Spatial models for probabilistic prediction of wind power with application to annual-average and high temporal resolution data

Producing accurate spatial predictions for wind power generation together with a quantification of uncertainties is required to plan and design optimal networks of wind farms. Toward this aim, we propose spatial models for predicting wind power generation at two different time scales: for annual average wind power generation, and for a high temporal resolution (typically wind power averages over 15-min time steps). In both cases, we use a spatial hierarchical statistical model in which spatial correlation is captured by a latent Gaussian field. We explore how such models can be handled with stochastic partial differential approximations of Matérn Gaussian fields together with Integrated Nested Laplace Approximations. We demonstrate the proposed methods on wind farm data from Western Denmark, and compare the results to those obtained with standard geostatistical methods. The results show that our method makes it possible to obtain fast and accurate predictions from posterior marginals for wind power generation. The proposed method is applicable in scientific areas as diverse as climatology, environmental sciences, earth sciences and epidemiology.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, Department of Electrical Engineering, Center for Electric Power and Energy, Energy Analytics and Markets
Authors: Lenzi, A. (Intern), Pinson, P. (Intern), Clemmensen, L. K. H. (Intern), Guillot, G. (Intern)
Number of pages: 17
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Stochastic Environmental Research and Risk Assessment
ISSN (Print): 1436-3240
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 2.54 SJR 1.149 SNIP 1.381
Web of Science (2016): Indexed yes
Accurate continuous geographic assignment from low- to high-density SNP data

Motivation: Large-scale genotype datasets can help tracking the dispersal patterns of epidemiological outbreaks and predicting the geographic origins of individuals. This shows direct applications in forensics for profiling both victims and criminals, and in wildlife management, where poaching hotspot areas can be located. Such approaches, however, require fast and accurate geographical assignment methods.

Results: We introduce a novel statistical method for geopositioning individuals of unknown origin from genotypes. Our method is based on a geostatistical model trained with a dataset of georeferenced genotypes. Statistical inference under this model can be implemented within the theoretical framework of Integrated Nested Laplace Approximation (INLA), which represents one of the major recent breakthroughs in statistics, devoid of Monte Carlo simulations. We compare the performance of our method and SPA in a simulation framework. We highlight the accuracy and limits of continuous spatial assignment methods at various scales by analyzing genotype datasets from a diversity of species, including Florida scrub
jay birds Aphelocoma coerulescens, Arabidopsis thaliana and humans, representing 41 to 197,146 SNPs. Our method appears to be best tailored for the analysis of medium-size datasets (a few tens of thousands of loci), such as reduced-representation sequencing data that become increasingly available in ecology.

**General information**

State: Published

Organisations: Department of Applied Mathematics and Computer Science, Cognitive Systems, Natural History Museum of Denmark, Technical University of Denmark, University of Copenhagen

Authors: Guillot, G. (Intern), Jónsson, H. (Ekstern), Hinge, A. (Ekstern), Manchih, N. (Ekstern), Orlando, L. (Ekstern)

Pages: 1106-1108

Publication date: 2016

Main Research Area: Technical/natural sciences

**Publication information**

Journal: Bioinformatics

Volume: 32

Issue number: 7

ISSN (Print): 1367-4803

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 6.42

Web of Science (2016): Indexed yes

BFI (2015): BFI-level 2

Scopus rating (2015): CiteScore 6.06

Web of Science (2015): Indexed yes

BFI (2014): BFI-level 2

Scopus rating (2014): CiteScore 5.5

Web of Science (2014): Indexed yes

BFI (2013): BFI-level 2

Scopus rating (2013): CiteScore 5.78

ISI indexed (2013): ISI indexed yes

Web of Science (2013): Indexed yes

BFI (2012): BFI-level 2

Scopus rating (2012): CiteScore 6.73

ISI indexed (2012): ISI indexed yes

Web of Science (2012): Indexed yes

BFI (2011): BFI-level 2

Scopus rating (2011): CiteScore 5.61

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
A genomewide catalogue of single nucleotide polymorphisms in white-beaked and Atlantic white-sided dolphins

The field of population genetics is rapidly moving into population genomics as the quantity of data generated by high-throughput sequencing platforms increases. In this study, we used restriction-site-associated DNA sequencing (RADSeq) to recover genomewide genotypes from 70 white-beaked (Lagenorhynchus albirostris) and 43 Atlantic white-sided dolphins (L. acutus) gathered throughout their north-east Atlantic distribution range. Both species are at a high risk of being negatively affected by climate change. Here, we provide a resource of 38 240 RAD-tags and 52 981 nuclear SNPs shared between both species. We have estimated overall higher levels of nucleotide diversity in white-sided (π = 0.0492 ± 0.0006%) than in white-beaked dolphins (π = 0.0300 ± 0.0004%). White-sided dolphins sampled in the Faroe Islands, belonging to two pods (N = 7 and N = 11), showed similar levels of diversity (π = 0.0317 ± 0.0007% and 0.0267 ± 0.0006%, respectively) compared to unrelated individuals of the same species sampled elsewhere (e.g. π = 0.0285 ± 0.0007% for 11 Scottish individuals). No evidence of higher levels of kinship within pods can be derived from our analyses. When identifying the most likely number of genetic clusters among our sample set, we obtained an estimate of two to four clusters, corresponding to both species and possibly, two further clusters within each species. A higher diversity and lower population structuring was encountered in white-sided dolphins from the north-east Atlantic, in line with their preference for pelagic waters, as opposed to white-beaked dolphins that have a more patchy distribution, mainly across continental shelves.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Cognitive Systems, University of Copenhagen, SAC Veterinary Services, Marine Research Institute, University of Veterinary Medicine Hannover, Fisheries and Maritime Museum, Institute of Marine Research, Irish Whale and Dolphin Group, University College Cork, Université de La Rochelle, King Saud University, Natural History Museum
Pages: 266-276
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology Resources
Volume: 16
Issue number: 1
ISSN (Print): 1755-098X
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 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
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.842 SNIP 2.217 CiteScore 5.04
Web of Science (2014): Indexed yes
A Spatial Model for the Instantaneous Estimation of Wind Power at a Large Number of Unobserved Sites

We propose a hierarchical Bayesian spatial model to obtain predictive densities of wind power at a set of un-monitored locations. The model consists of a mixture of Gamma density for the non-zero values and degenerated distributions at zero. The spatial dependence is described through a common Gaussian random field with a Matérn covariance. For inference and prediction, we use the GMRF-SPDE approximation implemented in the R-INLA package. We showcase the method outlined here on data for 336 wind farms located in Denmark. We test the predictions derived from our method with model-diagnostic tools and show that it is calibrated.
Enhanced computational methods for quantifying the effect of geographic and environmental isolation on genetic differentiation

Motivation: In a recent paper, Bradburd et al. [2013] proposed a model to quantify the relative effect of geographic and environmental distance on genetic differentiation. Here, we enhance this method in several ways.

Results: (i) We modify the covariance model so as to fit better with mainstream geostatistical models and avoid mathematically ill-behaved covariance functions, (ii) we extend the model - initially implemented only for co-dominant biallelic markers such as SNPs - to encompass highly polymorphic markers such as microsatellites, (iii) we implement and test a model selection procedure that allows users to assess which model (e.g. with or without an environment effect) is most suited, (iv) we extend the program to handle several environmental variables jointly, (v) we code all our MCMC algorithms in a mix of compiled languages which allows us to decrease computing time by at least one order of magnitude, (vi) we propose an approximate inference and model selection method allowing to deal with a large number of loci. We also illustrate the potential of the method by re-analyzing three datasets relative to harbour porpoises in Europe, coyotes in California and herrings in the Baltic Sea.

Availability: The computer program developed here is freely available as an R package called SUNDER. It takes as input geo-referenced allele counts at the individual or population level for codominant markers. Program home page: www2.imm.dtu.dk/~gigu/Sunder

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Cognitive Systems, University of Copenhagen, Technical University of Denmark, University of Groningen
Authors: Botta, F. (Intern), Eriksen, C. (Ekstern), Fontaine, M. C. (Ekstern), Guillot, G. (Intern)
Number of pages: 7
Pages: 1270-1277
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Methods in Ecology and Evolution
Volume: 6
Issue number: 11
ISSN (Print): 2041-210X
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 7.28 SJR 4.733 SNIP 2.621
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 5.382 SNIP 2.842 CiteScore 7.61
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
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 3.011 SNIP 2.427 CiteScore 5.34
Enhanced computational methods for quantifying the effect of geographic and environmental isolation on genetic differentiation

1. In a recent paper, Bradburd et al. (Evolution, 67, 2013, 3258) proposed a model to quantify the relative effect of geographic and environmental distance on genetic differentiation. Here, we enhance this method in several ways.

2. We modify the covariance model so as to fit better with mainstream geostatistical models and avoid mathematically ill-behaved covariance functions. We extend the model – initially implemented only for co-dominant bi-allelic markers such as single nucleotide polymorphisms – to encompass highly polymorphic markers such as microsatellites. We implement and test a model selection procedure that allows users to assess which model (e.g. with or without an environment effect) is most suited. We code all our MCMC algorithms in a mix of compiled languages which allows us to decrease computing time by at least one order of magnitude. We propose an approximate inference and model selection method allowing us to deal with genomic data sets (several hundred thousands loci).

3. We also illustrate the potential of the method by re-analysing three data sets, namely harbour porpoises in Europe, coyotes in California and herrings in the Baltic Sea.

4. The computer program developed here is freely available as an R package called sunder. It takes as input georeferenced allele counts at the individual or population level for co-dominant markers. Program homepage: http://www2.imm.dtu.dk/~gigu/Sunder/.
Patterns of trawling exploitation and the occurrence of hypoxia in the Baltic Sea

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Cognitive Systems, Swedish University of Agricultural Sciences
Authors: Bartolino, V. (Ekstern), Guillot, G. (Intern)
Number of pages: 9
Publication date: 2015

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Bibliographical note
This is a CONFIDENTIAL research report
Source: PublicationPreSubmission
Source-ID: 112873401
Publication: Research › Report – Annual report year: 2015

Variation in adaptive resilience underscores differences in vulnerability to a changing environment for an ecologically important freshwater fish species

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Cognitive Systems, Flinders University, University of Canberra, Universite Laval
Authors: Smith, S. (Ekstern), Brauer, C. (Ekstern), Unmack, P. (Ekstern), Guillot, G. (Intern), Bernatchez, L. (Ekstern), B. Beheregaray, L. (Ekstern)
Number of pages: 26
Publication date: 2015

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Bibliographical note
This is a CONFIDENTIAL research report
Source: PublicationPreSubmission
Source-ID: 112873376
Publication: Research › Report – Annual report year: 2015

Les éléphants en danger

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, University of Chicago, University of Washington
Authors: Guillot, G. (Intern), Wasser, S. (Ekstern), Stephens, M. (Ekstern)
Detecting correlation between allele frequencies and environmental variables as a signature of selection. A fast computational approach for genome-wide studies

Genomic regions (or loci) displaying outstanding correlation with some environmental variables are likely to be under selection and this is the rationale of recent methods of identifying selected loci and retrieving functional information about them. To be efficient, such methods need to be able to disentangle the potential effect of environmental variables from the confounding effect of population history. For the routine analysis of genome-wide datasets, one also needs fast inference and model selection algorithms. We propose a method based on an explicit spatial model which is an instance of spatial generalized linear mixed model (SGLMM). For inference, we make use of the INLA–SPDE theoretical and computational framework developed by Rue et al. (2009) and Lindgren et al. (2011). The method we propose allows one to quantify the correlation between genotypes and environmental variables. It works for the most common types of genetic markers, obtained either at the individual or at the population level. Analyzing the simulated data produced under a geostatistical model then under an explicit model of selection, we show that the method is efficient. We also re-analyze a dataset relative to nineteen pine weevils (Hylobius abietis) populations across Europe. The method proposed appears also as a statistically sound alternative to the Mantel tests for testing the association between the genetic and environmental variables.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, Centre de Biologie et de Gestion des Populations, Genome et Speciation
Authors: Guillot, G. (Intern), Vitalis, R. (Ekstern), Rouzic, A. L. (Ekstern), Gautier, M. (Ekstern)
Pages: 145-155
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Spatial Statistics
Volume: 8
ISSN (Print): 2211-6753
Ratings:
BFI (2018): BFI-level 2
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 1.15 SJR 0.523 SNIP 0.798
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.881 SNIP 1.581 CiteScore 2.33
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.574 SNIP 1.875 CiteScore 2.38
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.67 SNIP 2.131 CiteScore 2.25
ISI indexed (2013): ISI indexed no
Original language: English
SNP and AFLP data, Genomics, Spatial population structure, Model choice, MCMC-free method, INLA
DOIs: 10.1016/j.spasta.2013.08.001
Source: dtu
Source-ID: u::8336
Publication: Research - peer-review › Journal article – Annual report year: 2013
Validity of covariance models for the analysis of geographical variation

1. Due to the availability of large molecular data-sets, covariance models are increasingly used to describe the structure of genetic variation as an alternative to more heavily parametrised biological models.

2. We focus here on a class of parametric covariance models that received sustained attention lately and show that the conditions under which they are valid mathematical models have been overlooked so far.

3. We provide rigorous results for the construction of valid covariance models in this family.

4. We also outline how to construct alternative covariance models for the analysis of geographical variation that are both mathematically well behaved and easily implementable.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Cognitive Systems, Dresden University of Technology, Universidad de Valparaiso, Universidad Tecnica Federico Santa Maria
Authors: Guillot, G. (Intern), Schilling, R. L. (Ekstern), Porcu, E. (Ekstern), Bevilacqua, M. (Ekstern)
Pages: 329–335
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Methods in Ecology and Evolution
Volume: 5
ISSN (Print): 2041-210X
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 7.28 SJR 4.733 SNIP 2.621
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 5.382 SNIP 2.842 CiteScore 7.61
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
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 3.011 SNIP 2.427 CiteScore 5.34
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): SJR 2.106 SNIP 1.648 CiteScore 3.56
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
Original language: English
Isolation by distance, Isolation by ecology, Landscape genetics, Geostatistics, Positive-definite function
DOIs:
10.1111/2041-210X.12167
Links:
http://arxiv.org/abs/1311.4136
Source: dtu
Source-ID: u::9671
Publication: Research - peer-review › Journal article – Annual report year: 2014

Population dynamics of species-rich ecosystems: the mixture of matrix population models approach
Matrix population models are widely used to predict population dynamics, but when applied to species-rich ecosystems with many rare species, the small population sample sizes hinder a good fit of species-specific models. This issue can be overcome by assigning species to groups to increase the size of the calibration data sets. However, the species classification is often disconnected from the matrix modelling and from the estimation of matrix parameters, thus bringing
species groups that may not be optimal with respect to the predicted community dynamics.

We proposed here a method that jointly classified species into groups and fit the matrix models in an integrated way. The model was a special case of mixture with unknown number of components and was cast in a Bayesian framework. An MCMC algorithm was developed to infer the unknown parameters: the number of groups, the group of each species and the dynamics parameters.

We applied the method to simulated data and showed that the algorithm efficiently recovered the model parameters.

We applied the method to a data set from a tropical rain forest in French Guiana. The mixture matrix model classified tree species into well-differentiated groups with clear ecological interpretations. It also accurately predicted the forest dynamics over the 16-year observation period.

Our model and algorithm can straightforwardly be adapted to any type of matrix model, using the life cycle diagram. It can be used as an unsupervised classification technique to group species with similar population dynamics.
A Unifying Model for the Analysis of Phenotypic, Genetic and Geographic Data

Recognition of evolutionary units (species, populations) requires integrating several kinds of data such as genetic or phenotypic markers or spatial information, in order to get a comprehensive view concerning the differentiation of the units. We propose a statistical model with a double original advantage: (i) it incorporates information about the spatial distribution of the samples, with the aim to increase inference power and to relate more explicitly observed patterns to geography; and (ii) it allows one to analyze genetic and phenotypic data within a unified model and inference framework, thus opening the way to robust comparisons between markers and possibly combined analyzes. We show from simulated data as well are real data from the literature that our method estimates parameters accurately and improves alternative approaches in many situations. The interest of this method is exemplified using an intricate case of inter- and intra-species differentiation based on an original data-set of georeferenced genetic and morphometric markers obtained on Myodes voles from Sweden. A computer program is made available as an extension of the R package Geneland.

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Mathematical Statistics, Université Claude Bernard Lyon 1, INRA Institut National de La Recherche Agronomique, Université Montpellier
Authors: Guillot, G. (Intern), Rena, S. (Ekstern), Ledevin, R. (Ekstern), Michaux, J. (Ekstern), Claude, J. (Ekstern)
Pages: 897-911
Publication date: 2012
Main Research Area: Technical/natural sciences
Publication information
Journal: Systematic Biology
Volume: 61
Issue number: 6
ISSN (Print): 1063-5157
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): SJR 6.009 SNIP 2.691 CiteScore 8.4
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 10.301 SNIP 5.44 CiteScore 13.83
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 8.998 SNIP 4.825 CiteScore 11.8
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 9.295 SNIP 4.926 CiteScore 13.53
ISI indexed (2013): ISI indexed yes
Dismantling the Mantel tests

1. The simple and partial Mantel tests are routinely used in many areas of evolutionary biology to assess the significance of the association between two omoromeric matrices of distances relative to the same pairs of individuals or demes. Partial Mantel tests rather than simple Mantel tests are widely used to assess the relationship between two variables displaying some form of structure.

2. We show that contrary to a widely shared belief, partial Mantel tests are not valid in this case, and their bias remains close to that of the simple Mantel test.

3. We confirm that strong biases are expected under a sampling design and spatial correlation parameter drawn from an actual study.

4. The Mantel tests should not be used in case autocorrelation is suspected in both variables compared under the null hypothesis. We outline alternative strategies. The R code used for our computer simulations is distributed as supporting material.
Dismantling the Mantel tests

The simple and partial Mantel tests are routinely used in many areas of evolutionary biology to assess the significance of the association between two or more matrices of distances relative to the same pairs of individuals or demes. Partial Mantel tests rather than simple Mantel tests are widely used to assess the relationship between two variables displaying some form of structure. We show that contrarily to a widely shared belief, partial Mantel tests are not valid in this case, and their bias remains close to that of the simple Mantel test. We confirm that strong biases are expected under a sampling design and spatial correlation parameter drawn from an actual study. The Mantel tests should not be used in case autocorrelation is suspected in both variables compared under the null hypothesis. We outline alternative strategies. The R code used for our computer simulations is distributed as supporting material.

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Mathematical Statistics
Authors: Guillot, G. (Intern)
Publication date: 2012
Main Research Area: Technical/natural sciences

Bibliographical note
Invited talk
Integrating genetic, phenotypic and geographic data in ecological and evolutionary studies: The spatial mixture approach

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Mathematical Statistics
Authors: Guillot, G. (Intern)
Number of pages: 1
Publication date: 2012
Main Research Area: Technical/natural sciences
Electronic versions:
poster_gg_kyoto.pdf
Source: dtu

On the simple and partial Mantel tests with spatial data

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Mathematical Statistics, Institut des Sciences de l'Evolution
Authors: Guillot, G. (Intern), Rousset, F. (Ekstern)
Number of pages: 46
Publication date: 2012

Publication information
Media of output: Power Point presentation
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Avignon_2012_GG.pdf
Source: dtu

Population genetic and morphometric data analysis using R and the Geneland program

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Mathematical Statistics
Authors: The Geneland development group, Guillot, G. (Intern)
Number of pages: 62
Publication date: 2012

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Geneland-Doc.pdf
Links:
http://www2.imm.dtu.dk/~gigu/Geneland/

Bibliographical note
Geneland program documentation for versions >= 4.0.0.
Source: dtu
Source-ID: u::5975
Publication: Research › Report – Annual report year: 2012
Some models in evolutionary biology

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Mathematical Statistics
Authors: Guillot, G. (Intern)
Number of pages: 93
Publication date: 2012

Publication information
Media of output: Power Point presentation
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Prague_2012_GG.pdf
Source: dtu
Source-ID: u::5713
Publication: Research - peer-review › Sound/Visual production (digital) – Annual report year: 2012

Estimating the location and shape of hybrid zones
We propose a new model to make use of georeferenced genetic data for inferring the location and shape of a hybrid zone. The model output includes the posterior distribution of a parameter that quantifies the width of the hybrid zone. The model proposed is implemented in the GUI and command-line versions of the Geneland program versions ≥3.3.0. Information about the program can be found on .

General information
State: Published
Organisations: Mathematical Statistics, Department of Informatics and Mathematical Modeling, Universite Pierre et Marie Curie
Authors: Guedj, B. (Ekstern), Guillot, G. (Intern)
Pages: 1119-1123
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology Resources
Volume: 11
Issue number: 6
ISSN (Print): 1755-098X
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 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
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.842 SNIP 2.217 CiteScore 5.04
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 3.472 SNIP 2.986 CiteScore 7.31
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.172 SNIP 1.87 CiteScore 4.26
On the Informativeness of Dominant and Co-Dominant Genetic Markers for Bayesian Supervised Clustering

We study the accuracy of a Bayesian supervised method used to cluster individuals into genetically homogeneous groups on the basis of dominant or codominant molecular markers. We provide a formula relating an error criterion to the number of loci used and the number of clusters. This formula is exact and holds for arbitrary number of clusters and markers. Our work suggests that dominant markers studies can achieve an accuracy similar to that of codominant markers studies if the number of markers used in the former is about 1.7 times larger than in the latter.
Population genetics analysis using R and the Geneland program
Geneland program documentation 2011 Program distributed under GNU license as an R package on the Comprehensive R Archive Network.

General information
State: Published
Organisations: Mathematical Statistics, Department of Informatics and Mathematical Modeling
Authors: Guillot, G. (Intern), Santos, F. (Ekstern), Estoup, A. (Ekstern)
Publication date: 2011

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Geneland-Doc.pdf
Links:
http://www2.imm.dtu.dk/~gigu/Geneland/
Source: orbit
Source-ID: 314784
Publication: Research › Report – Annual report year: 2011

Splendor and misery of indirect measures of migration and gene flow

General information
State: Published
Organisations: Mathematical Statistics, Department of Informatics and Mathematical Modeling
Authors: Guillot, G. (Intern)
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information
Journal: Heredity
Volume: 106
Issue number: 11-12
Ratings:
BFI (2018): BFI-level 1
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 3.56 SJR 2.03 SNIP 1.243
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.094 SNIP 1.298 CiteScore 3.47
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.162 SNIP 1.304 CiteScore 3.42
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.029 SNIP 1.149 CiteScore 3.44
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.088 SNIP 1.356 CiteScore 3.5
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.279 SNIP 1.289 CiteScore 3.58
Clustering models in population genetics

General information
State: Published
Organisations: Mathematical Statistics, Department of Informatics and Mathematical Modeling
Authors: Guillot, G. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 269380
Publication: Research - peer-review › Journal article – Annual report year: 2011

Correcting for ascertainment bias in the inference of population structure

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Mathematical Statistics
Authors: Guillot, G. (Intern)
Publication date: 2010
Event: Poster session presented at 8th French-Danish Workshop in Spatial Statistics and Image Analysis in Biology, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 269388
Publication: Research - peer-review › Poster – Annual report year: 2010
Using AFLP markers and the Geneland program for the inference of population genetic structure

The use of dominant markers such as amplified fragment length polymorphism (AFLP) for population genetics analyses is often impeded by the lack of appropriate computer programs and rarely motivated by objective considerations. The point of the present note is twofold: (i) we describe how the computer program Geneland designed to infer population structure has been adapted to deal with dominant markers; and (ii) we use Geneland for numerical comparison of dominant and
codominant markers to perform clustering. AFLP markers lead to less accurate results than bi-allelic codominant markers such as single nucleotide polymorphisms (SNP) markers but this difference becomes negligible for data sets of common size (number of individuals $n \geq 100$, number of markers $L \geq 200$). The latest Geneland version (3.2.1) handling dominant markers is freely available as an R package with a fully clickable graphical interface. Installation instructions and documentation can be found on http://www2.imm.dtu.dk/~gigu/Geneland.
A computer program to simulate multilocus genotype data with spatially autocorrelated allele frequencies

Many models for inference of population genetic parameters are based on the assumption that the data set at hand consists of groups displaying within-group Hardy-Weinberg equilibrium at individual loci and linkage equilibrium between loci. This assumption is commonly violated by the presence of within-group spatial structure arising from nonrandom mating of individuals due to isolation by distance (IBD).

This paper proposes a model and simulation method implemented in a computer program to flexibly simulate data displaying such patterns. The program permits displaying of smooth spatial variations of allele frequencies due to IBD and more abrupt variations due to presence of strong barriers to gene flow. It is useful in assessing performance of various statistical inference methods and in designing spatial sampling schemes. This is shown by a simulation study aimed at assessing the extent to which IBD patterns affect accuracy of cluster inferences performed in models assuming panmixia. The program is also used to study the effects of spatial sampling scheme (e.g. sampling individuals in clumps or uniformly across the spatial domain). The accuracy of such inferences is assessed in terms of number of inferred populations, assignment of individuals to populations and location of borders between populations. The effect of spatial sampling was weak while the effect of IBD may be substantial, leading to the inference of spurious populations, especially when IBD was strong with respect to the size of the sampling domain. The model and program are new and have been embedded in the R package Geneland, for user convenience and compliance with existing data formats.

General information
State: Published
Organisations: Centre de Biologie et de Gestion des Populations, University of Oslo
Authors: Guillot, G. (Intern), Santos, F. (Ekstern)
Pages: 1112-1120
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology Resources
Volume: 9
Issue number: 4
ISSN (Print): 1755-098X
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 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
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.842 SNIP 2.217 CiteScore 5.04
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 3.472 SNIP 2.986 CiteScore 7.31
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Correcting for ascertainment bias in the inference of population structure

Background: The ascertainment process of molecular markers amounts to disregard loci carrying alleles with low frequencies. This can result in strong biases in inferences under population genetics models if not properly taken into account by the inference algorithm. Attempting to model this censoring process in view of making inference of population structure (i.e. identifying clusters of individuals) brings up challenging numerical difficulties.

Method: These difficulties are related to the presence of intractable normalizing constants in Metropolis-Hastings acceptance ratios. This can be solved via an Markov chain Monte Carlo (MCMC) algorithm known as single variable exchange algorithm (SVEA).

Result: We show how this general solution can be implemented for a class of clustering models of broad interest in population genetics that includes the models underlying the computer programs STRUCTURE, GENELAND and GESTE. We also implement the method proposed for a simple example and show that it allows us to reduce the bias substantially.

General information
State: Published
Organisations: University of Bern, University of Oslo
Authors: Guillot, G. (Intern), Foll, M. (Ekstern)
Pages: 552-554
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Bioinformatics
Volume: 25
Issue number: 4
ISSN (Print): 1367-4803
Ratings:
BFI (2018): BFI-level 2
On the inference of spatial structure from population genetics data

Motivation: In a series of recent papers, Tess, a computer program based on the concept of hidden Markov random field, has been proposed to infer the number and locations of panmictic population units from the genotypes and spatial locations of these individuals. The method seems to be of broad appeal as it is conceptually much simpler than other competing methods and it has been reported by its authors to be fast and accurate. However, this methodology is not grounded in a formal statistical inference method and seems to rely to a large extent on arbitrary choices regarding the parameters used. The present article is an investigation of the accuracy of this method and an attempt to assess whether recent results reported on the basis of this method are genuine features of the genetic process or artefacts of the method.

Method: I analyse simulated data consisting of populations at Hardy-Weinberg and linkage equilibrium and also data simulated under a scenario of isolation-by-distance at mutation-migration-drift equilibrium. Arabidopsis thaliana data previously analysed with this method are also reconsidered.

Results: Using the Tess program under the no-admixture model to analyse data consisting of several genuine HWLE
populations with individuals of pure ancestries leads to highly inaccurate results; Using the Tess program under the admixture model to analyse data consisting of a continuous isolation-by-distance population leads to the inference of spurious HWLE populations whose number and features depend on the parameters used. Results previously reported about the A. thaliana using Tess seem to a large extent to be artefacts of the statistical methodology used. The findings go beyond population clustering models and can be an help to design more efficient algorithms based on graphs.
Package 'Geneclust'

General information
State: Published
Organisations: Unknown
Authors: Ancelet, S. (Ekstern), Ancelet, M. S. (Ekstern), Guillot, G. (Intern)
Publication date: 2009

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Links:
http://www2.imm.dtu.dk/~gigu/Geneland/
Publication: Research › Computer programme – Annual report year: 2009

Population genetics analysis using R and Geneland

General information
State: Published
Organisations: Technical University of Denmark
Authors: Guillot, G. (Intern), Santos, F. (Ekstern), Estoup, A. (Ekstern)
Publication date: 2009

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Links:
http://www2.imm.dtu.dk/~gigu/Geneland/

Bibliographical note
Geneland manual, 10.
Publication: Research › Report – Annual report year: 2009

Response to comment on 'On the inference of spatial structure from population genetics data'

General information
State: Published
Organisations: Unknown
Authors: Guillot, G. (Intern)
Pages: 1805-1806
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Bioinformatics
Volume: 25
Issue number: 14
ISSN (Print): 1367-4803
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
Spatial prediction of weed intensities from exact count data and image-based estimates

Collecting weed exact counts in an agricultural field is easy but extremely time consuming. Image analysis algorithms for object extraction applied to pictures of agricultural fields may be used to estimate the weed content with a high resolution (about 1 m²), and pictures that are acquired at a large number of sites can be used to obtain maps of weed content over a whole field at a reasonably low cost. However, these image-based estimates are not perfect and acquiring exact weed counts also is highly useful both for assessing the accuracy of the image-based algorithms and for improving the estimates by use of the combined data. We propose and compare various models for image index and exact weed count and we use them to assess how such data should be combined to obtain reliable maps. The method is applied to a real data set from a 30-ha field. We show that using image estimates in addition to exact counts allows us to improve the accuracy of maps significantly. We also show that the relative performances of the methods depend on the size of the data set and on the specific methodology (full Bayes versus plug-in) that is implemented.

General information
State: Published
Organisations: Chalmers University of Technology, Swedish Institute for Food and Biotechnology, AgroParisTech
Authors: Guillot, G. (Intern), Lorén, N. (Ekstern), Rudemo, M. (Ekstern)
Pages: 525-542
Publication date: 2009
Main Research Area: Technical/natural sciences

**Publication information**

**Journal:** Journal of the Royal Statistical Society, Series C (Applied Statistics)

**Volume:** 58

**Issue number:** 4

**ISSN (Print):** 0035-9254

**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): SJR 1.407 SNIP 1.692 CiteScore 1.75
- BFI (2015): BFI-level 2
- Scopus rating (2015): SJR 1.085 SNIP 1.18 CiteScore 1.5
- BFI (2014): BFI-level 2
- Scopus rating (2014): SJR 1.394 SNIP 0.99 CiteScore 1.34
- BFI (2013): BFI-level 2
- Scopus rating (2013): SJR 1.32 SNIP 1.149 CiteScore 1.61
- ISI indexed (2013): ISI indexed yes
- BFI (2012): BFI-level 2
- Scopus rating (2012): SJR 0.989 SNIP 1.133 CiteScore 1.31
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 2
- Scopus rating (2011): SJR 0.809 SNIP 0.946 CiteScore 1.07
- ISI indexed (2011): ISI indexed yes
- BFI (2010): BFI-level 2
- Scopus rating (2010): SJR 0.663 SNIP 0.901
- BFI (2009): BFI-level 2
- Scopus rating (2009): SJR 0.849 SNIP 0.865
- Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 2
- Scopus rating (2008): SJR 1.63 SNIP 1.447
- Scopus rating (2007): SJR 1.208 SNIP 1.329
- Scopus rating (2006): SJR 1.172 SNIP 1.598
- Web of Science (2006): Indexed yes
- Scopus rating (2005): SJR 1.009 SNIP 1.566
- Scopus rating (2004): SJR 1.694 SNIP 1.317
- Scopus rating (2003): SJR 1.502 SNIP 1.521
- Scopus rating (2002): SJR 1.566 SNIP 1.506
- Scopus rating (2001): SJR 1.553 SNIP 1.6
- Scopus rating (2000): SJR 1.287 SNIP 1.574
- Scopus rating (1999): SJR 1.343 SNIP 1.484

**Original language:** English

**Approximate Cox process, Gaussian random field, Image analysis, Model-based geostatistics, Multivariate data, Poisson regression, Precision farming, Spatial prediction**

**DOIs:**

10.1111/j.1467-9876.2009.00664.x

**Publication:** Research - peer-review › Journal article – Annual report year: 2009

**Statistical methods in landscape genetics**

**General information**

**State:** Published
**Statistical methods in spatial genetics**

The joint analysis of spatial and genetic data is rapidly becoming the norm in population genetics. More and more studies explicitly describe and quantify the spatial organization of genetic variation and try to relate it to underlying ecological processes. As it has become increasingly difficult to keep abreast with the latest methodological developments, we review the statistical toolbox available to analyze population genetic data in a spatially explicit framework. We mostly focus on statistical concepts but also discuss practical aspects of the analytical methods, highlighting not only the potential of various approaches but also methodological pitfalls.
Supplementary material to Molecular Ecology: Statistical methods in spatial genetics

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, Mathematical Statistics, Museum National d'Histoire Naturelle, University of Sheffield
Authors: Guillot, G. (Intern), Leblois, R. (Ekstern), Coulon, A. (Ekstern), Frantz, A. C. (Ekstern)
Number of pages: 15
Publication date: 2009
Main Research Area: Technical/natural sciences

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Journal: Molecular Ecology
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
Analysing georeferenced population genetics data with Geneland: A new algorithm to deal with null alleles and a friendly graphical user interface

We introduce a new algorithm to account for the presence of null alleles in inferences of populations clusters from individual multilocus genetic data. We show by simulations that the presence of null alleles can affect the accuracy of inferences if not properly accounted for and that our algorithm improve significantly their accuracy.

Availability: This new algorithm is implemented in the program Geneland. It is freely available under GNU public license as an R package on the Comprehensive R Archive Network. It now includes a fully clickable graphical interface. Informations on how to get the software are available on folk.uio.no/gillesg/Geneland.html

General information
State: Published
Organisations: Centre de Biologie et de Gestion des Populations, University of Oslo
Authors: Guillot, G. (Intern), Filipe Santos (Ekstern), Arnaud Estoup (Ekstern)
Inference of structure in subdivided populations at low levels of genetic differentiation: The correlated allele frequencies model revisited
Motivation: This article considers the problem of estimating population genetic subdivision from multilocus genotype data. A model is considered to make use of genotypes and possibly of spatial coordinates of sampled individuals. A particular attention is paid to the case of low genetic differentiation with the help of a previously described Bayesian clustering model where allele frequencies are assumed to be a priori correlated. Under this model, various problems of inference are considered, in particular the common and difficult, but still unaddressed, situation where the number of populations is unknown.

Results: A Markov chain Monte Carlo algorithm and a new post-processing scheme are proposed. It is shown that they significantly improve the accuracy of previously existing algorithms in terms of estimated number of populations and estimated population membership. This is illustrated numerically with data simulated from the prior-likelihood model used in inference and also with data simulated from a WrightFisher model. Improvements are also illustrated on a real dataset of eighty-eight wolverines (Gulo gulo) genotyped at 10 microsatellites loci. The interest of the solutions presented here are not specific to any clustering model and are hence relevant to many settings in populations genetics where weakly differentiated populations are assumed or sought.

General information
State: Published
Organisations: University of Oslo
Authors: Guillot, G. (Intern)
Pages: 2222-2228
Publication date: 2008
Main Research Area: Technical/natural sciences

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Journal: Bioinformatics
Volume: 24
Issue number: 19
ISSN (Print): 1367-4803
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 6.42
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 6.06
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 5.5
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 5.78
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 6.73
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 5.61
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
Population substructure in Finland and Sweden revealed by the use of spatial coordinates and a small number of unlinked autosomal SNPs

Background: Despite several thousands of years of close contacts, there are genetic differences between the neighbouring countries of Finland and Sweden. Within Finland, signs of an east-west duality have been observed, whereas the population structure within Sweden has been suggested to be more subtle. With a fine-scale substructure like this, inferring the cluster membership of individuals requires a large number of markers. However, some studies have suggested that this number could be reduced if the individual spatial coordinates are taken into account in the analysis.

Results: We genotyped 34 unlinked autosomal single nucleotide polymorphisms (SNPs), originally designed for zygosity testing, from 2044 samples from Sweden and 657 samples from Finland, and 30 short tandem repeats (STRs) from 465 Finnish samples. We saw significant population structure within Finland but not between the countries or within Sweden, and isolation by distance within Finland and between the countries. In Sweden, we found a deficit of heterozygotes that we could explain by simulation studies to be due to both a small non-random genotyping error and hidden substructure caused by immigration. Geneland, a model-based Bayesian clustering algorithm, clustered the individuals into groups that corresponded to Sweden and Eastern and Western Finland when spatial coordinates were used, whereas in the absence of spatial information, only one cluster was inferred.

Conclusion: We show that the power to cluster individuals based on their genetic similarity is increased when including information about the spatial coordinates. We also demonstrate the importance of estimating the size and effect of genotyping error in population genetics in order to strengthen the validity of the results.
Discrimination and scoring using small sets of genes for two-sample microarray data

Comparison of gene expression for two groups of individuals form an important subclass of microarray experiments. We study multivariate procedures, in particular use of Hotelling's T-2 for discrimination between the groups with a special emphasis on methods based on few genes only. We apply the methods to data from an experiment with a group of atopic dermatitis patients compared with a control group. We also compare our methodology to other recently proposed methods on publicly available datasets. It is found that (1) use of several genes gives a much improved discrimination of the groups as compared to one gene only, (ii) the genes that play the most important role in the multivariate analysis are not necessarily those that rank first in univariate comparisons of the groups, (iii) Linear Discriminant Analysis carried out with sets of 2-5 genes selected according to their Hotelling T-2 give results comparable to state-of-the-art methods using many more genes, a feature of our method which might be crucial in clinical applications. Finding groups of genes that together give optimal multivariate discrimination (given the size of the group) can identify crucial pathways and networks of genes responsible for a disease. The computer code that we developed to make computations is available as an R package. (c) 2006 Elsevier Inc. All rights reserved.

General Information
State: Published
Organisations: Queen Silvia Children's Hospital, Chalmers University of Technology, INRA Institut National de La Recherche Agronomique
Authors: Guillot, G. (Intern), Olsson, M. (Ekstern), Benson, M. (Ekstern), Rudemo, M. (Ekstern)
Pages: 195-203
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Mathematical Biosciences
Volume: 205
Issue number: 2
ISSN (Print): 0025-5564
Ratings:
Differential analysis, Expression data, Discrimination, Small sets of genes, Hotelling statistic, Curse of dimension, Computational methods, Software, R package, Eczema

DOIs: 10.1016/j.mbs.2006.08.007

Publication: Research - peer-review › Journal article – Annual report year: 2007

Hidden markov random fields and the genetic structure of the scandinavian brown bear population

Spatial Bayesian clustering algorithms can provide correct inference of population genetic structure when applied to populations for which continuous variation of allele frequencies is disrupted by small discontinuities. Here we review works which used Bayesian clustering algorithms for studying the Scandinavian brown bears, with particular attention to a recent method based on hidden Markov random field. We provide a summary of current knowledge about the genetic structure of this endangered population potentially useful for its conservation.

General information
State: Published
Organisations: Unité de Mathématiques et Informatique Appliquées, TIMC Equipe TIMB, Faculté de Médecine
Authors: Ancelet, S. (Ekstern), Guillot, G. (Intern), François, O. (Ekstern)
A network-based analysis of allergen-challenged CD4+ T cells from patients with allergic rhinitis

We performed a network-based analysis of DNA microarray data from allergen-challenged CD4(+) T cells from patients with seasonal allergic rhinitis. Differentially expressed genes were organized into a functionally annotated network using the Ingenuity Knowledge Database, which is based on manual review of more than 200 000 publications. The main function of this network is the regulation of lymphocyte apoptosis, a role associated with several genes of the tumor necrosis factor superfamily. The expression of TNFRSF4, one of the genes in this family, was found to be 48 times higher in allergen-challenged cells than in diluent-challenged cells. TNFRSF4 is known to inhibit apoptosis and to enhance Th2 proliferation. Examination of a different material of allergen-stimulated peripheral blood mononuclear cells showed a higher number of interleukin-4(+) type 2 CD4(+) T (Th2) cells in patients than in controls (P < 0.01), as well as a higher number of non-apoptotic Th2 cells in patients (P < 0.01). The number of Th2 cells expressing TNFRSF4, TNFSF7 and TNFRSF18 was also significantly higher in patients. Treatment with anti-TNFSF4 resulted in a significantly decreased number of Th2 cells (P < 0.05). A logical inference from all this is that the proliferation of allergen-challenged Th2 cells is associated with a decreased apoptosis of Th2 cells and an increase in TNFRSF4 signalling.
Bayesian clustering using hidden Markov random fields in spatial population genetics

We introduce a new Bayesian clustering algorithm for studying population structure using individually geo-referenced multilocus data sets. The algorithm is based on the concept of hidden Markov random field, which models the spatial dependencies at the cluster membership level. We argue that (i) a Markov chain Monte Carlo procedure call implement the algorithm efficiently, (ii) it can detect significant geographical discontinuities in allele frequencies and regulate the number of clusters, (iii) it call check whether the clusters obtained without the use of spatial priors are robust to the hypothesis of discontinuous geographical variation in allele frequencies, and (iv) it can reduce the number of loci required to obtain accurate assignments. We illustrate and discuss the implementation issues with the Scandinavian brown bear and the human CEPH diversity panel data set.

General information

State: Published
Organisations: TIMC, TIMB (Department of Mathematical Biology), Unité de Mathématiques et Informatique Appliquées
Authors: François, O. (Ekstern), Ancelet, S. (Ekstern), Guillot, G. (Intern)
Pages: 805-816
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information

Journal: Genetics
Volume: 174
Issue number: 2
ISSN (Print): 0016-6731
Ratings:
Web of Science (2018): Indexed yes
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 4.7
Scopus rating (2015): CiteScore 4.67
Scopus rating (2014): CiteScore 5.14
Scopus rating (2013): CiteScore 4.56
Scopus rating (2012): CiteScore 4.11
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.78
Genetic structure is influenced by landscape features: Empirical evidence from a roe deer population

The delimitation of population units is of primary importance in population management and conservation biology. Moreover, when coupled with landscape data, the description of population genetic structure can provide valuable knowledge about the permeability of landscape features, which is often difficult to assess by direct methods (e.g. telemetry). In this study, we investigated the genetic structuring of a roe deer population which recently recolonized a fragmented landscape. We sampled 1148 individuals from a 40 x 55-km area containing several putative barriers to deer movements, and hence to gene flow, namely a highway, rivers and several canals. In order to assess the effect of these landscape features on genetic structure, we implemented a spatial statistical model known as GENELAND which analyses genetic structure, explicitly taking into account the spatial nature of the problem. Two genetic units were inferred, exhibiting a very low level of differentiation (F-ST = 0.008). The location of their boundaries suggested that there are no absolute barriers in this study area, but that the combination of several landscape features with low permeability can lead to population differentiation. Our analysis hence suggests that the landscape has a significant influence on the structuring of the population under study. It also illustrates the use of GENELAND as a powerful method to infer population structure, even in situations of young populations exhibiting low genetic differentiation.
Inference of a hidden spatial tessellation from multivariate data: Application to the delineation of homogeneous regions in an agricultural field

In a precision farming context, differentiated management decisions regarding fertilization, application of lime and other cultivation activities may require the subdivision of the field into homogeneous regions with respect to the soil variables of main agronomic significance. The paper develops an approach that is aimed at delineating homogeneous regions on the basis of measurements of a categorical and quantitative nature, namely soil type and resistivity measurements at different soil layers. We propose a Bayesian multivariate spatial model and embed it in a Markov chain Monte Carlo inference scheme. Implementation is discussed using real data from a 15-ha field. Although applied to soil data, this model could be relevant in areas of spatial modelling as diverse as epidemiology, ecology or meteorology.

General information
State: Published
Organisations: Universite Pierre et Marie Curie, Environnement et Grandes Cultures, INRA Institut National de La Recherche Agronomique
Un modèle géostatistique pour la détection et la localisation des discontinuités génétiques spatiales entre populations

A spatial statistical model for landscape genetics. Landscape genetics is a new discipline that aims to provide information on how landscape and environmental features influence population genetic structure. This approach is of primary importance in population management and conservation biology because it provides valuable knowledge about landscape connectivity. The first key step of landscape genetics is the spatial detection and location of genetic discontinuities between populations. However, efficient methods for achieving this task are lacking. In this research project, we first clarify what is conceptually involved in the spatial modelling of genetic data. Then we describe a Bayesian model that allows inference of the location of such genetic discontinuities from individual georeferenced multilocus genotypes, without a priori knowledge on the number of populational units and their limits. In this method, the global set of sampled individuals is modelled as a spatial mixture of panmictic populations, and the spatial organization of populations is modelled through coloured Voronoi tessellation. In addition to spatially locating genetic discontinuities, the method quantifies the amount of spatial dependence in the data set, estimates the number of populations in the studied area, assigns individuals to their population of origin, and detects migrants between populations. The performance of the method was evaluated through the analysis of simulated data sets. Results showed good performances for standard microsatellite data sets (e.g., 100 individuals genotyped at 10 loci with 10 alleles per locus), with high but also low levels of population differentiation (FST < 0.05). The method was then applied to two real data sets on large mammals with contrasted differentiation levels. The first application, to wolverines (Gulo gulo) sampled in the North-western United States, showed the ability of the method to detect populations consistent with landscape structures known to slow down dispersal movements of that species, and to locate putative migrants in a context of rather high genetic differentiation (FST from 0.08 to 0.17). The second application, to roe deer (Capreolus capreolus) in South-western France, illustrate the ability of the method to infer genetic discontinuities coherent with landscape structures (highways, canals) in a situation of very low genetic differentiation (FST = 0.008). A computer program named GENELAND is freely available at http://www.inapg.inra.fr/ens_rech/mathinfo/personnel/guillot/Geneland.html. A mailing list for users is managed by one of us (G. Guillot).

General information
State: Published
Organisations: INRA Institut National de La Recherche Agronomique, Centre de cooperation Internationale en Recherche Agronomique pour le Développement, Unité de Mathématiques et Informatique Appliquées
Authors: Cosson, J. (Ekstern), Estoup, A. (Ekstern), Coulon, A. (Ekstern), Galan, M. (Ekstern), Mortier, F. (Ekstern), Hewison, A. M. (Ekstern), Guillot, G. (Intern)
Pages: 41-55
Publication date: 2006

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Title of host publication: Les Actes du BRG
Volume: 6
Publisher: Bureau des Ressources Génétiques
Main Research Area: Technical/natural sciences
Barriers, Bayesian computations, Gene flow, Landscape connectivity, Landscape genetics
Publication: Research - peer-review › Book chapter – Annual report year: 2006

A spatial statistical model for landscape genetics
Landscape genetics is a new discipline that aims to provide information oil how landscape and environmental features influence population genetic structure. The first key step of landscape genetics is the spatial detection and location of genetic discontinuities between populations. However, efficient methods for achieving this task are lacking. In this article, we first clarify what is conceptually involved in the spatial modeling of genetic data. Then we describe a Bayesian model implemented in a Markov chain Monte Carlo scheme that allows inference of the location of such genetic discontinuities from individual georeferenced multilocus genotypes, without a priori knowledge on populational units and limits. In this method, the global set of sampled individuals is modeled as a spatial mixture of panmictic populations, and the spatial organization of populations is modeled through coloured Voronoi tessellation. In addition to spatially locating genetic discontinuities, the method quantifies the amount of spatial dependence in the data set, estimates the number of populations in the studied area, assigns individuals to their population of origin, and detects individual migrants between populations. However, efficient methods for achieving this task are lacking. In this article, we first clarify what is conceptually involved in the spatial modeling of genetic data. Then we describe a Bayesian model implemented in a Markov chain Monte Carlo scheme that allows inference of the location of such genetic discontinuities from individual georeferenced multilocus genotypes, without a priori knowledge on populational units and limits. In this method, the global set of sampled individuals is modeled as a spatial mixture of panmictic populations, and the spatial organization of populations is modeled through the colored Voronoi tessellation. In addition to spatially locating genetic discontinuities, the method quantifies the amount of spatial dependence in the data set, estimates the number of populations in the studied area, assigns individuals to their population of origin, and detects individual migrants between populations, while taking into account uncertainty on the location of sampled individuals. The performance of the method is evaluated through the analysis of simulated data sets. Results show good performances for standard data sets (e.g., 100 individuals genotyped at 10 loci with 10 alleles per locus), with high but also low levels of population differentiation (e.g., F-ST < 0.05). The method is then applied to a set of 88 individuals of wolverines (Gulo gulo) sampled in the northwestern United States and genotyped at 10 microsatellites.

General information
State: Published
Organisations: Centre de Biologie et de Gestion des Populations, Centre de cooperation Internationale en Recherche Agronomique pour le Développement, Unité de Mathématiques et Informatique Appliquées
Authors: Guillot, G. (Intern), Estoup, A. (Ekstern), Mortier, F. (Ekstern), Cosson, J. F. (Ekstern)
Pages: 1261-1280
Publication date: 2005
GENELAND: a computer package for landscape genetics
Geneland is a computer package that allows to make use of georeferenced individual multilocus genotypes for the inference of the number of populations and of the spatial location of genetic discontinuities between those populations. Main assumptions of the method are: (i) the number of populations is unknown and all values are considered a priori equally likely, (ii) populations are spread over areas given by a union of some polygons of unknown location in the spatial domain, (iii) Hardy-Weinberg equilibrium is assumed within each population and (iv) allele frequencies in each population are unknown and treated as random variable either following the so-called Dirichlet model or Falush model. Different algorithms implemented in Geneland to perform inferences are first briefly presented. Then major running steps and outputs (i.e. histogram of number of populations and map of posterior probabilities of population membership) are illustrated from the analysis of a simulated data set, which was also produced by Geneland.

General information
State: Published
Organisations: Centre de cooperation Internationale en Recherche Agronomique pour le Développement, Centre de Biologie et de Gestion des Populations, AgroParisTech
Authors: Guillot, G. (Intern), Mortier, F. (Ekstern), Estoup, A. (Ekstern)
Pages: 712-715
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology Notes
Volume: 5
Issue number: 3
ISSN (Print): 1471-8278
Ratings:
Original language: English
Landscape genetics, MCMC inference, Simulation, Software
DOIs:
Spatial disaggregation of Sahelian rain fields: A new application of the Gibbs sampler

The present study is in the framework of the pending research actions on the hydrological impacts of the drought that struck West Africa for almost 30 years, starting at the end of the 1960s. It centred on solving the spatial-scale problems existing between the rain fields, as they are presently available, and those necessary for the hydrological models. The proposed method is based on the coupling of the Gibbs sampler and the acceptance-rejection algorithm for the simulation of meta-Gaussian rain fields able to characterize an integral value representative for a given area by respecting the statistical properties of point rain depths. It is applied to the conditional simulation of rain fields observed at the Niamey Degree Square raingauge during the EPSAT-Niger campaign. The model performance is evaluated by comparing the simulated statistical rain field properties with those observed for high-resolution Sahelian area. According to the results of this validation, the proposed model provides an elegant and convenient answer to the conditional simulation of Sahelian rain fields.

Gibbs sampling for conditional spatial disaggregation of rain fields

Gibbs sampling is used to simulate Sahelian rain fields conditional to an areal estimate provided either as the output of an atmospheric model or by a satellite rainfall algorithm. Whereas various methods are widely used to generate simulated rain fields conditioned on point observations, there are many fewer simulation algorithms able to produce a spatially disaggregated rain field of known averaged value. The theoretical and practical aspects of Gibbs sampling for the purpose of conditional rain field simulation are explored in the first part of the paper. It is proposed to use a so-called acceptance-rejection algorithm to ensure convergence of the conditional simulation. On a Sahelian case study, it is then showed that Gibbs sampling performs similarly to the well-known turning band method in an unconditional mode. A preliminary validation of the method in conditional mode is presented. Several rain fields are simulated conditionally on an observed rainfall field, whose only the spatial average over a 100 x 100 km(2) area is supposed to be known. These conditional simulations are compared with the observed rain field and to other rain fields of similar magnitude. For a given class of events, the conditional rain fields have a distribution of point values similar to the distribution of observed point values. At the same time, the model is producing a wide range of spatial patterns corresponding to a single area average, giving an idea of the variety of possible fields of equal areal value.
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<th>Scopus Rating</th>
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<td>2003</td>
<td>2</td>
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Original language: English
Disaggregation, Rainfall, West Africa, Gibbs, Conditional simulation
DOI: 10.1029/2003WR002009
Interpolation of Rainfall at Small Scale in a Mediterranean Region: Relation between rainfall and altitude within a simple space-time model

This paper describes a statistical space-time model for rain-fall in Mediterranean regions. The rain-fall is supposed to be the sum of a deterministic component and a random function enjoying spatial second-order stationary and without temporal correlation. Under these assumptions, we analyse the dependence of the trend upon time and compute the optimal linear predictor. The proposed methods are implemented and discussed on a two year data set of daily recordings.

General information
State: Published
Organisations: Universite Claude Bernard Lyon 1, Unité Climat Sol et Environnement, Unité de Biométrie
Authors: Béal, D. (Ekstern), Guillot, G. (Intern), Courault, D. (Ekstern), Bruchou, C. (Ekstern)
Pages: 379-389
Publication date: 2004

Host publication information
Title of host publication: geoENV IV — Geostatistics for Environmental Applications : Proceedings of the Fourth European Conference on Geostatistics for Environmental Applications held in Barcelona, Spain, November 27–29, 2002
Editors: Sanchez-Vila, X., Carrera, J., Gómez-Hernández, J. J.
ISBN (Print): 978-1-4020-2007-0
Series: Quantitative Geology and Geostatistics
Volume: 13
ISSN: 0924-1973
Main Research Area: Technical/natural sciences
DOIs: 10.1007/1-4020-2115-1_32
Publication: Research - peer-review › Article in proceedings – Annual report year: 2004

Modélisation géostatistique en génétique des populations

Modélisation géostatistique en génétique des populations

Application of the Gibbs Sampler to the Conditional Simulation of Rain Fields

The low density of raingauge networks in West-Africa and the availability of climatological variable at large scale only (as outputs of climatological models or remote sensing estimation algorithms) can be bridged by the so-called disaggregation algorithms which are designed to provide rainfall data at any scale given large scale data, and a small set of ground (point scale) measurements. The proposed algorithms is based on a geostatistical model, namely a stochastic model taking explicitly into account the spatial structure of the variable. The disaggregation problem is then viewed as a Monte-Carlo simulation problem at the required scale conditioned by all the available information. As the problem of sampling from the multivariate density derived from our model does not have direct solution, the simulation is performed with an iteration of a Markov Chain whose limiting distribution is the desired one. Under the general Metropolis-Hastings scheme we use the well known Gibbs sampler, which allows here to deal with grids with arbitrary large number of points at the cost of small approximations. The behaviour of the model is demonstrated by disaggregation of a few rainfall events observed during the EPSAT-Niger experiment.

General information
State: Published
**Interpolation of Rainfall Fields Through Expectation Conditionally On Ground and Satellite Measurements**

We consider the problem of spatially interpolating rainfall fields at small scale from rain gauge measurements with the additional information provided by infrared satellite channels. Namely, to produce rainfall values at any arbitrary site \( r(x) \) given point measurements \( r(x_1), \ldots, r(x_n) \) and remote sensing measurements \( s(p_1), \ldots, s(p_m) \), each \( s(p_i) \) standing for a radiance integrated over pixel \( p_i \).

Formally, the best statistical prediction is given by the conditional expectation \( E[r(x)|r(x_1), \ldots, r(x_n), s(p_1), \ldots, s(p_m)] \) which can be computed only within a fully prescribed model of random function. We propose to perform the computation in the framework of the so-called transformed-Gaussian model with the additional specification that \( s = (r) + (\text{the link function and the noise being modeled separately}) \).

The transform-Gaussian model have proved to be a reasonable model for rainfall in the Sahel (which is the climatological application that we have in mind for these theoretical developments) and provides an optimal solution different from the classical kriging predictor. As a counterparts, it involves computational difficulties as it may requires MCMC simulations to obtain numerical approximation of the conditional expectation.

Theoretical results obtained are compared to those of more classical spatial and non spatial algorithms previously described in the literature.

**A positive definite estimator of the non stationary covariance of random fields**

This paper proposes a non parametric estimator of the covariance function for 2-dimensional random fields by regularization of the empirical covariance matrix by a convolution kernel. The main feature of this estimator is its positive definiteness everywhere on its domain while it does not assume stationarity of the field. We present several choices of the kernel, then we provide some insight for the selection of the smoothing parameter involved. We illustrate some of our results on a one dimensional simulated dataset and on actual 2-dimensional rainfall data.
Clustering geostatistical data
We explore and compare different methods for the spatial clustering of geostatistical data. A new methodology based on the likelihood is proposed and compared to the approach by Allard and Monestiez (1999). Both methods are compared on a heavy metal concentration data set in the Swiss Jura.

Approximation of Sahelian rainfall fields with meta-gaussian random functions: Part 2: parameter estimation and comparison to data
The meta-Gaussian model is fitted to a set of 258 sahelian rainfields. The hypotheses underlying this model are discussed with a special emphasis on its ergodic properties, the scale of the phenomenon and the scale of observation. Then the ability of this model to reproduce some observed features, in particular upscaling properties, is checked from a distributional point of view. Finally, some simple properties of the thresholds which are linked to the area threshold method are described.
Approximation of Sahelian rainfall fields with meta-gaussian random functions: Part 1: model definition and methodology
For the purpose of numerically studying sahelian storm rainfields, a family of random functions is described with a characterization of its finite dimensional law. Some problems appearing when fitting its functional parameters are put forward and two solutions to bypass those problems are provided, according to the regularity properties of the marginal cumulative distribution function. An illustration of this method is implemented on a set of sahelian rainfields of event accumulation displaying a strong spatial intermittency.

General information
State: Published
Organisations: Université de Grenoble
Authors: Guillot, G. (Intern)
Pages: 100-112
Publication date: 1999
Main Research Area: Technical/natural sciences

Publication information
Journal: Stochastic Environmental Research and Risk Assessment
Volume: 13
Disaggregation of Sahelian mesoscale convective system rain fields: Further developments and validation

Bridging the gaps between the GCM scales and the hydrological scales is a key issue when studying the impacts of potential climate changes on the water resources and, more generally, the links between climate variability and hydrological variability. This is especially true in tropical regions where (1) rainfall is highly variable in space and time due to its convective nature: and (2) measurements are scarce. Using high-resolution data collected in the semi arid region of
Niamey, Niger, Lebel et al. [1998] have proposed a space-time model (the LBC model), allowing the disaggregation of large-scale estimates produced either from satellite images or general circulation model (GCM) outputs. The behavior of this model was shown to be globally satisfying when tested on a small number of selected Sahelian mesoscale convective complexes (SMCCs). However, to be of use in simulation studies of the impact of climate changes as predicted by GCMs or in an operational context where only satellite data are readily available, a more systematic validation was required. Also, the initial version of the model was intended at dealing with SMCCs only, leaving aside the other convective systems displaying a less coherent spatial structure. This led to develop a new version of the LBC model, presented here, characterized by the following improvements: (I) a more precise modeling of the spatial structure of the total storm rain fields by taking into account their anisotropy and using a nested covariance, (2) a better representation of the storm kinematic by dealing with arrival times of rain rather than with speeds of movement, (3) a revision of the parameters used to define the standard hyetograph which is the basis of the time disaggregation algorithm. This new version of the model has two main advantages as compared to the older one: (i) the capacity of dealing with every kind of Sahelian mesoscale convective systems (SMCSs), which account for more than 90% of the total annual rainfall in the region; (2) the possibility of using the model both in simulation and in disaggregation modes. The validation of the model is carried out by comparing the rainfall statistics at various scales of aggregation, for a set of 170 observed SMCSs (corresponding to the 1990-1993 operating period) and a set of 170 simulated SMCSs.

**General information**

State: Published
Organisations: Laboratoire d'étude des Transferts en Hydrologie et Environnement, Université Pierre Mendès France
Authors: Guillot, G. (Intern), Lebel, T. (Ekstern)
Pages: 31533-31551
Publication date: 1999
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Geophysical Research: Atmospheres
Volume: 104
Issue number: D24
ISSN (Print): 2169-897X
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 3.36 SJR 1.996 SNIP 1.313
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.288 SNIP 1.362 CiteScore 3.39
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.324 SNIP 1.349 CiteScore 3.27
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.357 SNIP 1.44 CiteScore 3.38
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.365 SNIP 1.35 CiteScore 2.93
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.239 SNIP 1.301 CiteScore 3.03
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.449 SNIP 1.324
Modélisation statistique des champs de pluie sahéliens: Application à leur désagrégation spatiale et temporelle

General information
State: Published
Organisations: Unknown
Authors: Guillot, G. (Intern), Lebel, T. (Ekstern)
Number of pages: 135
Publication date: 1998

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

Bibliographical note
From: Université Joseph Fourier, Grenoble, France
Publication: Research › Ph.D. thesis – Annual report year: 1998

Projects:
Computational methods for wind-energy forecasting
Department of Applied Mathematics and Computer Science
Cognitive Systems
Department of Electrical Engineering
Center for Electric Power and Energy
Energy Analytics and Markets
Period: 01/02/2015 → 29/02/2016
Number of participants: 3
Project participant:
Bezzera, Erick (Ekstern)
Supervisor:
Pinson, Pierre (Intern)
Project Coordinator:
Guillot, Gilles (Intern)
Project

**Benchmarking and extending models of real estate price prediction, under financial regulation requirements**
Department of Applied Mathematics and Computer Science
Cognitive Systems
National Institute of Aquatic Resources
Section for Marine Living Resources
Period: 01/09/2014 → 01/10/2017
Number of participants: 4
Project participant:
Katossky, Arthur (Intern)
Thygesen, Uffe Høgsbro (Intern)
Dalhoff, Jakob (Ekstern)
Main Supervisor:
Guillot, Gilles (Intern)
Project

**Computational Landscape Genomics**
Department of Applied Mathematics and Computer Science
Cognitive Systems
Period: 01/10/2013 → …
Number of participants: 4
Project participant:
Guillot, Gilles (Intern)
Antolin, Mike (Ekstern)
Project Manager, academic:
Storfer, Andrew (Ekstern)
Poss, Mary (Ekstern)
Project

**Population structure**
Department of Applied Mathematics and Computer Science
Cognitive Systems
Period: 01/07/2013 → …
Number of participants: 2
Project participant:
Guillot, Gilles (Intern)
Orlando, Ludovic (Ekstern)
Project

**Computational statistical methods in evolutionary biology**
Department of Informatics and Mathematical Modeling
Development of new models, algorithms and programs to analyze genetic variation with application in conservation biology, epidemiology and medicine.
Statistical inference methods for evolutionary biology

Mathematical Statistics

Department of Informatics and Mathematical Modeling
Period: 01/09/2009 → 31/08/2012
Number of participants: 1
Acronym: EMILE
Project ID: 15778
Project Manager, organisational:
Guillot, Gilles (Intern)

Financing sources
Source: Uddannelse, udenlandske offentlige og private
Name of research programme: Uddannelse, udenlandske offentlige og private
Amount: 350,000.00 Danish Kroner

Activities:

ICES
Period: 9 Jun 2015
Gilles Guillot (Participant)
Department of Applied Mathematics and Computer Science
Cognitive Systems

Description
ICES working group on Spatial data

Related event
ICES Working Group on Spatial Fisheries Data
08/06/2015 → 12/06/2015
Denmark, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Member of PhD committee (External organisation)
Period: May 2015
Gilles Guillot (Participant)
Department of Applied Mathematics and Computer Science
Cognitive Systems

Description
Member of PhD committee, mathematics department, Aalborg university

Related external organisation
Model and inference algorithm to combine genetic, phenotypic and geographic information

Period: 29 Apr 2015
Gilles Guillot (Invited speaker)

Department of Applied Mathematics and Computer Science
Cognitive Systems

Description
Recognition of evolutionary units (species, populations) requires integrating several kinds of data, such as genetic or phenotypic markers or spatial information in order to get a comprehensive view concerning the differentiation of the units. We propose a statistical model with a double original advantage: (i) it incorporates information about the spatial distribution of the samples, with the aim to increase inference power and to relate more explicitly observed patterns to geography and (ii) it allows one to analyze genetic and phenotypic data within a unified model and inference framework, thus opening the way to robust comparisons between markers and possibly combined analyses. We show from simulated data as well as real data that our method estimates parameters accurately and is an improvement over alternative approaches in many situations. The power of this method is exemplified using an intricate case of inter- and intraspecies differentiation based on an original data set of georeferenced genetic and morphometric markers obtained on Myodes voles from Sweden. A computer program is made available as an extension of the R package Geneland.

Related event
Species delimitation in the age of genomics
28/04/2015 → 30/04/2015
Canberra, Australia
Activity: Talks and presentations › Conference presentations

10th Danish-French workshop in Spatial Statistics
21/05/2014 → 23/05/2014
Aalborg, Denmark
Activity: Talks and presentations › Conference presentations

Assessment committee PhD Scholarships, DTU compute (External organisation)
Period: 10 Nov 2014
Gilles Guillot (Participant)

Related external organisation
Assessment committee PhD Scholarships, DTU compute
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Workshop on effects of global change on species' range fluctuations using intra-specific genetic variation in both phenotypic and molecular data
Gilles Guillot (Invited speaker)
Department of Applied Mathematics and Computer Science
Cognitive Systems

Related event

Workshop on effects of global change on species' range fluctuations using intra-specific genetic variation in both phenotypic and molecular data
23/10/2014 → 24/10/2014
Seville, Spain
Activity: Talks and presentations › Conference presentations

Lecture
Period: Apr 2014
Gilles Guillot (Lecturer)
Department of Applied Mathematics and Computer Science
Cognitive Systems

Related event

PhD course 2014: Institute Gulbenkian
17/03/2014 → 22/11/2014
Lisbon, Portugal
Activity: Talks and presentations › Conference presentations

Seminar of the Department of Biology
Period: Apr 2014
Gilles Guillot (Participant)
Department of Applied Mathematics and Computer Science
Cognitive Systems

Description
Seminar at the University of Bern

Related event

Seminar of the Department of Biology
07/04/2014 → 10/04/2014
Berne, Switzerland
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Journal of the Royal Statistical Society (Journal)
Period: 1 Jan 2014 → 31 Dec 2014
Gilles Guillot (Editor)
Department of Applied Mathematics and Computer Science
Cognitive Systems

Description
Associate Editor, series A

Related journal

Journal of the Royal Statistical Society
Local database
Activity: Research › Journal editor
Member of the Editorial Board Population Ecology (External organisation)
Period: 1 Jan 2014 → 31 Dec 2014
Gilles Guillot (Participant)
Department of Applied Mathematics and Computer Science
Cognitive Systems

Description
Body type: Journal

Related external organisation

Member of the Editorial Board Population Ecology
Activity: Membership › Board duties in companies, associations, or public organisations

Estimating the phylogenetic history for two related populations A Hidden Markov Model approach to finding phylogenetic trees: A Hidden Markov Model approach to finding phylogenetic trees
Period: Jul 2013
Gilles Guillot (Internal examiner)
Cognitive Systems
Department of Applied Mathematics and Computer Science

Description
Master thesis
Activity: Examinations and supervision › Internal examination

Editorial Board, Journal of Statistical and Econometric Methods (Journal)
Period: 2012 → …
Gilles Guillot (Editor)
Department of Informatics and Mathematical Modeling
Mathematical Statistics

Related journal

Editorial Board, Journal of Statistical and Econometric Methods
Local database
Activity: Research › Journal editor

Journal of the Royal Statistical Society, series A (Journal)
Period: 2012 → 2014
Gilles Guillot (Editor)
Department of Applied Mathematics and Computer Science
Cognitive Systems

Related journal

Journal of the Royal Statistical Society, series A
Local database
Activity: Research › Journal editor

Journal of the Royal Statistical Society, Series A (Journal)
Period: 2012 → …
Gilles Guillot (Editor)
Department of Informatics and Mathematical Modeling
Mathematical Statistics
Related journal

*Journal of the Royal Statistical Society, Series A*
1467-985X
Scopus rating (2016): CiteScore 2.11 SJR 1.368 SNIP 1.69, Web of Science (2018): Indexed yes
Local database
Activity: Research › Journal editor

Spatial Statistics Conference 2012
Period: Dec 2012
Gilles Guillot (Participant)
Department of Informatics and Mathematical Modeling
Mathematical Statistics
Description
Conference talk

Related event

Spatial Statistics Conference 2012
13/12/2012 → 15/12/2012
Miami, United States
Activity: Attending an event › Participating in or organising a conference

Associate Editor, Journal of the Royal Statistical Society, Series A (External organisation)
Period: Jun 2012 → …
Gilles Guillot (Participant)
Department of Informatics and Mathematical Modeling
Mathematical Statistics
Degree of recognition: International

Related external organisation

Associate Editor, Journal of the Royal Statistical Society, Series A
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Population Ecology (External organisation)
Period: 1 Jan 2012 → 31 Dec 2012
Gilles Guillot (Participant)
Department of Informatics and Mathematical Modeling
Mathematical Statistics
Description
Member of the Editorial Board
Editing scientific articles
Degree of recognition: International

Related external organisation

Population Ecology
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

The Geneland program
Period: 1 Jan 2012 → 31 Dec 2012
Gilles Guillot (Participant)
Department of Informatics and Mathematical Modeling
Mathematical Statistics

Description
Maintenance of R package
Activity: Other

The Open Statistics and Probability Journal (External organisation)
Period: 1 Jan 2012 → 31 Dec 2100
Gilles Guillot (Participant)
Department of Informatics and Mathematical Modeling
Mathematical Statistics

Description
Member of the editorial board
Degree of recognition: International

Related external organisation
The Open Statistics and Probability Journal
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Population Ecology (Journal)
Period: 2011 → 2012
Gilles Guillot (Reviewer)
Department of Informatics and Mathematical Modeling
Mathematical Statistics

Description
Population Ecology

Related journal
Population Ecology
1438-3896
Scopus rating (2016): CiteScore 1.69 SJR 0.921 SNIP 0.961, Web of Science (2018): Indexed yes
Local database
Activity: Research › Journal editor

Associate Editor, Population Ecology (External organisation)
Period: 2010 → …
Gilles Guillot (Participant)
Department of Informatics and Mathematical Modeling
Mathematical Statistics
Degree of recognition: International

Related external organisation
Associate Editor, Population Ecology
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Population Ecology (Journal)
Period: 2010 → …
Gilles Guillot (Editor)
Department of Informatics and Mathematical Modeling
Mathematical Statistics
Related journal

Population Ecology
1438-3896
Scopus rating (2016): CiteScore 1.69 SJR 0.921 SNIP 0.961, Web of Science (2018): Indexed yes
Local database
Activity: Research › Journal editor

The Open Statistics & Probability Journal (Journal)
Period: 2010 → …
Gilles Guillot (Editor)
Department of Informatics and Mathematical Modeling
Mathematical Statistics
Description
Editorial Board, The Open Statistics and Probability Journal

Related journal

The Open Statistics & Probability Journal
1876-5270
ISI indexed (2013): ISI indexed no
Central database
Activity: Research › Journal editor

73rd Annual Meeting of the Institute of Mathematical Statistics
Gilles Guillot (Chairman)
Department of Informatics and Mathematical Modeling
Mathematical Statistics
Related event

73rd Annual Meeting of the Institute of Mathematical Statistics: Session on model selecion
09/08/2010 → 13/08/2010
Gothenburg, Sweden
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Population Ecology (Journal)
Period: 1 Jan 2010 → …
Gilles Guillot (Editor)
Department of Informatics and Mathematical Modeling
Mathematical Statistics
Description
Associate Editor

Related journal

Population Ecology
1438-3896
Scopus rating (2016): CiteScore 1.69 SJR 0.921 SNIP 0.961, Web of Science (2018): Indexed yes
Local database
Activity: Research › Journal editor

Period: 1 Jan 2010 → 31 Dec 2010
Gilles Guillot (Reviewer)
Department of Informatics and Mathematical Modeling
Mathematical Statistics

Related journal
Local database
Activity: Research › Peer review of manuscripts

The Open Statistics & Probability Journal (Journal)
Period: 1 Jan 2010 → …
Gilles Guillot (Editor)
Department of Informatics and Mathematical Modeling
Mathematical Statistics

Description
Associate Editor

Related journal
The Open Statistics & Probability Journal
1876-5270
ISI indexed (2013): ISI indexed no
Central database
Activity: Research › Journal editor

Open Statistics and Probability Journal (External organisation)
Period: 2009 → …
Gilles Guillot (Participant)
Department of Informatics and Mathematical Modeling
Mathematical Statistics

Description
Member of the Editorial Board

Related external organisation
Open Statistics and Probability Journal
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Introduction to non-linear models in food science
Period: 6 Dec 2009
Gilles Guillot (Participant)
Department of Informatics and Mathematical Modeling
Mathematical Statistics

Description
Course lecturer

Related event
Introduction to non-linear models in food science
06/12/2009 → 06/12/2009
Activity: Other
Associate Editor Molecular Ecology (External organisation)
Period: 1 Jan 2009 → …
Gilles Guillot (Participant)

Department of Informatics and Mathematical Modeling
Mathematical Statistics

Related external organisation

Associate Editor Molecular Ecology
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Reviewer for Global Ecology and BioGeography, Biometrics, Conservation Genetics (Journal)
Period: 1 Jan 2009 → 31 Dec 2009
Gilles Guillot (Reviewer)

Department of Informatics and Mathematical Modeling
Mathematical Statistics

Related journal

Reviewer for Global Ecology and BioGeography, Biometrics, Conservation Genetics

Local database
Activity: Research › Peer review of manuscripts

Prizes:

Molecular Ecology best reviewer 2013
Gilles Guillot (Recipient)
Department of Applied Mathematics and Computer Science , Cognitive Systems

Details
Awarded date: Jan 2013
Granting Organisations: Molecular Ecology
Prize: Prizes, scholarships, distinctions