The fungal genus of Aspergillus is highly interesting, containing everything from industrial cell factories, model organisms, and human pathogens. In particular, this group has a prolific production of bioactive secondary metabolites (SMs). In this work, four diverse Aspergillus species (A. campestris, A. novofumigatus, A. ochraceoroseus, and A. steynii) have been whole-genome PacBio sequenced to provide genetic references in three Aspergillus sections. A. taichungensis and A. candidus also were sequenced for SM elucidation. Thirteen Aspergillus genomes were analyzed with comparative genomics to determine phylogeny and genetic diversity, showing that each presented genome contains 15–27% genes not found in other sequenced Aspergilli. In particular, A. novofumigatus was compared with the pathogenic species A. fumigatus. This suggests that A. novofumigatus can produce most of the same allergens, virulence, and pathogenicity factors as A. fumigatus, suggesting that A. novofumigatus could be as pathogenic as A. fumigatus. Furthermore, SMs were linked to gene clusters based on biological and chemical knowledge and analysis, genome sequences, and predictive algorithms. We thus identify putative SM clusters for aflatoxin, chlorflavonin, and ochrindol in A. ochraceoroseus, A. campestris, and A. steynii, respectively, and novofumigatonin, ent-cycloechinulin, and epi-aszonalenins in A. novofumigatus. Our study delivers six fungal genomes, showing the large diversity found in the Aspergillus genus; highlights the potential for discovery of beneficial or harmful SMs; and supports reports of A. novofumigatus pathogenicity. It also shows how biological, biochemical, and genomic information can be combined to identify genes involved in the biosynthesis of specific SMs.
Approximation of ruin probabilities via Erlangized scale mixtures

In this paper, we extend an existing scheme for numerically calculating the probability of ruin of a classical Cramér–Lundberg reserve process having absolutely continuous but otherwise general claim size distributions. We employ a dense class of distributions that we denominate Erlangized scale mixtures (ESM) that correspond to nonnegative and absolutely continuous distributions which can be written as a Mellin–Stieltjes convolution $\Pi \ast G$ of a nonnegative distribution $\Pi$ with an Erlang distribution $G$. A distinctive feature of such a class is that it contains heavy-tailed distributions. We suggest a simple methodology for constructing a sequence of distributions having the form $\Pi \ast G$ with the purpose of approximating the integrated tail distribution of the claim sizes. Then we adapt a recent result which delivers an explicit expression for the probability of ruin in the case that the claim size distribution is modeled as an Erlangized scale mixture. We provide simplified expressions for the approximation of the probability of ruin and construct explicit bounds for the error of approximation. We complement our results with a classical example where the claim sizes are heavy-tailed.

General information

State: Published
Organisations: Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, University of Liverpool, University of Queensland
Authors: Peralta, O. (Intern), Rojas-Nandayapa, L. (Ekstern), Xie, W. (Ekstern), Yao, H. (Ekstern)
Pages: 136-156
Publication date: 1 Jan 2018
Main Research Area: Technical/natural sciences
Selecting of a cytochrome P450<sub>cam</sub> SeSaM library with 3-chloroindole and endosulfan – Identification of mutants that dehalogenate 3-chloroindole

Cytochrome P450<sub>cam</sub> (a camphor hydroxylase) from the soil bacterium Pseudomonas putida shows potential importance in environmental applications such as the degradation of chlorinated organic pollutants. Seven P450<sub>cam</sub> mutants generated from Sequence Saturation Mutagenesis (SeSaM) and isolated by selection on minimal media with either 3-chloroindole or the insecticide endosulfan were studied for their ability to oxidize of 3-chloroindole to isatin. The wild-type enzyme did not accept 3-chloroindole as a substrate. Mutant (E156G/V247F/V253G/F256S) had the highest maximal velocity in the conversion of 3-chloroindole to isatin, whereas mutants (T56A/N116H/D297N) and (G60S/Y75H) had highest \( \frac{k_{cat}}{K_M} \) values. Six of the mutants had more than one mutation, and within this set, mutation of residues 297 and 179 was observed twice. Docking simulations were performed on models of the mutant enzymes; the wild-type did not accommodate 3-chloroindole in the active site, whereas all the mutants did. We propose two potential reaction pathways for dechlorination of 3-chloroindole. This article is part of a Special Issue entitled: Cytochrome P450 biodiversity and biotechnology, edited by Erika Plettner, Gianfranco Gilardi, Luet Wong, Vlada Urlacher, Jared Goldstone.

General information

State: Published
Organisations: Novo Nordisk Foundation Center for Biosustainability, Research Groups, Bacterial Cell Factory Optimization, Simon Fraser University, RWTH Aachen University
Authors: Kammoonah, S. (Ekstern), Prasad, B. (Ekstern), Balaraman, P. (Ekstern), Mundhada, H. (Intern), Schwaneberg, U. (Ekstern), Plettner, E. (Ekstern)
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Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.78 SJR 1.276 SNIP 0.831
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.468 SNIP 0.914 CiteScore 3.02
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Latency and bit-error-rate evaluation for radio-over-ethernet in optical fiber front-haul networks

Nowadays several research projects are under progress to manage a soft migration toward the 5th generation networks. Radio over Ethernet (RoE) is one of recent topics that try to have a cost efficient and independent front-haul network. In this paper, we discuss the requirements of the 5G networks and analyze the conditions for the implementation of a RoE protocol. For this purpose we digitalize radio frames that are taken from BBU or RRH and create RoE basic frames considering all the requirements of protocol. We then encapsulate RoE basic frames into an Ethernet packet and finally experimentally evaluate this Ethernet packet as a case of study for RoE applications. The packet is transmitted through different fiber spans, measuring the BER and latency on each case. The system achieves BER values below the FEC limit and a manageable latency. These results serve as a guideline and proof of concept for applications on RoE, showing the viability of its implementation as part of the next generation of front-haul networks.

General information

State: Published
Organisations: Department of Photonics Engineering, Metro-Access and Short Range Systems, Networks Technology and Service Platforms, Electromagnetic Systems, Technical University of Denmark
Authors: Sayadi, M. (Ekstem), Rodriguez, S. (Intern), Olmos, J. J. V. (Intern), Tafur Monroy, I. (Intern)
Pages: 88-92
Heat Recovery from Multiple-Fracture Enhanced Geothermal Systems: The Effect of Thermoelastic Fracture Interactions

This study investigates the effect of thermoelastic interactions between multiple parallel fractures on energy production from a multiple-fracture enhanced geothermal system. A coupled thermo-hydro-mechanical finite element model has been developed that accounts for non-isothermal fluid flow within the fractures, conductive heat transfer in the rock matrix, and the mechanical deformation of the matrix. The model results show that the matrix deformation significantly increases the interactions between the two adjacent fractures. Matrix contraction due to the cooling of the matrix increases the fracture aperture in the adjacent fracture, and facilitates the creation of favourable flow pathways between the injection and production wells. These flow paths reduce the energy production from the system. The effects of fracture spacing, reservoir temperature gradient and mechanical properties of the rock matrix on the production temperature and the net production energy are investigated. It is shown that the spacing calculated based on the assumption of rigid matrix (constant uniform aperture) are too small, and in order to account for the thermoelastic interactions, the spacing between fractures should be further increased to maximise the net energy production from the system. Otherwise, the multiple-fracture system fails to improve the energy recovery from the geothermal reservoir, as initially intended.

General information
State: Accepted/In press
Organisations: Centre for oil and gas – DTU, Technical University of Denmark
Authors: Vik, H. S. (Ekstern), Salimzadeh, S. (Intern), Nick, H. (Intern)
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Renewable Energy
ISSN (Print): 0960-1481
Ratings:
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Web of Science (2018): Indexed yes
Transcriptomic profiling of interacting nasal staphylococci species reveals global changes in gene and non-coding RNA expression

Interspecies interactions between bacterial pathogens and the commensal microbiota can influence disease outcome. In the nasal cavities, Staphylococcus epidermidis has been shown to be a determining factor for Staphylococcus aureus
colonization and biofilm formation. However, the interaction between S. epidermidis and S. aureus has mainly been described by phenotypic analysis, and little is known about how this interaction modulates gene expression. This study aimed to determine the interactome of nasal S. aureus and S. epidermidis isolates to understand the molecular effect of interaction. After whole-genome sequencing of two nasal staphylococcal isolates, an agar-based RNA sequencing setup was utilized to identify interaction-induced transcriptional alterations in surface-associated populations. Our results revealed differential expression of several virulence genes in both species. We also identified putative non-coding RNAs (ncRNAs) and, interestingly, detected a putative ncRNA transcribed antisense to esp, the serine protease of S. epidermidis, that has previously been shown to inhibit nasal colonization of S. aureus. In our study, the gene encoding Esp and the antisense ncRNA are both downregulated during interaction with S. aureus. Our findings contribute to a better understanding of pathogen physiology in the context of interactions with the commensal microbiota, and may provide targets for future therapeutics.

General information
State: Accepted/In press
Organisations: Department of Biotechnology and Biomedicine, Infection Microbiology, University of Leicester, State Serum Institute, Technical University of Denmark
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Number of pages: 21
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.747 SNIP 0.597
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.131 SNIP 0.752 CiteScore 2.08
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.122 SNIP 0.767 CiteScore 2.17
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.043 SNIP 0.72 CiteScore 2.25
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.069 SNIP 0.817 CiteScore 2.25
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.096 SNIP 0.761 CiteScore 2.26
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.07 SNIP 0.756
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.111 SNIP 0.835
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Modeling the multi-scale mechanisms of macromolecular resource allocation

As microbes face changing environments, they dynamically allocate macromolecular resources to produce a particular phenotypic state. Broad ‘omics’ data sets have revealed several interesting phenomena regarding how the proteome is allocated under differing conditions, but the functional consequences of these states and how they are achieved remain open questions. Various types of multi-scale mathematical models have been used to elucidate the genetic basis for systems-level adaptations. In this review, we outline several different strategies by which microbes accomplish resource allocation and detail how mathematical models have aided in our understanding of these processes. Ultimately, such modeling efforts have helped elucidate the principles of proteome allocation and hold promise for further discovery.

General information
State: Published
Organisations: Novo Nordisk Foundation Center for Biosustainability, Big Data 2 Knowledge, Network Reconstruction in Silico Biology, University of California, San Diego
Authors: Yang, L. (Ekstern), Yurkovich, J. T. (Ekstern), King, Z. A. (Ekstern), Palsson, B. O. (Intern)
Pages: 8-15
Publication date: 2018
Main Research Area: Technical/natural sciences

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Journal: Current Opinion in Microbiology
Volume: 45
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Ratings:
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Web of Science (2018): Indexed yes
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Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 6.36 SJR 4.161 SNIP 1.609
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 4.153 SNIP 1.552 CiteScore 5.95
Web of Science (2015): Indexed yes
EasyCloneYALI: CRISPR/Cas9-based synthetic toolbox for engineering of the yeast Yarrowia lipolytica

The oleaginous yeast Yarrowia lipolytica is an emerging host for production of fatty acid-derived chemicals. To enable rapid iterative metabolic engineering of this yeast, there is a need for well-characterized genetic parts and convenient and reliable methods for their incorporation into yeast. Here, we present the EasyCloneYALI genetic toolbox, which allows streamlined strain construction with high genome editing efficiencies in Y. lipolytica via the CRISPR/Cas9 technology. The toolbox allows marker-free integration of gene expression vectors into characterized genome sites as well as marker-free deletion of genes with the help of CRISPR/Cas9. Genome editing efficiencies above 80% were achieved with transformation protocols using non-replicating DNA repair fragments (such as DNA oligos). Furthermore, the toolbox includes a set of integrative gene expression vectors with prototrophic markers conferring resistance to hygromycin and nourseothricin.

General information
State: Accepted/In press
Organisations: Novo Nordisk Foundation Center for Biosustainability, Research Groups, Yeast Metabolic Engineering, Technical University of Denmark
Authors: Holkenbrink, C. (Intern), Dam, M. I. (Intern), Kildegaard, K. R. (Intern), Beder, J. (Ekstern), Dahlin, J. (Intern), Belda, D. D. (Ekstern), Borodina, I. (Intern)
Number of pages: 23
Monge surfaces and planar geodesic foliations

A Monge surface is a surface obtained by sweeping a generating plane curve along a trajectory that is orthogonal to the moving plane containing the curve. Locally, they are characterized as being foliated by a family of planar geodesic lines of curvature. We call surfaces with the latter property PGF surfaces, and investigate the global properties of these two naturally defined objects. The only compact orientable PGF surfaces are tori; these are globally Monge surfaces, and they have a simple characterization in terms of the directrix. We show how to produce many examples of Monge tori and Klein bottles, as well as tori that do not have a closed directrix.

General information
Factors of electric vehicle adoption: A comparison of conventional and electric car users based on an extended theory of planned behavior

Increasing the share of battery electric vehicles (BEV) in the total car fleet is regarded as a promising way to reduce local car emissions. Based on online surveys in Denmark and Sweden, this study compares BEV users’ (n = 673) and conventional vehicle (CV) users’ (n = 1794) socio-demographic profiles, attitudinal profiles, and mobility patterns. In line
with previous research, BEV users are typically male, highly educated, have high incomes, and often more than one car in their household. Additionally, BEV users perceive less functional barriers toward BEV use and have more positive attitudes and norms than CV users. The different profiles of these user groups suggest a separate analysis of potential factors of BEV adoption in both groups. In regression analyses, CV and BEV users’ intention to use/purchase a BEV is modeled based on factors of the Theory of Planned Behavior extended by personal norm, perceived mobility necessities, and BEV experience. For CV users, symbolic attitudes related to BEVs are the most important factor of intention, while perceived functional barriers in terms of driving range are most relevant for BEV users’ intention. How BEV users cope with trips of longer distance seems of particular relevance. In multiple car households, we found the percentage of actual BEV usage related to the type of other cars in the household, perceived functional barriers of BEVs as well as (successful) behavioral adaption to longer trips by BEVs. Based on the results, we discuss ways to increase BEV adoption for current users and non-users.

General information
State: Accepted/In press
Organisations: Department of Management Engineering, Technology and Innovation Management, Transport DTU, Transport Modelling
Authors: Haustein, S. (Intern), Jensen, A. F. (Intern)
Number of pages: 13
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Main Research Area: Technical/natural sciences

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ISSN (Print): 1556-8318
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 1.91 SJR 0.957 SNIP 1.419
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.341 SNIP 2.269 CiteScore 2.94
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.192 SNIP 1.782 CiteScore 2.45
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.509 SNIP 1.5 CiteScore 1.43
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.002 SNIP 1.265 CiteScore 1.49
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.558 SNIP 0.445 CiteScore 0.98
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.288 SNIP 0.495
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.101 SNIP 0
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.101 SNIP 0

Original language: English
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Source: FindIt
Source-ID: 2395517131
Publication: Research - peer-review › Journal article – Annual report year: 2018
Adolescents' associations between travel behaviour and environmental impact: A qualitative study based on the Norm-Activation Model
The negative environmental impact of car-dependent daily transport is well known. Young people of today are the potential drivers of the future and their mode choice will influence the environment for many years. This study explores the associations drawn between daily transport and environmental impact among 15-year-old Danish adolescents. We conducted 50 in-depth interviews and analysed them using a data-driven inductive thematic approach. We interpret differences in pro-environmental awareness and engagement on the background of the Norm-Activation Model (Schwartz, 1977). Based on their personal norm and the denial of consequences and responsibility of own behaviour, we identified five sub-groups of adolescents called Environmentalists, Pragmatics, Indifferent, De-emphasisers, and Deniers. Results indicate a need for measures to increase adolescents' awareness and acceptance of daily transport as a relevant issue in relation to sustainability. Such measures should include tangible feedback in a daily context while taking different coping strategies with regard to climate change into account.

General information
State: Published
Organisations: Department of Management Engineering, Technology and Innovation Management, Transport DTU, Technical University of Denmark
Authors: Møller, M. (Intern), Haustein, S. (Intern), Bohlbro, M. S. (Ekstern)
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Main Research Area: Technical/natural sciences

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A spectral geometric model for Compton single scatter in PET based on the single scatter simulation approximation: Paper
We investigate the idealized mathematical model of single scatter in PET for a detector system possessing excellent energy resolution. The model has the form of integral transforms estimating the distribution of photons undergoing a single Compton scattering with a certain angle. The total single scatter is interpreted as the volume integral over scatter points that constitute a rotation body with a football shape, while single scattering with a certain angle is evaluated as the surface integral over the boundary of the rotation body. The equations for total and sample single scatter calculations are derived using a single scatter simulation approximation. We show that the three-dimensional slice-by-slice filtered backprojection algorithm is applicable for scatter data inversion provided that the attenuation map is assumed to be constant. The results of the numerical experiments are presented.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Department of Physics, Neutrons and X-rays for Materials Physics, Scientific Computing, Institute of Computational Mathematics and Mathematical Geophysics
Authors: Kazantsev, I. (Ekstern), Olsen, U. L. (Intern), Poulsen, H. F. (Intern), Hansen, P. C. (Intern)
Number of pages: 15
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Volume: 34
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BFI (2017): BFI-level 1
Recent years have seen the development of new iron-centered N-heterocyclic carbene (NHC) complexes for solar energy applications. Compared to typical ligand systems, the NHC ligands provide Fe complexes with longer-lived metal-to-ligand charge transfer (MLCT) states. This increased lifetime is ascribed to strong ligand field splitting provided by the NHC ligands that raises the energy levels of the metal centered (MC) states and therefore reduces the deactivation efficiency of MLCT states. Among currently known NHC systems, \([\text{Fe(btbip)}_2]^{2+}\) (btbip = 2,6-bis(3-tert-butyl-imidazol-1-ylidene)pyridine) is a unique complex as it exhibits a short-lived MC state with a lifetime on the scale of a few hundreds of picoseconds. Hence, this complex allows for a detailed investigation, using 100 ps X-ray pulses from a synchrotron, of strong ligand field effects on the intermediate MC state in an NHC complex. Here, we use time-resolved wide angle X-ray scattering (TRWAXS) aided by density functional theory (DFT) to investigate the molecular structure, energetics and lifetime of the high-energy MC state in the Fe-NHC complex \([\text{Fe(btbip)}_2]^{2+}\) after excitation to the MLCT manifold. We identify it as a 260 ps metal-centered quintet (5MC) state, and we refine the molecular structure of the excited-state complex verifying the DFT results. Using information about the hydrodynamic state of the solvent, we also determine, for the first time, the energy of the 5MC state as 0.75 ± 0.15 eV. Our results demonstrate that due to the increased ligand field...
strength caused by NHC ligands, upon transition from the ground state to the $^{5}$MC state, the metal to ligand bonds extend by unusually large values: by 0.29 angstrom in the axial and 0.21 angstrom in the equatorial direction. These results imply that the transition in the photochemical properties from typical Fe complexes to novel NHC compounds is manifested not only in the destabilization of the MC states, but also in structural distortion of these states.

General information
State: Published
Organisations: Neutrons and X-rays for Materials Physics, Department of Physics, European Synchrotron Radiation Facility, Lund University, European XFEL
Number of pages: 10
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Publication date: 2018
Main Research Area: Technical/natural sciences

Regulating combined sewage discharges to support EU Water Framework Directive ambitions in natural water bodies

General information
State: Published
Deciphering the microbial ecology in bio-gas reactors for optimizing the anaerobic digestion process

Anaerobic digestion (AD) is a microbial mediated process where organic compounds are degraded to biogas (CH4 and CO2). AD occurs in many natural anoxic environments and is an essential step for global carbon cycle. Engineered AD systems, i.e. biogas reactors, enhance methanogenic activity by applying empirical operational conditions, in order to accelerate the methane production for energetic purposes. In Denmark, biogas produced from AD has a considerable share in renewable energy with the expectation to expand. Thus, the more effective operation of biogas plants will significantly benefit Denmark’s sustainable development. As AD relies on complex microbial activity, a more comprehensive understanding of the AD microbial consortia and their activity provides the fundamental knowledge for process control and optimization. In AD, the microbial metabolisms are mostly thermodynamically constrained and the obligatory syntrophy is an essential intermediary step. Thus, the majority of AD microbiota remains uncharacterized since in the past it was mainly investigated using cultivated-based methods. The advent of more powerful sequencing technology (i.e. next generation sequencing, NGS) and newly developed bioinformatic methods enable researchers to perform in-situ analyses on uncharacterized microbial communities. The applications of NGS technology were proved to be effective tools to reveal AD microbial ecology. However, the detailed mechanisms of microbial activity are still far from fully elucidated due to the intricacy of AD microbial process.

This Ph.D. project relied on comprehensive investigations of microbial communities in order to optimize the AD process and elucidate the fundamental metabolisms. Specifically, in the case of process optimization, 16S rRNA amplicon sequencing was used to identify, analyse and solve the operational challenges during the start-up of thermophilic up-flow anaerobic sludge blanket (UASB) reactors. To elucidate the microbial metabolisms, genome-centric metagenomics was applied to characterize methanogenic communities degrading a set of defined substrates. In addition, the Ph.D. study also expands the understanding of AD microbial ecology by proposing and characterizing a novel Candidatus species ubiquitously present in AD systems. The start-up of thermophilic UASB reactors was investigated in lab-scale reactors inoculated with mesophilic granules. After increasing the operational temperature from mesophilic to thermophilic, volatile fatty acids (VFAs) and alcohols were found as the main digestion products. Methane production, on the other hand, only initiated after bicarbonate addition as external pH control. The dynamicity of microbial community composition in the granules during the temperature shift suggested that the majority of the mesophilic microbes could not tolerate the thermophilic conditions. Moreover, it was demonstrated that the fermentative thermophiles first evolved in the liquid phase of UASB reactor and then were encapsulated in the granular structure of the sludge. The growth of these bacteria rapidly restored the hydrolysis, acidogenesis and acetogenesis in the reactor. On the contrary, the thermophilic methanogens grew much slower than fermentative bacteria leading to severe process imbalance (i.e. accumulation of VFAs and alcohols). Thus, the evolvement of thermophilic methanogens was recognized as the biological ‘bottleneck’ during the temperature transition. To overcome the identified obstacle, bioaugmentation, i.e. provision of exogenous microbes, was proposed to accelerate the microbial community adaptation. The best strategy found to perform bioaugmentation was the injection of axenic methanogenic cultures. This practice significantly increased the thermophilic methane production rate by 40% compared with the control reactor (i.e. without bioaugmentation). The enhancement of methane production was attributed to the evolvement of exogenous Methanothermobacter thermautotrophicus and the concomitant growth of its syntrophic partners in the granular structure. The positive effects brought by bioaugmentation were persistent in UASB reactor due to the retention of the microbes in the granular sludge.

For the investigation of the basic microbial metabolism and ecology, methanogenic microbial communities were enriched in a lab-scale continuous stirred-tank reactor (CSTR) fed with synthetic feedstocks. In the experiment, the substrates used were stepwise simplified (i.e. polysaccharide, monosaccharide, short chain fatty acids, acetate) to mimic the four steps of AD process. During the continuous operation, the microbial community was substantially simplified, because the microbes that could not metabolize the specific compounds were washed out. The overall microbial community consisted of only 35 metagenome assembled genomes (MAGs) (31 bacterial and 4 archaeal). The abundance of these MAGs dramatically varied in the communities adapted to different substrates. The shifts in microbial community composition indicate that MAGs have specific functional roles in AD food chain and their roles cannot always be physiologically defined in accordance with 4 AD steps. Moreover, the explicit degradation pathways were reconstructed from the functional annotation of MAGs. It is notable that, a novel glucose degradation model was proposed with the syntrophic activity of Clostridiaceae sp. and Methanoculleus thermophilus. In this model, acetate is not produced as intermediate compound. The genome-centric metagenomics reveals a considerable number of MAGs that could not be taxonomically assigned to characterized species. A MAG extracted from co-assembly of 8 AD metagenomes was especially emphasized due to its
ubiquity in AD system and its high abundance under specific conditions. From the functional annotation and gene expression profile, it is confirmed that this MAG performs hydrogenotrophic methanogenesis in AD system and is found dominant from the reactors where H2 was added. This genome is present in 40 different samples from both full-scale and lab-scale AD reactors. The MAG was found in higher abundance during thermophilic reactor operations with relatively short hydraulic retention times. The phylogenetic assignment was based on 400 conserved genes and on 16S rRNA genes. The two methods concordantly showed that this MAG is closely related to Methanoculleus bourgensis MS2T. However, the average nucleotide identity between M. bourgensis MS2T and the selected MAG was only 89%, which is too low similarity to assign the MAG at the species level. Thus, we propose a novel Candidatus species inside the Methanoculleus genus. According to the metabolic traits, it is named as Candidatus Methanoculleus thermohydrogenotrophicum, sp. nov.

Overall, the results from this Ph.D. study bring new knowledge on the AD process based on NGS technology. Practically, the gained information regarding microbial community composition and dynamicity was directly used to solve technical challenges in AD operations. Fundamentally, deeper insights into the microbial metabolisms and ecology substantially expanded the current understanding of AD. The revealed knowledge provides pivotal prerequisites for future AD process control and optimization.

General information
State: Published
Organisations: Department of Environmental Engineering, Residual Resource Engineering
Authors: Zhu, X. (Intern), Angelidaki, I. (Intern), Kougiás, P. (Intern), Treu, L. (Intern)
Number of pages: 54
Publication date: 2018

Relation
Projects:
Deciphering the microbial ecology in bio- gas reactors for optimizing the anaerobic digestion process
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Operationelle udlederkrav for regnbetingede overløb fra fællessystemer til vandløb

General information
State: Published
Authors: Vezzaro, L. (Intern), Brudler, S. (Intern), McKnight, U. S. (Intern), Rasmussen, J. J. (Ekstern), Mikkelsen, P. S. (Intern), Ambjørn-Nielsen, K. (Intern)
Number of pages: 57
Publication date: 2018

Relation
Projects:
Operationelle udlederkrav for regnbetingede overløb fra fællessystemer til vandløb
Publication: Commissioned › Report – Annual report year: 2018

Advancing food, nutrition, and health research in Europe by connecting and building research infrastructures in a DISH-RI: Results of the EuroDISH project

Background
Research infrastructures (RIs) are essential to advance research on the relationship between food, nutrition, and health. RIs will facilitate innovation and allow insights at the systems level which are required to design (public health) strategies that will address societal challenges more effectively.

Approach
In the EuroDISH project we mapped existing RIs in the food and health area in Europe, identified outstanding needs, and synthesised this into a conceptual design of a pan-European DISH-RI. The DISH model was used to describe and
structure the research area: Determinants of food choice, Intake of foods and nutrients, Status and functional markers of nutritional health, and Health and disease risk.

Key findings
The need to develop RIs in the food and health domain clearly emerged from the EuroDISH project. It showed the necessity for a unique interdisciplinary and multi-stakeholder RI that overarches the research domains. A DISH-RI should bring services to the research community that facilitate network and community building and provide access to standardised, interoperable, and innovative data and tools. It should fulfil the scientific needs to connect within and between research domains and make use of current initiatives. Added value can also be created by providing services to policy makers and industry, unlocking data and enabling valorisation of research insights in practice through public-private partnerships. The governance of these services (e.g. ownership) and the centralised and distributed activities of the RI itself (e.g. flexibility, innovation) needs to be organised and aligned with the different interests of public and private partners.

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Co-digestion and model simulations of source separated municipal organic waste with cattle manure under batch and continuously stirred tank reactors

This study investigates the co-digestion of source separated municipal organic waste (SSMOW), pretreated using a biopulper, and cattle manure both in batch and continuous stirred tank reactors. The optimum co-digestion feeding mixture was consisted of 90% SSMOW and 10% cattle manure on organic matter basis, yielding 443 mLCH4/gVS. The high performance of the co-digestion was explained by the fact that the efficient pulping pretreatment boosted the methane production from SSMOW and that the added livestock slurry provided the buffer capacity to avoid inhibition occurred by intermediates' accumulation. Moreover, batch assays focused on the effect of inoculum to substrate ratio (ISR) were performed. Results showed that the reduction of ISR had slight impact on extending the lag phase, without affecting the rest kinetic parameters. The efficiency of the codigestion process in continuously fed reactor was comparable with the results obtained from the batch assay (i.e. <95% of the maximum expected value). Finally, the outputs from an applied mathematical model were in good agreement with the experimental data obtained from the continuous reactor operation, demonstrating that the BioModel can serve as a reliable tool to predict the process performance under real-scale conditions.

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Testing spatial heterogeneity with stock assessment models

This paper describes a methodology that combines meta-population theory and stock assessment models to gain insights about spatial heterogeneity of the meta-population in an operational time frame. The methodology was tested with stochastic simulations for different degrees of connectivity between sub-populations and applied to two case studies, North Sea cod (Gadus morua) and Northeast Atlantic sardine (Sardina pilchardus). Considering that the biological components of a population can be partitioned into discrete spatial units, we extended this idea into a property of additivity of sub-population abundances. If the additivity results hold true for putative sub-populations, then assessment results based on sub-populations will provide information to develop and monitor the implementation of finer scale/local
management. The simulation study confirmed that when sub-populations are independent and not too heterogeneous with regards to productivity, the sum of stock assessment model estimates of sub-populations’ SSB is similar to the SSB estimates of the meta-population. It also showed that a strong diffusion process can be detected and that the stronger the connection between SSB and recruitment, the better the diffusion process will be detected. On the other hand it showed that weak to moderate diffusion processes are not easy to identify and large differences between sub-populations productivities may be confounded with weak diffusion processes. The application to North Sea cod and Atlantic sardine exemplified how much insight can be gained. In both cases the results obtained were sufficiently robust to support the regional analysis.

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Monitoring and modeling of nitrogen conversions in membrane-aerated biofilm reactors: Effects of intermittent aeration

Nitrogen can be removed from sewage by a variety of physicochemical and biological processes. Due to the high removal efficiency and relatively low costs, biological processes have been widely adopted for treating nitrogen-rich wastewaters. Among the biological technologies, biofilm processes show great advantages as compared to suspended growth processes, allowing for biomass accumulation and retention without the need of external solid separation devices. The decoupling of solids retention from hydraulic retention is especially useful for slow-growing microorganisms, such as nitrifying bacteria, e.g. ammonium-oxidizing bacteria (AOB) and nitrite-oxidizing bacteria (NOB), and anaerobic ammonium-oxidizing bacteria (AnAOB), which are involved in ammonium (NH4+) removal process.

Stability of engineered biological processes requires an appropriate balance between activities of the main microbial groups involved in the system. However, finding proper operational conditions is especially challenging in biofilms. On the one hand, the existence of strong spatial chemical gradients within biofilms increases the difficulty to prescribe environmental conditions that favor any desired biological process. On the other hand, the presence of multiple simultaneous chemical gradients complicates the performance optimization. Mathematical modeling offers a way to describe and analyze multiple processes that occur simultaneously in time and space in biofilm systems.

This PhD project investigated NH4+ removal process in membrane-aerated biofilm reactors (MABRs), focusing on aeration control, especially the application of intermittent aeration. Compared to conventional biofilms which are characterized by co-diffusion, MABRs display counter-diffusion fluxes of substrates: oxygen is supplied through the membrane, whilst NH4+ is provided from the bulk liquid phase. The counter substrate supply not only offers flexible aeration control, but also supports the development of a unique microbial community and spatial structure inside the biofilm. In this study, lab-scale MABRs were operated under two types of aeration control: continuous versus intermittent aeration. Long-term reactor performance was monitored. Based on bulk measurements of NH4+, nitrite (NO2-) and nitrate (NO3-), microbial activities of individual functional guilds were evaluated. I found that NOB suppression occurred under intermittent aeration, but not under continuous aeration. Relative aeration duration and aeration intermittency were two effective operational factors in regulating MABR performance under intermittent aeration. Besides daily bulk monitoring, in situ microprofiles of dissolved oxygen (DO), pH and nitrous oxide (N2O) were performed. The significant temporal fluctuations in local biofilm pH (not DO) during aeration control suggested that pH-related effects drive the changing microbial activities under intermittent aeration, as compared to continuous aeration. Total N2O emissions were dramatically reduced at the onset of intermittent aeration, due to the development of an anoxic N2O reduction zone by heterotrophic bacteria (HB).

To further investigate the causal link between NOB suppression and aeration regime change, a 1-dimensional (1-D) multispecies nitrifying biofilm model was developed in Aquasim software, incorporating a pH calculation. Kinetic parameters to be estimated were chosen based on a local sensitivity analysis, and were estimated from in situ microprofiles. With the calibrated model, I identified that the periodically varying free ammonia inhibition, which was associated with transient pH variations, was the likely key factor causing NOB suppression in intermittently-aerated nitrifying MABRs.

To further investigate the mechanisms of N2O mitigation under aeration control, the 1-D biofilm model was extended to a partial nitritation-anammox (PNA) biofilm model, including description of all relevant biological N2O production pathways. Sensitive kinetic parameters were estimated with long-term bulk performance data. With the calibrated model, roles of HB and AnAOB were discussed and evaluated in mitigating N2O emissions in auto-trophic nitrogen removal MABRs. Moreover, I developed a 1-D biofilm model in Matlab software describing the counter-diffusion PNA process, aiming at an improved model calibration/evaluation for the highly variable N2O emissions.

Overall, a combination of experimental and modeling efforts were implemented to study nitrogen conversions in MABRs. The results showed that intermittent aeration was an efficient strategy to regulate microbial activities in counter-diffusion biofilms, achieving an energy-efficient NH4+ removal process with low N2O emissions.