Probabilistic structural assessment of conical grouted joint using numerical modelling

Conical grouted joints have been proposed as a solution for the relative settlement observed between the sleeve and the pile on monopiles for wind turbines. In this paper, the influence of the design parameters such as steel wall thicknesses and conical angle on the failure modes associated to continual loadings are assessed based on finite element analysis. It is found that both the sleeve's and pile's wall thicknesses have a significant impact on the grouted joint health. Namely, the larger are the wall thicknesses, the more vulnerable the grout is with respect to fatigue and material degradation but the more limited the progressive settlement is, and inversely. This implies that the appropriate wall thicknesses should be chosen by designers having in mind that neither extreme is conservative. Based on statistical modeling, the grout length is found to be the most influential parameter of the settlement caused by extreme loadings: longer grout significantly contributes to the reduction of extreme settlement. To ensure that the inevitable settlement does not jeopardize the joint's structural integrity, a probability-based method has been developed to estimate the minimal gap between the pile top and the brackets required to achieve a targeted annual reliability index (of 3.3).
Microbial electrolytic disinfection process for highly efficient Escherichia coli inactivation

Water quality deterioration caused by a wide variety of recalcitrant organics and pathogenic microorganisms has become a serious concern worldwide. Bio-electro-Fenton systems have been considered as cost-effective and highly efficient water treatment platform technology. While it has been extensively studied for recalcitrant organics removal, its application potential towards water disinfection (e.g., inactivation of pathogens) is still unknown. This study investigated the inactivation of Escherichia coli in a microbial electrolysis cell based bio-electro-Fenton system (renamed as microbial electrolytic-Fenton cell) with the aim to broaden the application of microbial electrochemistry. Results showed that a 4-log reduction of Escherichia coli (10⁷ to hundreds CFU/mL) was achieved with an external applied voltage of 0.2 V, 0.3 mM Fe²⁺ and cathodic pH of 3.0. However, non-notable inactivation was observed in the control experiments without external voltage or Fe²⁺ dose. The disinfection effect was enhanced when cathode air flow rate increased from 7 to 41 mL/min and was also in proportion to the increase of Fe²⁺ concentration from 0.15 to 0.45 mmol/mL. Fatal cell membrane destruction by [rad]OH was identified as one potential mechanism for disinfection. This study successfully demonstrated the feasibility of bio-electro-Fenton process for pathogens inactivation, which offers insight for the future development of sustainable, efficient, and cost-effective biological water treatment technology.

General information
State: Published
Organisations: Department of Environmental Engineering, Residual Resource Engineering, South China University of Technology, Technical University of Denmark
Authors: Zhou, S. (Ekstern), Huang, S. (Ekstern), Li, X. (Intern), Angelidaki, I. (Intern), Zhang, Y. (Intern)
Pages: 220-227
Publication date: 15 Jun 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Chemical Engineering Journal
Volume: 342
ISSN (Print): 1385-8947
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.18
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.16
Climate change risks for severe storms in developing countries in the context of poverty and inequality in Cambodia

Least developed countries are generally regarded as particularly sensitive to climate change due to among other vulnerable locations and low adaptation capabilities. In the present study, we address climate change hazards in least developed countries by presenting a methodological framework, which is suitable for the estimation damage costs as a function of risk aversion, equality, income distribution and climate scenario using state-of-the-art climate model projections. As a case study, the methodology is applied to study severe storms in Cambodia based on two future climate scenarios and data on historical damages from storm events, which are used as a proxy in performing a sensitivity analysis on all input parameters. For the assumptions and parameter ranges used here, the study shows a high sensitivity to the income distribution (reflected by discount rates) and risk aversion and smaller effects from equality measures and extreme wind climate scenario. We emphasize that the assumptions on risk aversion reflecting consumption smoothing possibilities of low-income households clearly depicts that climate risks can be particularly high as a consequence of poverty and therefore recommend that context-specific vulnerabilities and equity concerns in climate risk studies should be included when making assessments for least developed countries.

General information
State: Accepted/In press
Organisations: Department of Management Engineering, Systems Analysis
Authors: Halsnæs, K. (Intern), Larsen, M. A. D. (Intern), Kaspersen, P. S. (Intern)
Number of pages: 18
Publication date: 12 Jun 2018
Transcriptional profiles of PBMCs from pigs infected with three genetically diverse porcine reproductive and respiratory syndrome virus strains

Porcine reproductive and respiratory syndrome virus is the cause of reproductive failure in sows and respiratory disease in young pigs, which has been considered as one of the most costly diseases to the worldwide pig industry for almost 30 years. This study used microarray-based transcriptomic analysis of PBMCs from experimentally infected pigs to explore the patterns of immune dysregulation after infection with two East European PRRSV strains from subtype 2 (BOR and ILI) in comparison to a Danish subtype 1 strain (DAN). Transcriptional profiles were determined at day 7 post infection in three tested groups of pigs and analysed in comparison with the expression profile of control group. Microarray analysis
revealed differential regulation (> 1.5-fold change) of 4253 and 7335 genes in groups infected with BOR and ILI strains, respectively, and of 12518 genes in pigs infected with Danish strain. Subtype 2 PRRSV strains showed greater induction of many genes, especially those involved in innate immunity, such as interferon stimulated antiviral genes and inflammatory markers. Functional analysis of the microarray data revealed a significant up-regulation of genes involved in processes such as acute phase response, granulocyte and agranulocyte adhesion and diapedesis, as well as down-regulation of genes enrolled in pathways engaged in protein synthesis, cell division, as well as B and T cell signaling. This study provided an insight into the host response to three different PRRSV strains at a molecular level and demonstrated variability between strains of different pathogenicity level.

**General information**

State: Accepted/In press  
Organisations: National Veterinary Institute, National Veterinary Research Institute, Warsaw University of Life Sciences (SGGW)  
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Pages: 1-14  
Publication date: 7 Jun 2018  
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Molecular Biology Reports  
ISSN (Print): 0301-4851  
Ratings:  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Scopus rating (2017): CiteScore 1.8 SJR 0.721 SNIP 0.689  
Web of Science (2017): Indexed Yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): CiteScore 1.84 SJR 0.736 SNIP 0.768  
BFI (2015): BFI-level 1  
Scopus rating (2015): SJR 0.761 SNIP 0.75 CiteScore 1.83  
BFI (2014): BFI-level 1  
Scopus rating (2014): SJR 0.753 SNIP 0.919 CiteScore 2.04  
BFI (2013): BFI-level 1  
Scopus rating (2013): SJR 0.715 SNIP 0.853 CiteScore 1.97  
ISI indexed (2013): ISI indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): SJR 0.658 SNIP 1.014 CiteScore 2.23  
ISI indexed (2012): ISI indexed yes  
BFI (2011): BFI-level 1  
Scopus rating (2011): SJR 0.77 SNIP 1.13 CiteScore 2.17  
ISI indexed (2011): ISI indexed yes  
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 0.449 SNIP 0.655  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 0.449 SNIP 0.606  
BFI (2008): BFI-level 1  
Scopus rating (2008): SJR 0.541 SNIP 0.528  
Scopus rating (2007): SJR 0.502 SNIP 0.425  
Scopus rating (2006): SJR 0.546 SNIP 0.336  
Scopus rating (2005): SJR 0.586 SNIP 0.46  
Scopus rating (2004): SJR 0.543 SNIP 0.263  
Scopus rating (2003): SJR 0.357 SNIP 0.166  
Scopus rating (2002): SJR 0.729 SNIP 0.397  
Web of Science (2002): Indexed yes  
Scopus rating (2001): SJR 0.779 SNIP 0.259  
Scopus rating (2000): SJR 1.251 SNIP 0.369
Echinococcus multilocularis in Denmark 2012–2015: high local prevalence in red foxes

In Western Europe, the Echinococcus multilocularis lifecycle is predominantly sylvatic, typically involving red foxes (Vulpes vulpes) as the main definitive hosts with Microtus spp. and Arvicola spp. as intermediate hosts. During a 4-year surveillance study (2012–2015), Danish red foxes and raccoon dogs (n = 1345) were examined for E. multilocularis. Moreover, 134 insectivores and rodents collected in South Jutland during spring and summer 2016 were examined for the presence of metacestodes. The sedimentation and counting technique and molecular typing were used to identify E. multilocularis infections in the carnivores, while the rodent livers were examined macro- and microscopically for parasite lesions. Following morphological identification of E. multilocularis adult worms, the identity was verified by sequence analysis of the 12S rRNA gene in most cases (n = 13). Echinococcus multilocularis infection was demonstrated in 19 red foxes (Vulpes vulpes) originating from only two specific areas of South Jutland, namely Højer and Grindsted, and in two raccoon dogs (Nyctereutes procyonoides), originating from Højer. In Højer, 28.5% (CI 95% 11.7–45.3) of the examined red foxes were E. multilocularis positive per year. Moreover, positive red foxes were identified each year from 2012 to 2015, while E. multilocularis positive red foxes were only identified in Grindsted in 2013 (4.0%) and 2014 (6.4%). In contrast, all collected rodents were negative for E. multilocularis. We conclude that E. multilocularis is locally endemic in South Jutland with a high local prevalence in Højer.
Transcriptome analysis of the adult human Klinefelter testis and cellularity-matched controls reveals disturbed differentiation of Sertoli- and Leydig cells

The most common human sex chromosomal disorder is Klinefelter syndrome (KS; 47,XXY). Adult patients with KS display a diverse phenotype but are nearly always infertile, due to testicular degeneration at puberty. To identify mechanisms causing the selective destruction of the seminiferous epithelium, we performed RNA-sequencing of 24 fixed paraffin-embedded testicular tissue samples. Analysis of informative transcriptomes revealed 235 differentially expressed transcripts (DETs) in the adult KS testis showing enrichment of long non-coding RNAs, but surprisingly not of X-chromosomal transcripts. Comparison to 46,XY samples with complete spermatogenesis and Sertoli cell-only-syndrome allowed prediction of the cellular origin of 71 of the DETs. DACH2 and FAM9A were validated by immunohistochemistry and found to mark apparently undifferentiated somatic cell populations in the KS testes. Moreover, transcriptomes from fetal, pre-pubertal, and adult KS testes showed a limited overlap, indicating that different mechanisms are likely to operate at each developmental stage. Based on our data, we propose that testicular degeneration in men with KS is a consequence of germ cells loss initiated during early development in combination with disturbed maturation of Sertoli- and Leydig cells.

General information
State: Published
Organisations: Department of Bio and Health Informatics, DTU Multi Assay Core, Aarhus University, Copenhagen University Hospital, University of Copenhagen
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Number of pages: 14
Publication date: 1 Jun 2018
Kinetic Modeling of Texture and Color Changes During Thermal Treatment of Chicken Breast Meat

Heat treatment is commonly applied as a primary method for ensuring the microbial safety of poultry meat and to enhance its palatability. Although texture and color of cooked chicken breast meat are important quality parameters for the consumers that need to be controlled during thermal processing, studies assessing the temperature-time-dependent quality changes during thermal treatment are lacking. This work aims to investigate the texture and color changes of chicken breast meat during thermal processing and to develop kinetic models that describe these changes. We studied the storage modulus changes of chicken breast meat as function of temperature. The storage modulus increases from 55 °C until leveling off in an equilibrium value above 80 °C, which was attributed to microstructure changes and described with a sigmoidal function. The changes in the texture (TPA) and color (CIE L a b ) of chicken breast meat were measured as function of temperature and time. The texture and color parameters show a rise with heating time until reaching an equilibrium value, while the rate of change increased with temperature. Kinetic models that take the non-zero equilibrium into account were developed to describe the color (lightness) and texture (hardness, gumminess, and chewiness) changes with heating time and temperature. The kinetic models provide a deeper insight into the mechanisms of texture and color changes during thermal treatment. They can be used to predict the texture and color development of chicken breast meat during thermal processing and, thus, help to optimize the process.

General information
State: Published
Organisations: National Food Institute, Research Group for Food Production Engineering
Authors: Rabeler, F. (Intern), Feyissa, A. H. (Intern)
Pages: 1495–1504
Publication date: 1 Jun 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Food and Bioprocess Technology
Volume: 11
Issue number: 8
ISSN (Print): 1935-5130
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.14 SJR 1.29 SNIP 1.194
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Phone-based metric as a predictor for basic personality traits

Basic personality traits are believed to be expressed in, and predictable from, smart phone data. We investigate the extent of this predictability using data (n = 636) from the Copenhagen Network Study, which to our knowledge is the most extensive study concerning smartphone usage and personality traits. Based on phone usage patterns, earlier studies have reported surprisingly high predictability of all Big Five personality traits. We predict personality trait tertiles (low, medium, high) from a set of behavioral variables extracted from the data, and find that only extraversion can be predicted significantly better (35.6%) than by a null model. Finally, we show that the higher predictabilities in the literature are likely due to overfitting on small datasets.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Cognitive Systems, University of Copenhagen
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Pages: 16-22
Publication date: 1 Jun 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Research in Personality
Volume: 74
ISSN (Print): 0092-6566
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 1.248 SJR 1.787 CiteScore 3.07
Scopus rating (2016): CiteScore 2.71 SNIP 1.312 SJR 1.595
Scopus rating (2015): CiteScore 2.76 SNIP 1.367 SJR 1.815
Scopus rating (2014): CiteScore 2.46 SNIP 1.306 SJR 1.796
Scopus rating (2013): CiteScore 2.89 SNIP 1.345 SJR 1.819
Scopus rating (2012): CiteScore 2.38 SNIP 1.228 SJR 1.693
Effects of oil spill response technologies on the physiological performance of the Arctic copepod Calanus glacialis

A mesocosm study with oil in ice was performed in Van Mijenfjorden in Svalbard to compare effects of the oil spill responses (OSR) in situ burning, chemical dispersion and natural attenuation on the physiological performance of the Arctic copepod Calanus glacialis. Seawater collected from the mesocosms in winter and spring was used in laboratory incubation experiments, where effects on fecal pellet production, egg production and hatching success were investigated over a period of 14 days. Polycyclic aromatic hydrocarbon (PAH) seawater concentrations were lowest in winter. Brine channel formation in spring resulted in an 18 times increase in PAH concentration in the chemical dispersion treatment (1.67 μg L⁻¹), and a 3 fold increase in the natural attenuation (0.36 μg L⁻¹) and in situ burning (0.04 μg L⁻¹) treatments. The physiological performance of female C. glacialis was unaffected by the PAH seawater concentrations. However, a higher mortality and deformity of nauplii was observed in the chemical dispersion treatment, highlighting the importance of considering secondary effects on next generation in future environmental risk assessment of OSR. This study shows that during the ice-covered period, chemical dispersion of oil spills leads to higher PAH exposure than natural attenuation and in situ burning, with potential consequences for recruitment of Arctic copepods.

General information

State: Published
Organisations: National Institute of Aquatic Resources, Section for Oceans and Arctic, Centre for Ocean Life, COWI AS, University Centre in Svalbard, Cedre
Authors: Toxværd, K. (Intern), Pančić, M. (Intern), Eide, H. O. (Ekstern), Søreide, J. E. (Ekstern), Lacroix, C. (Ekstern), Le Floch, S. (Ekstern), Hjorth, M. (Ekstern), Nielsen, T. G. (Intern)
Pages: 65-76
Publication date: 1 Jun 2018
Main Research Area: Technical/natural sciences

Publication Information
Journal: Aquatic Toxicology
Volume: 199
ISSN (Print): 0166-445X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.233 SJR 1.456 CiteScore 4.18
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.38 SJR 1.627 SNIP 1.382
Web of Science (2016): Indexed yes
Enzyme-assisted peeling of cold water shrimps (Pandalus borealis)

An enzymatic method to facilitate the peeling of cold water shrimps (Pandalus borealis) was developed. The protease solutions were used to mature the shrimps to promote shell-loosening prior to peeling. The efficiency of peeling enzyme-treated shrimps was evaluated by a new quantitative measurement based on the tensile force, presented as a peelability profile. It was found that enzymatic maturation efficiently improved the peelability of shrimps. The factors affecting the peelability of the enzyme-matured shrimps were the type of enzyme, enzyme concentration and maturation duration, while changes in pH had no impact. Maturation of shrimps in solutions of the endoproteases Endocut-01L (180 NU/g) and
Endocut-03L (60 U/g) and the exoprotease Exocut-A0 (100 U/g) resulted in better peelability compared to shrimps matured in endoprotease Tail21 (65 U/mL) and 2% NaCl. A combination of 0.25% Endocut-03L and 0.25% Exocut-A0 for 20 h resulted in the best peeling of shrimps (100% completely peeled shrimps, 3 mJ/g work and 89% meat yield). Reuse of the enzyme solution was possible due to a 95% retention rate of proteolytic activity after two 20-h cycles of maturation. The studied enzymatic maturation offered a better shrimp product with respect to texture and color in comparison with an industrial brine-matured reference, i.e., ~22% higher redness and ~31% higher hardness. Industrial relevance: Enzymatic maturation is an attempt made as a pre-treatment to facilitate the removal of the shell from meat of shrimp. This approach would benefit the shrimp processing industry by 1) enhancing peeling efficiency that includes least efforts to remove the shell, high rate of completely peeled shrimps and high meat yield; 2) shortening the duration of maturation but still sufficiently loosening the shell for machine peeling; 3) performing as a chemical-free peeling aid, which may increase the preference of consumers over chemical compounds; and 4) being environmentally friendly since disposal of enzyme waste is harmless to the environment.

General information
State: Published
Organisations: National Food Institute, Research Group for Food Production Engineering, University of Copenhagen, Royal Greenland A/S
Authors: Dang, T. T. (Ekstern), Gringer, N. (Intern), Jessen, F. (Intern), Olsen, K. (Ekstern), Bøknæs, N. (Ekstern), Nielsen, P. L. (Ekstern), Orlien, V. (Ekstern)
Number of pages: 9
Pages: 127-135
Publication date: 1 Jun 2018
Main Research Area: Technical/natural sciences

Publication Information
Journal: Innovative Food Science and Emerging Technologies
Volume: 47
ISSN (Print): 1466-8564
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 1.201 SNIP 1.194 CiteScore 3.24
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.54 SJR 1.431 SNIP 1.386
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.675 SNIP 1.495 CiteScore 3.48
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.583 SNIP 1.672 CiteScore 3.67
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.374 SNIP 1.649 CiteScore 3.16
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.718 SNIP 1.902 CiteScore 3.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.711 SNIP 1.853 CiteScore 3.65
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.555 SNIP 1.482
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.252 SNIP 1.13
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.146 SNIP 1.213
Estimation and Control of Wind Turbine Tower Vibrations Based on Individual Blade-Pitch Strategies

In this brief, we present a method to estimate the tower fore-aft velocity based upon measurements from blade load sensors. In addition, a tower dampening control strategy is proposed based upon an individual blade pitch control architecture that employs this estimate. The observer design presented in this brief exploits the Coleman transformations that convert a time-varying turbine model into one that is linear and time-invariant, greatly simplifying the observability analysis and subsequent observer design. The proposed individual pitch-based tower controller is decoupled from the rotor speed regulation loop and hence does not interfere with the nominal turbine power regulation. Closed-loop results, obtained from high fidelity turbine simulations, show close agreement between the tower estimates and the actual tower velocity. Furthermore, the individual-pitch-based tower controller achieves a similar performance compared with the collective-pitch-based approach but with negligible impact upon the nominal turbine power output.

General information
State: Accepted/In press
Organisations: Technical University of Denmark, Department of Wind Energy, Wind turbine loads & control, University of Sheffield
Authors: Lio, W. H. (Intern), Jones, B. L. (Ekstern), Rossiter, J. A. (Ekstern)
Publication date: 16 May 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: IEEE Transactions on Control Systems Technology
ISSN (Print): 1063-6536
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 5.89 SJR 1.832 SNIP 2.728
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.17 SJR 1.655 SNIP 2.643
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.966 SNIP 2.798 CiteScore 4.72
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.786 SNIP 3.006 CiteScore 4.34
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.707 SNIP 3.41 CiteScore 4.41
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Corrigendum: An analysis of natural T cell responses to predicted tumor neoepitopes [Front Immunol, 8, 1566, (2017)]

An outdated version of Supplementary Table 1 was uploaded to the final version of the paper for publication. This table has not been under peer review and does not include the information described in the paper such as the similarity measurement column. The correct Supplementary Table 1 has now been published in the original article. The authors apologize for this oversight. This error does not change the scientific conclusion of the article in any way. The original article has been updated.

General information
State: Published
Organisations: Department of Bio and Health Informatics, Cancer Genomics, Immunoinformatics and Machine Learning, Technical University of Denmark, National Veterinary Institute, T-cells & Cancer, Universidad Nacional de San Martin
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Publication date: 14 May 2018
Main Research Area: Technical/natural sciences

Publication Information
Journal: Frontiers in Immunology
Volume: 9
Issue number: MAY
ISSN (Print): 1664-3224
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Understanding the impact of non-standard customisations in an engineer-to-order context: A case study

Companies operating with an engineer-to-order (ETO) manufacturing strategy produce customised solutions for their customers. While they may be able to build on a base of existing sub-solutions, e.g. standard product structures, modules or parts when engineering a customer-specific solution, they often have to create something completely new to satisfy customers’ requirements. However, it is not always clear to ETO companies what the costs associated with making customer specific solutions are, or which product or project characteristics drive costs and in what business processes. Therefore, it is not clear to companies if it is actually profitable for them to fulfil all of their customers’ requirements. Hence, making it relevant to understand how creating non-standard customisations impact project profitability. This paper presents a framework for how ETO companies can quantify the impact of the complexity associated with non-standard customisations when cost data is only available at the project level. The framework is theoretically founded; it is based on statistical regression and a definition of a complexity index for non-standard customisations. The framework is validated in the context of an ETO case company and empirical data is presented.
Objectives: We describe factors associated with and barriers to initiation of Direct Acting Antiviral (DAA) treatment in patients with chronic hepatitis C, who fulfill national fibrosis treatment guidelines in Denmark. Materials and Methods: In this nationwide cohort study, we included patients with chronic hepatitis C from The Danish Database for Hepatitis B and C (DANHEP) who fulfilled fibrosis treatment criteria. Factors associated with treatment initiation and treatment failure were determined by logistic regression analyses. Medical records were reviewed from patients who fulfilled fibrosis treatment criteria, but did not initiate DAA treatment to determine the cause. Results: In 344 (49%) of 700 patients, who fulfilled treatment criteria, factors associated with DAA treatment initiation were transmission by other routes than injecting drug use odds ratio (OR) 2.13 (CI: 1.38–3.28), previous treatment failure OR 2.58 (CI: 1.84–3.61) and ALT above upper limit of
normal OR 1.60 (CI: 1.18–2.17). The most frequent reasons for not starting treatment among 356 (51%) patients were non-adherence to medical appointments (n=107/30%) and ongoing substance use (n=61/17%). Treatment failure with viral relapse occurred in 19 (5.5%) patients, who were more likely to have failed previous treatment OR 4.53 (CI: 1.59–12.91). Conclusions: In this nationwide cohort study, we found non-adherence to medical appointments and active substance use to be major obstacles for DAA treatment initiation. Our findings highlight the need for interventions that can overcome these barriers and increase the number of patients who can initiate and benefit from curative DAA treatment.

**General information**

State: Accepted/In press
Organisations: Department of Bio and Health Informatics, Disease Intelligence and Molecular Evolution, University of Copenhagen, Aalborg University, Hospital Lillebaelt, University of Southern Denmark, Aarhus University
Authors: Sølund, C. (Ekstern), Hallager, S. (Ekstern), Pedersen, M. S. (Ekstern), Fahnæ, U. (Ekstern), Ernst, A. (Ekstern), Krrapu, H. B. (Ekstern), Rege, B. T. (Ekstern), Christensen, P. B. (Ekstern), Laursen, A. L. (Ekstern), Christensen, J. (Ekstern), Béland, E. (Ekstern), Madsen, L. G. (Ekstern), Schønning, K. (Ekstern), Pedersen, A. G. (Intern), Bukh, J. (Ekstern), Weis, N. (Ekstern)
Pages: 1-8
Publication date: 2 May 2018

**Publication information**

Journal: Scandinavian Journal of Gastroenterology
ISSN (Print): 0036-5521
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): SNIP 0.91 SJR 1.226 CiteScore 2.35
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 2.38 SJR 1.108 SNIP 0.918
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 0.947 SNIP 0.764 CiteScore 2.19
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 1.072 SNIP 0.999 CiteScore 2.44
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 0.122 SNIP 0.987 CiteScore 2.33
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.111 SNIP 1.023 CiteScore 2.23
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 0.107 SNIP 0.916 CiteScore 1.97
- ISI indexed (2011): ISI indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 0.107 SNIP 0.824
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 0.171 SNIP 0.823
- BFI (2008): BFI-level 1
- Scopus rating (2008): SJR 0.232 SNIP 0.882
- Scopus rating (2007): SJR 0.304 SNIP 1.248
- Scopus rating (2006): SJR 0.692 SNIP 1.429
- Scopus rating (2005): SJR 0.531 SNIP 0.834
- Scopus rating (2004): SJR 0.539 SNIP 0.971
- Scopus rating (2003): SJR 0.552 SNIP 0.738
- Web of Science (2003): Indexed yes
CD103⁺ CD11b⁺ mucosal classical dendritic cells initiate long-term switched antibody responses to flagellin

Antibody responses induced at mucosal and nonmucosal sites demonstrate a significant level of autonomy. Here, we demonstrate a key role for mucosal interferon regulatory factor-4 (IRF4)-dependent CD103⁺ CD11b⁺ (DP), classical dendritic cells (cDCs) in the induction of T-dependent immunoglobulin G (IgG) and immunoglobulin A (IgA) responses in the mesenteric lymph node (MLN) following systemic immunization with soluble flagellin (sFliC). In contrast, IRF8-dependent CD103⁺ CD11b⁻ (SP) are not required for these responses. The lack of this response correlated with a complete absence of sFliC-specific plasma cells in the MLN, small intestinal lamina propria, and surprisingly also the bone marrow (BM). Many sFliC-specific plasma cells accumulating in the BM of immunized wild-type mice expressed α4β7, suggesting a mucosal origin. Collectively, these results suggest that mucosal DP cDC contribute to the generation of the sFliC-specific plasma cell pool in the BM and thus serve as a bridge linking the mucosal and systemic immune system.

General information
State: Published
Organisations: Section for Immunology and Vaccinology, National Veterinary Institute, Mucosal Immunology, University of Birmingham, Lund University
Pages: 681-692
Publication date: 1 May 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Mucosal Immunology
Volume: 11
Issue number: 3
ISSN (Print): 1933-0219
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 6.63 SJR 4.314 SNIP 1.518
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 6.36 SJR 4.464 SNIP 1.525
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 4.401 SNIP 1.447 CiteScore 6.53
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 4.597 SNIP 1.686 CiteScore 6.82
Scopus rating (2013): SJR 4.076 SNIP 1.623 CiteScore 6.75
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): SJR 3.999 SNIP 1.631 CiteScore 6.69
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Scopus rating (2011): SJR 4.534 SNIP 1.452 CiteScore 6.66
ISI indexed (2011): ISI indexed yes
Transcription factor co-expression networks of adipose RNA-Seq data reveal regulatory mechanisms of obesity

Background: Transcription Factors (TFs) control actuation of genes in the genome and are key mediators of complex processes such as obesity. Master Regulators (MRs) are the genes at the top of a regulation hierarchy which regulate other genes. Objective: To elucidate clusters of highly co-expressed TFs (modules), involved pathways, highly interconnected TFs (hub-TFs) and MRs leading to obesity and leanness, using porcine model for human obesity.

Methods: We identified 817 expressed TFs in RNA-Sequencing dataset representing extreme degrees of obesity (DO; lean, obese). We built a single Weighted Transcription Factor Co-expression Network (WTFCN) and TF sub-networks (based on the DO). Hub-TFs and MRs (using iRegulon) were identified in biologically relevant WTFCNs modules. Results: Single WTFCN detected the Red module significantly associated with DO (P < 0.03). This module was enriched for regulation processes in the immune system, e.g.: Immune system process (Padj = 2.50E-06) and metabolic lifestyle disorders, e.g. Circadian rhythm - mammal pathway (Padj = 2.33E-11). Detected MR, hub-TF SPI1 was involved in obesity, immunity and osteoporosis. Within the obese sub-network, the Red module suggested possible associations with immunity, e.g. TGF-beta signaling pathway (Padj = 1.73E-02) and osteoporosis, e.g. Osteoclast differentiation (Padj = 1.94E-02). Within the lean sub-network, the Magenta module displayed associations with type 2 diabetes, obesity and osteoporosis e.g. Notch signaling pathway (Padj = 2.40E-03), osteoporosis e.g. hub-TF VDR (a prime candidate gene for osteoporosis). Conclusion: Our results provide insights into the regulatory network of TFs and biologically relevant hub TFs in obesity.
Dissection of the antimicrobial and hemolytic activity of Cap18: Generation of Cap18 derivatives with enhanced specificity

Due to the rapid emergence of resistance to classical antibiotics, novel antimicrobial compounds are needed. It is desirable to selectively kill pathogenic bacteria without targeting other beneficial bacteria in order to prevent the negative clinical consequences caused by many broad-spectrum antibiotics as well as reducing the development of antibiotic resistance. Antimicrobial peptides (AMPs) represent an alternative to classical antibiotics and it has been previously demonstrated that Cap18 has high antimicrobial activity against a broad range of bacterial species. In this study we report the design of a positional scanning library consisting of 696 Cap18 derivatives and the subsequent screening for antimicrobial activity against Y. ruckeri, A. salmonicida, S. Typhimurium and L. lactis as well as for hemolytic activity measuring the hemoglobin release of horse erythrocytes. We show that the hydrophobic face of Cap18, in particular I13, L17 and I24, is essential for its antimicrobial activity against S. Typhimurium, Y. ruckeri, A. salmonicida, E. coli, P. aeruginosa, L. lactis, L. monocytogenes and E. faecalis. In particular, Cap18 derivatives harboring a I13D, L17D, L17P, I24D or I24N substitution lost their antimicrobial activity against any of the tested bacterial strains. In addition, we were able to generate species-specific Cap18 derivatives by particular amino acid substitutions either in the hydrophobic face at positions L6, L17, I20, and I27, or in the hydrophilic face at positions K16 and K18. Finally, our data showed the proline residue at position 29 to be essential for the inherent low hemolytic activity of Cap18 and that substitution of the residues K16, K23 or G21 by any hydrophobic residues enhances the hemolytic activity. This study demonstrates the potential of generating species-specific AMPs for the selective elimination of bacterial pathogens.
Breakfast in human nutrition: The international breakfast research initiative

Breakfast is often referred to as the most important meal of the day and in recent years has been implicated in weight control, cardio-metabolic risk factors and cognitive performance although, at present, the literature remains inconclusive as to the precise health benefits of breakfast. There are extensive reports of breakfast’s contributions to daily food and nutrient intakes, as well as many studies that have compared daily food and nutrient intakes by breakfast consumers and skippers. However, significant variation exists in the definitions of breakfast and breakfast skippers, and in methods used to relate breakfast nutrient intakes to overall diet quality. The present review describes a novel and harmonised approach to the study of the nutritional impact of breakfast through The International Breakfast research Initiative involving national dietary survey data from Canada, Denmark, France, Spain, the UK and the USA. It is anticipated that the analysis of such data along harmonised lines, will allow the project to achieve its primary goal of exploring approaches to defining optimal breakfast food and nutrient intakes. Such data will be of value to public health nutrition policy-makers and food manufacturers and will also allow consistent messaging to help consumers to optimize food choices at breakfast.

General information
Compressive Online Robust Principal Component Analysis Via n-$\ell_1$ Minimization

This work considers online robust principal component analysis (RPCA) in time-varying decomposition problems such as video foreground-background separation. We propose a compressive online RPCA algorithm that decomposes recursively a sequence of data vectors (e.g., frames) into sparse and low-rank components. Different from conventional batch RPCA, which processes all the data directly, our approach considers a small set of measurements taken per data vector (frame). Moreover, our algorithm can incorporate multiple prior information from previous decomposed vectors via proposing an n-$\ell_1$ minimization method. At each time instance, the algorithm recovers the sparse vector by solving the n-$\ell_1$ minimization problem, which promotes not only the sparsity of the vector but also its correlation with multiple previously-recovered sparse vectors; and subsequently, updates the low-rank component using incremental singular value decomposition. We also establish theoretical bounds on the number of measurements required to guarantee successful compressive separation under the assumptions of static or slowly-changing low-rank components.
We evaluate the proposed algorithm using numerical experiments and online video foreground-background separation experiments. The experimental results show that the proposed method outperforms the existing methods.
Spatio-temporal pattern formation in predator-prey systems with fitness taxis

We pose a spatial predator–prey model in which the movement of animals is not purely diffusive, but also contains a drift term in the direction of higher specific growth rates. We refer to this as fitness taxis. We conduct a linear stability analysis of the resulting coupled reaction–advection–diffusion equations and derive conditions under which spatial patterns form. We find that for some parameters the problem is ill posed and short waves grow with unbounded speeds. To eliminate this, we introduce spatial kernels in the model, yielding coupled integro-differential equations, and conduct a similar stability analysis for this system. Through numerical simulation, we find that a variety of patterns can emerge, including stationary spatial patterns, standing and travelling waves, and seemingly chaotic spatio-temporal patterns. We argue that fitness taxis represents a simple and generic extension of diffusive motion, is ecologically plausible, and provides an alternative mechanism for formation of patterns in spatially explicit ecosystem models, with emphasis on non-stationary spatio-temporal dynamics.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Centre for Ocean Life, National Institute of Aquatic Resources, Dynamical Systems, Center for Intelligent Drug Delivery and Sensing Using Microcontainers and Nanomechanics, Technical University of Denmark, Center for Ocean Life
Authors: Heilmann, I. T. (Intern), Thygesen, U. H. (Intern), Sørensen, M. P. (Intern)
Pages: 44-57
Publication date: 1 May 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Ecological Complexity
Volume: 34
ISSN (Print): 1476-945X
Ratings:
  BFI (2018): BFI-level 1
  Web of Science (2018): Indexed yes
  BFI (2017): BFI-level 1
  Scopus rating (2017): SNIP 0.856 SJR 0.753 CiteScore 1.7
  Web of Science (2017): Indexed yes
  BFI (2016): BFI-level 1
  Scopus rating (2016): CiteScore 2.11 SJR 0.824 SNIP 1.017
  Web of Science (2016): Indexed yes
  BFI (2015): BFI-level 1
  Scopus rating (2015): SJR 0.914 SNIP 1.071 CiteScore 2.01
  Web of Science (2015): Indexed yes
  BFI (2014): BFI-level 1
  Scopus rating (2014): SJR 0.898 SNIP 1.48 CiteScore 2.53
  BFI (2013): BFI-level 1
  Scopus rating (2013): SJR 1.085 SNIP 1.635 CiteScore 3.29
  ISI indexed (2013): ISI indexed yes
  BFI (2012): BFI-level 1