 CiteScore 5.43
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 4.041 SNIP 2.107 CiteScore 5.38
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 4.242 SNIP 1.934 CiteScore 5.03
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 4.001 SNIP 2.048
Invasion rate and population characteristics of the invasive round goby Neogobius melanostomus: effects of density and invasion history

Round goby Neogobius melanostomus is currently one of the most wide-ranging invasive fish species in Europe and North America. The present study demonstrates how the distribution of round goby has expanded from 2008 to 2013 at a rate of about 30 km yr−1 along the Danish coastline in the western Baltic Sea. Further analyses showed that fish from an established high-density round goby population were slow-growing and displayed poorer condition (weight at age and hepatosomatic index) compared to fish sampled from recently invaded locations (i.e. at the forefront of the distribution range). The established population revealed a broad age distribution and a 1:1 gender ratio, while fish from a recently invaded site were primarily of intermediate ages with a male-biased gender ratio. Otolith analyses suggested that the oldest individuals from the recently invaded area experienced superior growth conditions only in the most recent years, suggesting immigration into the area as adults. Our results suggest that intraspecific competition for food may cause continued dispersal of the species and that population demographics likely relate to invasion history.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, University of Copenhagen
Authors: Azour, F. (Intern), Deurs, M. V. (Intern), Behrens, J. (Intern), Carl, H. (Ekstern), Hüussy, K. (Intern), Greisen, K. (Ekstern), Ebert, R. (Ekstern), Møller, P. R. (Ekstern)
Pages: 41-52
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Aquatic Biology
Volume: 24
ISSN (Print): 1864-7782
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.847 SNIP 0.895 CiteScore 1.82
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.767 SNIP 0.713 CiteScore 1.41
Klima og gener: perspektiver fra pukkellaks

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Limborg, M. (Intern)
Publication date: 2015
Event: Abstract from 18. Danske Havforskermøde, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2015

Korttidsprognoser for kortlivede industriisk under MSY – forvaltning af tobis i Nordsøen

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Marine Ecology and Oceanography
Authors: Deurs, M. V. (Intern), Christensen, A. (Intern), Bekkevold, D. (Intern), Lynam, C. (Ekstern), Nielsen, K. E. (Intern), Azour, F. (Intern), Lundgaard, L. S. (Intern), Hüsey, K. (Intern), Mostegaard, H. (Intern), Worsøe Clausen, L. (Intern)
Publication date: 2015

Publication information
Original language: Danish
Main Research Area: Technical/natural sciences

Bibliographical note
Slutrapport for EFF projekt J.nr. 33010-13-k-0280
Publication: Research › Report – Annual report year: 2015

Kulstof i havet - en tynd kop tø?

General information
Laksekvoter for fiskesæsonen 2015

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine Living Resources, Institute Management
Authors: Sivebæk, F. (Intern), Eg Nielsen, E. (Intern), Koed, A. (Intern)
Publication date: 2015

Laksens genetik forudsiger vindere og tabere ved klimaforandringer

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Limborg, M. (Intern)
Publication date: 2015

Larval grazing on zooplankton from a spatial model of the North Sea larval community

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management, Aarhus University, Danish Meteorological Institute
Authors: Christensen, A. (Intern), Maar, M. (Ekstern), Rindorf, A. (Intern), Møller, E. F. (Ekstern), Madsen, K. S. (Ekstern), Deurs, M. V. (Intern)
Publication date: 2015
Event: Abstract from 18. Danske Havforskermøde, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2015
Limits to the reliability of size-based fishing status estimation for data-poor stocks

For stocks which are considered “data-poor” no knowledge exist about growth, mortality or recruitment. The only available information is from catches. Here we examine the ability to assess the level of exploitation of a data-poor stock based only on information of the size of individuals in catches. The model is a formulation of the classic Beverton–Holt theory in terms of size where stock parameters describing growth, natural mortality, recruitment, etc. are determined from life-history invariants. A simulation study was used to compare the reliability of assessments performed under different information availability scenarios, from data-limited, where none of the parameters are known beforehand, to different degrees of information availability cases where one or more parameters are known. If no parameters are known it is possible to correctly assess whether the fishing mortality is below Fmsy in more than 60% of the cases, and almost always correctly assess whether a stock is subject to overfishing. Adding information about age, i.e., assuming that growth rate and asymptotic size are known, does not improve the estimation. Only knowledge of the ratio between mortality and growth led to a considerable improvement in the assessment. Overall, the simulation study demonstrates that it may be possible to classify a data-poor stock as undergoing over- or under-fishing, while the exact status, i.e., how much the fishing mortality is above or below Fmsy, can only be assessed with a substantial uncertainty. Limitations of the approach are discussed.
Meiotic recombination is fundamental for generating new genetic variation and for securing proper disjunction. Further, recombination plays an essential role during the rediploidization process of polyploid-origin genomes because crossovers between pairs of homeologous chromosomes retain duplicated regions. A better understanding of how recombination affects genome evolution is crucial for interpreting genomic data; unfortunately, current knowledge mainly originates from a few model species. Salmonid fishes provide a valuable system for studying the effects of recombination in nonmodel species. Salmonid females generally produce thousands of embryos, providing large families for conducting inheritance studies. Further, salmonid genomes are currently rediploidizing after a whole genome duplication and can serve as models for studying the role of homeologous crossovers on genome evolution. Here, we present a detailed interrogation of recombination patterns in sockeye salmon (Oncorhynchus nerka). First, we use RAD sequencing of haploid and diploid gynogenetic families to construct a dense linkage map that includes paralogous loci and location of centromeres. We find a nonrandom distribution of paralogs that mainly cluster in extended regions distally located on 11 different chromosomes, consistent with ongoing homeologous recombination in these regions. We also estimate the strength of interference across each chromosome; results reveal strong interference and crossovers are mostly limited to one per arm. Interference was further shown to continue across centromeres, but metacentric chromosomes generally had at least one crossover on each arm. We discuss the relevance of these findings for both mapping and population genomic studies.
Long-term effects of an offshore wind farm in the North Sea on fish communities

Long-term effects of the Horns Rev 1 offshore wind farm (OWF) on fish abundance, diversity and spatial distribution were studied. This OWF is situated on the Horns Reef sand bank in the North Sea. Surveys were conducted in September 2001, before the OWF was established in 2002, and again in September 2009, 7 yr post-establishment. The sampling surveys used a multi-mesh-size gillnet. The 3 most abundant species in the surveys were whiting Merlangius merlangus, dab Limanda limanda and sandeels Ammodytidae spp. Overall fish abundance increased slightly in the area where the OWF was established but declined in the control area 6 km away. None of the key fish species or functional fish groups showed signs of negative long-term effects due to the OWF. Whiting and the fish group associated with rocky habitats showed different distributions relative to the distance to the artificial reef structures introduced by the turbines. Rocky habitat fishes were most abundant close to the turbines while whiting was most abundant away from them. Species diversity was significantly higher close to the turbines. Overall, these results indicate that the artificial reef structures were large enough to attract fish species with a preference for rocky habitats, but not large enough to have adverse negative effects on species inhabiting the original sand bottom between the turbines.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, FishStats, Orbicon
Authors: Stenberg, C. (Intern), Stattrup, J. (Intern), Deurs, M. V. (Intern), Berg, C. W. (Intern), Dinesen, G. E. (Intern), Mosegaard, H. (Intern), Grome, T. (Intern), Leonhard, S. (Ekstern)
Pages: 257-265
Publication date: 2015
Main Research Area: Technical/natural sciences

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Lost in translation: Increased complexity in management results in lost pelagic catch opportunities

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Wageningen IMARES
Authors: Hintzen, N. T. (Ekstern), Pastoors, M. (Ekstern), Sparrevoht, C. R. (Ekstern), Rindorf, A. (Intern), Cooper, A. (Ekstern), Worsøe Clausen, L. (Intern)
Publication date: 2015
Event: Abstract from ICES MYFISH Symposium, Athens, Greece.
Main Research Area: Technical/natural sciences
Links:
Management of fisheries in harbour porpoise (Phocoena phocoena) marine protected areas

The harbour porpoise (Phocoena phocoena) is the focus of a range of conservation efforts and policies aiming at reducing bycatch of the species in gillnet fisheries. In European waters, the harbour porpoise is protected within the Habitats Directive (Annexes II and IV), implying that the population has to be maintained at a favourable conservation status and the deliberate actions of killing and disturbance and habitat deterioration shall be prohibited in accordance with the directive’s aims. A spatial network, Natura2000, will further protect all Annex II species. According to Natura2000, Member States are obliged to nominate candidate protected areas in their waters to the EU Commission and within six years establish legislation to implement them as special areas of conservation and prepare management plans. Up to this point in time, however, no such management plans exist. This PhD thesis focuses on research methods and management tools, which can contribute to a better scientific understanding in the preparation of fisheries management plans for Natura2000 sites designated for harbour porpoises. Firstly, it investigates the potential use of CCTV cameras to document bycatch of marine mammals. Here it is shown that Remote Electronic Monitoring (REM) systems installed on commercial fishing vessels can provide video footage, time and position of all net hauls and record bycatches of marine mammals. Comparisons between the visual analysis of the REM data and fishers logbooks showed that the REM system gave more reliable results since fishers did not, in many instances, observe the bycatch while working on the deck because it dropped out of the net before coming on board. Furthermore, REM provided high percentage coverage at low cost, compared to on-board observers. Secondly, the suitability of using high-resolution spatial and temporal data on porpoise density and fishing effort data from the Danish Skagerrak Sea as a method to predict harbour porpoise bycatches was examined. The results showed that a simple relation between the two could predict bycatch and that the final model can thus be used as a tool to identify areas of porpoise bycatch risk and thereby support the management of both fisheries and harbour porpoises in accordance with the Habitats Directive. Thirdly, the behaviour of porpoises in relation to two different pinger types with different acoustic properties was studied at three different locations. The results showed that at one location, the AQUAmark100 pinger had a significant effect on porpoise echolocation behaviour at 0 and 200 m distances, whereas another trial showed a significant reduction in such behaviour for up to 400 m. In none of the studies of the AQUA100 did the behaviour reveal any signs of habituation. Studies of the AQUAmark300, however, revealed clear habituation effects. Fourthly and finally, the thesis describes the governance process and analyses its mechanisms and conflicts surrounding ongoing fisheries management planning with a focus on two Natura2000 sites in the Danish part of the Skagerrak Sea designated to protect harbour porpoises.
Mating success and sexual selection in a pelagic copepod, Temora longicornis: Evidence from paternity analyses

Knowledge about mating patterns is essential for understanding and explaining rates of reproduction and genetic potential of copepods populations. The aim of this study was to examine (1) the occurrence of multiple paternity in Temora longicornis, (2) the effect of multiple paternity (if present) on the females reproductive output, and (3) whether mating is random or some individuals have a higher than average chance of fertilizing or being fertilized (super individuals). We show that multiple paternity is common in this copepod species, that females benefit from multiple matings by increased offspring production, and that a relatively small fraction of the males and females in a population account for most of the offspring production. In both males and females, mating is nonrandom. Superior individuals with a higher than average matings success were identified both among females and among males.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Centre for Ocean Life, Section for Marine Living Resources
Authors: Sichlau, M. H. (Intern), Eg Nielsen, E. (Intern), Thygesen, U. H. (Intern), Kiørboe, T. (Intern)
Pages: 600-610
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.472 SNIP 1.422 CiteScore 3.93
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.112 SNIP 1.584 CiteScore 3.73
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.256 SNIP 1.587 CiteScore 3.98
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.456 SNIP 1.5 CiteScore 3.81
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
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BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.38 SNIP 1.425
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Scopus rating (2008): SJR 2.381 SNIP 1.615
Web of Science (2008): Indexed yes
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Web of Science (2007): Indexed yes
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Web of Science (2006): Indexed yes
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Web of Science (2005): Indexed yes
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Scopus rating (2003): SJR 2.685 SNIP 2.004
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.605 SNIP 1.798
Web of Science (2002): Indexed yes
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Scopus rating (2000): SJR 3.103 SNIP 2.016
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Movements, migrations and space use of fish in the North Sea in relation to offshore wind farms

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Cefas, Marine Biological Association of the United Kingdom
Authors: Metcalfe, J. (Ekstern), Wright, S. (Ekstern), Pedersen, M. W. (Intern), Sims, D. (Ekstern), Righton, D. (Ekstern)
Number of pages: 2
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Main Research Area: Technical/natural sciences
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MSC certification of plaice fisheries in area IIIa: Basic investigations and development of a management plan

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management, Section for Monitoring and Data, Section for Marine Ecology and Oceanography
Authors: Hansen, J. H. (Intern), Ulrich, C. (Intern), Boje, J. (Intern), Christensen, A. (Intern), Degel, H. (Intern), Hüsey, K. (Intern), Worsøe Clausen, L. (Intern)
Number of pages: 52
Publication date: 2015
Nursery areas and recruitment variation of Northeast Atlantic mackerel (Scomber scombrus)

There are currently no dedicated recruitment survey data available in support of the assessment of the abundance and distribution of Northeast Atlantic (NEA) mackerel (Scomber scombrus), one of the most widespread and commercially important fish stocks in the North Atlantic. This is despite the fact that an estimate of recruitment is an important requirement for the provision of advice to fishery managers. The work here addresses this by compiling catch rates of juvenile mackerel from bottom-trawl surveys conducted between October and March during 1998–2012 and applying a log Gaussian Cox (LGC) process geostatistical model incorporating spatio-temporal correlations. A statistically significant correlation between the modelled catch rates in adjacent quarters 4 and 1 (Q4 and Q1) demonstrates that bottom-trawl surveys in winter are an appropriate platform for sampling juvenile mackerel, and that the LGC model is successful in extracting a population abundance signal from the data. In this regard, the model performed appreciably better than a more commonly used raising algorithm based on survey swept-area estimates. Therefore, the LGC model was expanded to include data from the entire survey time-series, and a recruitment index was developed for use in the annual ICES stock assessment. We hypothesize that catchability is positively density-dependent and provides supporting evidence from acoustic observations. Various density-dependent transformations of the modelled catch rates were furthermore found to improve the correlation between the derived annual recruitment index and recruitment estimated by backcalculation of adult mackerel data. Square root transformation led to the strongest correlation, so this is recommended for further analysis of mackerel abundance. Finally, we provide maps of spatial distributions, showing that the most important nursery areas are around Ireland, north and west of Scotland, in the northern North Sea north of 59°N and, to some extent, also in the Bay of Biscay.
Observing marine living resources

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Stage, B. (Intern), Pedersen, E. M. (Intern)
Number of pages: 1
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Oceanic boundary conditions for Jakobshavn Glacier Part I. Variability and renewal of Ilulissat Icefjord waters, 2001-2014

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, New York University, Greenland Institute of Natural Resources
Authors: Gladish, C. V. (Ekstern), Holland, D. M. (Ekstern), Rosing-Asvid, A. (Ekstern), Behrens, J. (Intern), Boje, J. (Intern)
Pages: 3-32
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Scopus rating (2014): SJR 2.568 SNIP 1.394 CiteScore 2.89
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Scopus rating (2012): SJR 3.216 SNIP 1.555 CiteScore 2.75
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BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.756 SNIP 1.318 CiteScore 2.54
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.585 SNIP 1.357
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.588 SNIP 1.405
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.553 SNIP 1.416
Scopus rating (2007): SJR 2.866 SNIP 1.501
Scopus rating (2006): SJR 2.267 SNIP 1.429
Scopus rating (2005): SJR 3.085 SNIP 1.581
Scopus rating (2004): SJR 3.091 SNIP 1.637
Optimal bæredygtig udnyttelse af tilgængelige torskebestande for dansk fiskeri

General information
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Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, Centre for Ocean Life
Authors: Eero, M. (Intern), Hansen, J. H. (Intern), Hüssy, K. (Intern), Huwer, B. (Intern), Berg, C. W. (Intern), Mariani, P. (Intern), Mosegaard, H. (Intern), Nielsen, A. (Intern), Eg Nielsen, E. (Intern), Rindorf, A. (Intern), Ulrich, C. (Intern), Vinther, M. (Intern), Worsøe Clausen, L. (Intern)
Number of pages: 52
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Oxygen minimum zone induced rapid temporal fluctuations of Eastern Baltic cod genetic diversity

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, Johann Heinrich von Thünen-Institute, Leibniz Institute of Marine Sciences
Authors: Dierking, J. (Ekstern), von Dewitz, B. (Ekstern), Elsbernd, L. (Ekstern), Schultz, H. (Ekstern), Bracamonte, S. (Ekstern), Hüsey, K. (Intern), Hansen, J. H. (Intern), Krumme, U. (Ekstern), Oeberst, R. (Ekstern), Hinrichsen, H. (Ekstern), Reusch, T. (Ekstern)
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Main Research Area: Technical/natural sciences

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Performance assessment of two whole-lake acoustic positional telemetry systems - is reality mining of free-ranging aquatic animals technologically possible?

Acoustic positional telemetry systems (APTs) represent a novel approach to study the behaviour of free ranging aquatic animals in the wild at unprecedented detail. System manufactures promise remarkably high temporal and spatial resolution. However, the performance of APTs has rarely been rigorously tested at the level of entire ecosystems. Moreover, the effect of habitat structure on system performance has only been poorly documented. Two APTs were deployed to cover two small lakes and a series of standardized stationary tests were conducted to assess system performance. Furthermore, a number of tow tests were conducted to simulate moving fish. Based on these data, we quantified system performance in terms of data yield, accuracy and precision as a function of structural complexity in relation to vegetation. Mean data yield of the two systems was 40%(Lake1) and 60%(Lake2). Average system accuracy (acc) and precision (prec) were Lake1: acc = 3.1 m, prec = 1.1 m; Lake2: acc = 1.0 m, prec = 0.2 m. System performance was negatively affected by structural complexity, i.e., open water habitats yielded far better performance than structurally complex vegetated habitats. Post-processing greatly improved data quality, and sub-meter accuracy and precision were, on average, regularly achieved in Lake2 but remained the exception in the larger and structurally more complex Lake1. Moving transmitters were tracked well by both systems. Whereas overestimation of moved distance is inevitable for stationary transmitters due to accumulation of small tracking errors, moving transmitters can result in both over-and underestimation of distances depending on circumstances. Both deployed APTs were capable of providing high resolution positional data at the scale of entire lakes and are suitable systems to mine the reality of free ranging fish in their natural habitat.
environment. This opens important opportunities to advance several fields of study such as movement ecology and animal social networks in the wild. It is recommended that thorough performance tests are conducted in any study utilizing APTs. The APTs tested here appear best suited for studies in structurally simple ecosystems or for studying pelagic species. In such situations, the data quality provided by the APTs is exceptionally high.

**General information**

State: Published

Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine Living Resources, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Berlin, University of Porto, University of the Balearic Islands, Humboldt-University of Berlin


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  - Web of Science (2016): Indexed yes
  - Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
  - Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
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  - Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
  - Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54
  - Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
  - Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94
  - Web of Science (2013): Indexed yes
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- BFI (2012): BFI-level 1
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  - ISI indexed (2012): ISI indexed yes
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  - Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58
  - ISI indexed (2011): ISI indexed no
- BFI (2010): BFI-level 1
  - Scopus rating (2010): SJR 2.631 SNIP 1.161
  - Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
  - Scopus rating (2009): SJR 2.473 SNIP 0.985
  - Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 1
  - Scopus rating (2008): SJR 2.323 SNIP 0.96
  - Web of Science (2008): Indexed yes
- Scopus rating (2007): SJR 1.289 SNIP 0.525
Reducing the impact of blue mussel (Mytilus edulis) dredging on the ecosystem in shallow water soft bottom areas

Dredging blue mussels (Mytilus edulis) and thus removing structural elements, inducing resuspension of sediment as well as reducing filtration capacity, will inevitably affect the ecosystem. The study demonstrates that the impacts of fishing can be reduced through gear developments. A new light dredge was tested on commercial vessels using two different experimental setups. First, a twin haul experiment tested the standard gear (i.e., a Dutch dredge) against the light dredge by fishing the two gears side by side onboard the same vessel. Second, a single dredge experiment tested the absolute performance of the two gears by fishing in areas with a known blue mussel density. Results from the twin haul experiment demonstrate that the weight of sediment retained in the gear per square metre fished is 49% less in the light dredge compared with the Dutch dredge which will reduce resuspension of sediment at the surface. Also, the drag resistance of the light dredge was significantly less (177.1 vs. 202.7 kgm⁻¹). In the twin haul experiment no significant difference was found in the catch per unit effort (CPUE) of the two gears. The single dredge experiment, on the other hand, demonstrated a significant increase in CPUE exceeding 200% when using the light dredge. Seafloor tracks made by the two dredges could not be distinguished by use of side-scan sonar and the tracks were still detectable 2 months after fishing. It was concluded that replacement of the Dutch dredge with the light dredge would reduce the impact of the fishery on the ecosystem by (i) reducing resuspension of sediment, (ii) reducing fuel consumption, and (iii) potentially reducing energy transfer to the sediment through a reduced gear drag resistance. A potential increase in catch efficiency may reduce the area affected. Fishing with the light dredge is discussed in relation to management of Natura 2000 sites.
Regime shifts in demersal assemblages of the Benguela Current Large Marine Ecosystem: a comparative assessment

Using long-term survey data, changes in demersal faunal communities in the Benguela Current Large Marine Ecosystem were analysed at community and population levels to provide a comparative overview of the occurrence and timing of regime shifts. For South Africa, the timing of a community-level shift observed in the early 1990s, and of a lesser shift observed in the mid-2000s, corresponded well with the results of other studies that showed environmental, community-level or population-level changes at similar times, suggesting that environmental forcing had played a role. Several population-level shifts were detected for Namibia; these and a regime shift in the overall community identified for this country corresponded well to the timing of severe environmental perturbations and an extensive regime shift in the pelagic ecosystem of this area. However, the interpretation of these shifts was confounded by changes in sampling gear; closer scrutiny of the types of species affected and the direction of shifts (increase/decrease) in relation to the timing and nature of sampling gear modifications, revealed that the observed shifts were potentially an artefact of gear changes. This highlighted the importance of accounting for changes in sampling protocols during the analysis and interpretation of long-term data. For Angola, a community level shift in the mid-2000s and population-level changes for a few species (mainly positive), could not have been influenced by gear changes which took place mainly before the onset of the time series under consideration. However, no clear environmental or anthropogenic changes that could have influenced these shifts were obvious.

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Fisheries Management, South African Environmental Observation Network (SAEON), Ministério da Agricultura e Desenvolvimento Rural e Pescas, Institute of Marine Research, University of Cape Town
Authors: Kirkman, S. P. (Ekstern), Yemane, D. (Ekstern), Atkinson, L. J. (Ekstern), Kathena, J. N. (Intern), Nsiangango, S. E. (Ekstern), Singh, L. (Ekstern), Axelsen, B. E. (Ekstern), Samaai, T. (Ekstern)
RevFisk – et projekt som kvantificerer stenrevs (et lavliggende stenrev i den fotiske zone og et dybere liggende stenrev i den afotiske zone) betydning for fisk

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Publication: Research › Conference abstract for conference – Annual report year: 2015

Robust statistical method in a single species age-structured state-space assessment model

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Nielsen, A. (Intern), Berg, C. W. (Intern)
Number of pages: 2
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Event: Abstract from ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
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Salinity tolerance and correlated physiology of the invasive round goby Neogobius melanostomus

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources
Authors: Behrens, J. (Intern), Deurs, M. V. (Intern), Christensen, E. A. F. (Intern)
Publication date: 2015
Event: Abstract from ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
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Signatures of natural selection between life cycle stages separated by metamorphosis in European eel

Species showing complex life cycles provide excellent opportunities to study the genetic associations between life cycle stages, as selective pressures may differ before and after metamorphosis. The European eel presents a complex life cycle with two metamorphoses, a first metamorphosis from larvae into glass eels (juvenile stage) and a second metamorphosis into silver eels (adult stage). We tested the hypothesis that different genes and gene pathways will be under selection at
different life stages when comparing the genetic associations between glass eels and silver eels. Results: We used two sets of markers to test for selection: first, we genotyped individuals using a panel of 80 coding-gene single nucleotide polymorphisms (SNPs) developed in American eel; second, we investigated selection at the genome level using a total of 153,423 RAD-sequencing generated SNPs widely distributed across the genome. Using the RAD approach, outlier tests identified a total of 2413 (1.57 %) potentially selected SNPs. Functional annotation analysis identified signal transduction pathways as the most over-represented group of genes, including MAPK/Erk signalling, calcium signalling and GnRH (gonadotropin-releasing hormone) signalling. Many of the over-represented pathways were related to growth, while others could result from the different conditions that eels inhabit during their life cycle. Conclusions: The observation of different genes and gene pathways under selection when comparing glass eels vs. silver eels supports the adaptive decoupling hypothesis for the benefits of metamorphosis. Partitioning the life cycle into discrete morphological phases may be overall beneficial since it allows the different life stages to respond independently to their unique selection pressures. This might translate into a more effective use of food and niche resources and/or performance of phase-specific tasks (e.g. feeding in the case of glass eels, migrating and reproducing in the case of silver eels)
Simulation testing the robustness of stock assessment models to error: some results from the ICES strategic initiative on stock assessment methods

The World Conference on Stock Assessment Methods (July 2013) included a workshop on testing assessment methods through simulations. The exercise was made up of two steps applied to datasets from 14 representative fish stocks from around the world. Step 1 involved applying stock assessments to datasets with varying degrees of effort dedicated to optimizing fit. Step 2 was applied to a subset of the stocks and involved characteristics of given model fits being used to generate pseudo-data with error. These pseudo-data were then provided to assessment modellers and fits to the pseudo-data provided consistency checks within (self-tests) and among (cross-tests) assessment models. Although trends in biomass were often similar across models, the scaling of absolute biomass was not consistent across models. Similar types of models tended to perform similarly (e.g. age based or production models). Self-testing and cross-testing of models are a useful diagnostic approach, and suggested that estimates in the most recent years of time-series were the least robust. Results from the simulation exercise provide a basis for guidance on future large-scale simulation experiments and demonstrate the need for strategic investments in the evaluation and development of stock assessment methods.

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Volume: 72
Spatial factor analysis: a new tool for estimating joint species distributions and correlations in species range

1. Predicting and explaining the distribution and density of species is one of the oldest concerns in ecology. Species distributions can be estimated using geostatistical methods, which estimate a latent spatial variable explaining observed variation in densities, but geostatistical methods may be imprecise for species with low densities or few observations. Additionally, simple geostatistical methods fail to account for correlations in distribution among species and generally estimate such cross-correlations as a post hoc exercise.

2. We therefore present spatial factor analysis (SFA), a spatial model for estimating a low-rank approximation to multivariate data, and use it to jointly estimate the distribution of multiple species simultaneously. We also derive an
3. As a first example, we show that distributions for 10 bird species in the breeding bird survey in 2012 can be parsimoniously represented using only five spatial factors. As a second case study, we show that forward prediction of catches for 20 rockfishes (Sebastes spp.) off the U.S. West Coast is more accurate using SFA than analysing each species individually. Finally, we show that single-species models give a different picture of cross-correlations than joint estimation using SFA.

4. Spatial factor analysis complements a growing list of tools for jointly modelling the distribution of multiple species and provides a parsimonious summary of cross-correlation without requiring explicit declaration of habitat variables. We conclude by proposing future research that would model species cross-correlations using dissimilarity of species' traits, and the development of spatial dynamic factor analysis for a low-rank approximation to spatial time-series data.
Spawning patterns of shallow-water hake (Merluccius capensis) and deep-water hake (M. paradoxus) in the Benguela Current Large Marine Ecosystem inferred from gonadosomatic indices

We use gonad- and body-weight data from 54,000 samples of Merluccius capensis and Merluccius paradoxus collected in all months of the years between 1991 and 2013 to infer peak spawning periods and areas in the Benguela Current Large Marine Ecosystem. We develop and apply a new gonadosomatic index threshold for identification of spawning individuals. Spawning M. capensis were observed throughout the study area, mainly in areas of about 100 m bottom depth. The highest proportions of spawning M. capensis females in the northern Benguela region were observed off central Namibia between 24.0 and 26.0°S. In the southern Benguela, peaks in the proportions of spawning M. capensis were observed in two areas off the South African West Coast (31.0-32.5°S and 34.5-36.0°S), whereas spawning females off the South African South Coast (east of 20°E) appeared to be more evenly distributed in space. Seasonality differed between areas. In the northern Benguela, the main spawning season of M. capensis appeared to be the austral winter (July-September, peaking in August), while off the South African South Coast, the main spawning season is suggested to be in summer (around January). Between these two extremes, on the western Agulhas bank in the southern Benguela, spawning peaks were observed in both summer and winter. These peaks largely coincided with peaks in phytoplankton production that are linked to upwelling conditions in the region. Hake condition decreased subsequent to the development of the gonads. The annual spawning cycle differed between small and large M. capensis. The current October-closure of the fishery in Namibia may not match the peak spawning in August/September and may need to be shifted to earlier in the year. Spawning M. paradoxus were mainly found in areas of 200-650 m bottom depths. In the northern Benguela, spawning M. paradoxus were observed as far north as 25°S in August. The proportion of spawning females peaked between 34.5°S and 36.5°S off the West Coast, and between 23.0°E and 26.5°E off the South Coast. It was suggested that M. paradoxus spawn throughout the year off the South African coast, with increased intensity around March and August-October. The finding of multiple spawning seasons and areas of both M. capensis and M. paradoxus strongly suggest multiple stocks (reproductive units).

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Monitoring and Data, Department for Agriculture, Forestry and Fisheries, Benguela Current Commission, Institute of Marine Research, Ministry of Fisheries and Marine Resources
Authors: Jansen, T. (Intern), Kainge, P. I. (Intern), Singh, L. (Ekstern), Wilhelm, M. (Ekstern), Durholtz, D. (Ekstern), Strømme, T. (Ekstern), Kathena, J. (Ekstern), Erasmus, V. (Ekstern)
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Spring and autumn spawning herring in the Gulf of Riga: intraspecific biodiversity across small local scales

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Bekkevold, D. (Intern), Gross, R. (Ekstern), Arula, T. (Ekstern), Ojaveer, H. (Ekstern)
Number of pages: 1
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Stock mixing of eastern and western Baltic cod in SD 24

General information
Sustainable development of the Nephrops fishery in the Kattegat-Skagerrak region

General information
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The Baltic ATLANTIS model: Implementing a holistic framework to evaluate ecosystem wide responses to changes in climate and anthropogenic forcing

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Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Ecosystem based Marine Management Systems, Section for Marine Living Resources, Section for Monitoring and Data, Centre for Ocean Life, Aarhus University
Authors: Palacz, A. (Intern), Nielsen, J. R. (Intern), Christensen, A. (Intern), Gislason, H. (Intern), Bastardie, F. (Intern), Geitner, K. (Intern), Maar, M. (Ekstern), Lindegren, M. (Intern), Hufnaagl, M. (Intern), Fulton, E. (Ekstern)
Number of pages: 1
Publication date: 2015

The history of cod in Greenland: A major fishery collapse explained by archived DNA

General information
The impact of environmental variability on Atlantic mackerel Scomber scombrus larval abundance to the west of the British Isles

The value of the Continuous Plankton Recorder (CPR) fish larvae dataset, with its extensive spatiotemporal coverage, has been recently demonstrated with studies on long-term changes over decadal scales in the abundance and distribution of fish larvae in relation to physical and biological factors in the North Sea. We used a similar approach in the west and southwest area of the UK shelf and applied a principal component analysis (PCA) using 7 biotic and abiotic parameters, combined with Hierarchical Cluster Analysis (HCA), to investigate the impact of environmental changes in the west and southwest area of the UK shelf on mackerel larvae during the period 1960-2004. The analysis revealed 3 main periods of time (1960-1968; 1969-1994; 1995-2004) reflecting 3 different ecosystem states. The results suggest a transition from an ecosystem characterized by low temperature, high salinity, high abundances of zooplankton and the larger phytoplankton groups, to a system characterized by higher temperature, lower salinities, lower abundances of zooplankton and larger phytoplankton and higher abundances of the small phytoplankton species. Analysis revealed a very weak positive correlation between the Second principal component and mackerel larvae yearly abundance, attributed to the North Atlantic Oscillation (NAO). The results presented here are in broad accord with recent investigations that link climatic variability and dynamics of mackerel reproduction. However, the growing body of literature that documents statistical correlations between environment and mackerel needs to be supplemented by local process studies, to gain more insight and to be able to predict mackerel response to climate change scenarios. Utilising the strength of the CPR dataset, namely its unique temporal coverage, in an analysis where other data (such as egg surveys) are drawn in to compensate for the spatial issues could prove to be the way forward. Crown Copyright (C) 2015 Published by Elsevier Ltd.
Thermal and maternal environments shape the value of early hatching in a natural population of a strongly cannibalistic freshwater fish

Hatching early in the season is often assumed to elevate fitness, particularly in cannibalistic fish in which size-dependent predation mortality is a major selective force. While the importance of the thermal environment for the growth of fish is undisputed, the relevance of maternal effects for offspring growth in the wild is largely unknown. Otoliths of 366 age-0 pike (Esox lucius L.) were sampled in a natural lake over three seasons. All offspring were assigned to more than 330 potential mothers using 16 informative microsatellites. We found temperature and past maternal environment (as represented by juvenile growth rate), but not female total length, to jointly contribute to explain within- and among-season size variation in juvenile pike. While there was no statistical evidence for maternal effects on offspring growth rate, fast female juvenile growth positively correlated with the offspring length in early summer. One mechanism could be related to fast-growing females spawning somewhat earlier in the season. However, the more likely mechanism emerging in our study was that fast-growing females could have been in better condition prior to spawning, in turn possibly producing higher numbers of
high-quality eggs. Our study is among the few to reveal carry-over effects related to past maternal environments on offspring performance in a naturally reproducing fish stock. At the same time, our study underscores recent arguments that size-dependent maternal effects may not be expressed in the wild and that early hatching does not generally produce size advantages in light of stochastically varying temperature conditions.

**General information**

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Berlin
Authors: Pagel, T. (Ekstern), Bekkevold, D. (Intern), Pohlmeier, S. (Ekstern), Wolter, C. (Ekstern), Arlinghaus, R. (Ekstern)
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Scopus rating (2011): SJR 2.235 SNIP 1.451 CiteScore 3.54
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.282 SNIP 1.556
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.075 SNIP 1.426
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.413 SNIP 1.522
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.253 SNIP 1.547
Scopus rating (2006): SJR 2.324 SNIP 1.577
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.19 SNIP 1.67
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.462 SNIP 1.757
Scopus rating (2003): SJR 2.398 SNIP 1.796
The use of at-sea-sampling data to dissociate environmental variability in Norway lobster (Nephrops norvegicus) catches to improve resource exploitation efficiency within the Skagerrak/Kattegat trawl fishery

Research into the influence of environmental variables on the behaviour of Norway lobster (Nephrops norvegicus), and hence catch rates, dates back to the 1960s (e.g., Höglund and Dybern, Diurnal and seasonal variations in the catch-composition of Nephrops norvegicus (L.) at the Swedish west coast. ICES CM 1965/I46; Simpson, Variations in the catches of Nephrops norvegicus at different times of day and night. Rapport et Proès-verbaux des Réunions Conseil permanent international pour l'Exploration de la Mer 156:186). However, the use of fishery-dependent data in identifying influential factors is relatively limited and only includes a number of papers on a limited dataset (e.g., Redant and De Clark, Diurnal variations in CPUE and length composition of the catches in a Nephrops directed fishery in the Central North Sea. ICES CM 1984/K:3; Maynou and Sardà, Influence of environmental factors on commercial trawl catches of Nephrops norvegicus (L.). ICES J. Mar. Sci. 58:1318). Here, we aimed to dissociate environmental variability in Norway lobster catches to improve resource exploitation efficiency within the Skagerrak and Kattegat trawl fisheries by utilising data collected as part of an extensive at-sea-sampling programme spanning 16 years. Catch rates were modelled using Generalized Additive Mixed Models (GAMMs) and considered a range of response variables, including depth, temperature, current speed, season, moon phase and time of day. The results obtained herein showed that time of day, season, depth, temperature, year, trawl type and location all significantly affect catch rates of Nephrops.
Umbrella species in marine systems: using the endangered humphead wrasse to conserve coral reefs

Extinction risk is closely tied to body size, home range, and species distribution. Quantifying home range is critical for conservation, and can enable the use of concepts such as 'umbrella species', whose conservation protects other species due to shared habitat. To determine the value of the humphead wrasse as an umbrella species for coral reef conservation, we conducted a multi-year study of humphead wrasse home range at Palmyra Atoll, Central Tropical Pacific, tagging juvenile, female, and male individuals with acoustic transmitters. We quantified home range using 2 metrics, length and area, and determined if these metrics were related to the sex and maturity status of the individual. We recorded individual movements during 5030 fish-days, yielding detailed records for 14 individuals comprising 3 juveniles, 5 females, and 6 males. The home range of humphead wrasse measured over a 2 yr study was 0.4 to 14 km and changed with ontogeny. Females had larger home ranges than other reef fishes studied to date (n = 68), indicating value as an umbrella species for coral reefs. We compared the home range of the species to the size distribution of tropical marine protected areas (MPAs), and used a model to estimate the MPA length necessary to retain humphead wrasse. Most MPAs are too small to effectively protect the humphead wrasse.
Using a science-industry partnership to identify herring spawning locations in the North Sea

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Thünen Institute of Baltic Sea Fisheries, Institute of Marine Research
Authors: Pastoors, M. (Ekstern), Worsøe Clausen, L. (Intern), Russell, M. (Ekstern), Reach, I. (Ekstern), Wiseman, A. (Ekstern), Ohms, V. (Ekstern), Sparrebohn, C. R. (Intern), Strehlow, H. V. (Ekstern), Dankel, D. J. (Ekstern), Goldsborough, D. (Ekstern)
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What are the major global threats and impacts in marine environments? Investigating the contours of a shared perception among marine scientists from the bottom-up

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What is it we want to maximise and sustain in Maximum Sustainable Yield?

**General information**

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**Organisations:** National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Imperial College London, Marine Institute

**Authors:** Rindorf, A. (Intern), Mumford, J. (Ekstern), Worsøe Clausen, L. (Intern), Hill, L. (Ekstern), Hintzen, N. (Ekstern), Hoefnagel, E. (Ekstern), Holt, J. (Ekstern), Kempf, A. (Ekstern), Leach, A. (Ekstern), Levontin, P. (Ekstern), Mace, P. (Ekstern), Mackinson, S. (Ekstern), Olesen, C. (Ekstern), Potter, C. (Ekstern), Prellezo, R. (Ekstern), Rossberg, A. (Ekstern), Tserpes, G. (Ekstern), Voss, R. (Ekstern), Reid, D. (Ekstern)

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What is MSY when stock productivity shifts? A worked example from the North Sea

General information
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Authors: Worsøe Clausen, L. (Intern), Rindorf, A. (Intern), Deurs, M. V. (Intern), Vinther, M. (Intern), Dickey-Collas, M. (Ekstern), Hintzen, N. (Ekstern)
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Main Research Area: Technical/natural sciences
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A cascade of warming impacts brings bluefin tuna to Greenland waters

Rising ocean temperatures are causing marine fish species to shift spatial distributions and ranges, and are altering predator-prey dynamics in food webs. Most documented cases of species shifts so far involve relatively small species at lower trophic levels, and consider individual species in ecological isolation from others. Here we show that a large highly migratory top predator fish species has entered a high latitude sub-polar area. Bluefin tuna, Thunnus thynnus Linnaeus 1758, were captured in waters east of Greenland (65° N) in August 2012 during exploratory fishing for Atlantic mackerel, Scomber scombrus Linnaeus 1758. The bluefin tuna were captured in a single net-haul in 9-11 °C water together with 6 tonnes of mackerel, which is a preferred prey species and itself a new immigrant to the area. Regional temperatures in August 2012 were historically high and contributed to a warming trend since 1985, when temperatures began to rise. The presence of bluefin tuna in this region is likely due to a combination of warm temperatures that are physiologically more tolerable and immigration of an important prey species into the area. We conclude that a cascade of climate change impacts is restructuring the food web in east Greenland waters.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Centre for Ocean Life, Section for Marine Living Resources, Technical University of Denmark, Danmarks Meteorologisk Institut, Greenland Institute of Natural Resources
Authors: MacKenzie, B. (Intern), Payne, M. (Intern), Boje, J. (Intern), Høyer, J. L. (Ekstern), Siegstad, H. (Ekstern)
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Rising ocean temperatures are causing marine fish species to shift spatial distributions and ranges, and are altering predator-prey dynamics in food webs. Most documented cases of species shifts so far involve relatively small species at lower trophic levels, and consider individual species in ecological isolation from others. Here, we show that a large highly migratory top predator fish species has entered a high latitude sub-polar area. Bluefin tuna, Thunnus thynnus Linnaeus 1758, were captured in waters east of Greenland (65° N) in August 2012 during exploratory fishing for Atlantic mackerel, Scomber scombrus Linnaeus 1758. The bluefin tuna were captured in a single net-haul in 9-11 °C water together with 6 tonnes of mackerel, which is a preferred prey species and itself a new immigrant to the area. Regional temperatures in August 2012 were historically high and contributed to a warming trend since 1985, when temperatures began to rise. The presence of bluefin tuna in this region is likely due to a combination of warm temperatures that are physiologically more tolerable and immigration of an important prey species into the area. We conclude that a cascade of climate change impacts is restructuring the food web in east Greenland waters.

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Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Centre for Ocean Life, Section for Marine Living Resources, Technical University of Denmark, Danmarks Meteorologisk Institut, Greenland Institute of Natural Resources
A low-density SNP array for analyzing differential selection in freshwater and marine populations of threespine stickleback (Gasterosteus aculeatus)

Background: The threespine stickleback (Gasterosteus aculeatus) has become an important model species for studying both contemporary and parallel evolution. In particular, differential adaptation to freshwater and marine environments has led to high differentiation between freshwater and marine stickleback populations at the phenotypic trait of lateral plate morphology and the underlying candidate gene Ectodysplasin (EDA). Many studies have focused on this trait and candidate gene, although other genes involved in marine-freshwater adaptation may be equally important. In order to develop a resource for rapid and cost efficient analysis of genetic divergence between freshwater and marine sticklebacks, we generated a low-density SNP (Single Nucleotide Polymorphism) array encompassing markers of chromosome regions under putative directional selection, along with neutral markers for background.

Results: RAD (Restriction site Associated DNA) sequencing of sixty individuals representing two freshwater and one marine population led to the identification of 33,993 SNP markers. Ninety-six of these were chosen for the low-density SNP array, among which 70 represented SNPs under putatively directional selection in freshwater vs. marine environments, whereas 26 SNPs were assumed to be neutral. Annotation of these regions revealed several genes that are candidates for affecting stickleback phenotypic variation, some of which have been observed in previous studies whereas others are new.

Conclusions: We have developed a cost-efficient low-density SNP array that allows for rapid screening of polymorphisms in threespine stickleback. The array provides a valuable tool for analyzing adaptive divergence between freshwater and marine stickleback populations beyond the well-established candidate gene Ectodysplasin (EDA).
A quantitative approach to static sensor network design

Static sensor networks to observe animals are widely used in ecological, management and conservation research, but quantitative methods for designing these networks are underdeveloped. In the context of aquatic systems, we present a method for quasi-optimal network design, which accounts for blocking of detections by obstacles, horizontal and vertical movement behaviour of the target animals, and type of research question (is the network intended for estimation of detailed movement or home range?). Optimal design is defined as the sensor configuration that maximizes the expected number of unique animal detections. As finding the global optimum is generally time consuming, we use a greedy algorithm instead, which places sensors optimally relative to already placed sensors. The design method requires access to topographic data of the study site and knowledge of the sensor detection range. We illustrate the method with real topographic data from a rugose coral reef where network performance is highly influenced by detection shadowing.

Network performance is visualized by a coverage map indicating the probability of detection at any location in the study area. The reported unique recovery rate summarizes the expected ability of the network to collect data given the design constraints. Because sensors are placed sequentially, the information gain per sensor can be evaluated and used as a
proxy for sensor value. The presented method formalizes important considerations, when designing sensor networks, that
were previously often based on heuristics and intuition. The method provides a guide to maximizing the information
potential of future monitoring studies as well as a means to improve existing networks. The method is available as an R
package and can be tested via an online web tool. 10.1111/(ISSN)2041-210X

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Authors: Pedersen, M. W. (Intern), Burgess, G. (Ekstern), Weng, K. C. (Ekstern)
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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 4.112 SNIP 2.452 CiteScore 6.29
Web of Science (2014): Indexed yes
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Scopus rating (2013): SJR 3.011 SNIP 2.427 CiteScore 5.34
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Assessing patterns of hybridization between North Atlantic eels using diagnostic single-nucleotide polymorphisms
The two North Atlantic eel species, the European eel (Anguilla anguilla) and the American eel (Anguilla rostrata), spawn in
partial sympatry in the Sargasso Sea, providing ample opportunity to interbreed. In this study, we used a RAD (Restriction
site Associated DNA) sequencing approach to identify species-specific diagnostic single-nucleotide polymorphisms
(SNPs) and design a low-density array that combined with screening of a diagnostic mitochondrial DNA marker. Eels from
Iceland (N=159) and from the neighboring Faroe Islands (N=29) were genotyped, along with 94 larvae (49 European and
45 American eel) collected in the Sargasso Sea. Our SNP survey showed that the majority of Icelandic eels are pure
European eels but there is also an important contribution of individuals of admixed ancestry (10.7%). Although most of
the hybrids were identified as F1 hybrids from European eel female × American eel male crosses, backcrosses were also
detected, including a first-generation backcross (F1 hybrid × pure European eel) and three individuals identified as
second-generation backcrosses originating from American eel × F1 hybrid backcrosses interbreeding with pure European
eels. In comparison, no hybrids were observed in the Faroe Islands, the closest bodies of land to Iceland. It is possible
that hybrids show an intermediate migratory behaviour between the two parental species that ultimately brings hybrid
larvae to the shores of Iceland, situated roughly halfway between the Sargasso Sea and Europe. Only two hybrids were
observed among Sargasso Sea larvae, both backcrosses, but no F1 hybrids, that points to temporal variation in the
occurrence of hybridization

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University, University of the Faroe Islands, Marine Biology and Biotechnology Center, BGI-Shenzhen, BGI-Europe, University of Leuven, Université Laval

Authors: Pujolar, J. M. (Forskerdatabase), Jacobsen, M. (Ekstern), Als, T. D. (Intern), Frydenberg, J. (Forskerdatabase), Magnusson, E. (Ekstern), Jónsson, B. (Ekstern), Jiang, X. (Ekstern), Cheng, L. (Ekstern), Bekkevold, D. (Intern), Maes, G. (Ekstern), Bernatchez, L. (Ekstern), Hansen, M. M. (Ekstern)

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A statistical model for estimation of fish density including correlation in size, space, time and between species from research survey data

Trawl survey data with high spatial and seasonal coverage were analysed using a variant of the Log Gaussian Cox Process (LGCP) statistical model to estimate unbiased relative fish densities. The model estimates correlations between observations according to time, space, and fish size and includes zero observations and over-dispersion. The model utilises the fact the correlation between numbers of fish caught increases when the distance in space and time between the fish decreases, and the correlation between size groups in a haul increases when the difference in size decreases. Here the model is extended in two ways. Instead of assuming a natural scale size correlation, the model is further developed to allow for a transformed length scale. Furthermore, in the present application, the spatial- and size-dependent correlation between species was included. For cod (Gadus morhua) and whiting (Merlangius merlangus), a common structured size correlation was fitted, and a separable structure between the time and space-size correlation was found for each species, whereas more complex structures were required to describe the correlation between species (and space-size). The within-species time correlation is strong, whereas the correlations between the species are weaker over time but strong within the year.
Characterizing neutral and adaptive variation in a duplicated salmonid genome

Combination of genetics and spatial modelling highlights the sensitivity of cod (Gadus morhua) population diversity in the North Sea to distributions of fishing

Conserving genetic diversity in animal populations is important for sustaining their ability to respond to environmental change. However, the “between-population” component of genetic diversity (biocomplexity) is threatened in many exploited populations, particularly marine fish, where harvest management regions may be larger than the spatial extent of genetically distinct subpopulations. Using single-nucleotide polymorphism data, we delineated the geographic limits of three population units of Atlantic cod (Gadus morhua) in northwest European waters. Two of the populations cohabit the North Sea, and trawl survey data showed differing trends in their abundances. We developed a spatial model of these units to simulate population dynamics under spatial patterns of harvesting. Competition between units during the pelagic juvenile stages in the model led to suppression of the more localized northern North Sea (Viking) unit by the more widespread (Dogger) unit, and its premature extinction under some spatial patterns of fishing. Fishery catch limits for cod are set at the scale of the whole North Sea without regard to such subpopulation dynamics. Our model offers a method to quantify adjustments to regional fishing mortality rates to strike a balance between maximizing sustainable yield and conserving vulnerable populations.
Comparative ecology of widely distributed pelagic fish species in the North Atlantic: Implications for modelling climate and fisheries impacts

This paper reviews the current knowledge on the ecology of widely distributed pelagic fish stocks in the North Atlantic basin with emphasis on their role in the food web and the factors determining their relationship with the environment. We consider herring (Clupea harengus), mackerel (Scomber scombrus), capelin (Mallotus villosus), blue whiting (Micromesistius poutassou), and horse mackerel (Trachurus trachurus), which have distributions extending beyond the continental shelf and predominantly occur on both sides of the North Atlantic. We also include albacore (Thunnus alalunga), bluefin tuna (Thunnus thynnus), swordfish (Xiphias gladius), and blue marlin (Makaira nigricans), which, by contrast, show large-scale migrations at the basin scale. We focus on the links between life history processes and the environment, horizontal and vertical distribution, spatial structure and trophic role. Many of these species carry out extensive migrations from spawning grounds to nursery and feeding areas. Large oceanographic features such as the North Atlantic subpolar gyre play an important role in determining spatial distributions and driving variations in stock size. Given the large biomasses of especially the smaller species considered here, these stocks can exert significant top-down pressures on the food web and are important in supporting higher trophic levels. The review reveals commonalities and differences between the ecology of widely distributed pelagic fish in the NE and NW Atlantic basins, identifies knowledge gaps and modelling needs that the EURO-BASIN project attempts to address. © 2014 Elsevier Ltd. All rights reserved.

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Scopus rating (2012): SJR 2.741 SNIP 1.794 CiteScore 4.17
Conserving marine biodiversity: insights from life-history trait candidate genes in Atlantic cod (Gadus morhua)

Recent technological developments have facilitated an increased focus on identifying genomic regions underlying adaptive trait variation in natural populations, and it has been advocated that this information should be important for designating population units for conservation. In marine fishes, phenotypic studies have suggested adaptation through divergence of life-history traits among natural populations, but the distribution of adaptive genetic variation in these species is still relatively poorly known. In this study, we extract information about the geographical distribution of genetic variation for 33 single nucleotide polymorphisms (SNPs) associated with life-history trait candidate genes, and compare this to variation in 70 putatively neutral SNPs in Atlantic cod (Gadus morhua). We analyse samples covering the major population complexes in the eastern Atlantic and find strong evidence for nonneutral levels and patterns of population structuring for several of the candidate gene-associated markers, including two SNPs in the growth hormone 1 gene. Thus, this study aligns with findings from phenotypic studies, providing molecular data strongly suggesting that these or closely linked genes are under selection in natural populations of Atlantic cod. Furthermore, we find that patterns of variation in outlier markers do not align with those observed at selectively neutral markers, and that outlier markers identify conservation units on finer geographical scales than those revealed when analysing only neutral markers. Accordingly, results also suggest that information about adaptive genetic variation will be useful for targeted conservation and management in this and other marine species.

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Hansen, J. H. (Intern), Therkildsen, N. O. (Intern), Meldrup, D. (Intern), Eg Nielsen, E. (Intern)
Coral by-catch in shrimp bottom trawl surveys in West Greenland waters (2010 – 2012)

There have been zoological expeditions in Greenland waters since the 19th century documenting the sea life, including cold water corals. Coral trees (vernacular name for Paragorgia arborea) are mentioned as early as 1741 in the first natural history book about Greenland (Egede 1741). Due to the many expeditions and opportunistic collections by Greenlandic fisheries surveys, the species composition of West Greenlandic corals is fairly well known (Tendal and Heiner 2002),
although observations of species new to Greenland are still being made (Jørgensen et al. 2013, Tendal et al. 2013). The earlier collections of corals were not systematic and distribution patterns are poorly understood. Thus, more recently the Greenland Institute of Natural Resources started to collect cold water corals in a more systematic way to document the occurrence of corals in the bottom trawls made for the annual shrimp stock assessments. A total of 628 hauls were conducted covering an area of 17.1 km². Sixty-six hauls contained corals and of these 13 hauls had two or more species of corals. Only two hauls contained more than one kilo of coral, which were in each case comprised of one only species. The identification of the corals is based on Kenchington et al. (2009). The identification of many specimens has further been verified by Ole Tendal (Zoological Museum, Copenhagen) on the basis of frozen samples. Few corals, mainly soft corals (Alcyonacea) and sea pens (Pennatulacea), were found in the depth range within which shrimp are fished. This first analysis suggests that dense fields of Sea Pens and patches of octocorals occur in the depth range and within the area covered by the shrimp fishery.

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Greenland Institute of Natural Resources
Authors: Jørgensbye, H. (Intern), Arboe, N. H. (Ekstern)
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Cormorant predation on PIT-tagged lake fish

The present study use data from recovered PIT (Passive Integrated Transponder) tags to explore species-and size-specific annual predation rates by cormorants on three common lacustine fishes (size range 120-367 mm) in a European lake; roach (Rutilus rutilus), common bream (Abramis brama) and perch (Perca fluviatilis). In addition, we quantify the level of age/size truncation that cormorant predation could introduce in a population of perch, an important fish for recreational angling as well as for trophic interactions and ecosystem function in European lakes. Based on three years of PIT tagging of fish in Lake Viborg and subsequent recoveries of PIT tags from nearby cormorant roosting and breeding sites, we show that cormorants are major predators of roach, bream and perch within the size groups we investigated and for all species larger individuals had higher predation rates. Perch appear to be the most vulnerable of the three species and based on a comparison with mortality estimates from lakes without significant avian predation, this study suggest that predation from cormorants can induce age/size truncation in Lake Viborg, leaving very few larger perch in the lake. This truncation reduces the likelihood of anglers catching a large perch and may also influence lower trophic levels in the lake and thus turbidity as large piscivorous perch often play an important structuring role in lake ecosystem functioning.

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BFI (2014): BFI-level 1
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Hatchery-reared juvenile turbot Psetta maxima were tagged with Passive Integrated Transponder (PIT) tags and released at three different depths in a sandy bay in Denmark. About 2–7% of the released fish were registered daily to monitor their distribution using a tag antenna mounted on a modified beam trawl, thus avoiding actually sampling the fish. The change in distribution of the three groups was adequately represented by a twodimensional movement model. Movement along the shore was described by a Brownian motion with group specific drift. Movement perpendicular to the shore line was described by a Cox–Ingersoll–Ross process with a group specific attraction point. All three groups exhibited similar depth preferences of 1.7 m. Immediately after the release, fish were concentrated around the release points but after one day, fish had moved to the preferred depth and subsequently maintained their position at this depth. Farmed turbot exhibited strong site fidelity and an innate behaviour for selecting a preferred depth.
Does copepod size determine food consumption of particulate feeding fish?
The climate-induced reduction in the mean copepod size, mainly driven by a decrease in the abundance of the large Calanus finmarchicus around 1987, has been linked to the low survival of fish larvae in the North Sea. However, to what extent this sort of reduction in copepod size has any influence on adult particulate feeding fish is unknown. In the present study, we investigated the hypothesis that the availability of the large copepods determines food consumption and growth conditions of lesser sandeel (Ammodytes marinus) in the North Sea. Analysis of stomach content suggested that food consumption is higher for fish feeding on large copepods, and additional calculations revealed how handling time limitation may provide part of the explanation for this relationship. Comparing stomach data and zooplankton samples indicated that lesser sandeel actively target large copepods when these are available. Finally, we observed that the length of lesser sandeel began to decrease in the late 1980s, simultaneously with the C. finmarchicus decline.
Do North Atlantic eels show parallel patterns of spatially varying selection?

Background: The two North Atlantic eel species, the European and the American eel, represent an ideal system in which to study parallel selection patterns due to their sister species status and the presence of ongoing gene flow. A panel of 80 coding-gene SNPs previously analyzed in American eel was used to genotype European eel individuals (glass eels) from 8 sampling locations across the species distribution. We tested for single-generation signatures of spatially varying selection in European eel by searching for elevated genetic differentiation using F-ST-based outlier tests and by testing for significant associations between allele frequencies and environmental variables. Results: We found signatures of possible selection at a total of 11 coding-gene SNPs. Candidate genes for local selection constituted mainly genes with a major role in metabolism as well as defense genes. Contrary to what has been found for American eel, only 2 SNPs in our study correlated with differences in temperature, which suggests that other explanatory variables may play a role. None of the genes found to be associated with explanatory variables in European eel showed any correlations with environmental factors in the previous study in American eel. Conclusions: The different signatures of selection between species could be due to distinct selective pressures associated with the much longer larval migration for European eel relative to American eel. The lack of parallel selection in North Atlantic eels could also be due to most phenotypic traits being polygenic, thus reducing the likelihood of selection acting on the same genes in both species.
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**Ecosystem-based management objectives for the North Sea: riding the forage fish rollercoaster**

The North Sea provides a useful model for considering forage fish (FF) within ecosystem-based management as it has a complex assemblage of FF species. This paper is designed to encourage further debate and dialogue between stakeholders about management objectives. Changing the management of fisheries on FF will have economic consequences for all fleets in the North Sea. The predators that are vulnerable to the depletion of FF are Sandwich terns, great skua and common guillemots, and to a lesser extent, marine mammals. Comparative evaluations of management
strategies are required to consider whether maintaining the reserves of prey biomass or a more integral approach of monitoring mortality rates across the trophic system is more robust under the ecosystem approach. In terms of trophic energy transfer, stability, and resilience of the ecosystem, FF should be considered as both a sized-based pool of biomass and as species components of the system by managers and modellers. Policy developers should not consider the knowledge base robust enough to embark on major projects of ecosystem engineering. Management plans appear able to maintain sustainable exploitation in the short term. Changes in the productivity of FF populations are inevitable so management should remain responsive and adaptive.

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Authors: Dickey-Collas, M. (Ekstern), Engelhard, G. H. (Ekstern), Rindorf, A. (Intern), Raab, K. (Ekstern), Smout, S. (Ekstern), Aarts, G. (Ekstern), Deurs, M. V. (Intern), Brunel, T. (Ekstern), Hoff, A. (Ekstern), Lauerburg, R. A. (Ekstern), Garthe, S. (Ekstern), Andersen, K. H. (Intern), Scott, F. (Ekstern), Kooten, T. V. (Ekstern), Beare, D. (Ekstern), Peck, M. A. (Ekstern)
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Effects of dietary fatty acids on the production and quality of eggs and larvae of Atlantic cod (Gadus morhua L.)
Cultivated Atlantic cod (Gadus morhua) entering their first year of gamete maturation were fed diets with different levels of arachidonic acid (ARA) and eicosapentaenoic acid (EPA) for 6.5 months prior to commencement of spawning. Gravid females were stripped three times: at the beginning, peak and end of spawning. Lipid composition and egg and larval quality of 34 family crosses were investigated. Results indicated that ARA uptake into eggs from broodstock diet was highly efficient achieving proportions of ARA up to 84% higher in eggs than in the diet. EPA was 42–76% higher, and DHA was 155–173% higher in eggs than in diets. Cod fed the diet with the lowest EPA/ARA ratio had the greatest egg production. Eggs from fish on a diet with high ARA level had significantly higher fertilization and hatching success than those fed low levels of ARA. This diet produced on average 71 viable eggs g⁻¹ female compared with 32.5 and 4 eggs in diet B and C, respectively. Furthermore, larval survival until 8 days posthatch was higher in diets with lower ARA levels. The combined results showed that ARA dietary supplementation and low EPA/ARA ratio yielded a greater number of viable larvae kg⁻¹ female

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Pages: 654-666
Estimates of reproductive potential of Greenland halibut (Reinhardtius hippoglossoides) in East Greenland based on an update of maturity status

When estimating reproductive potential (RP), correct interpretation of the maturity status is essential. It has now become apparent the presence of vitellogenic oocytes within the ovary of Greenland halibut (Reinhardtius hippoglossoides) does not necessarily indicate they will spawn within the next twelve months. This has led to a revision of the interpretation of the maturity scale where fish which contain only a developing cohort (DC) of oocytes are considered immature. Comparisons were made of estimates of L50 of female Greenland halibut in East Greenland using the previous interpretation of maturity status where the leading cohort (LC) and DC oocytes are not differentiated with the new interpretation where they are. Differentiation led to an increase from 63.8 to 80.2cm and from 61.2 to 74.1cm for the northern (between 63°40′N and 67°00′N) and southern area (between 61°45′N and 62°40′N), respectively. Combining the maturity data with abundance data of Greenland halibut in East Greenland, spawning stock biomass (SSB) and total egg production (TEP) was estimated in four quadrants between 1998 and 2012 using both the previous and current interpretation of the maturity scale. Using the new interpretation of the scale led to a decrease in SSB estimates of 28–92% in specific areas and years, with an average of 56%. Estimates of TEP were directly proportional to SSB so this approach did not offer any advantages over SSB as a measure of reproductive potential. Length composition of Greenland halibut caught by Norwegian fishing vessels fishing in East Greenland indicate that 85 and 57% of the females caught by the trawl and longline fleet respectively in the northern area and 46% caught by the longline fleet in the southern area were immature.
Estimating spatio-temporal dynamics of size-structured populations

Spatial distributions of structured populations are usually estimated by fitting abundance surfaces for each stage and at each point of time separately, ignoring correlations that emerge from growth of individuals. Here, we present a statistical model that combines spatio-temporal correlations with simple stock dynamics, to estimate simultaneously how size distributions and spatial distributions develop in time. We demonstrate the method for a cod population sampled by trawl surveys. Particular attention is paid to correlation between size classes within each trawl haul due to clustering of individuals with similar size. The model estimates growth, mortality and reproduction, after which any aspect of size-structure, spatio-temporal population dynamics, as well as the sampling process can be probed. This is illustrated by two applications: 1) tracking the spatial movements of a single cohort through time, 2) predicting the risk of by-catch of undersize individuals. The method demonstrates that it is possible to combine stock assessment and spatio-temporal dynamics, however at a high computational cost. The model can be extended by increasing its ecological fidelity, although computational feasibility eventually becomes limiting.

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Authors: Kristensen, K. (Intern), Thygesen, U. H. (Intern), Andersen, K. H. (Intern), Beyer, J. E. (Intern)
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Estimation of time-varying selectivity in stock assessments using state-space models

Time-varying selectivity is one of the main challenges in single species age-based assessment models. In classical deterministic VPA-type models the fishing mortality rates are unfiltered representations of the observed catches. As a consequence the selectivity becomes time-varying, but this representation is too fluctuating, because it includes the observation noise. In parametric statistical catch at age models a common assumption is that the selectivity is constant in all years, although time-varying selectivity can be introduced by splitting the data period in blocks with different selectivities, or by using smoothing splines and penalized time-deviances. However, these methods require subjective choices w.r.t. the degree of time-varying allowed. A simple state-space assessment model is presented as an alternative, which among other benefits offers an objective way of estimating time-varying selectivity pattern. The fishing mortality rates are considered (possibly correlated) stochastic processes, and the corresponding process variances are estimated within the model. The model is applied to North Sea cod and it is verified from simulations that time-varying selectivity can be estimated.
Evaluation of alternative age-based methods for estimating relative abundance from survey data in relation to assessment models

Indices of abundance from fishery-independent trawl surveys constitute an important source of information for many fish stock assessments. Indices are often calculated using area stratified sample means on age-disaggregated data, and finally treated in stock assessment models as independent observations. We evaluate a series of alternative methods for calculating indices of abundance from trawl survey data (delta-lognormal, delta-gamma, and Tweedie using Generalized Additive Models) as well as different error structures for these indices when used as input in an age-based stock assessment model (time-constant vs time-varying variance, and independent versus correlated age groups within years). The methods are applied to data on North Sea herring (Clupea harengus), sprat (Sprattus sprattus), and whiting (Merlangius merlangus), and the full stock assessments are carried out to evaluate the different indices produced. The stratified mean method is found much more imprecise than the alternatives based on GAMs, which are found to be similar. Having time-varying index variances is found to be of minor importance, whereas the independence assumption is not only violated but has significant impact on the assessments.
Exploring the multidimensional nature of stock structure: a case study on herring dynamics in a transition area

Fish are not just fish. Differences within marine fish species in terms of morphology, behaviour, life history and certainly also genetic differentiation have been shown for an impressive number of species, including herring (Clupea harengus). These differences persist despite marine fish usually occupy areas without much environmental structuring and extensive mixing between populations. Many species of marine fishes have the capacity of dispersing over vast geographical areas, either passively by drifting eggs and larvae following ocean currents, or actively by migration of juveniles and adults, however, even for highly migratory species, significant population structure have been documented. Thus population structures are maintained despite extensive mixing of populations across vast distances; however the structuring factors are not easily disentangled. The factors behind this structure of populations have in some cases been referred to as spatial distance between populations, when the distribution of the species is larger than the dispersal range of individuals. Also oceanographic processes and the topography of the ocean floor have been linked to population structure in a number of species, yet few studies have tested specifically for relationships between environmental parameters of adaptive significance and population structuring in marine migratory fish, and even fewer have examined evidence of local adaptation. The relative roles of migratory behaviour and local differences in environmentally induced selective pressures in effecting such structure remain elusive. Maintaining population structures is of vital importance for the resilience of fish populations to changes in the environment and their exploitation. The preservation of intraspecific population integrity is a prerequisite for maintaining population and life history diversity which in turn affect the performance of individual species in providing important ecosystem services. In this PhD thesis, I explore the population complexity of the herring stock called the Western Baltic Spring Spawning herring; localized in the transition area between the North Sea and the Baltic. I analyse which herring populations that are available to a mixed herring fishery in the area and their spatial and temporal occurrence. I explore the potential structuring factors causing the population diversity in the area and discuss the mechanisms behind these structuring factors. The results in this present thesis contribute to the understanding of the dynamics of the herring populations in the mixed pool of herring in the transition area between the North Sea and the Baltic. I identify several genetically different herring populations which are available for a fishery; their occurrence is structured by divergent migration strategies driven primarily by growth potential and the persistence of a genetic population differentiation is linked to the environmental heterogeneity in terms of salinity facilitating homing to spawning site. Such insight will aid a sustainable aggregated management of a fishery on a mixed herring stock. It will facilitate protecting the weaker populations from over harvesting in a mixed fishery and thus maintain the diversity and in turn the resilience of the stock to a fishery.
Forage fish, their fisheries, and their predators: who drives whom?
The North Sea has a diverse forage fish assemblage, including herring, targeted for human consumption; sandeel, sprat, and Norway pout, exploited by industrial fisheries; and some sardine and anchovy, supporting small-scale fisheries. All show large abundance fluctuations, impacting on fisheries and predators. We review field, laboratory, and modelling studies to investigate the drivers of this complex system of forage fish. Climate clearly influences forage fish productivity; however, any single-species considerations of the influence of climate might fail if strong interactions between forage fish exist, as in the North Sea. Sandeel appears to be the most important prey forage fish. Seabirds are most dependent on forage fish, due to specialized diet and distributional constraints (breeding colonies). Other than fisheries, key predators of forage fish are a few piscivorous fish species including saithe, whiting, mackerel, and horse-mackerel, exploited in turn by fisheries; seabirds and seals have a more modest impact. Size-based foodweb modelling suggests that reducing fishing mortality may not necessarily lead to larger stocks of piscivorous fish, especially if their early life stages compete with forage fish for zooplankton resources. In complex systems, changes in the impact of fisheries on forage fish may have potentially complex (and perhaps unanticipated) consequences on other commercially and/or ecologically important species.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, Cefas, University of Hamburg, University of St Andrews, Wageningen IMARES, University of Kiel
Authors: Engelhard, G. H. (Ekstern), Peck, M. A. (Ekstern), Rindorf, A. (Intern), Smout, S. (Ekstern), Deurs, M. V. (Intern), Raab, K. (Ekstern), Andersen, K. H. (Intern), Garthe, S. (Ekstern), Lauerburg, R. A. (Ekstern), Scott, F. (Ekstern), Brunel, T. (Ekstern), Aarts, G. (Ekstern), Kooten, T. V. (Ekstern), Dickey-Collas, M. (Ekstern)
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Genetic variation among major sockeye salmon populations in Kamchatka peninsula inferred from SNP and microsatellite DNA analyses
Sockeye salmon samples from six populations from Kamchatka Peninsula were tested for polymorphism at six microsatellite (STR) and forty-five single nucleotide polymorphism (SNP) loci. These populations included the five largest populations in the region. Statistically significant genetic differentiation among the local populations from this part of the species range examined was demonstrated. The STR variability points to pronounced genetic divergence of the populations from two geographical regions, Eastern and Western Kamchatka. The results of SNP analysis further revealed that the populations of the two northern Kamchatka rivers (Palana River and Pakhacha River) differed significantly from the other populations studied. We estimated the efficiency for both types of markers for individual assignment of fish taken in mixtures. Accuracy was generally higher for assignment with SNP data; however, pooling of the STR and SNP data sets provided higher accuracy than with either one alone.

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Khrustaleva, A. (Ekstern), Limborg, M. (Intern), Seeb, J. E. (Ekstern)
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Genome-wide single-generation signatures of local selection in the panmictic European eel
Next-generation sequencing and the collection of genome-wide data allow identifying adaptive variation and footprints of directional selection. Using a large SNP data set from 259 RAD-sequenced European eel individuals (glass eels) from eight locations between 34 and 64°N, we examined the patterns of genome-wide genetic diversity across locations. We tested for local selection by searching for increased population differentiation using FST-based outlier tests and by testing for significant associations between allele frequencies and environmental variables. The overall low genetic differentiation found (FST = 0.0007) indicates that most of the genome is homogenized by gene flow, providing further evidence for genomic panmixia in the European eel. The lack of genetic substructuring was consistent at both nuclear and mitochondrial SNPs. Using an extensive number of diagnostic SNPs, results showed a low occurrence of hybrids between European and American eel, mainly limited to Iceland (5.9%), although individuals with signatures of introgression several generations back in time were found in mainland Europe. Despite panmixia, a small set of SNPs showed high genetic differentiation consistent with single-generation signatures of spatially varying selection acting on glass eels. After screening 50,354 SNPs, a total of 754 potentially locally selected SNPs were identified. Candidate genes for local selection constituted a wide array of functions,
including calcium signalling, neuroactive ligand–receptor
interaction and circadian rhythm. Remarkably, one of the candidate genes identified is PERIOD, possibly related to
differences in local photoperiod associated with the >30° difference in latitude between locations. Genes under selection
were spread across the genome, and there were no large regions of increased differentiation as expected when selection
occurs within just a single generation due to panmixia. This supports the conclusion that most of the genome is
homogenized by gene flow that removes any effects of diversifying selection from each new generation

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Marine Biology and
Biotechnology Center, BGI-Shenzhen, BGI-Europe, Aarhus University, James Cook University, Universite Laval
, Jónsson, B. (Ekstern), Jian, J. B. (Ekstern), Cheng, L. (Ekstern), Maes, G. E. (Ekstern), Bernatchez, L. (Ekstern),
Hansen, M. M. (Ekstern)
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BFI (2015): BFI-level 2
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BFI (2014): BFI-level 2
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Web of Science (2014): Indexed yes
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Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): SJR 3.068 SNIP 1.705 CiteScore 5.36
ISI indexed (2012): ISI indexed yes
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BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.469 SNIP 1.823 CiteScore 5.56
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Scopus rating (2010): SJR 3.513 SNIP 1.915
Web of Science (2010): Indexed yes
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Scopus rating (2009): SJR 3.455 SNIP 2.024
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
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Web of Science (2008): Indexed yes
Genomics and the future of conservation genetics revisited

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Publication date: 2014
Event: Abstract from North America Congress for Conservation Biology, Missoula, Montana, United States.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2014

Genomic signatures of selection in a classic fisheries experiment

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Stanford University
Authors: Therkildsen, N. O. (Intern), Munch, S. (Ekstern), Conover, D. (Ekstern), Palumbi, S. (Ekstern)
Publication date: 2014
Event: Abstract from Evolution meeting, Raleigh, United States.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2014

Genudsætning og erhvervsfiskeristop: Vejen til et bedre geddefiskeri

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine Living Resources
Authors: Skov, C. (Intern), Jansen, T. (Intern), Sivebæk, F. (Intern)
Pages: 52-53
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Main Research Area: Technical/natural sciences
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Journal: Fisk & Fri
Gynogenetic haploid and diploid mapping reveals chiasma interference and hidden islands of adaptive importance in a salmonid genome

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Limborg, M. (Intern), Waples, R. K. (Ekstern), Seeb, L. W. (Ekstern), Seeb, J. E. (Ekstern)
Publication date: 2014
Event: Poster session presented at The International Conference on Integrative Salmonid Biology, Vancouver, Canada.
Main Research Area: Technical/natural sciences
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Haploid-assisted mapping disentangles complexities of duplicated salmonid genomes

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Herring otolith shape – a tool for gauging stock complexity?

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Worsøe Clausen, L. (Intern)
Publication date: 2014
Event: Abstract from 5th International Otolith Symposium, Mallorca, Spain.
Main Research Area: Technical/natural sciences
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How does prey quality affect life-history traits under different temperature regimes?

General information
Implications of stock recovery for a neighbouring management unit: experience from the Baltic cod

Cod in the Baltic Sea is assessed and managed as two separate stocks, i.e. eastern and western Baltic cod. The eastern Baltic cod has recently started to recover after several decades of severe depletion. In the present study, we suggest that the recovery of the eastern Baltic cod population has also substantially increased cod abundance in a specific area of the adjacent western Baltic management unit. This is investigated through long time-series of spatially resolved stock assessment data supplemented by genetic analyses of origin of the cod currently found in the transition area between the two populations. Due to immigrating cod from the east, there are currently large spatial differences in cod abundance and mean weight in the western Baltic management unit that raise new management concerns. First, the high abundance of cod of eastern origin found in the western Baltic management unit can mask the relatively poor state of the western Baltic cod population. Second, the current fishing mortality estimates for the entire western Baltic management unit, used as basis for fisheries management, are difficult to interpret as these are highly influenced by mixing of biological populations and the spatial distribution of fisheries.

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State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Marine Ecology and Oceanography
Authors: Eero, M. (Intern), Hansen, J. H. (Intern), Hüssy, K. (Intern)
Pages: 1458-1466
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Main Research Area: Technical/natural sciences
Introducing time-varying natural mortality in the length-based assessment model for the Pandalus Borealis stock in ICES Div. Illa and IVa east

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Lund University
Authors: Jørgensen, M. (Ekstern), Munch-Petersen, S. (Intern), Nielsen, A. (Intern), Søvik, G. (Ekstern), Ulmestrand, M. (Ekstern), Devine, J. (Ekstern), Eigaard, O. R. (Intern)
Publication date: 2014
Main Research Area: Technical/natural sciences
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Learning from the past and stepping into the future: Population dynamics of Atlantic cod (Gadus morhua) revealed by historical DNA

Marine fish biodiversity is often highly variable in space and time, and the additional impacts of human exploitation and climate change might greatly affect the survival of many organisms within the ocean. Dramatic changes in the abundance of many fish populations have been widely observed over time together with shifting distributional range. However, it is known that population diversity or biocomplexity underpins ecosystem functioning and productivity, and stabilizes ecosystem processes and services. Thus, preserving intraspecific genetic diversity is of paramount importance for successful management and conservation of marine fish. The present thesis uses a spatiotemporal population genetic approach to examine historical dynamics of Atlantic cod populations (Gadus morhua) in Greenland and to elucidate how they have differentially responded to intense fishing pressure and environmental changes over the past century. Utilizing unique collections of archived fish samples, the overarching goals of this PhD project were to (1) examine the temporal stability of population structure of cod, (2) disentangle the population dynamics and how they have responded to intense fishing and environmental variability, and (3) understand important patterns of population connectivity. The thesis opens with a general introduction which briefly describes the historical and recent perception of world fisheries resources in human society (Chapter 1). The following chapters review relevant knowledge and methodological issues which have provided a critical rationale for addressing the research questions in this work. Chapter 2 emphasizes the importance of recognizing complex population structure in classical marine fish to reach effective management goals. Chapter 3 defines the most important drivers of genetic variation, and how these can generate detrimental demographic and evolutionary effects in marine fish populations. Chapter 4 presents the field of fisheries genetics, giving particular emphasis on genetic stock identification and retrospective genetic monitoring. Subsequently, a collection of manuscripts is provided. The different studies have revealed (Paper 1) complex and dynamic interactions of four genetically distinct populations of cod, (Paper 2) that the different populations exhibited dramatic spatiotemporal changes in abundance and distribution and responded markedly different to historical commercial fishing and recent increases of ocean temperatures, (Paper 3) historical fish tags as a useful source of DNA for conducting retrospective genetic analysis, and (Paper 4) long-distance natal homing in cod. Overall, this thesis provides unprecedented insights into the population dynamics of Atlantic cod at the northern margin of its distribution. It illustrates how temporally spaced DNA samples offer a unique opportunity for disentangling the effects of primary forces shaping marine fish populations accumulated over decades or even a century. Of particular note, Paper 1, 2 and 4 represent some of the first concrete examples of how spatiotemporal data delivered by geneticists can be successfully applied in current fisheries management schemes.
Local adaptation at the transcriptome level in brown trout: Evidence from early life history temperature genomic reaction norms

Local adaptation and its underlying molecular basis has long been a key focus in evolutionary biology. There has recently been increased interest in the evolutionary role of plasticity and the molecular mechanisms underlying local adaptation. Using transcriptome analysis, we assessed differences in gene expression profiles for three brown trout (Salmo trutta) populations, one resident and two anadromous, experiencing different temperature regimes in the wild. The study was based on an F2 generation raised in a common garden setting. A previous study of the F1 generation revealed different reaction norms and significantly higher $Q_{ST}$ than $F_{ST}$ among populations for two early life-history traits. In the present study we investigated if genomic reaction norm patterns were also present at the transcriptome level. Eggs from the three populations were incubated at two temperatures (5 and 8 degrees C) representing conditions encountered in the local environments. Global gene expression for fry at the stage of first feeding was analysed using a 32k cDNA microarray. The results revealed differences in gene expression between populations and temperatures and population × temperature interactions, the latter indicating locally adapted reaction norms. Moreover, the reaction norms paralleled those observed previously at early life-history traits. We identified 90 cDNA clones among the genes with an interaction effect that were differently expressed between the ecologically divergent populations. These included genes involved in immune- and stress response. We observed less plasticity in the resident as compared to the anadromous populations, possibly reflecting that the degree of environmental heterogeneity encountered by individuals throughout their life cycle will select for variable level of phenotypic plasticity at the transcriptome level. Our study demonstrates the usefulness of transcriptome approaches to identify genes with different temperature reaction norms. The responses observed suggest that populations may vary in their susceptibility to climate change.

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State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University,
Universite Laval
Authors: Meier, K. (Intern), Hansen, M. M. (Ekstern), Normandeau, E. (Ekstern), Mensberg, K. D. (Intern), Frydenberg, J. (Ekstern), Larsen, P. F. (Intern), Bekkevold, D. (Intern), Bernatchez, L. (Ekstern)
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BFI (2015): BFI-level 1
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Web of Science (2015): Indexed yes
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Web of Science (2014): Indexed yes
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ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): SJR 1.945 SNIP 1.142 CiteScore 4.15
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Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58
Modelling group dynamic animal movement

Group dynamic movement is a fundamental aspect of many species' movements. The need to adequately model individuals' interactions with other group members has been recognised, particularly in order to differentiate the role of social forces in individual movement from environmental factors. However, to date, practical statistical methods which can include group dynamics in animal movement models have been lacking. We consider a flexible modelling framework that distinguishes a group-level model, describing the movement of the group's centre, and an individual-level model, such that each individual makes its movement decisions relative to the group centroid. The basic idea is framed within the flexible class of hidden Markov models, extending previous work on modelling animal movement by means of multi-state random walks. While in simulation experiments parameter estimators exhibit some bias in non-ideal scenarios, we show that generally the estimation of models of this type is both feasible and ecologically informative. We illustrate the approach using real movement data from 11 reindeer (Rangifer tarandus). Results indicate a directional bias towards a group centroid for reindeer in an encamped state. Though the attraction to the group centroid is relatively weak, our model successfully captures group-influenced movement dynamics. Specifically, as compared to a regular mixture of correlated random walks, the group dynamic model more accurately predicts the non-diffusive behaviour of a cohesive mobile group.
Outlier SNP markers reveal fine-scale genetic structuring across European hake populations (Merluccius merluccius)

Shallow population structure is generally reported for most marine fish and explained as a consequence of high dispersal, connectivity and large population size. Targeted gene analyses and more recently genome-wide studies have challenged such view, suggesting that adaptive divergence might occur even when neutral markers provide genetic homogeneity across populations. Here, 381 SNPs located in transcribed regions were used to assess large and fine-scale population structure in the European hake (Merluccius merluccius), a widely distributed demersal species of high priority for the European fishery. Analysis of 850 individuals from 19 locations across the entire distribution range showed evidence for several outlier loci, with significantly higher resolving power. While 299 putatively neutral SNPs confirmed the genetic break between basins (FCT = 0.016) and weak differentiation within basins, outlier loci revealed a dramatic divergence between Atlantic and Mediterranean populations (FCT range 0.275–0.705) and fine-scale significant population structure. Outlier loci separated North Sea and Northern Portugal populations from all other Atlantic samples and revealed a strong differentiation among Western, Central and Eastern Mediterranean geographical samples.

Significant correlation of allele frequencies at outlier loci with seawater surface temperature and salinity supported the hypothesis that populations might be adapted to local conditions. Such evidence highlights the importance of integrating information from neutral and adaptive evolutionary patterns towards a better assessment of genetic diversity. Accordingly, the generated outlier SNP data could be used for tackling illegal practices in hake fishing and commercialization as well as to develop explicit spatial models for defining management units and stock boundaries.
Parallel signatures of selection in temporally isolated lineages of pink salmon

Studying the effect of similar environments on diverse genetic backgrounds has long been a goal of evolutionary biologists with studies typically relying on experimental approaches. Pink salmon, a highly abundant and widely ranging salmonid, provide a naturally occurring opportunity to study the effects of similar environments on divergent genetic backgrounds due to a strict two-year semelparous life history. The species is composed of two reproductively isolated lineages with overlapping ranges that share the same spawning and rearing environments in alternate years. We used restrictionsite-
associated DNA (RAD) sequencing to discover and genotype approximately 8000 SNP loci in three population pairs of even- and odd-year pink salmon along a latitudinal gradient in North America. We found greater differentiation within the odd-year than within the even-year lineage and greater differentiation in the southern pair from Puget Sound than in the northern Alaskan population pairs. We identified 15 SNPs reflecting signatures of parallel selection using both a differentiation-based method (BAYESCAN) and an environmental correlation method (BAYENV). These SNPs represent genomic regions that may be particularly informative in understanding adaptive evolution in pink salmon and exploring how differing genetic backgrounds within a species respond to selection from the same natural environment.
Pink salmon: Genomic islands in the stream of evolution

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Seeb, L. W. (Ekstern), Limborg, M. (Intern), Waples, R. K. (Ekstern), Tarpey, C. (Ekstern), Seeb, J. E. (Ekstern)
Publication date: 2014
Event: Abstract from North America Congress for Conservation Biology, Missoula, Montana, United States.
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Journal article – Annual report year: 2014

Population genomics of marine fishes: next generation prospects and challenges
Over the past few years, technological advances have facilitated giant leaps forward in our ability to generate genome-wide molecular data, offering exciting opportunities for gaining new insights into the ecology and evolution of species where genomic information is still limited. Marine fishes are valuable organisms for advancing our understanding of evolution on historical and contemporary time scales, and here we highlight areas in which research on these species is likely to be particularly important in the near future. These include possibilities for gaining insights into processes on ecological time scales, identifying genomic signatures associated with population divergence under gene flow, and determining the genetic basis of phenotypic traits. We also consider future challenges pertaining to the implementation of genome-wide coverage through next-generation sequencing and genotyping methods in marine fishes. Complications associated with fast decay of linkage disequilibrium, as expected for species with large effective population sizes, and the possibility that adaptation is associated with both soft selective sweeps and polygenic selection, leaving complex genomic signatures in natural populations, are likely to challenge future studies. However, the combination of high genome coverage and new statistical developments offers promising solutions. Thus, the next generation of studies is likely to truly facilitate the transition from population genetics to population genomics in marine fishes. This transition will advance our understanding of basic evolutionary processes and will offer new possibilities for conservation and management of valuable marine resources

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University
Authors: Hansen, J. H. (Intern), Therkildsen, N. O. (Intern), Pujolar, J. (Ekstern)
Pages: 117-132
Publication date: 2014
Main Research Area: Technical/natural sciences
Prey or predator – expanding the food web role of sandeel (Ammodytes marinus)

We report an unexpected observation of lesser sandeel Ammodytes marinus foraging on juveniles and late larval stages of the same species. This recording sheds new light on the cannibalistic and piscivorous capacity of forage fish and raises a number of questions about the role of forage fish in marine food webs. In 2012 and 2013 the stomachs of 748 sandeels from 36 different commercial sandeel hauls in the central North Sea were opened. 9% of these stomachs contained late stage sandeel larvae. In order to better understand the cannibalistic nature of sandeels, we made a detailed analysis of another 450 sandeels from a single haul with a high frequency of apparent cannibals. One-third of the stomachs contained a minimum of one young sandeel (mean length 2.7 cm; max. length 4.9 cm), 10 percent contained 5 or more, and one stomach contained 18. Analyses of sample DNA confirmed that predator and prey were conspecifics. Larger specimens were more likely to be cannibals. However, among cannibals the specific sandeel larva consumption was independent of...
cannibal size. We argue that this piscivorous cannibalistic behaviour may not only be a key factor in explaining recruitment fluctuations in North Sea sandeel stocks, but it may also add a new element to the complexity of energy flow in marine food chains.

**General information**

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Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, Centre for Ocean Life
Authors: Eigaard, O. R. (Intern), Deurs, M. V. (Intern), Behrens, J. (Intern), Bekkevold, D. (Intern), Brander, K. (Intern), Plambech, M. (Intern), Schreiber Piet-Hansen, K. (Intern), Mosegaard, H. (Intern)
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BFI (2016): BFI-level 2
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Web of Science (2015): Indexed yes
Scopus rating (2016): CiteScore 2.4
Web of Science (2014): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.75
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.79
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 2.9
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 2.85
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Pseudocollapse and rebuilding of North Sea mackerel (Scomber scombrus)

The largest observed change in mackerel (Scomber scombrus) abundance in the North Atlantic happened when the so-called "North Sea mackerel" collapsed due to overfishing. Despite protection, it has remained in a depleted state. Central to this interpretation was that the "North Sea mackerel" was considered to be a distinct spawning component. However, a recent study has shown that this is not likely. In the light of this study, a review of the history of mackerel spawning in the North Sea found that the traditional explanation of the collapse did not account for a range of unfavourable environmental changes: high fishing pressure was followed by decreasing temperatures that reduced the spawning migration into the North Sea. This was further supplemented by unfavourable changes in food and wind-induced turbulence. On the population level, this was, therefore, not a local stock collapse, but a southwest shift in spawning distribution combined with a reduction in that portion of the population cline with an affinity for spawning in the northeastern part of the spawning area, including the North Sea. No indication of irreversible genetic or behavioural losses caused by the events was found. The previously unexplained lack of rebuilding of spawning in the North Sea consequently seems related to two environmental factors that have remained unfavourable: (i) zooplankton concentration, and (ii) wind-induced turbulence. Furthermore, the large commercial autumn–winter fishery in the North Sea continues to land unknown quantities of mackerel that have an affinity for spawning in the northeastern part of the spawning area, including the North Sea.

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Jansen, T. (Intern)
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.63
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.18
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.46
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.35
ISI indexed (2012): ISI indexed yes
Report of the ICES/NAFO Joint Working Group on Deep-water Ecology (WGDEC), 24–28 February 2014, Copenhagen, Denmark

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Joint Nature Conservation Committee, Peterborough
Publication date: 2014

Publication information
Original language: English
Series: ICES CM 2014/ACOM: 29
Main Research Area: Technical/natural sciences
Links:
Source: FindIt
Source-ID: 2194677407
Publication: Research › Report – Annual report year: 2015
Route optimisation and solving Zermelo's navigation problem during long distance migration in cross flows

The optimum path to follow when subjected to cross flows was first considered over 80 years ago by the German mathematician Ernst Zermelo, in the context of a boat being displaced by ocean currents, and has become known as the ‘Zermelo navigation problem’. However, the ability of migrating animals to solve this problem has received limited consideration, even though wind and ocean currents cause the lateral displacement of flyers and swimmers, respectively, particularly during long-distance journeys of 1000s of kilometres. Here, we examine this problem by combining long-distance, open-ocean marine turtle movements (obtained via long-term GPS tracking of sea turtles moving 1000s of km), with a high resolution basin-wide physical ocean model to estimate ocean currents. We provide a robust mathematical framework to demonstrate that, while turtles eventually arrive at their target site, they do not follow the optimum (Zermelo’s) route. Even though adult marine turtles regularly complete incredible long-distance migrations, these vertebrates primarily rely on course corrections when entering neritic waters during the final stages of migration. Our work introduces a new perspective in the analysis of wildlife tracking datasets, with different animal groups potentially exhibiting different levels of complexity in goal attainment during migration.
Seasonal migration, vertical activity and winter temperature experience of Greenland halibut Reinhardtius hippoglossoides (Walbaum) in West Greenland waters

The deep-water flatfish Greenland halibut Reinhardtius hippoglossoides (Walbaum) is common along the West Greenland coast. In the northwestern fjords, Greenland halibut is an important socio-economic resource for the Greenland community, but due to the deep and partly ice-covered environment, very little is known about its behavior and habitat characteristics. We tagged adult Greenland halibut in the waters off Ilulissat with electronic data storage tags that collected information on depth, temperature, and time. Although clear differences between individuals in migration and vertical behavior were present, we discovered a consistent seasonal migration from the relatively shallow-water Disko Bay area into the deep waters of the Ilulissat Icefjord, where the fish resided in the winter months before returning to Disko Bay. Vertical activity was pronounced at both locations, with fish covering vertical distances of up to 100 m within 15 min. During the winter months, the fish experienced temperatures between ca. 0 and 4°C, with most experiencing temperatures of 2 to 3°C. Irrespective of year and quarter of the year, the fish experienced warmer water and a broader range of temperatures when resident in Disko Bay (mean range 2.6°C) than when resident in the ice fjord (mean range 1.4°C). Using the tagged halibut as a ‘live tool,’ we show that parts of the ice fjord are hundreds of meters deeper than previously thought. We also document the first seawater temperature measurements made beneath the Jakobshavn Isbræ outlet glacier, revealing a positive relationship between depth and temperature for the upper 600 m and a between-year variation in temperatures beneath the ice sheet in 2001, 2002, and 2003.
Size-dependent diffusion promotes the emergence of spatiotemporal patterns

Spatiotemporal patterns, indicating the spatiotemporal variability of individual abundance, are a pronounced scenario in ecological interactions. Most of the existing models for spatiotemporal patterns treat species as homogeneous groups of individuals with average characteristics by ignoring intraspecific physiological variations at the individual level. Here we explore the impacts of size variation within species resulting from individual ontogeny, on the emergence of spatiotemporal patterns in a fully size-structured population model. We found that size dependency of animal's diffusivity greatly promotes the formation of spatiotemporal patterns, by creating regular spatiotemporal patterns out of temporal chaos. We also found that size-dependent diffusion can substitute large-amplitude base harmonics with spatiotemporal patterns with lower
amplitude oscillations but with enriched harmonics. Finally, we found that the single-generation cycle is more likely to drive spatiotemporal patterns compared to predator-prey cycles, meaning that the mechanism of Hopf bifurcation might be more common than hitherto appreciated since the former cycle is more widespread than the latter in case of interacting populations. Due to the ubiquity of individual ontogeny in natural ecosystems we conclude that diffusion variability within populations is a significant driving force for the emergence of spatiotemporal patterns. Our results offer a perspective on self-organized phenomena, and pave a way to understand such phenomena in systems organized as complex ecological networks.

**General information**

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Umea University, Indian Institute of Technology, Kanpur
Authors: Zhang, L. (Intern), Thygesen, U. H. (Intern), Banerjee, M. (Ekstern)
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**Publication information**

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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.993 SNIP 0.896
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.047 SNIP 0.978 CiteScore 1.89
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.22 SNIP 1.123 CiteScore 2.05
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.311 SNIP 1.239 CiteScore 2.28
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.42 SNIP 1.226 CiteScore 2.28
ISI indexed (2012): ISI indexed yes
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Scopus rating (2011): SJR 1.485 SNIP 1.225 CiteScore 2.28
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.69 SNIP 1.215
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.694 SNIP 1.259
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.96 SNIP 1.314
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.926 SNIP 1.332
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.787 SNIP 1.324
Processes leading to speciation in oceanic environments without obvious physical barriers remain poorly known. European and American eel (Anguilla anguilla and A. rostrata) spawn in partial sympatry in the Sargasso Sea. Larvae are advected by the Gulf Stream and other currents towards the European/North African and North American coasts, respectively. We analyzed 104 mitogenomes from the two species along with mitogenomes of other Anguilla and outgroup species. We estimated divergence time between the two species to identify major events involved in speciation. We also considered two previously stated hypotheses: one where the ancestral species was present in only one continent but was advected across the Atlantic by ocean current changes and another where population declines during Pleistocene glaciations led to increasing vicariance, facilitating speciation. Divergence time was estimated to ∼3.38 Mya, coinciding with the closure of the Panama Gateway that led to reinforcement of the Gulf Stream. This could have advected larvae towards European/North African coasts, in which case American eel would be expected to be the ancestral species. This scenario could, however, not be unequivocally confirmed by analyses of dN/dS, nucleotide diversity and effective population size estimates. Extended bayesian skyline plots showed fluctuations of effective population sizes and declines during glaciations, and thus also lending support to the importance of vicariance during speciation. There was evidence for positive selection at the ATP6 and possibly ND5 genes, indicating a role in speciation. The findings suggest an important role of ocean current changes in speciation of marine organisms.
Statistical analysis of population assignment for fisheries management employing otolith characteristics

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Mosegaard, H. (Intern)
Publication date: 2014
Event: Abstract from 5th International Otolith Symposium, Mallorca, Spain.
Main Research Area: Technical/natural sciences
Links:

Original language: English
DOIs: 10.1038/hdy.2014.44
Publication: Research - peer-review › Journal article – Annual report year: 2014
Temporally isolated lineages of Pink salmon reveal unique signatures of selection on distinct pools of standing genetic variation

A species’ genetic diversity bears the marks of evolutionary processes that have occurred throughout its history. However, robust detection of selection in wild populations is difficult and often impeded by lack of replicate tests. Here, we investigate selection in pink salmon (Oncorhynchus gorbuscha) using genome scans coupled with inference from a haploid-assisted linkage map. Pink salmon have a strict 2-year semelparous life history which has resulted in temporally isolated (allochronic) lineages that remain sympatric through sharing of spawning habitats in alternate years. The lineages differ in a range of adaptive traits, suggesting different genetic backgrounds. We used genotyping by sequencing of haploids to generate a high-density linkage map with 7035 loci and screened an existing panel of 8036 loci for signatures of selection. The linkage map enabled identification of novel genomic regions displaying signatures of parallel selection shared between lineages. Furthermore, 24 loci demonstrated divergent selection and differences in genetic diversity between lineages, suggesting that adaptation in the 2 lineages has arisen from different pools of standing genetic variation. Findings have implications for understanding asynchronous population abundances as well as predicting future ecosystem impacts from lineage-specific responses to climate change.
The Baltic ATLANTIS model: Implementing a holistic framework to evaluate ecosystem wide responses to changes in climate and anthropogenic forcing

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Monitoring and Data, Centre for Ocean Life, Aarhus University
Authors: Palacz, A. (Intern), Nielsen, J. R. (Intern), Christensen, A. (Intern), Gislason, H. (Intern), Bastardie, F. (Intern), Geitner, K. (Intern), Maar, M. (Ekstern), Lindegren, M. (Intern), Hufnagl, M. (Intern), Fulton, E. (Ekstern)
Number of pages: 1
Publication date: 2014
Event: Poster session presented at EU-FP7-VECTORS Symposium, La Grande Motte, France.
Main Research Area: Technical/natural sciences
Publication: Research › Poster – Annual report year: 2014

The Baltic cod: A case study for testing stock discrimination based on otolith shape analysis in a mixed stock fishery

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, Section for Ecosystem based Marine Management
Authors: Hüssy, K. (Intern), Mosegaard, H. (Intern), Hansen, J. H. (Intern), Eero, M. (Intern)
Publication date: 2014
Event: Abstract from 5th International Otolith Symposium, Mallorca, Spain.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2014

The effects of medieval dams on genetic divergence and demographic history in brown trout populations

Background: Habitat fragmentation has accelerated within the last century, but may have been ongoing over longer time scales. We analyzed the timing and genetic consequences of fragmentation in two isolated lake-dwelling brown trout populations. They are from the same river system (the Gudenå River, Denmark) and have been isolated from downstream anadromous trout by dams established ca. 600-800 years ago. For reference, we included ten other anadromous populations and two hatchery strains. Based on analysis of 44 microsatellite loci we investigated if the lake populations have been naturally genetically differentiated from anadromous trout for thousands of years, or have diverged recently due to the establishment of dams. Results: Divergence time estimates were based on 1) Approximate Bayesian Computation and 2) a coalescent-based isolation-with-gene-flow model. Both methods suggested divergence times ca. 600-800 years bp, providing strong evidence for establishment of dams in the Medieval as the factor causing divergence. Bayesian cluster analysis showed influence of stocked trout in several reference populations, but not in the focal lake and anadromous populations. Estimates of effective population size using a linkage disequilibrium method ranged from 244 to > 1,000 in all but one anadromous population, but were lower (153 and 252) in the lake populations. Conclusions: We show that genetic divergence of lake-dwelling trout in two Danish lakes reflects establishment of water mills and impassable dams ca. 600-800 years ago rather than a natural genetic population structure. Although effective population sizes of the two lake populations are not critically low they may ultimately limit response to selection and thereby future adaptation. Our results demonstrate that populations may have been affected by anthropogenic disturbance over longer time scales than normally assumed.
The importance of spatial models for estimating the strength of density dependence

Identifying the existence and magnitude of density dependence is one of the oldest concerns in ecology. Ecologists have aimed to estimate density dependence in population and community data by fitting a simple autoregressive (Gompertz) model for density dependence to time series of abundance for an entire population. However, it is increasingly recognized that spatial heterogeneity in population densities has implications for population and community dynamics. We therefore adapt the Gompertz model to approximate local densities over continuous space instead of population-wide abundance, and to allow productivity to vary spatially. Using simulated data generated from a spatial model, we show that the conventional (nonspatial) Gompertz model will result in biased estimates of density dependence, e.g., identifying oscillatory dynamics when not present. By contrast, the spatial Gompertz model provides accurate and precise estimates of density dependence for a variety of simulation scenarios and data availabilities. These results are corroborated when comparing spatial and nonspatial models for data from 10 years and ~100 sampling stations for three long-lived rockfishes (Sebastes spp.) off the California Coast. In this case, the nonspatial model estimates implausible oscillatory dynamics on an annual time scale, while the spatial model estimates strong autocorrelation and is supported by model selection tools.

We conclude by discussing the importance of improved data archiving techniques, so that spatial models can be used to re-examine classic questions regarding the presence and strength of density dependence in wild populations.

Read More: http://www.esajournals.org/doi/abs/10.1890/14-0739.1
The nuclear genome: Neutral and adaptive markers in fisheries science

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Salford
Authors: Mariani, S. (Ekstern), Bekkevold, D. (Intern)
Pages: 297-328
Publication date: 2014

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Edition: 2.
ISBN (Print): 978-0-12-397003-9
Chapter: 14
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Book chapter – Annual report year: 2013

The use of archived tags in retrospective genetic analysis of fish
Collections of historical tissue samples from fish (e.g. scales and otoliths) stored in museums and fisheries institutions are precious sources of DNA for conducting retrospective genetic analysis. However, in some cases only external tags used for documentation of spatial dynamics of fish populations have been preserved. Here we test the usefulness of fish tags as a source of DNA for genetic analysis. We extract DNA from historical tags from cod collected in Greenlandic waters between 1950 and 1968. We show that the quantity and quality of DNA recovered from tags is comparable to DNA from archived otoliths from the same individuals. Surprisingly, levels of cross-contamination do not seem to be significantly higher in DNA from external (tag) than internal (otolith) sources. Our study therefore demonstrates that historical tags can be a highly valuable source of DNA for retrospective genetic analysis of fish

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Biologisk institut
Authors: Bonanomi, S. (Intern), Therkildsen, N. O. (Intern), Hedeholm, R. B. (Forskerdatabase), Hansen, J. H. (Intern), Eg Nielsen, E. (Intern)
The use of at-sea-sampling data to dissociate environmental variability in Norway lobster (Nephrops norvegicus) catches to improve resource efficiency

The primary aim of this study was to determine whether the information collected as part of the at-sea-sampling program could be used to identify hydrographical and environmental variables that are influential on catch rates of Norway lobster. Ultimately, we wanted to know whether environmental variables' influence on catches could be accounted for in order to improve resource efficiency and economic viability.

Trading yield against precautionarity and the need for stability in the fishing sector

Værdioptimering af fiskefangsten i dansk blandet fiskeri (VærdiFisk) - forbedret kvalitet og selektion som følge af redskabsudvikling

Zooplankton mortality in 3D ecosystem modelling considering variable spatial–temporal fish consumptions in the North Sea

We tested the feasibility of imposing mesozooplankton mortality into a 3D model based on estimated consumption rates of the dominant planktivorous fish in the North Sea-Kattegat area. The spatial biomass distribution of Atlantic herring (Clupea
herring (Clupea harengus), horse mackerel (Trachurus trachurus), Atlantic mackerel (Scomber scombrus), sandeel (Ammodytidae) and European sprat (Sprattus sprattus) was derived from quarterly scientific trawl surveys and Danish commercial catches. Spatio-temporal indices of mortality were created based on the estimated biomasses and ingestion rates from the literature. The fish larvae grazing pressure was obtained from a spatial, size-based larval community model. In this model, larvae, herring and sandeel were the most important fish predators on mesozooplankton, but these groups had different spatial and temporal (seasonal) distributions. Fish larvae were particularly dominant in the eastern and southern areas in early summer. Herring and sandeel had the highest consumption in the central and north-western areas and were more important in late summer. The fish index changed the perceived annual, seasonal and spatial patterns in modelled mesozooplankton biomass, production and mortality. In the present study, the index was kept relatively simple and can be further developed with respect to the description of fish as well carnivorous zooplankton ingestion rates. The data input required to create the fish index is i) planktivorous fish stock biomasses and ii) relative fish spawning distribution information and iii) physics (ocean currents and temperatures) for the region and situation of interest. The fish index seems promising as a realistic mortality term for lower trophic levels in 3D ecosystem models in areas with available data on fish stocks to improve management of marine resources.
Scopus rating (2009): SJR 2.669 SNIP 1.829  
Web of Science (2009): Indexed yes  
BFI (2008): BFI-level 1  
Scopus rating (2008): SJR 2.065 SNIP 1.422  
Web of Science (2008): Indexed yes  
Scopus rating (2007): SJR 1.859 SNIP 1.503  
Web of Science (2007): Indexed yes  
Scopus rating (2006): SJR 1.551 SNIP 1.175  
Web of Science (2006): Indexed yes  
Scopus rating (2005): SJR 2.619 SNIP 1.839  
Web of Science (2005): Indexed yes  
Scopus rating (2004): SJR 2.526 SNIP 1.571  
Scopus rating (2003): SJR 2.523 SNIP 1.658  
Scopus rating (2002): SJR 2.168 SNIP 1.807  
Scopus rating (2001): SJR 2.389 SNIP 1.732  
Scopus rating (2000): SJR 1.924 SNIP 1.245  
Scopus rating (1999): SJR 2.094 SNIP 1.268  
Original language: English  
DOIs:  
10.1016/j.pocean.2014.03.002  
Publication: Research - peer-review › Journal article – Annual report year: 2014

Addressing challenges in single species assessments via a simple state-space assessment model.  
Single-species and age-structured fish stock assessments still remain the main tool for managing fish stocks. A simple state-space assessment model is presented as an alternative to (semi) deterministic procedures and the full parametric statistical catch at age models. It offers a solution to some of the key challenges of these models. Compared to the deterministic procedures it solves a list of problems originating from falsely assuming that age classified catches are known without errors and allows quantification of uncertainties of estimated quantities of interest. Compared to full parametric statistical catch at age models the state-space assessment model avoids the problem of fishing mortality being restricted to a parametric structure (e.g. multiplicative), and problems related to having a high number of model parameters compared to the number of observations. The main criticism of state-space assessment models is that they tend to be more conservative (react slower to changes) than the alternatives. A solution to this criticism is offered by introducing a mixture distribution for the transitions steps. The model presented is used for several commercially important stocks at the International Council for the Exploration of the Sea.

General information  
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources  
Authors: Nielsen, A. (Intern)  
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Event: Abstract from World conference on stock assessment methods, Boston, United States.  
Main Research Area: Technical/natural sciences  
Publication: Research › Conference abstract for conference – Annual report year: 2013

A genomic island linked to ecotype divergence in Atlantic cod  
The genomic architecture underlying ecological divergence and ecological speciation with gene flow is still largely unknown for most organisms. One central question is whether divergence is genome-wide or localized in ‘genomic mosaics’ during early stages when gene flow is still pronounced. Empirical work has so far been limited, and the relative impacts of gene flow and natural selection on genomic patterns have not been fully explored. Here, we use ecotypes of Atlantic cod to investigate genomic patterns of diversity and population differentiation in a natural system characterized by high gene flow and large effective population sizes, properties which theoretically could restrict divergence in local genomic regions. We identify a genomic region of strong population differentiation, extending over approximately 20 cM, between pairs of migratory and stationary ecotypes examined at two different localities. Furthermore, the region is characterized by markedly reduced levels of genetic diversity in migratory ecotype samples. The results highlight the genomic region, or ‘genomic island’, as potentially associated with ecological divergence and suggest the involvement of a selective sweep. Finally, we also confirm earlier findings of localized genomic differentiation in three other linkage groups associated with divergence among eastern Atlantic populations. Thus, although the underlying mechanisms are still unknown, the results suggest that ‘genomic mosaics’ of differentiation may even be found under high levels of gene flow and that marine fishes may provide insightful model systems for studying and identifying initial targets of selection during ecological divergence.
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BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.9 SJR 3.508 SNIP 1.651
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.862 SNIP 1.606 CiteScore 5.73
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.068 SNIP 1.705 CiteScore 5.36
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.469 SNIP 1.823 CiteScore 5.56
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.513 SNIP 1.915
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.455 SNIP 2.024
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.326 SNIP 2.086
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.937 SNIP 1.918
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.932 SNIP 2.111
Web of Science (2005): Indexed yes
A resource of genome-wide single-nucleotide polymorphisms generated by RAD tag sequencing in the critically endangered European eel

Reduced representation genome sequencing such as restriction-site-associated DNA (RAD) sequencing is finding increased use to identify and genotype large numbers of single-nucleotide polymorphisms (SNPs) in model and nonmodel species. We generated a unique resource of novel SNP markers for the European eel using the RAD sequencing approach that was simultaneously identified and scored in a genome-wide scan of 30 individuals. Whereas genomic resources are increasingly becoming available for this species, including the recent release of a draft genome, no genome-wide set of SNP markers was available until now. The generated SNPs were widely distributed across the eel genome, aligning to 4779 different contigs and 19703 different scaffolds. Significant variation was identified, with an average nucleotide diversity of 0.00529 across individuals. Results varied widely across the genome, ranging from 0.00048 to 0.00737 per locus. Based on the average nucleotide diversity across all loci, long-term effective population size was estimated to range between 132000 and 1320000, which is much higher than previous estimates based on microsatellite loci. The generated SNP resource consisting of 82425 loci and 376918 associated SNPs provides a valuable tool for future population genetics and genomics studies and allows for targeting specific genes and particularly interesting regions of the eel genome.
A stochastic length-based assessment model for the Pandalus stock in Skagerrak and the Norwegian Deep

This working document describes a length based stochastic assessment model of Pandalus in ICES areas IIIA and IVA. The model describing stock development is age based, but the model also estimates the relation between age and length assuming a von Bertalan growth curve. The model presented in this paper is based on the assessment data presented at the 2012 NIPAG meeting, but with updated survey information. Also the estimates shown here are based on equal standard deviations for survey and catch L = (c) L , which is the natural assumption, as this parameter describes the standard deviation of the length distribution in the population.

Can fisheries-induced evolution shift reference points for fisheries management?

Biological reference points are important tools for fisheries management. Reference points are not static, but may change when a population's environment or the population itself changes. Fisheries-induced evolution is one mechanism that can alter population characteristics, leading to "shifting" reference points by modifying the underlying biological processes or by changing the perception of a fishery system. The former causes changes in "true" reference points, whereas the latter is caused by changes in the yardsticks used to quantify a system's status. Unaccounted shifts of either kind imply that reference points gradually lose their intended meaning. This can lead to increased precaution, which is safe, but potentially costly. Shifts can also occur in more perilous directions, such that actual risks are greater than anticipated. Our qualitative analysis suggests that all commonly used reference points are susceptible to shifting through fisheries-induced evolution, including the limit and "precautionary" reference points for spawning-stock biomass, Blim and Bpa, and the target reference point for fishing mortality, F0.1. Our findings call for increased awareness of fisheries-induced changes and highlight the value of always basing reference points on adequately updated information, to capture all changes in the biological processes that drive fish population dynamics.
Can IBM’s tell us why some cod undertake vertical (feeding) migrations into hypoxic waters?

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources
Authors: Behrens, J. W. (Intern), Neuenfeldt, S. (Intern), Deurs, M. V. (Intern)
Publication date: 2013
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2013

Cod recovery as a new challenge for fisheries management: experience from the Baltic Sea

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, Institute Management
Authors: Eero, M. (Intern), Hüssy, K. (Intern), Mosegaard, H. (Intern), Hansen, J. H. (Intern), Bastardie, F. (Intern), Köster, F. (Intern)
Publication date: 2013
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2013

Dansk fiskeris udnyttelse af discardforbudet: En udredning

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Public Sector Consultancy, Section for Marine Living Resources, Institute Management, AquaMind
Authors: Larsen, E. (Intern), Dalskov, J. (Intern), Eg Nielsen, E. (Intern), Kirkegaard, E. (Intern), Nielsen, J. W. (Ekstern), Tørring, P. (Ekstern), Schou, M. (Ekstern)
Number of pages: 106
Publication date: 2013

Excess post hypoxic oxygen consumption in Atlantic cod (Gadus morhua)
Atlantic cod Gadus morhua experienced oxygen deficit (DO2) when exposed to oxygen levels below their critical level (c. 73% of pcrit) and subsequent excess post-hypoxic oxygen consumption (CEPHO) upon return to normoxic conditions, indicative of an oxygen debt. The mean±s.e. CEPHO:DO2 was 6·9±1·5, suggesting that resorting to anaerobic energy production in severe hypoxia is energetically expensive.
Exploring geovisualization symbology for landscape genetics
Landscape genetics, which considers genetic population structure in the context of spatially referenced parameters in the surrounding landscape, has been shown to be extremely useful for wildlife management. Unfortunately its widespread uptake beyond the research community is hampered due to a lack of effective communication of usable information in a suitable format for application by stakeholders such as wildlife regulators or managers. To improve the communication of suitable information, geovisualization of results should be facilitated in a comprehensible format for stakeholders without GIS or genetic expertise. While specialist applications exist, alternative accessible solutions do not provide adequate support for the visualization of multi-attribute spatially referenced genetic population structure information. As a solution, we document our exploration for an appropriate symbology to communicate landscape genetic information through an accessible, web-based interface. A full problem description, review of available technologies, development rationale, and discussion of the symbology exploration are provided.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, European Commission - Joint Research Center, Katholieke Universiteit, University of Bologna
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BFI (2014): BFI-level 2
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BFI (2013): BFI-level 2
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BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.474 SNIP 1.153 CiteScore 1.19
Genomic signatures distinguish ancient from recent selection in pink salmon (Oncorhynchus gorbuscha)

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Limborg, M. (Intern), Waples, R. K. (Ekstern), Seeb, J. E. (Ekstern), Seeb, L. W. (Ekstern)
Publication date: 2013
Event: Abstract from Evolution meeting, Little Cottonwood Canyon, United States.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2014

Greenland's first living deep-water coral reef

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State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Bedford Institute of Oceanography, University of Copenhagen
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Pages: 14-18
Publication date: 2013
Main Research Area: Technical/natural sciences

Grønlands første koralrev opdaget

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Natural History Museum of Denmark
Authors: Jørgensbye, H. Ø. (Intern), Tendal, O. S. (Forskerdatabase)
Pages: 38-39
Publication date: 2013
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Havvindmølleparker og deres indflydelse på fisk - et casestudy fra Horns Rev havvindmøllepark

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Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Department of Applied Mathematics and Computer Science, Dynamical Systems
Publication date: 2013
Event: Abstract from 17. Danske havforskermøde, Roskilde, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2013

Identification of seasonal migration, vertical activity and thermal experience of Greenland halibut Reinhardtius hippoglossoides (Walbaum) in west Greenland waters

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Ecosystem based Marine Management, Section for Marine Living Resources
Authors: Behrens, J. W. (Intern), Neuenfeldt, S. (Intern), Sparrevohn, C. R. (Intern), Eigaard, O. R. (Intern), Boje, J. (Intern)
Publication date: 2013
Event: Poster session presented at Society of Experimental Biology, Annual Main Meeting, Valencia, Spain.
Main Research Area: Technical/natural sciences
Publication: Research › Poster – Annual report year: 2013

Improved management based on stock identification of eastern and western Baltic cod
The objective of this project was to establish an empirically founded knowledge base for the sustainable exploitation of the western Baltic cod stock by including the complex stock structure and migration patterns.
Stock mapping: Extensive immigration of "Eastern" cod into the Arkona Basin (SD 24) within the "Western" cod's management unit was documented using high-powered genetic tools. The majority (91%) of all spawning fish caught in SD 24 in 2011 were "Eastern" cod and only 9% were from the "Western" stock. The results suggest that the stock structure in the Arkona Basin is highly influenced by mixing of genetically separate stocks.
Trends in mixing: Since the 1980’s where cod in SD 24 consisted primarily of "Western" type, the proportion of "Eastern" cod has increased, particularly since 2005. Throughout that period, the immigration of "Eastern" cod into SD 24 consisted
In-situ identification of marine organisms using high frequency, wideband ultrasound

Reliable remote fish identification would be an important improvement in resource management as well as in commercial fishing. Optical and acoustical methods could be used either in combination or separately. However, the acoustical methods have better detection ranges than any known optical methods. Conventional acoustical methods use frequencies in the range of 10 to 500 kHz and give reasonable estimations of size distribution, if the species is known, but can only significantly support the determination of the actual species, if there are only a few known species available. It is expected that higher frequencies and broader bandwidths than used until now will give more information useful for fish species identification.

The objective of this Ph.D. study has been to develop a method to investigate the possibility of in-situ identification of fish with high-frequency, wideband ultrasound. The approach was to build a 1 MHz wideband single-element transducer system to obtain range profiles of fish, and to do fish species identification by comparing measured range profiles with libraries of reference range profiles as it is done in some radar systems used to identify aircraft. To do this, it is also necessary to investigate the properties of ultrasound backscatter of fish in the MHz frequency range to help the interpretation of the range profiles. Three case studies were investigated in this Ph.D. study.

The first case study was to investigate the ultrasound backscatter of fish in the MHz frequency range using empirical methods. Measurements using a BK Medical ultrasound scanner equipped with a dedicated research interface were performed on a saithe (Pollachius virens) and three cods (Gadus morhua) at different frequencies as well as angles between the center line of the transducer beams and the fish bodies. The frequencies are 2, 3.5, and 6 MHz. The angles are -30°, -15°, 0°, 15°, and 30°. The results show that even though there are variations, a scan of the ultrasound backscatter along a fish of a specific species contains patterns that are characteristic for that species. This is true at all frequencies in the low MHz range. The part of a fish that contributes most is not necessarily the swimbladder as the results indicate that in the low MHz frequency range bone structures, and skin surfaces are more important.

The second case study was to develop a method to generate simulated ultrasound images from computed tomography images to build simulated ultrasound range profiles of fish. It can be observed from the first case study that shadow effects are normally pronounced in ultrasound images, so they should be included in the simulation. In this study, a method to capture the shadow effects has been developed, which makes the simulated ultrasound images appear more realistic. The method using a focused beam tracing model gives diffuse shadows that are similar to the ones observed in measurements on real objects.

The last case study was to do measurements of ultrasound range profiles of free-swimming fish using a 1 MHz wideband single-element transducer system. The portable system consists of a Reson TC3210 1 MHz single-element transducer, a
BlueView P900-2250 dual-frequency multi-beam sonar, and three Oregon ATC9K cameras on a fixture. The positions, orientations, and lengths of the fish were estimated by three-dimensional image analysis, while species were identified manually from the video sequences. Ex-situ experiments were performed on fish that have swimbladder (cod, European sea bass (Dicentrarchus labrax), gilthead sea bream (Sparus aurata), and Atlantic horse mackerel (Trachurus trachurus)) as well as on fish that do not have swimbladder (Atlantic mackerel (Scomber scombrus)). There are indications that the variations in the range profiles seem to have some unique details to discriminate between species like mackerel and sea bream. In some cases the range profiles also indicate whether the head or the tail is closest to the transducer. It has also been shown that the surface areas of the fish are the most important elements that decide how much energy is backscattered in the low MHz frequency range.

In conclusion, the ultrasound backscatter from fish in the MHz frequency range was investigated empirically as well as by simulation and the 1 MHz wideband single-element transducer system was developed. The results data from the ex-situ experiments in a large aquarium tank presented in the last case study can be considered comparable to data obtained in in-situ experiments in a calm shallow sea area. The single-element transducer system can therefore be considered ready for preliminary in-situ experiments. Hereby the main objectives of the Ph.D. study have been reached.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Department of Electrical Engineering, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Biomedical Engineering, Center for Fast Ultrasound Imaging
Authors: Pham, A. H. (Intern), Lundgren, B. (Intern), Stage, B. (Intern), Jensen, J. A. (Intern)
Number of pages: 171
Publication date: 2013
Localisation of nursery areas based on comparative analyses of the horizontal and vertical distribution patterns of juvenile Baltic cod (Gadus morhua)

Knowledge of the spatial distribution of juvenile cod is essential for obtaining precise recruitment data to conduct sustainable management of the eastern and western Baltic cod stocks. In this study, the horizontal and vertical distribution and density patterns of settled juvenile 0- and 1-group Baltic cod are determined, and their nursery areas are localised according to the environmental factors affecting them. Comparative statistical analyses of biological, hydrographic and hydroacoustic data are carried out based on standard ICES demersal trawl surveys and special integrated trawl and acoustic research surveys. Horizontal distribution maps for the 2001–2010 cohorts of juvenile cod are further generated by applying a statistical log-Gaussian Cox process model to the standard trawl survey data. The analyses indicate size-dependent horizontal and distinct vertical and diurnal distribution patterns related to the seabed topography, water layer depth, and the presence of hydrographic frontal zones (pycnoclines) as well as intraspecific patterns in relation to the presence of adult cod. The extent of the nursery areas also depends on the cod year class strength. Juvenile cod (≥3 cm) are present in all areas of the central Baltic Sea (CBS), showing broad dispersal. However, their highest density in the Baltic Basins is found at localities with a 40–70 m bottom depth in waters with oxygen concentrations above 2 ml O2.l−1 and temperatures above 5°C. The smallest juveniles are also found in deep sea localities down to a 100 m depth and at oxygen concentrations between 2–4 ml O2.l−1. The vertical, diurnally stratified and repeated trawling and hydroacoustic target strength-depth distributions obtained from the special surveys show juvenile cod concentrations in frontal zone water layers (pycnocline). However, the analyses indicate that in the CBS, juvenile cod of all sizes do not appear to aggregate in dense schooling patterns, which differs from what has been reported from the North Sea.
Marine climate change research in Nordic regions: recent trends and current state

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, National Institute of Aquatic Resources, Centre for Ocean Life, Section for Marine Ecology and Oceanography, Section for Marine Living Resources
Microevolution in time and space: SNP analysis of historical DNA reveals dynamic signatures of selection in Atlantic cod

Little is known about how quickly natural populations adapt to changes in their environment and how temporal and spatial variation in selection pressures interact to shape patterns of genetic diversity. We here address these issues with a series of genome scans in four overfished populations of Atlantic cod (Gadus morhua) studied over an 80-year period. Screening of >1000 gene-associated single-nucleotide polymorphisms (SNPs) identified 77 loci that showed highly elevated levels of differentiation, likely as an effect of directional selection, in either time, space or both. Exploratory analysis suggested that temporal allele frequency shifts at certain loci may correlate with local temperature variation and with life history changes suggested to be fisheries induced. Interestingly, however, largely nonoverlapping sets of loci were temporal outliers in the different populations and outliers from the 1928 to 1960 period showed almost complete stability during later decades. The contrasting microevolutionary trajectories among populations resulted in sequential shifts in spatial outliers, with no locus maintaining elevated spatial differentiation throughout the study period. Simulations of migration coupled with observations of temporally stable spatial structure at neutral loci suggest that population replacement or gene flow alone could not explain all the observed allele frequency variation. Thus, the genetic changes are likely to at least partly be driven by highly dynamic temporally and spatially varying selection. These findings have important implications for our understanding of local adaptation and evolutionary potential in high gene flow organisms and underscore the need to carefully consider all dimensions of biocomplexity for evolutionarily sustainable management.
Patchy zooplankton grazing and high energy conversion efficiency: ecological implications of sandeel behavior and strategy

Sandeel display strong site-fidelity, and spend most of their life buried in the seabed. This strategy carries important ecological implications. Sandeels save energy when they are not foraging but in return are unable to move substantially and therefore possibly are sensitive to local depletion of prey. Here we studied zooplankton consumption and energy conversion efficiency of lesser sandeel (Ammodytes marinus) in the central North Sea, using stomach data, length and weight-at-age data, bioenergetics, and hydrodynamic modeling. The results suggested: (i) Lesser sandeel in the Dogger area depend largely on relatively large copepods in early spring. (ii) Lesser sandeel is an efficient converter making secondary production into fish tissue available for higher trophic levels. Hence, changes in species composition towards a more herring dominated system, as seen in recent times, may lead to a decrease in system transfer efficiency. (iii) Sandeels leave footprints in the standing copepod biomass as far as 100 km from the edge of their habitat, but smaller and more isolated sandeel habitat patches have a much lower impact than larger patches, suggesting that smaller habitats can sustain higher sandeel densities and growth rates per area than larger habitats.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management
Authors: Deurs, M. V. (Intern), Christensen, A. (Intern), Rindorf, A. (Intern)
Pages: 123-133
Population structure of Atlantic Mackerel (Scomber scombrus)

Atlantic mackerel (Scomber scombrus) occurs on both sides of the north Atlantic and has traditionally been grouped into 5 spawning components, some of which were thought to be isolated natal homing stocks. Previous studies have provided no evidence for cross Atlantic migration and no or weak support for isolated spawning components within either side of the North Atlantic. We question the de-facto accepted hypothesis of isolation between spawning components on the basis of spawning and age distribution data. The spawning intensities, proxied by larval abundances, are negatively correlated between the North Sea and Celtic Sea, which indicates that the two spawning components may be connected by straying individuals. This finding is based on unique larvae samples collected before the collapse of North Sea component, thus showing that the exchange is not a recent phenomenon due to the collapse. The analyses of old as well as more recent age distributions show that strong year classes spread into other areas where they spawn as adults ("twinning"). Our findings are in accordance with the lack of solid evidence for stock separation from previous analyses of tagging data, genetics, ectoparasite infections, otolith shapes, and blood phenotypes. Because no method has been able to identify the origin of spawning mackerel unequivocally from any of the traditional spawning components, and in the light of our results, we conclude that straying outweighs spatial segregation. We propose a new model where the population structure of mackerel is described as a dynamic cline, rather than as connected contingents. Temporal changes in hydrography and mackerel behavior may affect the steepness of the cline at various locations. The new interpretation of the population structure of Atlantic mackerel has important implications for research, assessment and management.
Recruitment decline in North Sea herring is accompanied by reduced larval growth rates

The stock of North Sea autumn spawning herring (Clupea harengus L.) has shown an unprecedented sequence of ten years of sharply reduced recruitment, in spite of a high spawning biomass. Recent work has identified this below-expected recruitment as being determined during the larval phase; however, the underlying mechanism remains elusive. In this study we analysed archived larval samples captured before and after the onset of the reduced survival to test the hypothesis of a concurrent change in the larval growth rate. Individual larval growth rates, averaged over the 21 days prior to capture, were estimated for two hundred larvae from four different years using a model-based analysis of the otolith ring-widths. Hydrographic-backtracking models complemented the otolith analysis by reconstructing the environmental history and spawning origin of each larva. A significant reduction in net larval growth rate of 8%, concurrent with the reduced larval survival and recruitment, was identified: after correcting for the effect of other explanatory variables (e.g. temperature changes), the gross reduction was found to be 12%. This reduction is most probably due to changes in either the amount or quality of available food. The study demonstrates the potential in coupling of two different techniques, the otolith microstructure analysis and the hydrographic modelling, for affording new insights into fish early-life history. Finally, the study provides a novel indication of the association between reduced growth and larvae survival, thereby narrowing the range of potential mechanisms underlying the observed reduction in the recruitment of North Sea autumn spawning herring.
In the present study the genetic variability of European sardine from Adriatic and Ionian seas was investigated in order to detect the occurrence of genetic structure within and between these basins. In several samples the analysis of genetic variability at eight microsatellite loci showed a number of homozygote individuals higher than expected at Hardy-Weinberg equilibrium. The inter-population differentiation level estimated by AMOVA, qST and rRST and Bayesian descriptors detected no signs of population differentiation between the samples analysed. These results are consistent with previous studies based on allozymes and several mitochondrial DNA markers and add further evidence contradicting the early identification, based on morphological and reproductive data, of two sub-populations in the Adriatic Sea.
Size-based estimation of the status of fish stocks: simulation analysis and comparison with age-based estimations

Estimation of the status of fish stocks is important for sustainable management. Data limitations and data quality hinder this task. The commonly used age-based approaches require information about individual age, which is costly and relatively inaccurate. In contrast, the size of organisms is linked to physiology more directly than is age, and can be measured easier with less cost. In this work we used a single-species size-based model to estimate the fishing mortality (F) and the status of the stock, quantified by the ratio F/Fmsy between actual fishing mortality and the fishing mortality which leads to the maximum sustainable yield. A simulation analysis was done to investigate the sensitivity of the estimation and its improvement when stock specific life history information is available. To evaluate our approach with real observations, data-rich fish stocks, like the North Sea cod, were investigated and our estimations were compared to the ICES advice. Only size-specific catch data were used, in order to emulate data limited situations. The simulation analysis reveals that the status of the stock, i.e. F/Fmsy, is estimated more accurately than the fishing mortality F itself. Specific knowledge of the natural mortality improves the estimation more than having information about all other life history parameters. Our approach gives, at least qualitatively, an estimated stock status which is similar to the results of an age-based assessment. Since our approach only uses size-based catch data, it is a suitable tool for data-limited situations.

Spatial segregation within the spawning migration of North Eastern Atlantic mackerel (Scomber scombrus) as indicated by juvenile growth patterns

A comparison of growth data (fish length) with latitude shows that southern juvenile mackerel attain a greater length than those originating from further north before growth ceases during their first winter. A similar significant relationship was found between the growth in the first year (derived from the otolith inner winter ring) and latitude for adult mackerel spawning between 44°N (Bay of Biscay) and 54°N (west of Ireland). These observations are consistent with spatial segregation of the spawning migration; the further north that the fish were hatched, the further north they will tend to spawn. No such relationship was found in mackerel spawning at more northerly latitudes, possibly as a consequence of increased spatial mixing in a more energetic regime with stronger currents. This study provides previously lacking support for spawning segregation behaviour among North East Atlantic mackerel – an important step towards understanding the migratory behaviour of mackerel and hence the spatiotemporal distribution dynamics around spawning time.
Spatial segregation within the spawning migration of North Eastern Atlantic mackerel (Scomber scombrus) as indicated by juvenile growth patterns
Spatiotemporal SNP analysis reveals cryptic distribution shifts and signs of ongoing adaptation at the northern range margin for Atlantic cod

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Publication date: 2013
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Main Research Area: Technical/natural sciences

Relations
Activities:

Spatiotemporal distribution and composition of mixed stock fishery of Atlantic cod (Gadus morhua) in West Greenlandic waters based on retrospective genetic analysis

Historical samples of fish are a unique source of DNA to investigate the temporal dynamics of fish population structure and distribution over time. During the last century Atlantic cod (Gadus morhua) stocks have declined dramatically in Greenlandic Waters. Recent genetic investigations have identified the presence of four genetically distinct spawning groups in the area. We used SNP (Single Nucleotide Polymorphism) analysis of DNA from archived historical cod otoliths (1946-2011) to conduct a retrospective spatiotemporal genetic analysis. The aim was to detect historical changes in the contribution from the different spawning groups in population mixtures of cod in West Greenland Waters in response to climate variability and fisheries. Performing genetic assignment test, we found stable genetic composition of feeding aggregations over decades in some areas, whereas shifts in composition were evident in others. Our findings are consistent with previous results demonstrating that the distribution of different spawning components has changed over time. We discuss how these results will allow a better prediction of future population structure and abundance of cod in a changing environment as in Greenlandic Waters and thus lead to more robust management plans

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Biologisk institut
Authors: Bonanomi, S. (Intern), Therkildsen, N. O. (Intern), Hedeholm, R. B. (Forskerdatabase), Retzel, A. (Ekstern), Eg Nielsen, E. (Intern)
Publication date: 2013
Event: Abstract from ICES Conference and NorMER Annual Meeting, Reykjavik, Iceland.
Main Research Area: Technical/natural sciences

Relations
Activities:

Spatiotemporal SNP analysis reveals pronounced biocomplexity at the northern range margin of Atlantic cod Gadus morhua

Accurate prediction of species distribution shifts in the face of climate change requires a sound understanding of population diversity and local adaptations. Previous modeling has suggested that global warming will lead to increased abundance of Atlantic cod (Gadus morhua) in the ocean around Greenland, but the dynamics of earlier abundance fluctuations are not well understood. We applied a retrospective spatiotemporal population genomics approach to examine the temporal stability of cod population structure in this region and to search for signatures of divergent selection over a 78-year period spanning major demographic changes. Analyzing >900 gene-associated single nucleotide polymorphisms in 847 individuals, we identified four genetically distinct groups that exhibited varying spatial distributions with considerable overlap and mixture. The genetic composition had remained stable over decades at some spawning grounds, whereas complete population replacement was evident at others. Observations of elevated differentiation in certain genomic regions are consistent with adaptive divergence between the groups, indicating that they may respond differently to environmental variation. Significantly increased temporal changes at a subset of loci also suggest that adaptation may be ongoing. These findings illustrate the power of spatiotemporal population genomics for revealing biocomplexity in both space and time and for informing future fisheries management and conservation efforts
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Web of Science (2014): Indexed yes
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ISI indexed (2012): ISI indexed yes
Scopus rating (2011): SJR 2.427 SNIP 1.216 CiteScore 4.5
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Scopus rating (2009): SJR 1.241 SNIP 0.87
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Relations
Activities:
Populationsgenetiske undersøgelser af torsk fra Vestgrønland
Publication: Research - peer-review › Journal article – Annual report year: 2013
Statistical aspects of fish stock assessment

Fish stock assessments are conducted for two main purposes: 1) To estimate past and present fish abundances and their commercial exploitation rates. 2) To predict the consequences of different management strategies in order to ensure a sustainable fishery in the future.

This thesis concerns statistical aspects of fish stocks assessment, which includes topics such as time series analysis, generalized additive models (GAMs), and non-linear state-space/mixed models capable of handling missing data and a high number of latent states and parameters. The aim is to improve the existing methods for stock assessment by application of state-of-the-art statistical methodology. The main contributions are presented in the form of six research papers.

The major part of the thesis deals with age-structured assessment models, which is the most common approach. Conversion from length to age distributions in the catches is a necessary step in age-based stock assessment models. For this purpose, GAMs and continuation ratio logits are combined to model the probability of age as a smooth function of length and spatial coordinates, which constitutes an improvement over traditional methods based on area-stratification. GAMs and delta-distributions are applied for the calculation of indices of abundance from trawl survey data, and different error structures for these are investigated.

Two extensions to the state-space approach to age-structured stock assessment modelling are presented. The first extension introduces multivariate error distributions on survey catch-at-age data. The second extension is an integrated assessment model for overlapping sub-stocks subject to joint exploitation in the area of overlap. Estimation and inference is carried out using maximum likelihood.

Finally, a biomass dynamic model based on stochastic differential equations is presented. This work extends the classical approaches to biomass modelling by incorporating observation errors on the catches, and allowing for missing and non-equidistant samples in time.

General information

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Organisations: Department of Applied Mathematics and Computer Science, Dynamical Systems, National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources
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Publication date: 2013

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Strategies for fitting nonlinear ecological models in R, AD Model Builder, and BUGS

Ecologists often use nonlinear fitting techniques to estimate the parameters of complex ecological models, with attendant frustration. This paper compares three open-source model fitting tools and discusses general strategies for defining and fitting models. R is convenient and (relatively) easy to learn, AD Model Builder is fast and robust but comes with a steep learning curve, while BUGS provides the greatest flexibility at the price of speed. Our model-fitting suggestions range from general cultural advice (where possible, use the tools and models that are most common in your subfield) to specific suggestions about how to change the mathematical description of models to make them more amenable to parameter estimation. A companion web site (https://groups.nceas.ucsb.edu/nonlinear-modeling/projects) presents detailed examples of application of the three tools to a variety of typical ecological estimation problems; each example links both to a detailed project report and to full source code and data.

General information

State: Published
Organisations: Department of Applied Mathematics and Computer Science, Dynamical Systems, National Institute of Aquatic Resources, Section for Marine Living Resources, McMaster University, USGS Patuxent Wildlife Research Center, Inter-American Tropical Tuna Commission, University of Florida, National Center for Ecological Analysis and Synthesis, Harvard University, French National Centre for Scientific Research, Dalhousie University, University of California at
The proportion of Atlantic cod (Gadus morhua) discarded in the Danish Baltic Sea cod trawl fishery has been as high as 40%. This, combined with a stock that has declined dramatically over the past 30 years, has led to numerous technical regulations being introduced to reduce the capture of juveniles and thus discards. One method that has been widely adopted in the Baltic Sea has been to improve gear selectivity, subsequently allowing young individuals to escape capture. To understand the effects that changes to gear selectivity and minimum landing size have had on discard rates, as well as the effects of a range of additional explanatory factors, generalized additive mixed models were used. Gear regulation changes enforced in the Danish demersal trawl fishery in the Baltic Sea and other factors, such as minimum landings size, juvenile abundance, catch mass, price, and their spatial and temporal distribution, were found to significantly affect discard rates. The newest and currently legislated gears were identified as having the lowest discard rates. The increase in minimum landing size from 35 to 38 cm has increased discard rates.
Tissue specific haemoglobin gene expression suggests adaptation to local marine conditions in North Sea flounder (*Platichthys flesus L.)*

Recent genetic analyses of candidate genes and gene expression in marine fishes have provided evidence of local adaptation in response to environmental differences, despite the lack of strong signals of population structure from conventional neutral genetic markers. In this study expression of the haemoglobin alpha and beta subunit genes was studied in reciprocally transplanted European flounder *Platichthys flesus* from the highly saline North Sea and the brackish Baltic Sea. Clear differences in expression patterns of haemoglobin alpha and beta subunit genes were found among different types of tissue in flounder. In gill tissue a plastic response to salinity treatments was observed with general up-regulation of these genes concomitant with higher salinity. For liver tissue a population specific expression differences was observed with lower expression at simulated non-native compared to native salinities. Finally, for kidney tissue a stress response was observed in one population, with gene up-regulation when North Sea flounders were transplanted to low salinity. This study underlines the importance of tissue specific gene expression and the significance of gene expression for evolution of local adaptation in high gene flow marine fishes. © 2013 The Genetics Society of Korea
Towards an integrated forecasting system for fisheries on habitat-bound stocks

First results of a coupled modelling and forecasting system for fisheries on habitat-bound stocks are being presented. The system consists currently of three mathematically, fundamentally different model subsystems coupled offline: POLCOMS providing the physical environment implemented in the domain of the north-west European shelf, the SPAM model which describes sandeel stocks in the North Sea, and the third component, the SLAM model, which connects POLCOMS and SPAM by computing the physical–biological interaction. Our major experience by the coupling model subsystems is that well-defined and generic model interfaces are very important for a successful and extendable coupled model framework. The integrated approach, simulating ecosystem dynamics from physics to fish, allows for analysis of the pathways in the ecosystem to investigate the propagation of changes in the ocean climate and to quantify the impacts on the higher trophic level, in this case the sandeel population, demonstrated here on the basis of hindcast data. The coupled forecasting system is tested for some typical scientific questions appearing in spatial fish stock management and marine spatial planning, including determination of local and basin-scale maximum sustainable yield, stock connectivity and source/sink structure. Our presented simulations indicate that sandeel stocks are currently exploited close to the maximum sustainable yield, even though periodic overfishing seems to have occurred, but large uncertainty is associated with determining stock maximum sustainable yield due to stock inherent dynamics and climatic variability. Our statistical ensemble simulations indicates that the predictive horizon set by climate interannual variability is 2–6 yr, after which only an asymptotic probability distribution of stock properties, like biomass, are predictable.
Udvikling af effektivt og skånsomt redskab til tobisfiskeri på Dogger Banke
Variability and connectivity of plaice populations from the Eastern North Sea to the Western Baltic Sea, and implications for assessment and management

An essential prerequisite of sustainable fisheries is the match between biologically relevant processes and management action. Various populations may however co-occur on fishing grounds, although they might not belong to the same stock, leading to poor performance of stock assessment and management. Plaice in Kattegat and Skagerrak have traditionally been considered as one stock unit. Current understanding indicates that several plaice components may exist in the transition area between the North Sea and the Baltic Sea. A comprehensive review of all available biological knowledge on plaice in this area is performed, including published and unpublished literature together with the analyses of commercial and survey data and historical tagging data. The results suggest that plaice in Skagerrak is closely associated with plaice in the North Sea, although local populations are present in the area. Plaice in Kattegat, the Belts Sea and the Sound can be considered a stock unit, as is plaice in the Baltic Sea. The analyses revealed great heterogeneity in the dynamics and productivity of the various local components, and suggested for specific action to maintain biodiversity.
Retrospective genomic analysis of Atlantic cod in Greenlandic Waters

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Bonanomi, S. (Intern), Therkildsen, N. O. (Intern), Eg Nielsen, E. (Intern)
Publication date: 2012
Main Research Area: Technical/natural sciences

SNPs: windows into demography, evolutionary history, and adaptation

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State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Limborg, M. (Intern)
Publication date: 2012
Event: Abstract from Annual Conference of the Wildlife Society, Portland, OR, United States.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2014

The use of archived tags in retrospective genetic analysis of fish

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Biologisk institut
Authors: Bonanomi, S. (Intern), Therkildsen, N. O. (Intern), Hedeholm, R. B. (Forskerdatabase), Eg Nielsen, E. (Intern)
Publication date: 2012
Event: Poster session presented at NorMER Annual Meeting 2012, Helsinki, Finland.
Main Research Area: Technical/natural sciences

Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges
Recent improvements in the speed, cost and accuracy of next generation sequencing are revolutionizing the discovery of single nucleotide polymorphisms (SNPs). SNPs are increasingly being used as an addition to the molecular ecology toolkit in nonmodel organisms, but their efficient use remains challenging. Here, we discuss common issues when employing SNP markers, including the high numbers of markers typically employed, the effects of ascertainment bias and the inclusion of nonneutral loci in a marker panel. We provide a critique of considerations specifically associated with the application and population genetic analysis of SNPs in nonmodel taxa, focusing specifically on some of the most commonly applied methods.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Marine Living Resources, Royal Zoological Society of Scotland, University of Bologna, Katholieke Universiteit, Bangor University
Genomic approaches of adaptation of marine organisms in changing environments: what can populations tell us about genes underlying phenotypic changes and what can genes tell us about adaptive evolution of populations?

**General information**
- **State:** Published
- **Organisations:** National Institute of Aquatic Resources, Section for Marine Living Resources, Institute for Agricultural and Fisheries Research, Radiological Protection Institute of Ireland
- **Authors:** Boudry, P. (Ekstern), Limborg, M. (Intern), Robbens, J. (Ekstern), van Wijk, S. (Ekstern), Pascoal, S. (Ekstern), Prodohl, P. (Ekstern), McGinnity, P. (Ekstern), Volkaert, F. (Ekstern)
- **Pages:** 64-73
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- **Publisher:** International Council for the Exploration of the Sea (ICES)
- **Main Research Area:** Technical/natural sciences

**Historical changes in population distribution and micro-evolution in response to climate variability: Retrospective genomic analysis of archived fish tissue collection**

**General information**
- **State:** Published
- **Organisations:** National Institute of Aquatic Resources, Section for Marine Living Resources
- **Authors:** Bonanomi, S. (Intern), Hansen, J. H. (Intern), Eg Nielsen, E. (Intern)
- **Publication date:** 2011
- **Event:** Abstract from NorMER Annual Meeting 2011, Oslo, Norway.
- **Main Research Area:** Technical/natural sciences

**Relations**
- **Activities:** Populationsgenetiske undersøgelser af torsk fra Vestgrønland
- **Publication:** Research › Conference abstract for conference – Annual report year: 2011

**Populationsstruktur hos små pelagiske fisk i et heterogent marint miljø viden fra – og anvendelse af genetiske metoder**

**General information**
- **State:** Published
- **Organisations:** National Institute of Aquatic Resources, Section for Marine Living Resources
- **Authors:** Limborg, M. (Intern), Bekkevold, D. (Intern)
- **Publication date:** 2011
- **Event:** Abstract from 16. Dansk Havforskermøde, Knebel, Denmark.
- **Main Research Area:** Technical/natural sciences
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**Managing fleets and fisheries rather than single stocks – conceptual change in European fisheries management advice**

**General information**
- **State:** Published
- **Organisations:** National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources
- **Authors:** Nielsen, J. R. (Intern), Limborg, M. (Intern)
- **Pages:** 8-9
- **Publication date:** 2009
- **Main Research Area:** Technical/natural sciences
Improved advice for the mixed herring stocks in the Skagerrak and Kattegat: EU Rolling Programme; FISH/2004/03

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management, Institute of Marine Research
Authors: Worsøe Clausen, L. (Intern), Ulrich, C. (Intern), Deurs, M. V. (Intern), Skagen, D. (Ekstern)
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