NTNU
Kunnskap for en bedre verden

Master's theses proposals

Department of Biotechnology and Food Science

Department of Biology

This document contains proposed projects relevant for students at MSc Biotechnology (2- and 5-year study), MSc Aquatic Food Production, the 2- and 5-year MSc Chemical Engineering and Biotechnology (MIKJ/MTKJ) and MSc Nanotechnology (MTNANO/sivilingeniørstudiet).

The different proposals might have different credits. This relates to the proposed theses being planned for different study programmes: the MSc Biotechnology (60 credits), MSc Aquatic Food Production (30 credits) or MSc Chemical Engineering and Biotechnology / Nanotechnology (30 credits). Some proposals may also be relevant as specialization project for the technology studies (15 credits). New proposals since 22.03.17 is marked in Content.

Please contact supervisor directly if you have any questions regarding theses' proposals.

Academic year 2017/18

Date: 20.04.2017 v4

Contents

Department of Biotechnology and Food Science

Hovedveileder: *Main supervisor:*	Finn L. Aachmann
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Biveileder/-e: *Co-supervisor/-s:*	Gaston Courtade
Arbeidstittel på oppgaven/ *Preliminary title:*	**Development of chitin-based sorbents for protein purification**

Kort beskrivelse av oppgaven / *Short description of the project*:
The focus of this project will be to design and construct chitin-based materials for the extraction and purification of proteins from complex biological mixtures.

Bakgrunn og mål / *Background and Objectives:*
The production of proteins is a high-value industry with applications in all branches of biotechnology. A key step of the protein-production process is to achieve a high degree of purity of the protein products. Affinity chromatography is a powerful tool for the purification of specific proteins from a complex biological mixture, such as a fermenter. Chitin is a polysaccharide that is a good candidate for use in affinity chromatography because it selectively adsorbs proteins that bind chitin. In fact, chitin resins are already employed in affinity chromatography columns. However, the use of columns requires some degree of sample preparation and filtration. The aim of this project is to develop chitin-based materials that can be used for direct extraction of proteins from biological mixtures. Such materials would provide a rapid alternative method to extract and purify target proteins at different stages of a process without the need for sample preparation.

Eksperimentelt / *Experimental methods:*
- Development of methods for the production of chitin fibers.
- Characterization of chitin fibers (strength, swelling, protein adsorption).
- Design of a protocol for the use of chitin fibers in protein purification applications.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

Hovedveileder: *Main supervisor:*	Finn L. Aachmann
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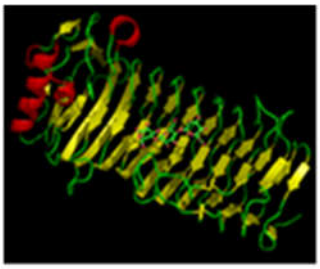
Biveileder/-e: *Co-supervisor/-s:*	Marit Sletmoen og/eller Anne Tøndervik (Sintef)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Purification and characterization of design mannuronan-c-5 epimerases**

Kort beskrivelse av oppgaven / *Short description of the project*:
The focus of this project will be to study the interaction of alginate C-5 epimerases with substrate, and its product profile using biophysical techniques. The specific content of project may be adapted to the candidate's preferences.

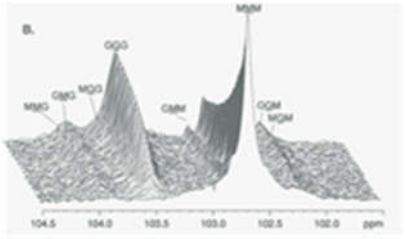
Bakgrunn og mål / *Background and Objectives:*

Azotobacter vinelandii is a soil bacteria, which are able to produce alginate, a polysaccharide. Alginate consists of mannuronic acid (M) and guluronic acid (G), and the properties of the polymer are, among other things, dependent on the distribution of these units. *A. vinelandii* synthesises alginate by first making polymannuronic acid (poly-M), of which some M-units are converted to G-units. This reaction is catalyzed by enzymes called epimerases, and *A. vinelandii* produce seven enzymes of this kind; AlgE1 to AlgE7. Poly-M can be epimerized in vitro and the various epimerases are shown to give different G-contents and different distributions of G-unites in the alginate that is produced



A-module of AlgE4

Certain alginates have turned out to be bioactive, and are therefore interesting with regards to medical applications. Researchers at NTNU/Sintef are trying to find new enzymes that can create alginates with tailored properties for these kinds of applications. This project will be about characterization of alginate epimerases. This involves protein production and purification of the enzymes. Characterization of the properties of the enzymes with regard to epimerization of poly-M. Gelling properties of the generated alginates and characterization.



Epimerase activity profile by NMR

Eksperimentelt / *Experimental methods:*

- Production and purification of the alginate epimerases.
- Characterization of the enzymes with regard to activity, substrate specificity and reaction pattern. Relevant methods for the characterization are Isothermal titration calorimetry (ITC), atomic force microscopy (AFM), Ion chromatography system (ICS), NMR and Time-resolved NMR.
- Characterization of epimerized alginates with regard to gelling properties, relevant for their biomedical applications.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

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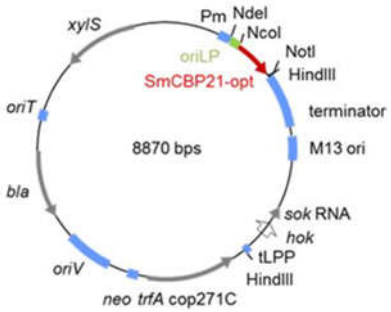
Biveileder/-e: *Co-supervisor/-s:*	Trygve Brautaset
Arbeidstittel på oppgaven/ *Preliminary title:*	**New heterologous protein expression system for isotope labeled proteins**

Kort beskrivelse av oppgaven / *Short description of the project*:
This project will focus on the further development of a new set of expression vectors for production of isotope labeled protein (for NMR applications) based on the *Pm*/XylS promoter system. The specific content of the project may be adapted to the candidate's preferences.

Bakgrunn og mål / *Background and Objectives:*
A common bottleneck in heterologous protein expression of isotope labelled protein in bacteria is the promoter system used. These promoter systems are mainly based on the carbohydrate metabolism of the cell, like the *Lac* and *ara—BAD* operons. This poses a problem when growing cells in a minimal medium with glucose as the sole carbon source, which results in poor regulation of the promoter system and low expression of the target protein.



Vector map of LPMO Expression cassette

A solution to the problem is to use a promoter system that is not influenced by the carbohydrate metabolism of the cell. The group of Prof. Svein Valla at our department has developed an expression system based on the *Pm*/XylS promoter system, which uses benzoate derivatives as inducers of the protein expression. Recently, we have published a work where *Pm*/XylS promoter system was used for the expression of an isotope labeled LPMO (lytic polysaccharide monooxygenase).

Aim of this project is to construct a new set of expression vectors for production of isotope labeled protein where expression level of the target protein is independent of media composition. The developed expression system will offer a large potential within structural biology and for protein expression in general.

Eksperimentelt / *Experimental methods:*
- *State-of-the-art* molecular genetics.
- Characterization of the of the expression system.
- Production and purification of the target protein.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

Hovedveileder: *Main supervisor:*	Finn L. Aachmann
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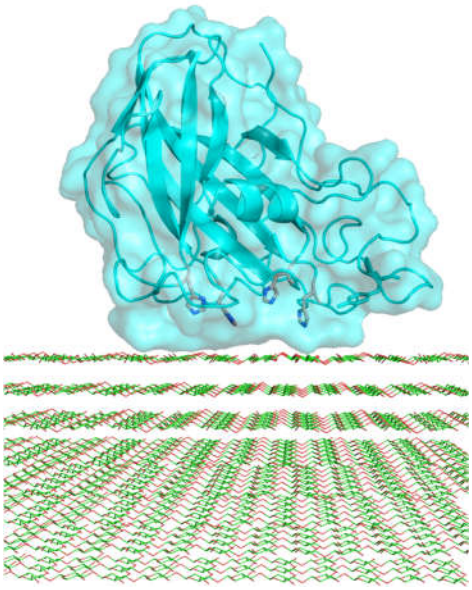
Biveileder/-e: *Co-supervisor/-s:*	Gaston Courtade
Arbeidstittel på oppgaven/ *Preliminary title:*	**Characterization of novel proteins for biorefinery applications**

Kort beskrivelse av oppgaven / *Short description of the project*:
The focus of this project will be to study new carbohydrate active enzymes by using biophysical techniques such as NMR spectroscopy. The specific content of project may be adapted to the candidate's preferences.

Bakgrunn og mål / *Background and Objectives:*
Biorefineries where biomass from marine and forestry resources are converted to monosaccharides are a cornerstone of bioeconomy. These monosaccharides can be used to produce bioethanol and value-added products. However, the inefficient hydrolysis of insoluble biomass (chitin and cellulose) is a bottleneck in the biorefining process. A way to overcome this obstacle is through a new family of enzymes - lytic polysaccharide monooxygenases (LPMOs) – that enhance the biomass degradation process by the oxidative cleavage of glycosidic bonds in chitin and cellulose. Since 2010, we have studied LPMOs in cooperation with NMBU, and we are interested in gaining a better understanding of the function and mode of action of LPMOs.



Eksperimentelt / *Experimental methods:*
- Recombinant protein production and purification.
- Acquisition of multidimensional NMR spectra and assignment of the protein backbone and side-chains.
- Protein structure determination.
- Dynamics studies with NMR spectroscopy and other techniques such as circular dichroism (CD).
- Measurements of interactions between LPMOs and other substrates/proteins.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

Veileder: *Supervisor:*	Prof. Eivind Almaas
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Biveileder/-e: *Co-supervisor/-s:*	Assoc. Prof. Martin Hohmann-Marriott
Arbeidstittel på oppgaven/ *Preliminary title:*	**Comparative study of gene expression networks in Synechocystis sp. PCC6803**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Network analysis has been central to uncovering important principles of interactome organization. Gene expression correlation networks consist of genes that showing strong similarities or dissimilarities in their expression patterns, making it possible to identify important gene clusters associated with a given phenotype or biological function.

In this project, the candidate will use a recently developed network approach (Voigt, Nowick & Almaas) to study evolution and conservation of gene expression correlations. The candidate will use the comprehensive database cyanoExpress, which contains gene expression data from 177 distinct genetic and environmental perturbation experiments for the cyanobacterium Synechocystis sp. PCC6803. Synechocystis is an important model organism for developing our understanding of photosynthesis, and the research focus will be on using network analysis methodology to study photosynthetic function.

Eksperimentelt / *Experimental methods:*
N/A

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Prof. Eivind Almaas
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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Comparative study of gene expression networks in *Homo sapiens***

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Network analysis has been central to uncovering important principles of interactome organization. Gene expression correlation networks consist of genes that showing strong similarities or dissimilarities in their expression patterns, making it possible to identify important gene clusters associated with a given phenotype or biological function.

The ability to understand consequences of genetic variation among humans is a significant challenge in biology. The goal of this project is to use a recently developed network approach (Voigt, Nowick & Almaas) to study the variation of *gene co-expression patterns* in a recent high-quality gene-expression data set, GTEx (http://www.gtexportal.org/), and compare with disease data. The candidate will further develop the approach as well as applying it to GTEx data using a variety of human tissue types.

Eksperimentelt / *Experimental methods:*
N/A

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Prof. Eivind Almaas
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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Computational modeling of two-species microbial consortium**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Flux Balance Analysis (FBA) is the central approach in modeling genome-scale metabolism, with its capability for predicting metabolic phenotypes and identifying possible approaches for engineering cellular behavior. A genome-scale model may be generated within 48 hours, and the COBRA toolbox in MatLab or for the programming language Python will be used to analyze the models.

Using the "Computation Of Microbial Ecosystems in Time and Space" (COMETS)[1] computational framework for simulating microbial metabolism using FBA in a spatial structure, the aim of this project is to evaluate the effect of different competitive strategies between two chosen microbes.

Eksperimentelt / *Experimental methods:*
N/A

[1] http://www.bu.edu/segrelab/comets/

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

[1] http://www.bu.edu/segrelab/comets/

Veileder: *Supervisor:*	Prof. Eivind Almaas
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Webside / *webpage*:	www.ntnu.edu/almaaslab
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Analysis of genotype-phenotype networks constructed from constraint-based modeling**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Flux Balance Analysis (FBA) is the central approach in modeling genome-scale metabolism, with its capability for predicting metabolic phenotypes and identifying possible approaches for engineering cellular behavior. A genome-scale model may be generated within 48 hours, and the COBRA toolbox in MatLab or for the programming language Python will be used to analyze the models.

Using the FBA approach together with an in-house compendium of possible metabolic models, the aim of this project is to generate genotype-phenotype mappings for a large set of metabolic models and analyze the properties of these networks using complex network approaches.

Eksperimentelt / *Experimental methods:*
N/A

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Prof. Eivind Almaas
Kontaktinformasjon / epost *Contact information / email:*	K3-125/ 735 97860 / eivind.almaas@ntnu.no
Webside / *webpage*:	www.ntnu.edu/almaaslab
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Computational modeling of evolution of antibiotic resistance in a bacterial species**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

The spread of antibiotic resistance in pathogens is becoming a severe threat to modern medicine. While the level of antibiotics use in Norway is comparatively low to other parts of the world, widespread travel patterns are sure to bring resistant strains to Norway even if resistance is not developed locally.

The first part of this project consists of a literature survey of methods for computational modeling of antibiotic resistance evolution in bacterial species, as well as mechanisms for resistance evolution. The second part is to develop a model that will be solved computationally.

Eksperimentelt / *Experimental methods:*
N/A

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Ingrid Bakke / Marit Sletmoen / Catherine Taylor Nordgård
Kontaktinformasjon / epost *Contact information / email:*	ingrid.bakke@ntnu.no, marit.sletmoen@ntnu.no, catherine.t.nordgard@ntnu.no
Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Understanding the mucosal barrier: Bacteria-mucus interactions**

Bakgrunn og mål / *Background and Objectives:*

The aim of this interdisciplinary project, involving microbiology, rheology, and advanced high resolution microscopy, is to elucidate how bacteria influence on the mechanical properties and the barrier function of mucus.

Mucosal tissue, covering the body cavities of animals and the skin of fishes, constitutes a major barrier against microbes and other agents in the external environment. This barrier is permeable but selective, allowing the absorption of nutrients, electrolytes, and water, but preventing the penetration of pathogens, toxins, and antigens. It consists of a single layered sheet of epithelial cells covered with mucus. The mucus is continuously secreted and transported away from the epithelial cell layer, so that entrapped microbes or other agents are removed together with the mucus. Mucin glycoproteins are the major constituent of the mucus, and are responsible for the viscous properties. The mucus is colonized by resident microbiota, and this microbiota contributes to the barrier function and also influences on the mechanical properties of the mucus. However, the specific molecular mechanisms for interactions between bacteria and mucus and the implications for the barrier function are poorly understood. We will take advantage of the expertise existing within several research groups at the Department of Biotechnology, to study mucus-bacteria interactions at a basic, molecular level. In particular, we will apply rheology, microscopy as well as microbiological approaches to examine consequences on barrier function and mechanical properties after exposure of mucus to various bacterial strains and communities. The focus will be on mucus from salmon skin, since this mucosal barrier is particularly important for fish health.

Eksperimentelt / *Experimental methods:*

The final design of the master projects will be determined by the supervisors together with the master students. Up to three master students can be involved in the project. Relevant methods are:

- Cultivation of strains and selection for microbial communities with distinct properties
- Deep-sequencing approaches for taxonomic analysis of microbial communities associated with the salmon mucus
- Use of rheology and sensitive force probes to determine the viscoelastic properties of the mucus layer and how this changes after introduction of the microbial communities.
- Use of sensitive force probes to study the interaction between bacteria and mucus layer
- Characterisation of the mucosal barrier, including diffusion abilities of molecules through the barrier, using laser scanning fluorescence microscopy.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Kari Attramadal (kari.attramadal@ntnu.no) Ingrid Bakke (ingrid.bakke@ntnu.no)
Kontaktinformasjon / epost *Contact information / email:*	
Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	Olav Vadstein (olav.vadstein@ntnu.no)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Microbial stabilization: a tool for combating pathogens in aquaculture systems?**

Background and Objectives:

Fish are sharing their living environment with high loads of bacteria. In nature, the fishes experience relatively stable microbial environments. In aquaculture systems, the reared animals are exposed to high and unstable loads of bacteria compared to the natural environments. For a number of reared marine species, we have previously demonstrated that stable microbial environments improve growth and survival. Stabilization of microbial communities in the rearing water can be obtained by so-called K-selection, i.e. keeping microbial loads close to the carrying capacity (the maximal microbial population size that the system can support). Recirculating aquaculture systems (RAS) are well suited for exerting microbial K-selection, because the water going in to the rearing tanks has a carrying capacity similar to that of the water inside the rearing tank. K-selected bacteria are typically specialists, characterized by low maximum growth rate, but with the ability to compete when the available resources are limited. In a system where the carrying capacity is dramatically increased in the rearing tank, e.g. by addition of fish feed in a flow-through system, rapid-growing, opportunistic bacteria will bloom. This would be an example of an r-selected system. R-selected bacteria have a high maximum growth rate, but are poor competitors when resources are limited. According to ecological theory, opportunistic rapid-growing bacteria would more easily bloom in an r-selected system with excess of resources, but would be outcompeted in a K-selected system. If stabilization of the water microbial community is found to prevent blooming of opportunistic bacteria, this could be a promising and sustainable strategy for preventing pathogenic invasion in aquaculture systems.

The aim of this project is to evaluate whether microbial stabilization is feasible a strategy to prevent blooming of pathogens in aquaculture systems

Experimental methods:

This master project will be part of a project involving a Fulbright research fellow, and the student will work closely together with this researcher. We will use lab-scale continuous bioreactors and aim at also build up a lab scale RAS for creating r- and K-selected microbial communities. Potential fish pathogens will be introduced to the systems under both K- and r-selected conditions, and the fate of these strains will be monitored by methods like qPCR and flow-cytometry combined with specific probing. For examining the dynamics of the microbial communities in the systems, methods based on analysis of sequence variation in the 16S rRNA gene will be used, like DNA sequencing of 16S rRNA amplicons and qPCR.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng

Veileder: *Supervisor:*	Ingrid Bakke / Eivind Almaas / Olav Vadstein
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Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Network analysis as a tool for studying interactions in aquatic bacterial communities**

Bakgrunn og mål / *Background and Objectives:*
Aquatic microbial communities are highly dynamic. Environmental conditions, stochastic processes, and interactions (e.g. competition) between community members will influence the community composition. We have found that in aquaculture systems, stable microbial environments promote fish health. To be able to control aquatic microbial systems, we need knowledge about the factors structuring them. In biofilm communities, bacteria are known to interact with each other through many mechanisms, but for planktonic bacterial communities, little is known when it comes to communication and interactions. In this project, the aim is to investigate to what extent interactions between community members are taking place in planktonic bacterial communities. During the last decade, network approaches have been applied to a wide variety of biological challenges with great success. We will apply network analysis to large data sets generated by Illumina amplicon sequencing of bacterial communities, with the aim of identifying species co-occurrence relationships. To allow for comparisons between different types of microbial communities, the dataset will include also biofilm and/or fish microbiota samples.

Eksperimentelt / *Experimental methods:*
Depending on the interests of the student, the project may include experimental work, involving operating lab scale continuous bioreactors, sampling, DNA isolation, PCR, and Illumina amplicon sequencing. Alternatively, datasets already generated in the research group may be immediately used for network analyses. The student will use simple programming in python and an existing R-package for network analysis (WGCNA) to generate networks that reflect the interactions taking place in the bacterial communities.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Ingrid Bakke
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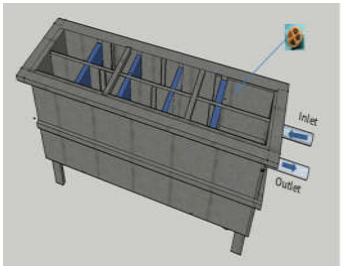
Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	Blanca M. Gonzalez Silva (blanca.g.silva@ntnu.no) Stein Wold Østerhus (stein.w.osterhus@ntnu.no)
Arbeidstittel på oppgaven/ *Preliminary title:*	**The microbial community associated with enhanced biological phosphorus removal (EBPR) from wastewater in continuous moving bed biofilm reactors (MBBR)**

Bakgrunn og mål / *Background and Objectives:*

Wastewater with high levels of organic matter (COD) Phosphorus (P) and Nitrogen (N) cause several problems, such as eutrophication, oxygen consumption and fish toxicity, when discharged to the aquatic environment. It is, therefore, necessary to remove these substances from wastewaters for reducing their potential negative impact. P removal is achieved by polyphosphate-accumulating organisms (PAOs) through enhanced biological phosphorus removal (EBPR) under alternating anaerobic-aerobic conditions. The aim of this project is to characterize microbial communities of an EBPR carried out in a pilot-scale Moving Bed Biofilm Reactor (MBBR) operated as a continuous biofilm process with circulating carrier media. Illumina sequencing of 16S rRNA amplicons and statistical analysis will be used for investigating the structure and dynamics of the bacterial communities.

Objectives:

- To provide a comprehensive insight into the key PAOs and determine their relative abundance.
- To identify the possible existence of nitrifying and denitrifying bacteria
- To identify the most dominant ordinary heterotrophic organisms.
- To link the performance of the EBPR with the microbial community structures.



Eksperimentelt / *Experimental methods:*

The student will take part in operating the MBBR reactors at the department of Water and wastewater systems engineering. Analyses of the microbial communities will be done by DNA extraction, PCR amplification of the 16S rRNA bacterial gene, analyses of the sequence diversity of the 16S rRNA amplikons. The student will also be involved in the data analyses.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng

Master thesis in Biotechnology, 15, 30, 60 sp

Microbial control in land based recirculating aquaculture systems

Goal

The objective of this master thesis is to identify factors that are decisive for creating microbial stability in recirculating aquaculture systems.

Background

This master thesis will be part of the EU ERANET project MicStaTech, and the master student will work together with the project researchers. Water treatment and design of aquaculture systems are typically focused on optimising physicochemical water quality and efforts to maintain bacteria numbers low (i.e. by removing organic matter and disinfection). However, high bacteria numbers are not necessarily problematic for the cultured organisms as long as the system is bio-stable and all other requirements are met. In this project the main objective is to optimise the systems for microbial stability in the water instead of keeping low bacteria numbers, which has often been the main focus in RAS. This has implications for the technological solutions and optimal systems design. We are aiming at elucidating the underlying mechanisms to better understand the effects of water treatment on the microbial dynamics and for optimizing the microbial conditions for the reared fish.

Work description

The project will involve experiments for freshwater and seawater in lab-scale continuous reactors. Effects of for example different hydraulic retention times and biofilm area per volume on the development of microbial communities will be examined. The composition of the microbial communities in both biofilm and in the water will be studied by a 16S rDNA amplicon based strategy (DNA extraction, PCR, DGGE, DNA sequencing). Microbial numbers will be analysed by flow-cytometry, and also other water quality parameters will be measured.

Supervisors: Kari Attramadal Kari Attramadal (kari.attramadal@ntnu.no), Olav Vadstein (olav.vadstein@ntnu.no), and Ingrid Bakke (ingrid.bakke@ntnu.no)

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Biveileder/-e: *Co-supervisor/-s:*	Sigrid Hakvåg
Arbeidstittel på oppgaven/ *Preliminary title:*	**Study and development of genetic tools for the thermotolerant methylotrophic bacterium Bacillus methanolicus strain PB1**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
Bacillus methanolicus is a thermotolerant bacterium that can efficiently utilize methanol as a sole carbon source. It has an optimum growth temperature of 50°C.
The methanol dehydrogenase gene, *mdh*, is crucial for methanol consumption in this bacterium.

Bacillus methanolicus is able to overproduce amino acids from methanol. Genetically engineered *B. methanolicus* strains overproducing different commercially interesting compounds such as L-lysine, L-glutamate, cadaverine and GABA, using methanol as raw material have been established[1, 2, 3, 4]

Genetic tools for modification of the strain MGA3 are developed, but remains to be tested in other wild type strains. Expanding the range of strains available for modifications will optimally also expand the range of products and production levels, and give further understanding of this bacterium. Of the wild type strains available in the lab, strain PB1 genetically differs the most from the model strain MGA3. The main focus of this project will be testing out, and possibly further develop, the different vectors and promoters used for MGA3 in PB1.

Alternative wild type strains will also be considered tested. At present, no transformation of strains other than MGA3 and PB1 has been performed, and protocols will need to be developed.

Eksperimentelt / *Experimental methods:*
- Cultivation
- Genetic modification
- Development of transformation protocols

References:

1. Brautaset T, Jakobsen ØMM, Degnes KF, Netzer R, Nærdal I, Krog A, Dillingham R, Flickinger MC, Ellingsen TE. (2010). *Bacillus methanolicus* pyruvate carboxylase and homoserine dehydrogenase I and II and their roles for L-lysine production from methanol at 50 degrees C. Appl. Microbiol. Biotechnol. 87,951-964
2. Schendel FJ, Dillingham R, Hanson RS, Sano K, Matsui K. (2000). Production of glutamate using wild type *Bacillus methanolicus*. US 6083728.
3. Irla M, Heggeset TMB,Nærdal I, Paul L, Haugen T, Le SB, Brautaset T, Wendisch VF.(2016) Genome-based genetic tool development for *Bacillus methanolicus*: Theta- and rolling circle-replicating plasmids for inducible gene expression and application to methanol-based cadaverine production. Front. Microbiol. 7:1481
4. Irla M, Nærdal I, Brautaset T, Wendisch VF. Methanol-based γ-aminobutyric acid (GABA) production by genetically engineered *Bacillus methanolicus* strains. (2016) Ind. Crops Prod

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	Can be adapted to 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Sigrid Hakvåg, Tonje Heggeset (SINTEF)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Study of different promoters in the thermotolerant methylotrophic bacterium *Bacillus methanolicus***

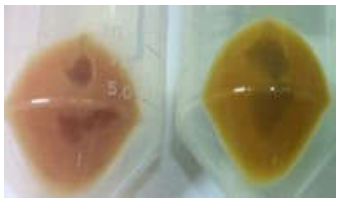
Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Bacillus methanolicus is a thermotolerant bacterium that can efficiently utilize methanol as a sole carbon source. It has an optimum growth temperature of 50°C.
The methanol dehydrogenase gene, *mdh*, is crucial for methanol consumption in this bacterium.

Introduction of the genes crtM and crtN from *Staphylococcus aureus* into *Bacillus methanolicus* MGA3 results in yellow pigmentation. The genes encode a dehydrosqualene synthase and dehydrosqualene desaturase, respectively, and expression of the genes results in the production of two C30 terpenoids, diaponeurosporene and diapolycopene providing yellow pigmentation. The resulting colour will allow the study of different promoters, including the mdh (methanol dehydrogenase) promoter. This will be the main focus of the project.

Alternative wild type strains will also be considered tested as potential hosts for carotenoid biosynthesis. At present, no transformation of strains other than MGA3 and PB1 has been performed, and protocols will need to be developed. Introducing the crtMN genes into these strains, and cultivating them on different C-sources, will yield more information on the physiology of the strains and on the regulation of the promoter(s).



WT crtMN

Eksperimentelt / *Experimental methods:*

- Cultivation
- Genetic modification
- Extraction and quantification of pigment
- Development of transformation protocols

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	Can be adapted to 60 credits / 30 credits / 15 credits (specialization project)

Production of therapeutic proteins in alternative bacterial species

Faglærer: Trygve Brautaset
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Background

Modern therapeutic proteins, such as insulin, are almost exclusively produced in *E. coli*. One of the challenges when producing recombinant proteins is solubility: a large fraction of the product is often found in an insoluble form, making it less useful for therapeutic applications.

The expression technology of Vectron Biosolutions was developed in *E. coli*, but can cover a broad range of bacterial species. By exploring the use of this technology in different bacterial species, the chances of finding a suitable production process for each protein is enhanced.

Project description

The goal of this project is to test and further develop the expression technology of Vectron Biosolutions for the production of proteins in alternative bacterial species.

Projects can be adjusted to fit different sp-profiles (15sp, 15+30sp or 60sp).

Tasks

Tasks depend on the final structure of the project, but will routinely include:

- Cloning of genes for therapeutic proteins into Vectron's vectors (PCR, gel electrophoresis, plasmid DNA isolation, plasmid purification, primer design).
- Transformation of *E. coli* with newly constructed vectors (make competent *E. coli* cells, transformation of *E. coli*)
- Using the expression of the reporter genes mCherry and beta-lactamase (growth experiments, enzyme activity assays).
- Expression of therapeutic proteins using the newly constructed vectors (bacterial growth experiments, protein isolation, SDS page, Western blot).
- Comparing the expression of the reporter genes and therapeutic proteins (bacterial growth experiments, protein isolation, SDS page, Western blot).
- Transferring the newly constructed vector into a new alternative host (transformation / conjugation / electroporation of alternative bacterial species).
- Comparing and evaluating the expression of soluble and insoluble protein fractions between *E. coli* and alternative hosts (bacterial growth experiments, protein isolation, SDS page, Western blot, protein (semi-)quantification).

About Vectron Biosolutions

Vectron Biosolutions is a small, dynamic company based at NTNU Gløshaugen. We provide state-of-the-art expression technology to both pharmaceutical and industrial companies worldwide. We welcome enthusiastic, independent students to further explore the possibilities our technology holds.

Reading

Brautaset, T., R. Lale, and S. Valla, *Positively regulated bacterial expression systems.* Microb Biotechnol, 2009. **2**(1): p. 15-30.

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Biveileder/-e: *Co-supervisor/-s:*	Professor Marit Otterlei, IKM, MH-faculty, NTNU
Arbeidstittel på oppgaven/ *Preliminary title:*	**Characterization of bioactive garlic extracts**

Background and Aims:
The complex phytochemistry of garlic (*Allium sativum*) has been the subject of more than 4000 research papers in many fields of life science the last 20 years. Much is now known about the composition of the plant, its commonly made extracts, their effects and properties. Apart from its use as a spice, relevant research in the field has justified its use as a medicinal herb as well. Numerous studies have confirmed its beneficial effects on the cardiovascular system and immune responses; as well as its antioxidant or oxidant properties. Direct antibacterial and antiviral properties have also been described, with allicin being almost exclusively responsible for the antibacterial effects. Garlic and its preparations are recommended by the US National Cancer Institute, amongst other things, for cancer prevention and as a supplement of standard cancer therapy, while WHO lists the recommended daily dose at 2-5 g of fresh garlic per day, the equivalent of 2-5 mg of allicin.

We have already tested various garlic extracts and they exhibit a clear anti-growth efficacy on cancer cell lines both *in vitro* and *in vivo,* multiple cellular signaling pathways are affected under exposure, and importantly, the garlic extracts increased the efficacy of both chemotherapeutics and target agents. This student project is based on our previously generated data (soon to be published) with aims 1. To characterize at the molecular and cellular levels the effects of garlic extracts, and 2. To explore the chemical composition and stability of the bioactive compounds in garlic extracts.

Experimental methods:
Preparation of garlic extracts, cultivation of cancer cell lines, cytotoxicity and other cellular assays incl dynamic online measurements, fractionation of extracts and partial purification of bioactive compounds, characterization by GC-MS and LC-MS methods

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/ MIKJ
Omfang (studiepoeng): Credits (ECTS):	30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Professor Per Bruheim
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Biveileder/-e: *Co-supervisor/-s:*	Post doc Katsuya Fuchino, PhD
Arbeidstittel på oppgaven/ *Preliminary title:*	**Physiological studies of biofuel producing *Zymomonas mobilis***

Bakgrunn og mål / *Background and Goal:*

This MSc project is associated the European Era-IB research project: "Z-Fuels: A novel bacterial system with integrated micro-bubble distillation for the production of acetaldehyde". The ultimate goal of Z-Fuels is to develop an integrated process in which low value waste (e.g. crude glycerol) is converted to a valuable biofuel and/or precursor chemical (acetaldehyde). The concept of Z-Fuels is to design, construct and operate a bacterial process, based on genetically engineered *Z. mobilis* with an integrated microbubble distillation system to convert complex sugary feedstocks and crude glycerol to acetaldehyde. Effective removal of acetaldehyde during the metabolic process will alleviate the inhibition and give higher yields. From the higher production quantities of acetaldehyde a more competitive and efficient route to butanol production can be obtained compared to current practise.

Eksperimentelt / *Experimental:*

Bioreactor cultivations (100 mL to 2 L operating volume), sampling and sample processing for Metabolome and Fluxome (13C experimentation) analyses, mass spectrometric analysis (LC-MS, GC-MS, capIC-MS), enzymatic analysis and other biochemical assays (especially for studies of respiratory chain)

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH, MTKJ, MIKJ
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Professor Per Bruheim
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Biveileder/-e: *Co-supervisor/-s:*	Inga Marie Aasen, SINTEF Materialer og Kjemi
Arbeidstittel på oppgaven/ *Preliminary title:*	**Metabolic profiling of omega-3 fatty acid producing thraustochytrids**

Bakgrunn og mål / *Background and Objectives:*

The MSc project is associated the NFR Digital Life/ Biotek2021 research project "AurOmega - Microbial production of omega-3 fatty acids – a model-based approach"
This is a joint NTNU and SINTEF project to establish a knowledge platform on DHA synthesis and lipid accumulation in native DHA-producing thraustochytrids, and to develop these into high productivity omega-3 fatty acid producing cell factories.

Background for the project is that the fish oil production, which is the current supply for omega-3 fatty acids in salmon farm feed, from wild fish catches cannot be further increased, continued growth of marine aquaculture will be completely dependent on development of new, sustainable sources of the essential omega-3 fatty acids, which are vital for salmon health and important for the status of salmon as a healthy food.

Thraustochytrids are unicellular, eukaryote, heterotrophic, obligate marine microorganisms, commonly found in seawater and sediments. They are able to accumulate high levels of lipids as triacylglycerols, with a high content of DHA. . Total lipid contents of the cell mass above 80 %21 and DHA-contents above 80 % of total fatty acids 14 have been reported. However, such extremes have never been obtained simultaneously Some strains producing high levels of carotenoids, squalene or exopolysaccharides have also been identified.

Eksperimentelt / *Experimental methods:*

Bioreactor cultivations (100 mL to 2 L operating volume), sampling and sample processing for Metabolome and Fluxome (13C experimentation) analyses, mass spectrometric analysis (LC-MS, GC-MS, capIC-MS), enzymatic analysis and other biochemical assays of relevance to study lipid accumulation mechanisms.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH, MTKJ, MIKJ,
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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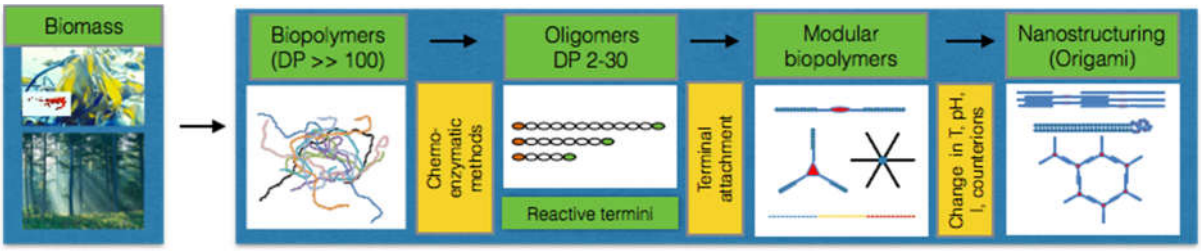
Biveileder/-e: *Co-supervisor/-s:*	Ingrid Vikøren Mo
Arbeidstittel på oppgaven/ *Preliminary title:*	**New biopolymer hybrids by oligosaccharide conjugation**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*



The exploitation of biopolymers from carbon neutral biomass (wood, seaweeds, microorganisms) can be significantly increased and expand into novel applications (medicine, pharmacy, nanotechnology) by tailoring a new class of hitherto unexplored hybrid polymers. In brief, they are linear or branched constructs ($A_nB_mC_x$) of more than one oligomer [A, B or C (or more)] of predetermined lengths (n, m, x ..) (figure) combining through terminal coupling different self-assembling functionalities, aiming towards:

a) Nanoparticle formation (for drug delivery) in both aqueous and non-aqueous (lipophilic) systems
b) Dendritic-like structures for conjugation of oligosaccharide ligands to antibodies, proteins, aptamers etc. for targeted applications
c) Macroscopic biomaterials with tuneable nano- and microstructure (for cell proliferation and tissue engineering)
d) Self-assembling 'block carbohydrate polymers': Towards polysaccharide origami.
e)

Eksperimentelt / *Experimental methods:*

a) Controlled degradation of alginates to oligosaccharides
b) Oligosaccharide fractionation (gel filtration)
c) Terminal (reducing and non-reducing end) activation and conjugation
d) Analysis of conjugates (MS, NMR, chemical, chromatographic analysis)
e)

Note: Project starts up earliest 1. October 2016

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	15 ECTS project + 30 ECTS Master: MTKJ, MIKJ, MTNANO 60 ECTS: MBIOT5,
Omfang (studiepoeng): Credits (ECTS):	Flexible, dep. on study programme

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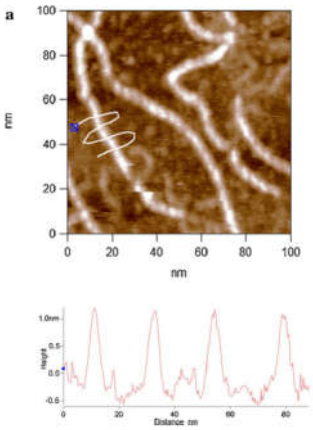
Biveileder/-e: *Co-supervisor/-s:*	Dr. Marianne Øksnes Dalheim (Post doc. VISTA)
Arbeidstittel på oppgaven/ *Preliminary title:*	**EOR Biopolymers: Xanthan**

Background and Goal:



Xanthan is a bacterial polysaccharide produced by fermentation. It is, among others, commonly used as a food ingredient, but is also relevant for Enhanced Oil Recovery (EOR). We have support from VISTA (Statoil) to investigate xanthan for EOR.

Chemical substitution of double-stranded xanthan gives rise to modified properties, most importantly viscosity, thermal stability and biodegradability.

Experimental:

a) Purify double-stranded xanthan directly from fermentation broth
b) Prepare a range of Mw's by high shear (StarBurst Mini)
c) Determine pyruvate and acetate by NMR following cellulase degradation
d) Substitute by octylamine (carbodiiimide route), DS 0-0.5
e) Conformational properties by optical rotation and CD (new instrument at IBT)
f) Determine MWD for all samples by SEC-MALLS (+/- visc. detector)
g) Biodegradability in the disordered state

For MTKJ and MTNANO: Continued work as master project
For MBIOT5: Experimental work starts 2018 (take courses autumn 2017)

TBT4135 mandatory.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	15 ECTS project + 30 ECTS Master: MTKJ, MIKJ, MTNANO 60 ECTS: MBIOT5,
Omfang (studiepoeng): Credits (ECTS):	Flexible, dep. on study programme

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
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Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina;
Arbeidstittel på oppgaven/ *Preliminary title:*	**Determination and analysis of novel bioactive compounds obtained from macro- and micro-algae**

Background and Objectives:
The aim of this project is to use NMR spectroscopy to determine industry relevant bioactive molecules from various algal extracts and to structurally characterise them.

Marine algae (contain a large amount of bioactive compounds (e.g. carotenoids, fucoidan, omega-3 and omega-6 fatty acids, pigments, amino acids, etc) that can be employed as pharmaceuticals, nutraceuticals, food additives, nutracosmeticals as well as for animal feed, fertiliser and biogas generation. The molecular content of different algae species differs greatly due to geography, time of the year and method of harvest and processing. However, little information is available on the most suitable harvesting time/geography and harvesting procedure to obtain the highest amount of bio-active compounds.

Experimental methods:
Within this project, several different extracts of algae will be studied using Nuclear Magnetic Resonance (NMR) in order to determine which bio-active compounds are present within them and measure their concentration. Certain bio-active compounds will be then further investigated and their structure determined using NMR.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
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Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina
Arbeidstittel på oppgaven/ *Preliminary title:*	**Determination of quality metabolites in different brands of cod fillets**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The aim of the work is to determine the quality and molecular changes due to storage of different brands of cod fillets utilising Nuclear Magnetic Resonance (NMR).

Fish is an important nutritive source for human consumption. The world fish food supply has grown dramatically in the last years, with an average growth rate of 3.2 percent per year in the period 1961–2009 (FAO, 2012). Atlantic cod (Gadus morhua) is a popular food product in Norway and worldwide.

Different companies sell cod of varying qualities. For the consumer it is important to know whether the price correlates with the quality of the product and how and for how long the fish should be stored, in order to keep all the metabolites that account for its health benefits.

Eksperimentelt / *Experimental methods:*
Within this project, the student will utilise a method developed in our laboratory to test A) the quality (amount of vitamins, amino acids, fatty acids, etc.) of cod purchased from different producers utilising NMR spectroscopy; B) characterise how these products change their metabolic profile over time and C) characterise how their metabolic profile changes depending on storage temperatures and time.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits

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Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina
Arbeidstittel på oppgaven/ *Preliminary title:*	**Development of a methodology to determine frauds in salmon products**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The aim of the work is to develop a method and protocol to determine salmon frauds utilising Nuclear Magnetic Resonance (NMR).

Fish is an important nutritive source for human consumption. The world fish food supply has grown dramatically in the last years, with an average growth rate of 3.2 percent per year in the period 1961–2009 (FAO, 2012). Atlantic salmon (Salmo salar) is a popular food product in Norway and worldwide due to its delicate taste and health benefits obtained from its metabolites (peptides, carbohydrates, vitamins, lipids).
However, as it happens with different fish, salmon products can be counterfeit to sell a lower quality product for a higher price. Several methods exist on how to determine frauds in fish, such as genetic verifications, isotope analysis, etc. However, most of them have several limitations.

Eksperimentelt / *Experimental methods:*
Within this project a method will be developed that will allow the detection of fraud products utilising NMR spectroscopy. Firstly, a model of salmon metabolites will be made by analysing both fresh and frozen samples of the fish. Subsequently, various frauds will be purposefully created to assess the validity of the developed methodology. The final stage of the project will be to create a protocol that might be used by authorities to detect counterfeits.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
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Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina
Arbeidstittel på oppgaven/ *Preliminary title:*	**Determination of stress biomarkers in human saliva**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The aim of this project is to determine which molecules in human saliva correlate with stress and can be thus used as biomarkers.

Stress is a condition that affects both body and mind of people. High levels of stress trigger changes in the metabolism, hormonal levels and physiological reactions. Stress is currently mostly monitored by analysing the concentration of the hormone cortisol in blood. However, such method is invasive, costly, requires specialised personnel for collection and if carried out with not sterile equipment can result in contamination with diseases. Presently, methods that are non-invasive are gaining popularity, such as the analysis of cortisol in saliva samples. For such purpose an enzyme-linked immunosorbent assay (ELISA) is usually used. However, such method is relatively time consuming and as result gives the concentration of only one molecule in the sample.

Eksperimentelt / *Experimental methods:*
Within this project, it will be investigated whether other molecules can be found in saliva samples that change in quantity depending upon stress levels. In order to study a high number of molecules, Nuclear Magnetic Resonance (NMR) spectroscopy will be used. Saliva samples of stressed and not stressed people will be analysed both by NMR and by ELISA and the results will be compared.

The results of such research may help find an efficient and fast way to detect stress both in humans and animals.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits

Hovedveileder: *Main supervisor:*	Helga Ertesvåg
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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**G-block containing alginate produced by *Pseudomonas fluorescens***

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*

Alginate is a polysaccharide composed of mannuronic acid (M) and guluronic acid (G) that is widely used in industry and medicine. It is manufactured from brown algae, but is also produced by some bacteria, including *Pseudomonas fluorescens. P. fluorescens* is an efficient alginate producer, however, it is not able to make alginate containing consecutive G-residues. *Azotobacter vinelandii* is another alginate-producing bacterium. It secreted mannuronan C-5-epimerases that are create alginate with a high G-content. A similar enzyme has been found in *Pseudomonas syringae.* The aim of this project will be to try to express secreted mannuronan C-5-epimerases in *P. fluorescens* thereby obtaining a strain that produces a more valuable product. The new strain would have to express both the enzyme and a functional secretion system for the enzyme.

Eksperimentelt / *Experimental:*

1. Express selected mannuronan C-5 epimerases in *P. fluorescens*. In parallel, clone the secretion system (The standard techniques: Cloning, PCR, sequencing)
2. Transfer the vectors containing epimerase genes to *P. fluorescens.* (Conjugation)
3. Measure internal epimerase activity. (Enzyme work)
4. Transfer the vectors with the secretion system to *P. fluorescens* strain expressing the epimerase and measure extracellular enzyme activity.
5. Isolate alginate and use NMR to demonstrate production of alginate containing consecutive G-residues.

Within a 15 stp project point 1-3 may be achieved, Plasmids expressing some of the epimerase genes have already been constructed.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5,
Omfang (studiepoeng): Credits (ECTS):	30 sp studiepoeng / 15 studiepoeng 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Helga Ertesvåg
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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Develop Rhodococcus opacus as a platform organism for lipid production**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*

Rhodococcus opacus is an actinomycete that is able to store large amounts of lipids in lipid bodies within its cytoplasm. At NTNU it has been chosen as one contender in a project aimed at producing the essential omega-3 fatty acids DHA and EPA for aquaculture feed. Aquaculture is the most likely way of providing animal protein for the increasing human population, and new sources for omega-3 are necessary in order to increase the production from aquaculture.

In connection with the ongoing MIRA project it is possible to define molecular biology projects tailored to the wishes of the student. Topics could be: optimized vectors and methods. Cloning and characterization of specific proteins like acetyl transferases, elucidation of gene function, making specific gene knock-outs etc. Literature studies or bioinformatic studies could also be included as part of the project.

Since this is a very open project, it will be available for up to three students. Each will be given their separate project. These projects will be specified in a dialog between the student and the supervisor, and will also depend on how far the MIRA project has developed when the individual students are starting up their thesis work.

Eksperimentelt / *Experimental:*

The techniques utilized will vary with the actual topic for and length of the project. All will contain standard techniques (Cloning, PCR, DNA sequencing). Other possible experiments might be: construction and characterization of new strains, vector construction/characterization or protein purification and characterization.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Veileder: *Supervisor:*	Helga Ertesvåg
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Biveileder/-e: *Co-supervisor/-s:*	To be decided based on the needs of the specific project
Arbeidstittel på oppgaven/ *Preliminary title:*	**Genetic modification of omega-3 fatty acid producing thraustochytrids**

Bakgrunn og mål / *Background and Objectives:*

The Master project is associated the NFR Digital Life/ Biotek2021 research project "AurOmega - Microbial production of omega-3 fatty acids – a model-based approach"

This is a joint NTNU and SINTEF project to establish a knowledge platform on DHA synthesis and lipid accumulation in native DHA-producing thraustochytrids, and to develop these into high productivity omega-3 fatty acid producing cell factories.

Fish oil production from wild fish catches, which is the current supply for omega-3 fatty acids in salmon farm feed, cannot be further increased, continued growth of marine aquaculture will be completely dependent on development of new, sustainable sources of the essential omega-3 fatty acids, which are vital for salmon health and important for the status of salmon as a healthy food.

Thraustochytrids are unicellular, eukaryote, heterotrophic, obligate marine microorganisms, commonly found in seawater and sediments. They are able to accumulate high levels of lipids as triacylglycerols, with a high content of DHA. . Total lipid contents of the cell mass above 80 % and DHA-contents above 80 % of total fatty acids have been reported. However, such extremes have never been obtained simultaneously. Some strains producing high levels of carotenoids, squalene or exopolysaccharides have also been identified.

In connection with the AurOmega project it is possible to define molecular biology projects tailored to the wishes of the student and the length of the master project. These will be performed in collaboration with researchers working on the project. One possible topic could be optimized vectors and methods, for instance to evaluate different promoters or to find new selectable markers. Through the project, we are obtaining hypothesis about genes that would be important for DHA biosynthesis. To generate mutants in such interesting genes and analyze the effect on fatty acid accumulation is another option for master projects.

Eksperimentelt / *Experimental methods:*

The techniques utilized will vary with the actual topic for and length of the project. All will contain standard techniques (Cloning, PCR, DNA sequencing). Other possible experiments might be: construction and characterization of the new strains, enzyme assays, measurement of reporter gene products, etc – all depending on the specific project.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH, MTKJ, MIKJ,
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Title

Nanowire-mediated electron transport in Bacteria

Contact

PhotoSynLab (*http://photosynlab.org)*
Assoc Prof Martin Hohmann-Marriott & Dr Rahmi Lale

Goal

Identify pathways that allow bacteria to donate electrons to external electron acceptors, such as iron oxide, manganese oxide or electrodes.

Introduction

There is strong evidence that bacterial pili have a function in donating electrons to iron oxides. However, this electron disposal has so far only been interpreted as to enable respiration of soil bacteria in anaerobic conditions. In contrast, we have collected data that indicates that pili are crucial for iron acquisition in bacteria. We hypothesise that pili are meditating electron donation to iron oxides, thereby converting insoluble ferric iron (Fe3+) into soluble ferrous iron (Fe2+), which can readily been taken up by bacteria. In addition to addressing the role of pili in iron acquisition, our proposal may also provide crucial understanding required to limit iron uptake by infectious bacteria and construction truly renewable photovoltaic devices.

Techniques

The student will use bioinformatics and access databases. To genetically manipulate bacteria the student will perform molecular biological approaches (e.g. PCR-amplification, plasmid construction and transformation.) Sterile culturing techniques will be used to grow bacterial cells and to select transformants. Analytical techniques (imaging and statistical techniques for the determination of growth parameters, HPLC & mass spectrometry for pigment analysis as well as potentimetric techniques) may be used to characterize the performance of the generated strains.

Literature

Reguera G., McCarthy K.D., Mehta T., Nicoll J.S., Tuominen M.T., Lovley D.R. (2005) Extracellular electron transfer via microbial nanowires. Nature, 435: 1098-1101.

Gorby Y.A., Yanina S., McLean J.S., Rosso K.M., Moyles D., Dohnalkova A., Beveridge T.J., et al. (2006) Electrically conductive bacterial nanowires produced by Shewanella oneidensis strain MR-1 and other microorganisms. Proc Natl Acad Sci USA 103: 11358-11363.

Lamb JJ, Hill RE, Eaton-Rye JJ, ***Hohmann-Marriott MF*** *(2014) Functional Role of PilA in iron acquisition in the cyanobacterium* **Synechocystis** *sp. PCC 6803. PLoS ONE 9(8):e105761****Title***

Title

Synthetic Biology - Development and implementation

Contact

PhotoSynLab (*http://photosynlab.org)*
Assoc Prof Martin Hohmann-Marriott & Dr Rahmi Lale

Project descriptions

We employ synthetic biology [1] to develop biology-based solutions for a sustainable future. We have projects on developing new biological chassis (including cyanobacteria and algae) and synthetic biology approaches. These approaches include the design of standardized biological modules [2] and implementation using high-throughput phenotyping and robotics.

Techniques

The student will genetically manipulate microorganisms. This work will involve molecular biology (e.g. PCR-amplification, plasmid construction and transformation). Sterile culturing techniques will be used to grow the selected model organism (*E. coli*, *Synechococcus, Nannochloropsis, Chlamydomonas, Sacchromyces)*. Suitable analytical techniques will be used to verify the developed synthetic biology approaches.

Literature

[1] Cameron DE, Bashor CJ, Collins JJ (2014) A brief history of synthetic biology. Nat Rev Microbiol 12: 381–390

[2] Ho-Shing O, Lau KH, Vernon W, Eckdahl TT, Campbell AM (2012) Assembly of standardized DNA parts using BioBrick ends in *E. coli*. Methods Mol Biol. 852: 61-76.

Title

Microfluidics application in microbiology

Contact

PhotoSynLab (*http://photosynlab.org*)
Adjunct Assoc. Prof. Rahmi Lale & Dr Swapnil Bhujbal

Goal

The utilization of droplet microfluidics and micro contact printing for single cell analysis and screening with applications in single cell functional metagenomics.

Introduction

Conventional cell-based assays measure the average response from a population of cells, assuming that an average response is representative of a typical cell within a population. However, this simplification and assumption of average behavior can result in a misleading interpretation. Single cell analysis using droplet microfluidics has become an important and emerging field in biological and biomedical research to understand the insights of heterogeneity between large populations at high resolution. Droplet microfluidics combined with micro contact provides a platform for characterization high number of single cells over prolonged periods of time[1]. We will explore above techniques to enrich metagenomic libraries in targeted populations to maximize functional expression and screening throughput, while reducing screening time and costs.

Techniques

The student will use interdisciplinary approach and state of art techniques like microfluidics (alginate based encapsulation), soft lithography, microcontact printing, confocal microscopy and image analysis.

Literature

1. Håti, A. G. *et al.* Microarrays for the study of compartmentalized microorganisms in alginate microbeads and (W/O/W) double emulsions. *RSC Adv.* **6,** 114830–114842 (2016)

2. Weibel, D. B., Diluzio, W. R. & Whitesides, G. M. Microfabrication meets microbiology. *Nat. Rev. Microbiol.* **5,** 209–18 (2007).

3. Zhu, Z. & Yang, C. J. Hydrogel Droplet Microfluidics for High-Throughput Single Molecule/Cell Analysis. *Acc. Chem. Res.* **50,** 22–31 (2017).

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Biveileder/-e: *Co-supervisor/-s:*	Trygve Brautaset
Arbeidstittel på oppgaven/ *Preliminary title:*	**Metabolic engineering of *B. methanolicus* for production of 2,3-butanediol.**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The use of methanol as a carbon source in the biotechnological processes has recently become an issue of great interest due to its relatively low price, abundance, purity, and the fact that it is a non-food raw material. *Bacillus methanolicus* is a Gram-positive thermotolerant methylotroph considered to be a suitable candidate for methanol-based production of amino acids and their derivatives.
In this project, *B. methanolicus* will be engineered for production of 2,3-butanediol (2,3-BD). 2,3-BD is has versatile applications, it can be used as a liquid fuel, fuel additive, or antifreeze agent. Moreover, it can serve as a precursor of bulk chemicals such as 1,3-butadiene, methyl ethyl ketone, polyesters and gammabutyrolactone. The project will consist of the search through the genome for the genes potentially involved in the native 2,3-BDO biosynthesis pathways, characterization of the wild type strains with regard to native 2,3-BDO production and resistance to this compound, and creation of 2,3-BDO producing strains.

Eksperimentelt / *Experimental methods:*
The project will include

- basic molecular biology work (e.g. plasmid construction, transformation into *E. coli* and *B. methanolicus*),
- analysis of wild type strains for their applicability for production of 2,3-BD (e.g. tolerance to 2,3-BDO),
- construction of producing strains and characterization
- if time permits, methanol-based fed-batch fermentations of producing strains.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits / 15 credits

Veileder: *Supervisor:*	Marta Irla
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Biveileder/-e: *Co-supervisor/-s:*	Trygve Brautaset
Arbeidstittel på oppgaven/ *Preliminary title:*	**Development of gene deletion tools for *B. methanolicus* for generation of sporulation deficient and biologically contained platform strains**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The use of methanol as a carbon source in the biotechnological processes has recently become an issue of great interest due to its relatively low price, abundance, purity, and the fact that it is a non-food raw material. *Bacillus methanolicus* is a Gram-positive thermotolerant methylotroph considered to be a suitable candidate for methanol-based production of amino acids and their derivatives.
In this project, the gene deletion system based on the application of thermosensitive plasmid and counter selection markers will be developed. The newly established system will be applied for deletion of genes involved in sporulation, cell autolysis and protection from UV-light. This way a safe, biologically contained strain for future industrial applications will be developed and if possible, directly applied for methanol-based production of γ-aminobutyric acid (precursor of bioplastics).

Eksperimentelt / *Experimental methods:*
The project will include

- basic molecular biology work (e.g. plasmid construction, transformation into *E. coli* and *B. methanolicus*),
- analysis of plasmids with regards to their themosensitivity and putative counter selection markers,
- strain characterization (ability to sporulate, UV-sensitivity),
- construction of GABA producing strains and characterization (HPLC),
- if time permits, methanol-based fed-batch fermentations of GABA producing strains,
- if time permits, establishment of new method in our lab: Ordered Gene Assembly in *Bacillus subtilis* (OGAB), developed in 2003 by Tsuge et al.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits / 15 credits

Veileder: *Supervisor:*	Marta Irla
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Biveileder/-e: *Co-supervisor/-s:*	Trygve Brautaset
Arbeidstittel på oppgaven/ *Preliminary title:*	**Use of regulatory circuits for controlled gene expression in *B. methanolicus***

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The use of methanol as a carbon source in the biotechnological processes has recently become an issue of great interest due to its relatively low price, abundance, purity, and the fact that it is a non-food raw material. *Bacillus methanolicus* is a Gram-positive thermotolerant methylotroph considered to be a suitable candidate for methanol-based production of amino acids and their derivatives.
In this project, the novel system for controlled gene expression will be developed. The system is based on the function of lysine riboswitches which regulate expression of genes involved in the lysine metabolism. First, lysine riboswitches derived from *B. methanolicus* and *B. subtilis* will be tested for regulation of plasmid-based expression of reporter gene *sfGfp.* In next steps, the lysine riboswitch will be used for controlled expression of genes involved in lysine metabolism.

Eksperimentelt / *Experimental methods:*
The project will include

- basic molecular biology work (e.g. plasmid construction, transformation into *E. coli* and *B. methanolicus*),
- analysis of sfGFP fluorescence of created by the means of flow cytometry,
- construction of producing strains and characterization (HPLC),
- if time permits, methanol-based fed-batch fermentations producing strains.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits / 15 credits

Hovedveileder: *Main supervisor:*	Turid Rustad
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Biveileder/-e: *Co-supervisor/-s:*	Ulf Erikson, SINTEF
Arbeidstittel på oppgaven/ *Preliminary title:*	**Bestemmelse av kvalitetsendringer i fisk ved bruk av ny metodikk**

Bakgrunn og mål / *Background and Objectives:*

Det er et økende salg av frossen tint fisk. Denne selges også som fersk. Det er derfor behov for målemetoder som kan skille mellom fersk og frossen tint fisk. Noen målemetoder finnes – men disse er tidkrevende og lite presise. For å kunne forbedre og utvikle nye og bedre prosesseringsmetoder for bla fisk er det behov for gode målemetoder for å bestemme endringer i råstoffet som funksjon av prosessbetingelser. Dette vil for eksempel være å bestemme når proteindenatureringen begynner – bla ved varmebehandling – hvis vi ønsker mildere varmebehandling – hva skjer med proteinene (og tekstur med mer). Det er også mulig å studere effekt av ulike tinemetoder osv.

Eksperimentelt / *Experimental methods:*

Oppgaven vil gå ut på å bruke måle endringer i proteiner ved hjelp av endringer i overflatespenning ved hjelp av et nytt utviklet instrument og koble dette til målinger med konvensjonelle metoder.

Det vil bli gjort målinger på fersk fisk som er behandlet på ulik måte, fersk, lagret og frossen tint. Prøvene vil bli analysert ved hjelp av overflatespenningsmetoden og ved metoder slik som endringer i proteinløselighet, vannbindingsevne, tekstur og evt endringer i enzymaktivitet.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ
Omfang (studiepoeng): Credits (ECTS):	15 studiepoeng

Hovedveileder: *Main supervisor:*	Turid Rustad
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Arbeidstittel på oppgaven/ *Preliminary title:*	**Processing to retain quality and stability of healthy nutrients in model mackerel products**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

The aim of this work is to optimize the processing steps of model products from mackerel. Re-formulated products (mimics fishcake/finger) will be made and Sous vide (light heat treatment) will be used. The focus will be on the quality and stability of healthy nutrient like omega – 3 fatty acids.

Consumption of fatty fish such as mackerel provides numerous important nutrients linked both to their lipids, proteins and water soluble components. The lipids in mackerel are rich in long chain n-3 polyunsaturated fatty acids (LC n-3 PUFA) with well documented beneficial effects e.g. on cardiovascular diseases. However, the LC n-3 PUFA are highly susceptible to oxidation resulting in rapid quality loss such as reduced sensory quality (undesirable taste and flavour) of the product. **This work will screen the changes in lipids during processing of mackerel into model ready to eat/sous vide mackerel products.** The ability of natural antioxidants like herbs to increase the oxidative stability of the model products will be studied.

Eksperimentelt / *Experimental methods:*

The methods involved in the study will be mainly: compositional analysis (lipid, water, protein content) and quality analysis (amount of peroxides, conjugated dienes, thiobarbituric reactive substances and free fatty acids). Additional investigation on the lipid oxidation methods will be carried out in order to choose and optimise the available methods for the analysis of marinated herring.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Arbeidstittel på oppgaven/ *Preliminary title:*	**Storage quality of ready-to-eat Atlantic salmon treated with soluble gas stabilization (SGS)-technology and gentle heating**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

For å øke inntak av sjømat er det behov for utvikling av attraktive, stabile og velsmakende produkter. Det vil si produkter som er lettvinte å bruke og har god holdbarhet. For å utvikle slike produkter er det nødvendig med mer kunnskap både om råstoffene som skal inngå og hvordan disse påvirkes av prosess og lagring samt om hvordan prosessering og ingredienser påvirker holdbarhet. Oppgaven går ut på å optimalisere kombinasjonen av SGS- og varmebehandling av Atlantisk laks for å sikre god kjemisk og mikrobiell holdbarhet av laks. Ulike SGS betingelser (tid, temperatur, emballasje), varmebehandling (type, temperatur + tid kombinasjon) vil bli studert. Spesielt for varmebehandling vil man se på hvordan kvaliteten av laksen påvirkes ved lett varmebehandling samt hvilke varmebehandlingsmetoder som kan benyttes. I tillegg vil man måle hvor mye varmebehandlingen påvirker innløsningen av CO_2.

Eksperimentelt / *Experimental methods:*

SGS-teknologi vil bli testet i kombinasjon med forskjellige varmebehandlinger. Hvor mye CO_2-som blir løst opp vil bli bestemt. For å følge kvalitetsendringer vil mikrobiell, kjemisk og/eller fysikalsk kvalitet ved forskjellige behandlinger (enkeltvis og i kombinasjon) bli bestemt.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Turid Rustad
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Biveileder/-e: *Co-supervisor/-s:*	Rasa Slizyte og Kirsti Greiff
Arbeidstittel på oppgaven/ *Preliminary title:*	**Funksjonelle ingredienser i mat**

Hovedmålet med oppgaven vil være å undersøke hvilke effekter tilsetning av ulike ingredienser har på fysio-kjemiske, sensoriske og teknologiske egenskaper i mat.

Bakgrunn og mål:
Enzymatisk hydrolyse er en prosesseringsteknikk som kan benyttes for å produsere høyverdige ingredienser fra restråstoff. Prosessen er basert på bruk av kommersielle enzymer (proteaser) som bryter peptidbindinger, forenkler degraderingen av råstoffet og fører til utskillelse av oljen. Resultatet er tre fraksjoner; proteinhydrolysat (vannløselig protein), olje og grakse (uløselig proteiner, fosfolipider og bein). Råstoffsammensetning, enzymtype og prosessbetingelsene vil påvirke egenskapene til sluttproduktene, noe som gjør det nødvendig å utvikle prosesser skreddersydd for det restråstoffet det er tenkt brukt på. SINTEF Fiskeri og havbruk har gjennom flere prosjekter utviklet teknologier for utnyttelse av restråstoff fra fisk og kylling. Et resultat av dette er ulike ingredienser som kan ha funksjonelle egenskaper ved prosessering av mat, gi økt næringsverdi og påvirke sensoriske og teknologiske egenskaper i ferdig produkt.

Eksperimentelt*:*
Prosjektarbeidet vil bli knyttet opp mot aktiviteter som SINTEF Fiskeri og havbruk har i prosjekter på dette området. Det vil være behov for forsøk og analysering av både ingredienser og ferdig produkt.
Aktiviteter som kan inngå i dette prosjektet:

- Karakterisering av kjemisk sammensetning i ingrediensene
- Pilotforsøk hvor modellprodukter testes ut
- Fysio-kjemiske, sensoriske og teknologiske analyser.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Alex Dikiy, Rasa Slizyte/Revilija Mozuraityte (SINTEF)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Technological solutions for production of safe and high quality proteins from salmon rest raw materials**

Bakgrunn og mål / *Background and Objectives:*

Rest- and by-products from slaughtering and processing of farmed salmon contain valuable protein and lipid as well as vitamins and minerals. Today, most of these by-products goes to low value fish silage for use as animal feed. The slaughtering and processing of the farmed fish generate fresh, high quality rest- and by-products that may be separated into different fractions. These raw materials therefore has great potential to be used for products to more demanding, but also better paying markets such as ingredients, e.g. protein hydrolysates, for use in functional stage specific diets for poultry, pet food including nutritional supplements for human consumption. This requires hygienic handling of the by-products to ensure food safety as well as methods to generate storage-stable products.

One of the most fundamental challenges are decomposition of rest raw material and formation of undesirable compounds like biogenic amines (BAs) such as histamine, tyramine, putrescine, cadaverine and phenylethylamine in poorly stored raw materials or later during processing. The overall project idea is to develop **technological toolbox to control safety, quality and stability of proteins from salmon rest raw materials for dietary functional application**. The technological toolbox will include the solutions to prevent formation of undesirable components (BA), microbiological control and establishing product stability through the processing chain.

Eksperimentelt / *Experimental methods:*

*Experimental part will cover de*fining raw material composition, storage as well as processing parameters for production of safe and high quality products to be used in functional applications as high value ingredients.

This will involve:

- Determination of chemical composition of raw material
- Characterization of degradation products (including biogenic amines) by traditional and rapid analytical techniques like NMR
- Identification where during different technological steps, undesirable components are formed.
- Identification the stability of the protein concentrate as a function of dry matter, pH, degree of hydrolysis and storage temperature.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Arbeidstittel på oppgaven/ *Preliminary title:*	**Marine protein ingredients in functional food**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*
Fish rest raw material is mainly used for production of feed. Processing into products/ingredients for human consumption will increase profitability. The local industry at Møre has started the production of protein meal from rest raw material both from herring and white fish. Human consumption of the valuable fish proteins are depending on finding a good way to administer this. How these powders may be suited to increase protein content in different foods is not well described. They may be added to different processed seafood or administered in liquids for nutrient drinks/sports nutrition. Different protein ingredients are available for testing.

The aim of this study is to test different ways to administer these fish powders, and to test how this addition will affect the functional properties as well as the sensory properties of the products. This study can also be extended to include marine lipids.

Eksperimentelt / *Experimental:*
The task will be to find a suitable model product and test inclusion of different levels of protein. The functional properties (water holding, texture ..) and quality measured by sensory attributes will then be tested.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	name/-s
Arbeidstittel på oppgaven/ *Preliminary title:*	**Extraction and properties of salmon gelatine**

Bakgrunn og mål / *Background and Objectives:*
Several million tonnes of marine rest raw materials (MRRM) are generated in Europe each year. Some countries have traditionally utilised significant parts of the MRRM as silage, which is often processed into fish and animal feed or well, as a biofuel feedstock for anaerobic digesters. Only a small fraction of MRRM is used for human consumption or other value-added applications. In other countries, due to the lack of specialised infrastructure, MRRM are wasted or sent directly for animal feed without any attempt to extract the valuable components.
Fish skin and other MRRM (like backbones, viscera) are rich in collagen, and a good source for gelatine extraction. Extraction of fish gelatine usually involve acid or alkaline pre-treatment of gelatine rich raw material prior to gelatine extraction .Due to a lower content of the amino acids proline and hydroxyproline, gelatines from cold-water fish species are known to have lower gel strength, as well as lower gelling and melting temperatures, compared to gelatine from mammals and warm-water fish species. Fish gelatine is used in cosmetic, food and pharmaceutical applications, and in contrast to bovine gelatine, it is not associated with the risk of Bovine Spongiform Encephalopathy, and unlike porcine gelatine, it is Halal compliant. However, the suboptimal physical properties have limited the commercial interest in cold-water fish gelatine.
Optimisation of extraction from different start material like fish RRM and co-fractions after other technological processing (like thermal extraction and enzymatic hydrolysis), technological steps like different extraction parameters (extraction temperature and time, pH, fractionation of extracted) as well as separation of different gelatine fractions and chemical or enzymatic modifications will be applied to improve the properties of fish gelatine.

Eksperimentelt / *Experimental methods:*
Gelatine will be isolated from sorted and unprocessed fractions of fish RRM (skin, backbones) and from the insoluble fractions obtained after fractionation/hydrolysis of fish viscera into oil, stick water/hydrolysate and sediments. Several extraction parameters (like extraction temperature and time, pH, fractionation of extracted gelatine) for improving gelatine extraction technologies with the focus on yield, bioactive and textural properties will be tested. Molecular weight distribution, amino acid composition as well as viscosity, film forming capacity and gel strength, bioactive properties like ACE inhibition, antioxidativy will be analysed on extracted gelatines.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	nameKristine Kvangarsnes
Arbeidstittel på oppgaven/ *Preliminary title:*	**Characterization of rest raw material from organic Atlantic salmon**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Goal:*
NTNU Ålesund rules a full scale production of organic Atlantic Salmon. The diet is specialized and contain higher amount of marine ingredients during this production. The rest raw material may have special properties due to this.

The aim of this study is to characterize the rest raw material of organic salmon to exploit possible properties and evaluate utilization both as a consumption products and as an ingredient. Organic salmon oil or organic salmon meal – evaluate market and possibilities

Eksperimentelt / *Experimental:*
Chemical analysis of different fractions of raw material of organic salmon. Fatty acid profiles. Amino acid analysis. Comparison with conventional produced salmon. Coordinated experiments with our phd.student.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Arbeidstittel på oppgaven/ *Preliminary title:*	**Processing of mackerel oil for quality and stability**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

2014 Norwegian and foreign vessels landed ca 280 000 and 150 000 metric tonnes of mackerel, respectively. At present only 2-4 % of the mackerel is filleted by the domestic processing industry, but there are several initiatives to increase this share, to increase the profitability of the mackerel industry. An increasing filleting share – will results in increased volume of available rest raw materials from mackerel. Mackerel rest raw materials are very rich in long-chain omega-3 polyunsaturated fatty acids (LC-PUFA) such as EPA and DHA. Therefore, Norwegian fish oil processing industry is interested to use rest raw material from mackerel to produce mackerel oil for supplement market. Unfortunately, long-chain omega-3 PUFAs are especially labile with respect to oxidation. Without enhanced protection marine lipids oxidize virtually instantly which causes formation of undesirable rancid flavours and odours. Moreover, the color of the oil can change as the result of lipid-protein oxidation also. Therefore, the stabilisation and optimal processing technologies are necessary for mackerel oils.
Therefore, **the aim of this study to find important processing steps for extraction and processing of mackerel oil for good quality and stability.**

Eksperimentelt / *Experimental methods:*
The student will study the extraction of oil from mackerel rest raw material and possibilities to stabilise it by adding antioxidants early in the process. The color development and effect of processing parameters will be studied. Short path distillation will be used to study the distillation of the mackerel oils to improve the quality. The analysis that student will perform will be: fatty acid composition using GC-FID, lipid quality – peroxide value, anisidine value, lipid protein interaction – measurement of Schiff bases (at NTNU) and others according the needs.
The work will take place at SINTEF SeaLab, but some analysis will be also performed at NTNU.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Revealing the mechanisms underlying the adhesion of bacteria to mucosa**

Background and Goal:
Mucus, and more precisely mucin O-glycans, contribute to the selection of the microbiota by representing ligands for microbial adhesins, displaying antimicrobial properties towards certain bacteria and by limiting the surface attachment of other bacteria. These bacteria – mucus interactions are thus important for both human and bacterial health. The exact structures involved in these critical glycan – bacteria interactions are for many systems unknown. In this project we propose to focus on the interaction of various bacterial strans to the mucosal surface on fish skin. *We hypothesize that the potential of a bacterium to colonize fish skin depends on its ability to adhere to the mucosal surface.* In order to test this hypothesis, we propose to quantify bacterial-mucous interactions, both for bacteria isolated from the skin and bacteria not isolated from skin but preferably present in the fish environment.

Experimental:
The main experimental approach will be the direct determination of bacteria – surface interactions using the sensitive force probe atomic force microscopy (AFM). The study will include quantification of the interaction abilities of various bacterial strains immobilized onto AFM tips, to fish skin mucus. These investigations will be combined with microscopic inspection of the mucosal surfaces. Additionally, the role of glycan structures for bacterial adhesions will be elucidated**.** The adhesion force between bacteria and surfaces covered with one of the main glycan structures found on salmon skin will be quantified using AFM. The amount of adhering bacteria will be determined by microscopy of mucus surfaces exposed to bacteria.

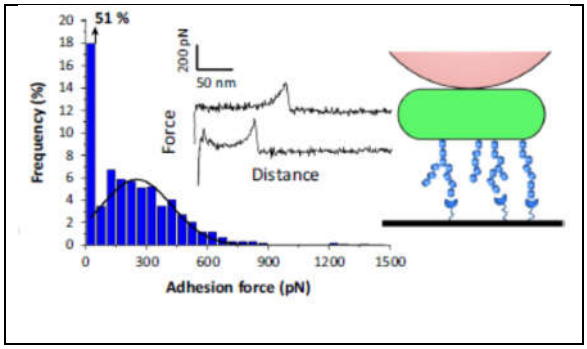

Illustration of single cell force spectroscopy (SCFS) assay in microbiology. The illustration is taken from a review paper (Dufrêne, Trends in Microbiology June 2015, Vol. 23, No. 6) and illustrates the approach used in the study "Single-cell force spectroscopy of probiotic bacteria" (Beaussart, A. *et al*. (2013) Biophys. J. 104, 1886–1892) were carbohydrate interactions of probiotic bacteria were quantified using AFM.

The topic can be adjusted to fit with the expected workload for 60, 30 or 15 credits.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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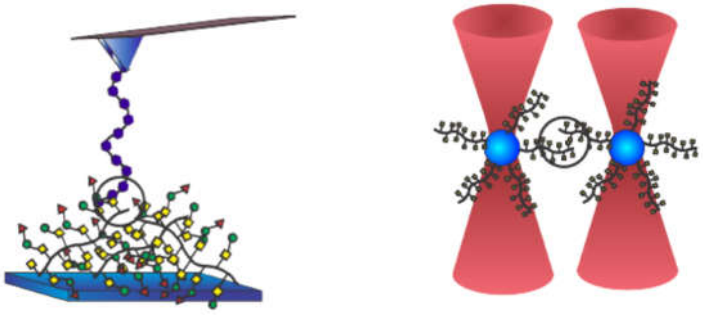
Webside / *webpage*:	https://www.ntnu.edu/employees/-/employee/sletmoen
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Importance of altered mucin glycosylation for molecular interactions and cancer progression.**

Background and Goal:
Changes in glycosylation occur in essentially all types of cancers and changes in mucin-type O-linked glycans are the most prevalent aberrant glycophenotype. The aberrant glycosylation seen in cancer results in the multiple O-linked glycans carried by mucins being mainly short and sialylated, in contrast to the long, branched chains seen on mucins expressed by normal epithelial cells. In carcinomas this aberrant glycosylation can alter the interaction of the mucin with lectins of the immune system8 and thereby influence tumor-immune interplay. While it is clear that expression of mucins carrying short, sialylated glycans enhances tumor growth, the mechanisms underlying this are ill-defined.

We are investigating the effect of this aberrant glycosylation occurring in the majority of human cancers. We are investigating both how certain carbohydrate based tumor-associated antigens interact with specific lectins found on antigen presenting cells, and also the self-interaction abilities of these truncated glycans.



Biomacromolecules to be investigated are immobilized onto flat surfaces for investigations using AFM microscopy (left) or onto the surface of polystyrene beads for investigation using optical tweezers (right).

Experimental:
The main experimental approach will be the direct determination of glycan interactions using the sensitive force probes atomic force microscopy (AFM) or optical tweezers (OT). These techniques allow determining intermolecular interaction forces with picoNewton resolution. They are thus powerful tools to provide new information concerning specific biological interactions.

The topic can be adjusted to fit with the expected workload for 60, 30 or 15 credits. Due to limited instrument time max 2 students can be admitted.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Marit Sletmoen
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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Characterizing pilus-mediated adhesion of *E. coli* to mannose coated surfaces**

Background and Goal:

Understanding the fundamental forces involved in the adhesion of microbial cells to a surface is important not only in microbiology, to elucidate cellular functions (such as ligand-binding or biofilm formation), but also in medicine (biofilm infections) and biotechnology (cell aggregation). In the case of *E.coli*, the first contact between the eukaryotic cell and the bacterium, crucial for the subsequent development of the disease, is mediated by adhesive organelles that are anchored on the outer membrane of the bacterium. These so-called fimbriae consist of various protein units with a lectin domain at the very end. One of the best characterized fimbriae and among the most important virulent factors of *E. coli* are the type 1 fimbriae. Their associated lectin is FimH which is specific for α-D mannosides. FimH is known to bind to high-mannose type oligosaccharides of the glycocalyx of eukaryotic cells. Multivalency of this protein-carbohydrate interaction leads to adhesion of bacterial cells.

Experimental:

In the current project, single *E.coli* cells will be immobilized onto an AFM cantilever (Figure 1). This cantilever will then be brought into contact with a mannan-coated surface. The forces acting between the *E.coli* cell and the mannan-coated surface will be recorded upon retraction of the AFM cantilever. The resulting AFM force versus distance curve will reveal details of the *E.coli* interaction with the surface. In addition to the AFM based studies, studies of cell mobility through a thin channel might be performed (Figure 1, right panel). Such a system will allow investigations of the combined effect of the hydrodynamic conditions and surface properties on initial bacterial adhesion.

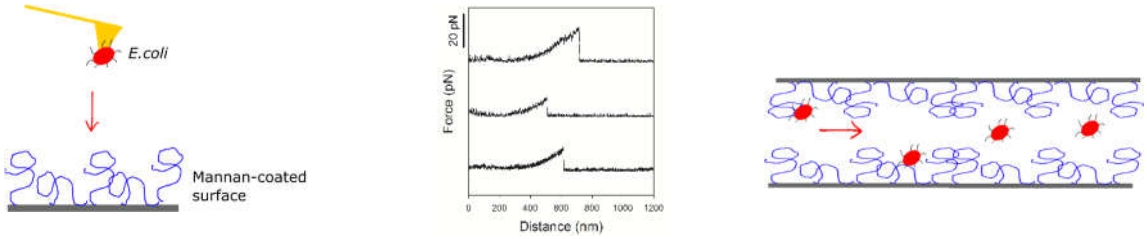

Figure 1: Schematic illustration of the experimental approach. Left: AFM based determination of interaction strength between a piliated *E.coli* cell and a mannan coated surface. The *E.coli* cell is immobilised onto an AFM cantilever (shown in yellow in the figure) and the probe is allowed to approach the surface. If an interaction forms between a structure on the surface of the *E.coli* and the immobilized mannans, this interaction will be ruptured upon retraction of the AFM cantilever. This event is observed as a force jump in the force versus distance curve (middle panel). Right: Micro-flow system developed to study the adhesion of piliated *E.coli* cells to mannan coated surfaces. The translocation of the *E.coli* cells will be recorded using continuous microscopic inspection of the channel.

The topic can be adjusted to fit with the expected workload for 60 or 30 credits.

Suitable for main profiles:	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Investigation of bacterial adhesion to glycan-presenting surfaces**

Background and Goal:
Glycans comprise the outer face of cells, and cellular interactions within and between species therefore often involve glycan binding and recognition. Many of these glycans exist as part of mucin molecules. Throughout evolution, opportunistic pathogens have developed the ability to target glycan structures on host cells to facilitate infection. Glycans therefore present attractive drug targets for infectious disease prevention and treatment.

Experimental:
We propose to develop glycan microarrays and to use these as a tool to study glycan interactions as well as bacterial attachment to glycosylated molecules. The microarrays will present patches of mucins displaying glycans of a predefined structure, surrounded by mucins displaying glycans of a different structure (Figure 1). The PDMS stamps needed to deposit mucins in micron-sized patches will be prepared using lithographic techniques present in NTNU Nanolab. In a first series of experiments we will investigate the ability of glycan self-interaction to assure stable immobilization of micronsized particles onto glycan presenting surfaces (Figure 1). Of particular interest will be functionalization with mucins carrying truncated glycans as found on cancerous tissue. The amount and position of the bound polystyrene beads will be determined by light microscopy. Furthermore, we hypothesize that the potential of a bacterium to colonize a mucosal surface depends on its ability to bind to specific glycans carried by mucins exposed on the surface. Studies of bacterial adhesion to glycan presenting surface spots will be performed as explained in figure 1 C.

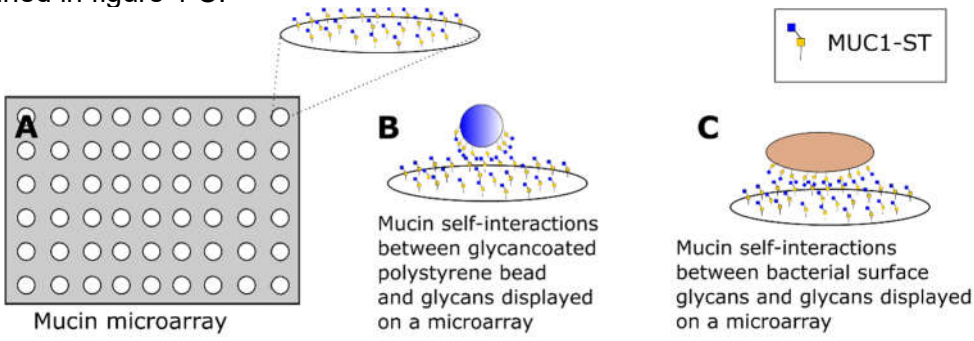

Figure 1: A: We propose to prepare glycan microarrays consisting of patches functionalized with a mucin displaying the glycan sialyl-Tn (STn). B: MUC1-STn functionalized polystyrene beads (diameter 1 – 3 micrometers) will be used to investigate the ability of STn glycans to mediate adhesion of micronsized particles to STn-presenting surfaces. The amount and position of the bound polystyrene beads will be determined by light microscopy. C: The glycan arrays will be used to asses and compare the adhesion abilities of chosen bacteria to mucins with well-characterized glycosylation patterns.

The topic can be adjusted to fit with the expected workload for 60 or 30 credits.

Suitable for main profiles:	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Arbeidstittel på oppgaven/ *Preliminary title:*	**Alginate matrices for tissue engineering**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Alginate is a attractive biopolymer for use as scaffold (matrix) in tissue engineering. Although alginate entrapment is a very gentle technique for immobilizing living cells, many cells need specific interaction with the matrix for their proliferation and viability. Such anchoring depending behaviour is common for most mammalian cells and the alginate network itself is non-interacting. Peptides known from the extracellular matrix (ECM) to interact with integrins in the cell membrane can be linked to alginate and induce attachment of cells to the alginate. Interactions between ECM and integrins have been shown to determine cell morphology, viability and differentiation, and is thus highly relevant study objects in tissue engineering. Of particular interest is the covalent linkage of peptides that can be used to crosslink the alginate and that cells by secreted enzymes can degrade and by this modify their microenvironment. **The aim of the project is to design novel alginate matrices covalent cross-linked with peptides that can be degraded by proteases and with cell adhesion properties.**

Eksperimentelt / *Experimental methods:*

Different peptides will be covalently link to alginate using a novel method developed at IBT, NTNU. NMR spectroscopy, light scattering (SEC-MALS) and viscosity measurements, will be relevant method for product characterisation (e.g. degree of coupling and crosslinking). Hydrogel properties, such as gel elasticity and stability will be studied. Studies of cell interactions with the developed materials on 2D gels and in 3D gels using confocal microscopy may be a part of the project depending on the student interests and the progress of the project.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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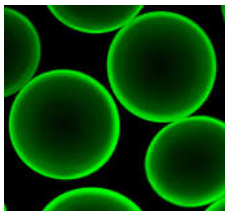
Arbeidstittel på oppgaven/ *Preliminary title:*	**Strategies for stabilising alginate beads of intermediate G content**

Project description:

Alginate microbeads have through many years of research shown great potential as an immunoisolation system for the entrapment of insulin-producing cells. The preferential use of alginate gels in cell immobilisation is primarily due to the gentle environment they provide for the entrapped material. Alginate is a binary heteropolymer containing 1,4-linked β-**D**-mannuronic acid (M) and α-**L**-guluronic acid (G) residues, known for its gel forming properties in the presence of divalent cations. The use of alginate gels for cell encapsulation provides many challenges related to its application, which includes destabilisation of the gel network in terms of swelling and gel dissolution, as well as increased pore size, at physiological conditions (Mørch et al., 2006). Traditionally, a polycation layer has been applied to stabilise the alginate gel beads. However, the conventional polycation layer (poly-L- lysine) has been found to be highly immune stimulating, associated with cellular overgrowth on the surface of the alginate capsule (Strand et al., 2001), in addition to activating the complement system (Rokstad et al., 2011). The functional properties of alginate are essentially governed by the content of M and G. In a recent *in vivo* study performed by Tam et al. (2011), alginate isolated from *Laminaria hyperborea* leaf with an intermediate G content was found to be biocompatible. However, the alginate displayed a low degree of stability in terms of swelling and bead fragmentation upon transplantation.

The aim of the current project, with the possibility of a continuation to a master's project, is to explore different strategies for stabilising alginate beads made from *L. hyperborea* leaf alginate, which has already shown to be a promising candidate for cell transplantation in terms of biocompatibility. These strategies include the incorporation of short and extremely long G-blocks into the gelling system, in combination with varying the type and concentration of gelling ions used. The size stability of the alginate beads will be studied at physiological conditions (saline experiments). In addition, the diffusional properties of the added G-blocks will be assessed through fluorescence-labelling of the alginates, followed by confocal-laser-scanning microscopy (CLSM) analysis.



Fluorescence-labelled *L. hyperborea* leaf alginate beads, visualised by CLSM.

References

Mørch, Y. A., Donati, I., Strand, B. L. & Skjåk-Bræk, G. 2006. *Biomacromolecules,* 7**,** 1471-80.

Rokstad, A. M., Brekke, O.-L., Steinkjer, B., Ryan, L., Kollárikóva, G., Strand, B. L., Skjåk-Bræk, G., Lacík, I., Espevik, T. & Mollnes, T. E. 2011. *Acta Biomaterialia,* 7**,** 2566-2578.

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Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	30 sp studiepoeng / 15 studiepoeng 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	**Olav Vadstein**
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Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	**Charlotte Volpe**
Arbeidstittel på oppgaven/ *Preliminary title:*	**Evaluation of reactive oxygen species (ROS) production in microalgae**

Background and Objectives:

During the last decades there has been an increased interest in biotechnological applications of microalgae related to bioenergy and as lipid source (LC-PUFAs). In order to use these organisms for large-scale production it is essential to investigate in details how various variables influence productivity. Light is a factor of major importance as it represents the energy source of photosynthetic organisms; but too low or too high light supply will cause disadvantages in terms of growth. When present in excess, it may cause serious damages to the cells due to the formation of harmful reactive oxygen species (ROS) that leads to oxidative stress and in some cases cell death. Algae in a photobioreactor (PBR) are inevitably exposed to variation in light conditions due to mixing and natural changes in irradiation. For a cell shifting between the highly illuminated zones to the darkness, the overall photosynthetic quantum yield depends on the residence time in each zone. Once a photon is absorbed the system needs 1-15 ms to reset itself before being ready to receive another photon. If the exposure to high light conditions and the photon absorption exceed the maximum capacity of the photosystems, the reaction center can incur in over-reduction, ROS production and cell damage/death. The goal of the project is to get a better understanding of ROS production in microalgae, and to evaluate the best time intervals between light and dark to reduce ROS formation as much as possible.

Experimental methods:

The experiment will be done with one or two species of microalgae, cultured in 96 well plates. The cultures will be exposed to different light conditions carried out by a microplate light incubator. Three different light intensities will be used (three plates – high, medium, low light). For each plate, 12 different light/dark time intervals will be tested (with 8 replicates). The DCFH-DA method for ROS measurements will be used and detected with fluorescence spectrophotometric analysis. In parallel growth, autofluorescence and quantum yield analysis will be performed. The extent of the work will be adapted to the type of thesis.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, and MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	Kan tilpasses 60, 30 eller 15 studiepoeng Can be adapted to 60, 30 credits or 15 credits

Hovedveileder: *Main supervisor:*	**Olav Vadstein**
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Biveileder/-e: *Co-supervisor/-s:*	**Charlotte Volpe**
Arbeidstittel på oppgaven/ *Preliminary title:*	**Random mutagenesis as a tool for strain improvement in microalgae**

Background and Objectives:

Even if the commercial potential of microalgae has been widely recognized by society, to date large scale production of microalgae for most industrial purpose (e. g. bioenergy, fish-farming, food supplement) are not yet feasible due to high production costs. For biotechnological applications like those mentioned, the phenotypical traits are critical for whether a process is profitable or not. The main strategies that can be used to maximize productivity and reduce costs of large-scale production are: Increase the lipid content per unit of biomass and increase the biomass density per culture volume or area. Strain improvement can be achieved by genetic engineering or by exposing microalgal strains to selection regime that favors certain traits. In this project the second method will be used. Random mutagenesis will be performed to increase the genetic variation in the population; afterwards those cultures will be exposed to selection regimes, which will favor certain traits.

Experimental methods:

The experiment will be performed on one or two microalgal strains. After the identification of an ideal mutagenic factor the mutagenesis will be performed on the cultures. Afterwards the cells will be exposed to two selection regime: 1) a light regime simulating the light perception of one cell in a photobioreactor that will favor cells with altered photosynthetic antennas; and 2) darkness incubation at a set point of the growth, that will favor cells with the highest lipid content. In parallel, as a control, wild type cells will be exposed to the same selection regime. Growth rate, quantum yield and autofluorescence measurement will be performed in addition to lipid analysis performed with the fluorescence method, Nile Red. The extent of the work will be adapted to the type of thesis.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, and MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	Kan tilpasses 60, 30 eller 15 studiepoeng Can be adapted to 60, 30 credits or 15 credits

Hovedveileder: *Main supervisor:*	Olav Vadstein
Kontaktinformasjon / epost *Contact information / email:*	Phone: 9189 7034 / olav.vadstein@ntnu.no
Webside / *webpage*:	http://www.ntnu.edu/biology/research/ecology/einum-lab https://www.ntnu.edu/ibt/research/acms
Biveileder/-e: *Co-supervisor/-s:*	Sigurd Einum (IBI) / Ingrid Bakke (IBT)
Arbeidstittel på oppgaven/ *Preliminary title:*	**The effects of microbiota on fitness variation within and among Daphnia genotypes**

Background and Objectives:

For many organisms it has been shown that the microbiota contributes to the health and disease of the host. In cultures of many animals, both invertebrates and vertebrates, considerable culture-to-culture variation has been observed in the performance/fitness of the organism. It has been suggested that parts of this variation can be caused by differences in the microbiota of the culture. Variation among replicate cultures containing the same genotype of the cultured species can be caused by founding effects and drift, and is therefore of a random type. In contrast, systematic variation among cultures containing different genotypes that have been previously exposed to a common environment would suggest that different genotypes impose different selective pressures on the microbiota community. In the case where different genotypes have different fitness, the question is to what extent these differences are explained by their associated microbiota?

In our Daphnia lab we are currently running population dynamics experiments where we observe considerable random variation in population growth and carrying capacity among replicates within clones, as well as systematic variation among clones. The role of microbiota in this variation remains unknown, but the biology of Daphnia makes it an attractable model system to study such effects. The goal of this project is to:

1. Test for differences in the microbiota in water and associated with animals between and within (among replicates) clones of Daphnia.
2. Test if it is possible to reduce culture-to-culture and temporal variation in fitness of Daphnia by experimental manipulation of microbiota of the culture within clones (i.e. reduce random source of variation)
3. Test if variation in fitness among clones can be partly caused by their associated microbiota.

Experimental methods:

Experiments will be conducted at Dept. Biology and molecular work Dept. Biotechnology.
The student will run parallel replicates of two genetically unique clones of *Daphnia* with verified differences in fitness and estimate population growth rate and carrying capacity of each replicate. The study will test 1) for systematic differences in microbiota composition between the two clones, 2) whether across-culture (within clone) transfer of microbiota reduces random culture-to-culture variation in fitness. If microbiota composition differs between the two clones, containers containing individual *Daphnia* juveniles of the two clones will be inoculated with microbiota from cultures of the two clones in a 2x2 fashion, and juvenile growth, age at reproduction and offspring production will be recorded to test how microbiota composition contributes to differences in these life history traits among clones.

Methods include cultivation studies and characterization of the microbial community based PCR-based amplification of the 16S-rRNA gene.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH og MACODEV
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng 60 credits

Department of Biology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Arild Husby, Thor Harald Ringsby, Bernt-Erik Sæther, and/or Jonathan Wright may be co-supervisor(s)
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Spatio-temporal dynamics of genes for ecologically important traits in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Knowing the genetic architecture of ecologically important traits is fundamental to our understanding of many ecological and evolutionary processes in natural populations. I can offer a number of exciting MSc-projects which focus on identifying the genetic architecture of such traits, and the causes and consequences of the traits' genetic architectures. The MSc-projects will use state-of-the-art genomic and eco-evolutionary data from a unique long-term study of a house sparrow (*Passer domesticus*) model system. Ecologically important traits are traits related to fitness (survival and reproduction) and they will therefore be important for both ecological and evolutionary dynamics in natural populations. Examples of such types of traits are morphological traits behavioural traits, physiological traits, parasite load, and life-history traits. A trait's genetic architecture consists of information on which genes affect the trait, locations of these genes in the genome, and how the genes affect the phenotype. Eco-evolutionary data have been collected on an individual based level from natural and experimental insular house sparrow populations in northern Norway since 1993. More than 27,000 individuals are included in our data base. The genomic data consists of a reference house sparrow genome, SNP-genotype data on 6500 SNPs for ca. 2300 individuals and 185,000 SNPs for ca. 4000 individuals, and information on polymorphisms within ca. 140 candidate genes for various ecologically important traits. The eco-evolutionary and genomic data will be used in statistical analyses to determine genetic architecture by mapping genes for various ecologically important traits using QTL-mapping (linkage mapping/GWAS) and/or study effects of candidate genes directly. Further statistical analyses will then be carried out to examine causes and consequences for spatio-temporal eco-evolutionary dynamics in the model system. Students choosing one of these MSc-projects will have the opportunity to get experience from fieldwork, molecular genetic laboratory work and cutting edge statistical analyses of eco-evolutionary and genomic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Postdoc Alina Niskanen
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**The genetic basis for inbreeding depression in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Anthropogenic changes of the environment, such as habitat destruction, are the major causes of high rates of population declines and extinctions. As population sizes decline they become vulnerable to inbreeding, which is expected to decrease individual fitness (called inbreeding depression) and population growth rates. As a consequence, inbreeding depression is one of the most important genetic processes affecting the persistence of small and threatened populations. Despite its importance, the genetic mechanisms underlying inbreeding depression are not well known. For example, it is unclear whether inbreeding depression is mainly caused by small genome-wide effects or single genes with large effects. We can offer MSc-projects that will focus on I) investigating the genome-wide architecture of inbreeding depression, identify specific loci important for inbreeding depression, and identify the functional genetic variation within these loci, and II) examining the interaction between environmental conditions and inbreeding depression. To achieve these goals, the projects will use state-of-the-art genomic tools, long-term individual-based data on fitness and environmental records from a unique study system of pedigreed wild house sparrow (*Passer domesticus*) populations. Data on approximately 4,000 adult house sparrows from 11 Norwegian experimental and non-experimental island populations will be used. The birds have been genotyped for 185,000 genome-wide single nucleotide polymorphisms. Students choosing one of these MSc-projects will have the opportunity to get experience from fieldwork, molecular genetic laboratory work and cutting edge statistical analyses of eco-evolutionary and genomic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Thor Harald Ringsby, Bernt-Erik Sæther, and/or PhD-stipendiat Dilan Saatoglu may be co-supervisor(s)
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**The genetics of dispersal in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Dispersal (migration) of individuals between populations may affect both ecological and evolutionary dynamics and is consequently a very important process in natural populations. For example, immigration will increase population size, reduce inbreeding and introduce genetic variation. Furthermore, dispersal reduces genetic differentiation between populations. Accurate knowledge about the number of immigrants and where they dispersed from is crucial to understand both causes and consequences of dispersal. I can offer exciting MSc-projects where the goal is to combine ecological data with genetic analyses to identify the number and origin of immigrants to natural island-populations of house sparrows (*Passer domesticus*) at the Helgeland coast in northern Norway. This information will then be used to identify population and landscape characteristics that explain variation in dispersal in space and time, and to examine the consequences of dispersal for both ecological, population genetic and evolutionary processes. Eco-evolutionary data on e.g. dispersal has been collected on an individual based level from 18 natural house sparrow populations in an island metapopulation at Helgeland since 1993. In total more than 17,500 individuals are included in this data base. The genetic data consists of genotypes on 14 microsatellites for >12000 individuals, SNP-genotype data on 6500 variable SNPs distributed across the genome for ca. 1100 individuals, and SNP-genotype data on 185,000 SNPs for ca. 3300 individuals. Students choosing one of these MSc-projects will have the opportunity to get experience from fieldwork, molecular genetic laboratory work and cutting edge statistical analyses of eco-evolutionary and genomic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Thor Harald Ringsby and postdoc Thomas Kvalnes
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Heritability and fitness effects of egg colour in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Egg colour and egg colour pattern has been shown to affect fitness in a number of bird species. This may be because colour and pattern influence the level of camouflage against predation or because colour and pattern may affect the probability of egg parasitism, either intra-specificially (e.g. by cockoo) or intra-specificially («egg dumping»). The goal of the MSc-project is to estimate the heritability (additive genetic variance) of egg colour and egg pattern, as well as genetic correlations between these traits and other fitness-related traits in house sparrows (*Passer domesticus*). Such estimates are very rare because few data sets exist where such analyses are possible. The project will then examine the effect of egg colour and pattern on individual fitness (measured by survival and reproductive output). Data on egg colour and egg pattern has been collected in up to five insular house sparrow populations at Helgeland between 2003 and 2009. Digital photographs that can be used to determine egg colour and egg pattern have been taken of more than 400 clutches. Clutches were assigned to individual females by genetic parentage analyses. Large and genetically determined pedigrees (containing almost 10,000 individuals) will be used with the data on egg colour and pattern to estimate quantitative genetic parameters using “animal models”. Students choosing this MSc-project will have the opportunity to get experience from fieldwork, molecular genetic laboratory work, quantitative genetic analyses, and statistical analyses of eco-evolutionary data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Bernt-Erik Sæther, Thor Harald Ringsby, Henrik Pärn, and/or PhD-student Sindre Sommerli may be co-supervisor(s)
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Population genetics of water voles**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	To understand populations' ability to evolve in response to environmental change and persist in the face of habitat fragmentation and spatio-temporal fluctuations in demography due to e.g. anthropogenic effects, it is important to understand the causes and consequences of temporal changes in genetic variation within and between populations. In 2015 we started a large-scale field study on water voles (*Arvicola amphibius*) on islands at the coast of Helgeland. Our aim is that this will be a model system we can use to examine questions related to population dynamics and population genetics processes in such a fragmented system, which has large spatio-temporal fluctuations in population size. I can offer exciting MSc-projects with focus on important population genetics processes in water voles; inbreeding, genetic drift, genetic bottlenecks, founder events, and genetic population structure. Methods for genotyping individual voles on 13 microsatellites are already established. In addition, we will in collaboration with a research group at the University of Aberdeen develop high-throughput genomic resources for water voles that we aim to use in the proposed MSc-projects. Students choosing these MSc-projects will gain skills in carrying out high-quality fieldwork on the beautiful Helgeland coast, experience with molecular genetic laboratory work, and good knowledge about statistical analyses of population genetic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Åse Krøkje
Biveileder(e): Co supervisor	
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Induction of genotoxic endpoints and biotransformation enzymes in liver cells (cell line) exposed to defined mixtures of chemical compounds.**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Cells from rat or fish liver (cell line) will be exposed for mixtures of pollutants, in environmentally relevant concentrations, *in vitro*. Compounds in mixtures will often interact, and result in a higher (synergistic) or a lower (antagonistic) effect compared with that of a single-component exposure. To improve hazard identification and environmental risk evaluation, it is important to study how pollutants behave in mixtures. The aim of these projects is to develop and test out methods to evaluate complex mixtures with regard to interaction effects, which can occur between single compounds in a mixture. Pollutants, which occur in the terrestrial or aquatic environment, will be used in environmentally relevant concentrations. A statistical method for experimental design will be used to achieve a cost- and time effective performance of mixture studies, most probably factorial design. Eventual interactions will be studied by use of genotoxic endpoints (f ex DNA-adducts, DNA-strand breaks, micronucleus or chromosomal aberrations) or induction of biotransformation enzymes (CYP1A1 and conjugation enzymes). Multivariate regression models, such as projection to latent structures (PLS), can be used to evaluate possible interactions in mixtures. 1-2 master projects
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Environmental Toxicology and Chemistry

Hovedveileder: Main supervisor:	Jens Rohloff
Biveileder(e): Co supervisor	Richard Strimbeck
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Ecological Urban Production of Vegetables**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The master project(s) is/are integrated as part of a regional research project aiming at the utilisation of compost derived from manure and food waste for the ecological production of vegetables. Major active partners involve Skjetlein vgs (*Naturbrukslinje*) and the company Global Green Energy (GGE). Sub-goals include (a) Development and optimisation of compost products (mixtures) to be used as growth substrate (b) Increase knowledge about innovative soil substrate(s) by the use of a compost bioreactor (c) Improve recruitment to education and research within urban farming and ecological food production Possible master projects: 1. Investigation of effects of compost products in vegetable production (e.g. tomato, salad, herbs) on crop growth, yield and quality. Focus areas: plant physiology, phytochemistry, food chemistry 2. Investigation of effects of manure/food waste ratio and bioreactor conditions on composting process and composition with regard to soil substrate quality and commercial value. Focus areas: microbiology, biochemistry, agriculture
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biology, Biotechnology, LUR

Hovedveileder: Main supervisor:	Thorsten Hamann
Biveileder(e): Co supervisor	Timo Engelsdorf
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Functional analysis of candidate genes mediating plant cell wall integrity maintenance**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The plant cell wall is the first line of defense of all plants against stress. It is a highly dynamic structure, which also provides different materials relevant for society. Plant cell wall signaling processes are essential during defense and are also intricately involved in maintaining functional integrity of the cell wall during growth and response to biotic stress. Recently the host lab has performed extensive transcriptomics and phospho-proteomics experiments to identify genes maintaining plant cell wall integrity during development and defense in *Arabidopsis thaliana*. The aim of the project is to functionally characterize several of these candidate genes in order to dissect the molecular mechanism underlying plant cell wall integrity maintenance. The project will initially involve sterile tissue culture work to generate biological material, qRT-PCR-based confirmation of transcriptomics results, LC-MS-based measurements of phytohormones in gene knockout plants, cloning of reporter-protein fusion and promoter reporter constructs, which will be followed by generation of transgenic plants to perform cellbiological and expression studies using advanced microscopy (confocal microscopy in combination with image analysis). Generating the data on gene function is the prerequisite to achieve the long-term of this project, which is to use the genes identified in Arabidopsis as leads to improve performance of food crops and facilitate bioenergy production from ligno-cellulosic biomass.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biologi, bioteknologi

Hovedveileder: Main supervisor:	Thorsten Hamann
Biveileder(e): Co supervisor	Timo Engelsdorf
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Development of novel analytical tools to analyze plant cell wall signaling**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Plant cell wall signaling processes are essential during interaction between the plant and the environment as well as during development. They are also intricately involved in maintaining functional integrity of the cell wall during growth and response to biotic stress. Currently there are no suitable tools available to study early, fast cell biological processes during cell wall integrity maintenance. The host lab has performed recently extensive transcriptomics experiments and identified genes, which are responding to cell wall integrity impairment. The aim of the project is to use the candidate genes as starting place to develop novel markers. The project will initially involve tissue culture work to generate biological material, qRT-PCR-based confirmation of transcriptomics results and cloning of reporter-protein fusion constructs, which will be followed by generation of transgenic plants to perform cellbiological studies of the reporter fusion constructs using advanced microscopy (confocal microscopy in combination with image analysis).
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biologi, bioteknologi

Hovedveileder: Main supervisor:	Professor Berit Johansen
Biveileder(e): Co supervisor	Dr. Astrid Feuerherm, Dr Thuy Nguyen, Dr. Linn-Karina Selvik
Arbeidstittel på oppgaven (max 20 word): Preliminary tittel:	**Lipid signaling mechanisms in inflammation.**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Obesity is a major risk factor for lifestyle diseases. Lifestyle is affecting severity of chronic diseases, including cardiovascular diseases and rheumatism. Common symptom between obesity, lifestyle and chronic disease is inflammation (1,2). Investigations regarding molecular mechanisms of inflammation will give insights on how different aspects of lifestyle, hormonal responses, e.g. insulin, will affect disease progression and severity (3,4). Hormones under study include cytokines, insulin, chemokines, eicosanoids and adipokines. Model systems: Synoviocytes, cellular model for rheumatoid arthritis; Monocytes, cellular model for white blood cells. **Possible master theses:** 1) Characterization of insulin signaling in synoviocytes 2) Characterization of adipokin signaling in synoviocytes 3) Characterization of microRNA as a regulatory mechanism of synoviocyte biology 4) Characterisation of TLR2/4-induced responses, and possible involvement of cPLA2 in an osteoclast cell model 5) Metabolomics detection human samples (collaboration with Dr Jens Rohloff) 6) Systems biology of human intervention samples (collaboration with Prof. Martin Kuiper.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	MBIOT5, MBI-celle/molekylærbiologi, MSc Biotechnology (2yr)

1. WHO, *Global status report on noncommunicable diseases 2010. Description of the global burden of NCDs, their risk factors and determinants.*, WHO, Editor. 2011. p. 1-176.

2. Kelly, T., et al., *Global burden of obesity in 2005 and projections to 2030.* International Journal of Obesity, 2008. **32**(9): p. 1431-1437.

3. Ouchi, N., et al., *Adipokines in inflammation and metabolic disease.* Nat Rev Immunol. **11**(2): p. 85-97.

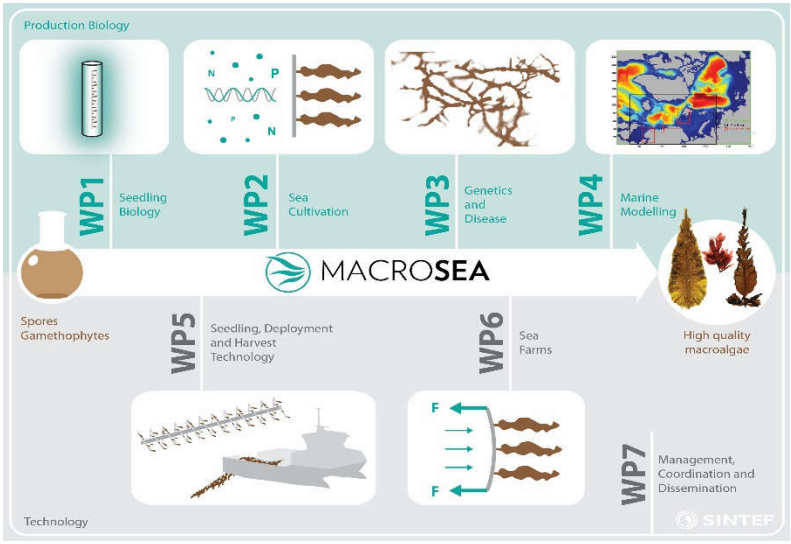
4. Gregor, M.F. and G.S. Hotamisligil, *Inflammatory mechanisms in obesity.* Annu Rev Immunol, 2011. **29**: p. 415-45.

Hovedveileder: Main supervisor:	Martin Kuiper - kuiper@ntnu.no – 73550348 – DU1-111 IBI
Biveileder(e): Co supervisor	Astrid Lagreid, IKM-DMF; several other co-supervisors (IBI, IBT) are possible, depending on the design of the master proposal.
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Implementation of Boolean models for cell perturbation analysis and drug development**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The use of network and model based approaches to describe, explain and understand biological processes is an essential approach in Systems Biology. Tools that enable this approach range from Cytoscape (network based) to CellDesigner (pathway-based) to full-fledged mathematical modeling platforms. One of the more basic modeling paradigms is based on Boolean logics, where interactions between model components (proteins, genes) only need to be described in terms of activation and inhibition, and the regulatory rules are described using AND, OR, and NOT logics. We are developing user-friendly, semi-automated software tools (see Flobak et al 2015), in the new initiative DrugLogics (www.DrugLogics-NTNU.org), part of the NTNU Digital Life theme. DrugLogics aims to develop Boolean model based approaches to help develop Personalized Medicine approaches to treat cancer. This initiative offers possibilities for a variety of Master projects: - The assembly of a 'causal statement' knowledge base that integrates information from resources like Reactome and SIGNOR that can be used to build Boolean models - The use of our curation tool SciCura to convert information from literature in the form of causal statements to the knowledge base - The building of Boolean models to simulate the effect of experimental perturbations on the behavior of specific cells (plant, animal, microorganism) - The simulation of these Boolean models to predict the effects of mutations or other perturbations and the subsequent experimental validation - and many more …
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biology / Biotechnology
Reference:	Flobak Å et al. Discovery of drug synergies in gastric cancer cells predicted by logical modelling. PloS Comp. Biol. 2015 DOI: 10.1371/journal.pcbi.1004426. www.druglogics-ntnu.org www.colosys.org https://www.ntnu.edu/crossover-research https://www.ntnu.edu/health/druglogics www.reactome.org, http://signor.uniroma2.it/

Hovedveileder: Main supervisor:	Augustine Arukwe
Biveileder(e): Co supervisor	
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Identification of key cellular targets of toxicants as potential *xenosensor* biomolecules in fish**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Our group is part of a big NFR funded biotechnology "Digital life" project entitled "dCod 1.0: decoding systems toxicology of Atlantic cod (*Gadus morhua*) – environmental genomics for ecosystem quality monitoring and risk assessment" in collaboration with several national (UiB, UiO, NMBU) and international partners The project will pursue a research line in environmental omics that identifies key cellular targets of toxicants as potential *xenosensor* biomolecules. An illustrating example is the use of transcription factors such as the peroxisome proliferator-activated receptors (PPARs), aryl hydrocarbon receptor (AhR) and estrogen receptor (ER) in multiple assays for toxicants and endocrine disruptors in fish systems. We are looking for 4-5 master students to work together with a PhD fellow in delivering our part of the project. We will develop and structure out a candidate-specific *in vivo* or *in vitro* research plan that fits with the overall aims of dCod. Otherwise, the overall objective of our research is to develop diagnostic gene, enzyme and protein response tools in the study of the molecular and physiological mechanisms of the effects of xenoestrogens and xenobiotic, and their interactions in wildlife species. In our laboratory, these studies are performed in both *in vitro* and *in vivo* systems.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Environmental Toxicology and Chemistry; cell and molecular biology

Main supervisor:	Tor Jørgen Almaas
Co supervisor	
Preliminary title:	**Electrophysiological characterization of receptor neurons on insects: taste receptors (feet, flagellum, mouth-parts), receptors for temperature, humidity and touch (antenna, feet), olfactory receptors (flagellum).** (One student – one sensory modality)
Short description of the project:	By electrophysiological techniques the neurophysiological properties of sensory neurons will be described: sensitivity, specificity and temporal response pattern. Electrochemically sharpened tungsten electrodes or glass capillary electrodes are being positioned by micromanipulators in the extracelluar space close to the receptor cell in order to record actionpotentials as respons to the relevant stimulus. Special designed stimulation equipment are applied for the stimulation procedures. Please contact the supervisor for more information about the lab and how to design the individual project.
Suitable for (main profiles):	Physiology, ecology, cell biology

Hovedveileder: Main supervisor:	Rolf Erik Olsen
Biveileder(e): Co supervisor	Bjørg Egelandsdal, Erik Slinde, NMBU
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Krebs cycle in fish performance and quality**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The Krebs cycle is running in cell mitochondria and is the main provider of NADH for the synthesis of ATP which is the energy all living organisms need for growth and survival. Limitations in intermediates in the cycle will limit available energy for the animal. In a growing animal increasing the Krebs cycle output can increase energy availability and therefore growth performance over time. In pigs being slaughtered, boosting the Krebs cycle has been shown to increase product quality. The cause is unknown, but it is probably linked to a faster depletion of tissue oxygen and thereby lower lipid peroxidation. It is currently unknown if these mechanisms are valid in fish. But salmon in particular is a fatty species with high potential for rancidity. **The project will include feeding studies, quality assessment and cell tissue cultures.**
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Nutrient chemistry, chemistry, aquaculture, cell biology

Main supervisors:	Kjell Inge Reitan, Geir Johnsen, Atle Bones, Yngvar Olsen (one)
Co supervisors:	Jorunn Skjermo, Silje Forbord, Aleksander Handå (one or two)
Preliminary title:	**MACROSEA - A knowledge platform for industrial macroalgae cultivation in Norway (2016-2019)**
Short description of the project:	You will take part in the enthusiastic MACROSEA project team at SINTEF and NTNU and contribute to successful and predictable production of high quality biomass making significant steps towards industrial macroalgae cultivation in Norway.  The primary objective is to establish an interdisciplinary knowledge platform on fundamental production biology and technology for macroalgae cultivation over a wide range of climatic, ecological and physical conditions. Secondary objectives are: **(i)** to increase the principal knowledge on biological performance and environmental requirements for optimized chemical composition and biomass production, and **(ii)** to obtain technological specifications and develop generic model and simulation tools for farm systems and biomass production. The brown kelps *Saccharina latissima* and *Alaria esculenta* (large volumes, low value), and the red alga *Palmaria palmata* (small volumes, high value) will be studied as promising species for industrial cultivation in Norway. **<u>Topics for 5-7 master thesis in MACROSEA:</u>** • Develop cultivation and quality parameters • Develop quality indicators (genetic markers) • Characterize importance of light • Characterize N metabolism and photosynthetic capabilities • Characterize NH4 uptake (IMTA) • Measure quality parameters for seedlings with different latitudinal origin (Western, Mid and Northern Norway) • Perform a regional study of growth and quality together in Western, Mid and Northern Norway Contact: Project leader Aleksander Handå. Aleksander.handa@sintef.no - mob. 91577232
Suitable for:	Marine Biology, Aquaculture, Photobiology,Cell biology,Genetics

Main supervisor:	Professor Kjell Inge Reitan (NTNU) Kjell.i.reitan@ntnu.no
Co supervisors	Seniorforsker Aleksander Handå (SINTEF) Forsker Kari Attramadal (SINTEF)
Preliminary title (max 20 word):	**Cultivation of Polychaeta for waste treatment, improved resource utilisation and production of raw material for feed in aquaculture**: **Thesis I:** Growth and reproduction of polychaetes under intensive culture conditions **Thesis II:** Metabolism and nutritional value of polychaetes under intensive culture conditions
Short description of the project (max 300 word):	**Motivation:** The Norwegian salmon production is estimated to increase from 1.2 to 3 million tons, with a use of 3.6 million tons feed per year in 2030. To realize this growth, there are at least two major challenges that must be solved; *environmental impact and feed supply.* There is accordingly a need to develop strategies to a) decrease waste effluents and bio-deposit impacts from aquaculture and b) replace feed ingredients with proteins and lipids from new resources outside the human food chain. Polychaetes of the *Nereis* family seem promising for both. **Polychaeta** are filter- and detritus feeding marine worms that have several industrial applications. Polychaete biomass is rich in marine fatty acids and a valuable raw material for feed. In addition, the polychaetes grow fast at optimal conditions. The ability to convert organic waste to high quality biomass is useful in a range of issues related to aquaculture. E.g. polychaete cultivation combines waste treatment with improved resource utilisation and production of raw materials that are in high demand. **Master thesis** This will be the first studies of intensive polychaete production as a method to treat fish farm wastes in Norway. The main focus will be on production biology of polychaetes under intensive culture conditions to increase our understanding of: • Growth and reproduction (Thesis I) • Metabolism and biochemical composition (Thesis I and II) • Nutrient budgets (C,N,P) (Thesis II) • The potential of polychaetes to recycle wastes from aquaculture (Thesis I and II) ***Research team:*** *You will be part of a new enthusiastic research team on polychaetes. The team consists of researchers and engineers at NTNU Biology and SINTEF Fisheries and Aquaculture. You will contribute to the establishment of a knowledge platform for decision support to stakeholders considering using polychaete cultures to recycle waste effluents from various types of aquaculture systems.*

Suitable for (main profiles):	Biology/aquaculture
Hovedveileder: Main supervisor:	Professor Kjell Inge Reitan, NTNU Kjell.i.reitan@ntnu.no
Biveileder(e): Co supervisor	Research Scientist Matilde S. Chauton, SINTEF Research Scientist Kari J. K. Attramadal, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Nitrogen-rich waste water from fish farming as a resource in cultivation of microalgae**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The outlet water from the fish farming tanks contains a lot of nitrogen, in some cases at levels that are relevant as growth fertilizer for successful cultivation of microalgae. This nitrogen concentration of the outlet water may give a microalgae biomass of 10^6 -10^7 cells/ml (depending on the algae species). Most of the nitrogen originate from the excretion of the fish and microbial degradation of fish feed. The nitrogen in the water is available as ammonia, nitrite and nitrate. Ammonia (NH_3) is toxic to fish, and must therefore be removed from the fish tank systems, and is a waste product in the fish farming units. The microalgae need nitrogen, mainly in the form of nitrate, nitrite or ammonium (NH_4^+). The reuse of the N-rich water from the fish tanks is interesting as a resource in the microalgae production, but we need to have more knowledge about the amount of N that are in water system and what forms it exists in. In this task, we will pick up the water with a fish breeder, and analyze and analyze the main nutrient nitrogen compounds as well as phosphorous, and use the water in cultivation trials with 2-3 different algae. The algaewill be selected among candidates with interesting chemical profile and uses for biomass production. Timescale: Spring 2016-Autumn 2017
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biology, Biotechnology, Marine Coastal Development

Hovedveileder: Main supervisor:	Prof. Kjell Inge Reitan
Biveileder(e): Co supervisor	Forskere Andreas Hagemann og Matilde S. Chauton, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Rhodomonas sp. og N-omsetning: Optimalisering av dyrkingsmedium i produksjonssammenheng**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Mikroalgen Rhodomonas sp. er interessant som fôr i produksjon av hoppekreps, bl.a fordi den har en god fettsyreprofil og balansert proteininnhold. Rhodomonas og andre svelgflagellater har dessuten spesielle pigmenter, fykobiliner, som er rike på N. Den kjemiske profilen varierer imidlertid med dyrkingsbetingelser og varighet på produksjonsperioden, og dette er en utfordring for å etablere stabil produksjon av algebiomasse med forutsigbar kjemisk profil. Et annet viktig element i storskalaproduksjon av mikroalger er kostnadene ved tilførsel av makronæringsstoffer (N, P el silikat) eller mikronæringsstoffer (spormetaller, vitaminer) og det er veldig relevant å vite mer om hvordan man kan utnytte disse komponentene bedre i dyrkingen. I denne oppgaven vil det derfor være fokus på å dyrke Rhodomonas under ulike vekstbetingelser med fokus på N-omsetningen og biomasseutbytte. Det vil også bli lagt vekt på å se hvor effektivt komponentene i næringsmediet utnyttes, for å foreta en optimalisering av næringsmedium for produksjon av Rhodomonas sp. Denne oppgaven vil knyttes til arbeidet som foregår hos C-feed, et nyetablert firma som produserer og selger copepode-egg.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	

Hovedveileder: Main supervisor:	Prof. Kjell Inge Reitan
Biveileder(e): Co supervisor	Forskere Matilde S. Chauton og Kari J. K. Attramadal, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Bruk av nitrogenrikt vann fra fiskeoppdrett til produksjon av mikroalger**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Vann fra fiskeoppdrettskar inneholder mye nitrogen, i noen tilfeller så mye at det er på nivå med det som tilsettes i standard algedyrkingsmedium og nok til å produsere 10^6-10^7 celler/ml (avhengig av hvilken alge). Mye av nitrogenet stammer fra ekskresjon og urea-produksjon hos fisken og foreligger som ammoniakk, nitritt og nitrat i vannet. Ammoniakk (NH3) er giftig for fisken og man må derfor fjerne det. Mikroalger trenger N, hovedsakelig i form av nitritt eller ammonium (NH4+). Gjenbruk av N-rikt vann fra fiskeanlegg er interessant i mikroalgeproduksjon, men vi må ha mer kunnskap om hvor mye N som er i omløp i vannet og hvilke former det foreligger i. I denne oppgaven vil vi hente vann hos en fiskeoppdretter og analysere og analysere hovednæringsstoffene N og P, og så bruke det i dyrkingsforsøk med 2-3 forskjellige alger. Algene velges ut fra sin kjemiske profil og anvendelsesområder for biomassen.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	

Hovedveileder: Main supervisor:	Ann- Kristin Tveten
Biveileder(e): Co supervisor	Helene Fjørtoft, Anne Stene
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Sea lice (L. salmonis) microbiota and their role in dispersal of pathogens**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The coastal region of north west Norway have high densities of farmed fish, in addition to several different stocks of wild salmonid species. Increased production have the potential risk of increasing the number and dispersal of pathogenic like virus, parasites and bacteria. Interactions of pathogens between farmed and wild salmonids have been identified. Sea lice is a major problem in both wild and farmed salmonids in areas of high aquaculture activity. Sea lice can potentially delay the national goals of increased growth in the fish farming industry. The microbiota may vary geographically and may play a role in dispersal of the multiple pathogens. Known diseases caused by pathogens are; viruses: ILA, IPN, PD, VHS, HSMB, CMS, bacteria; vibriose, BKD, Furunkulose, and Yersiniose- and parasites; Paramoeba perurans (AGD) and Parvicapsul. In this project we would like to: • Map the microflora of sea lice to determine the sea lice role as a vector for the pathogen. • Establish methods for detection of a selection of the pathogens and determine their prevalence in sea lice. • If possible, study geographical variations We would like to focus on the interactions between farmed and wild salmon fish. We would like to focus on the intersection between the environment, the salmonid fish and pathogen in defined areas. The fish will be grouped in farmed salmon, rainbow trout, escaped farmed salmon (time in the sea after the escapes are determined by external confirmation), wild salmon. Collection of wild salmonid fish are in cooperation with the Institute of marine research and NINA and the local fishermen with wedge-net license. The project is a part of the PhD for Helene Fjørtoft, and financed through RFF and Miljøskapings fondet
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Marine biology - biotechnology - molecular biology - microbiology

Hovedveileder: Main supervisor:	Prof. Kjell Inge Reitan
Biveileder(e): Co supervisor	Forskere Matilde S. Chauton, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Upscaling microalgae biomass production and post-harvesting processing to extract high-value compounds**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	We are looking for new resources to meet the demands for protein and essential lipids in the near future. Microalgae are a promising resource for applications such as feed production or extraction of high-value compounds such as lipids. Upscaled biomass production is a focus area, and we must solve challenges both upstream in the production end and downstream on the harvest and processing end. This work will focus on the production of microalgae biomass in a pilot system, a 250 L photobioreactor, and harvesting e.g. by centrifugation. After harvesting the biomass must be stabilized e.g. by lyophilization before it is ready for processing. Here the focus will be on obtaining protein-rich bulk material and high-value lipids such as EPA/DHA, and analysis of the fractions.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	

Hovedveileder: Main supervisor:	Prof. Kjell Inge Reitan
Biveileder(e): Co supervisor	Forsker Matilde S. Chauton, SINTEF
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Høyverdi-komponenter fra marine mikroalger: Protein-og lipidinnhold utvalgte mikroalger under varierende dyrkingsbetingelser.**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Mikroalger er en fremtidig kilde til proteiner og fett, inkludert høyverdi-komponenter EPA/DHA som brukes i helsekost og fôr. Mikroalger har et gunstig proteininnhold, og mange har også et høyt innhold av essensielle fettsyrer. Innholdet varierer imidlertid fra art til art, og med dyrkingsbetingelser. Vi trenger mer kunnskap om proteininnhold og hvilke alger som inneholder mest EPA/DHA, og under hvilke betingelser man får størst utbytte av disse komponentene. Oppgaven består i å dyrke 3-4 ulike mikroalger under forskjellige betingelser og analysere biomasseutbytte, protein- og lipidinnhold og aminosyre/fettsyreprofiler. Relevante dyrkingsbetingelser kan være variasjoner i lyskvalitet (LED vs konvensjonelt lys), temperatur og variasjoner i næringstilgang som f.eks nitrogenbegrensning.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	