Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: The effect of genetic variation on smolt development

Key words: Gene regulation, smolt biology, a lot of data analyses, very limited lab (if any)

Contact persons / supervisors:

Simen Rød Sandve
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Task description:
We are kickstarting a project on genetics and development of seawater readiness (smoltification) in Atlantic salmon in 2024 (collaboration with UiT). NMBU has a leading role in the data generation and analyses related to genetics and gene regulation. This project has four main tasks:

1. Take part in sampling of tissue in Tromsø (dependent on timing of sampling)
2. Organizing / generating transcriptomics (single cell or bulk tissue) data
3. Analysing differences in gene regulation between different genetic backgrounds
4. Interpreting differences in gene regulation in the context of a genetic variant on chromosome 14

Other ideas could be related to Pore-C, detailed characterization of genetic variation, measurements of endocrine (hormone) levels and changes.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: The consequence of whole genome duplications on genome regulatory evolution

Key words: Gene regulation, evolutionary biology, comparative genomics

Contact persons / supervisors:

Simen Rød Sandve
email: simen.sandve@nmbu.no

Lars Grønvold
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Task description:
We have chromatin accessibility and gene expression data from 8 species of salmonids and 4 outgroup species. Now we are interested in using these data to identify genes that have changed regulation following whole genome duplication and test if these shifts are associated with changes in chromatin regulation/accessibility. This project revolves around two main tasks:

1. Test for changes in gene expression levels among gene duplicates across 100 million years of salmonid evolution using the eveR software (https://gitlab.com/sandve-lab/gillard-groenvold)
2. If we get time, we can then compare the evolutionary expression shifts with changes in accessibility of chromatin by analysing ATAC-seq data

This project is computationally a bit hard, so you should be a bit talented in coding (and enjoy it tremendously) and like open-ended creative processes.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Selection on protein sequence content in Mucormycota fungi

Key words: Genome evolution, comparative genomics, selection, fungi

Contact persons / supervisors:

Simen Rød Sandve
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Helle Tessand Baalsrud
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Task description:

We have sequenced 20-30 fungal genomes in the Mycormycota group. These species have widely different adaptations and abilities to metabolize different molecules. In this project we are interested in asking the question: To what extent has selection on protein coding gene sequences shaped sequence evolution in Mycormycota fungi. To do this we have defined three main tasks:

1. Run genome wide dN/dS tests in Hyphy to identify protein coding gene sequences under positive selection in Mycormycota fungi species
2. Test if different molecular pathways have been under selection in different fungal lineages
3. Interpret the resutls in the context of gene expression data we have generated

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Signals for cell migration in salmonid cells- investigations of variation in sea lice resistance

Key words: Fish cell cultures, CRISPR, cell migration, imaging, lab-based

Contact persons / supervisors:

Guro Sandvik
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Mari Austad Brandt
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Task description:
When fish skin is wounded, keratinocytes are migrating to the wound to cover the wound. In some salmon species, cells also migrate toward attached sea lice, and cover them with the result of killing the sea lice. We are investigating the signal for cell migration of different cells from different salmonids, and aim at using CRISPR knock-out to test the significance of different receptors in different species. Linked to the NFR-project LiceResist.

Methods:
-CRISPR knock-out of relevant receptor genes in different skin and gill cell lines of fish species
-DNA extraction, PCR and sequencing to assess efficiency of gene editing
-Migration assays with time lapse microscopy

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Imaging and gene editing to study early development and cell fate in Atlantic salmon

Key words: Early development, imaging of embryos, CRISPR, lab-based

Contact persons / supervisors:

Guro Sandvik

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Christiaan Henkel

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Task description:

We are interested in early development in Atlantic salmon and have seen several interesting phenomenons when doing a single cell sequencing experiment of early stages of Atlantic salmon. We want to further investigate the physiological mechanisms lying behind these observations. The actual phenomenon that is going to be investigated depends on further studies done this spring, in addition to the interest of the student. Examples is the study of the mechanism of hatching through imaging and CRISPR knock-out of live salmon embryos, or tracking of primordial germ cells in early development. Linked to the FHF-project Salmocode.

Relevant methods:

- cell tracking with fluorescent *in situ* hybridisation or immunohistochemistry
- imaging through early development of the fish inside the egg
-CRISPR knock-out on live Atlantic salmon embryos
-analyses of single-cell data

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Long-read data creates new insight into cattle and pig genomics.

Key words: Norwegian red cattle, landrace pigs, pan-genomes, long-read sequence, structural variants, genotype-phenotype associations.

Contact persons / supervisors:

Matthew Kent

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Harald Grove

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Kristina Stenslokk

email:kristina.stenlokk@nmbu.no

Matthew Kent

Task description:

In cattle and pig breeding, information about genetic variation between individuals is used to guide breeding programs, reveal links between genes and traits and more. In our current research project CAUSATIVE (link), we are generating a comprehensive overview of structural variants (larger insertions, deletions etc) using nanopore long read sequencing. This will be used to construct complex, but accurate pan-genome representations of variation in Norwegian cattle and pig breed and allow us to explore gene-trait associations with a completely new type of data. The wealth of raw data, numerous bioinformatic tools, and extensive pre-existing trait information made available through our collaboration with the breeding industry creates room to develop a project(s) that focus on data analysis and representation, benchmarking alternative bioinformatic approaches, digging more deeply into variant-trait associations. The exact project description will be jointly developed by the student and CAUSATIVE team closer to the start time.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Nanopore sequencing of multiplex-PCR amplicons for genotyping structural variants.

Key words: Long-read nanopore sequencing, multiplexing PCR, protocol benchmarking and optimization

Contact persons / supervisors:

Matthew Kent

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Task description:

Several technologies exist that allow us to cheaply and easily test (genotype) small single-nucleotide polymorphism SNP variants, but as we begin to explore the role of larger structural variants (SVs)and their association with biological traits we soon realize that there are few versatile and cost-effective solutions to genotyping SVs in large numbers of samples. Earlier, we have successfully used nanopore to sequence single large PCR products capturing genetic variation in hundreds of samples simultaneously, but we have not fully explored the potential of this approach. We would now like to investigate the potential for sequencing multiplexed-PCR reactions and optimize the associated experimental design, wet-lab protocol and bioinformatics. Test material will be from agri- or aquaculture materials and DNA targets will be selected based on their connection to suspected or known relevant traits.

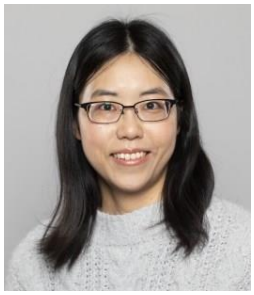
Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Investigating how the genetics and the environment affect the Atlantic salmon meta-transcriptome.

Keywords: Genomics, bioinformatics, microbiology, -omics.

Contact persons / supervisors:



Marie Saitou
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Arturo Vera Ponce De Leon)
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Summary
Atlantic salmon disease outbreaks in aquaculture lead to financial losses, yet they also detrimentally impact surrounding ecosystems by facilitating the transmission of pathogens. The use of antibiotics to combat these outbreaks further compounds environmental harm by encouraging the emergence of resistant bacteria. To tackle this problem by clarifying the underlying biological basis, metatranscriptomics has emerged as a pivotal tool. Metatranscriptomics can detect and analyze microbial communities and their gene expression under various conditions of the yet unexplored microbiota and their potential roles in aquaculture.

The tasks in this project are:
- Investigate microbiome composition and diversity using the gill transcriptome of thousands of Atlantic salmon individuals under three light treatments that can affect growth speed and fish robustness.
- Conduct genome-wide association analysis between the host salmon genome and microbiome metrics to see how the host genome and light treatments affect the microbiome composition and transcriptomic activity.
- Investigate the function and evolutionary history of the associated host genes depending on the student's interest.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Genetic variants in the Atlantic salmon genome and their impact on fish health

Key words: long read sequencing, genetic variants, fish diseases

Contact persons / supervisors:

Sigbjørn Lien
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Tim Knutsen
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Task description:

At CIGENE we are now using long-read nanopore sequencing to *de novo* whole-genome sequence multiple individuals of Atlantic salmon. The initial analysis of the data has revealed a huge number of mutations (SNPs - single nucleotide polymorphisms) and structural variants (SVs - insertions, deletions, inversion, etc.) that may alter the presence, structure and regulation of genes in the salmon genome.

We are now looking for master students interested in investigating specific chromosome regions for functional variants (SNPs/SVs) with the prospect of affecting severe diseases in Norwegian aquaculture.

In the master project, we will combine information about SNPs and SVs, with functional annotation data from the AQUA-FAANG project (https://www.aqua-faang.eu/), and disease challenge data generated by the fish breeding company AquaGen (https://aquagen.no/en/) to identify genetic variation underlying severe diseases in salmon aquaculture.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: The role of repeated DNA in creating chromosomal rearrangements in salmonid fishes

Key words: genome evolution, structural variation, long-read sequencing

Contact person / supervisor:

Sigbjørn Lien
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Task description:
Repeat DNA represents a major proportion of salmonid genomes but have been challenging to characterize using short-read sequencing technology. At CIGENE we are now using long-read nanopore sequencing to *de novo* whole-genome sequence multiple salmonid species, and in so doing characterize the repeat content of their genomes.

In this master project, we will look specifically into boundaries of chromosomal rearrangements in different salmonid genomes and investigate if they comprise certain classes of repeated DNA (tandem repeats or transposable elements) contributing to the rearrangements.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Discovery of host factors for PCV2 infection in porcine cells using genome-wide CRISPR knockout screening.

Key words: CRISPR, pigs, PCV2, host-virus interactions, genome-wide screen

Contact persons / supervisors:

Thomas Harvey
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Victor Boyartchuk
Email: victor.boyartchuk@nmbu.no

Task description:

Porcine circovirus type 2 (PCV2) is a pig pathogen that is associated with postweaning multisystemic wasting syndrome and other reproductive disorders. Our lab has developed a genome-wide CRISPR knockout (GeCKO) screening toolkit for use in pig cells. We would like to apply this technology to identify host factors involved in PCV2 infection. This project will be mostly lab based, but will involve some bioinformatics towards the end to analyze the screen data. The main tasks include:

1. Develop a reproducible assay for infection of PK15 cells with PCV2 and monitor cytopathic effects.
2. Generate a GeCKO cell library and apply the PCV2 assay.
3. Extract DNA and prepare GeCKO sequencing libraries.
4. Analyse GeCKO sequencing data to identify over- and under-represented populations of guides to discover genes involved in PCV2 infection.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Validation of genes promoting resistance to PCV2 in porcine cells.

Key words: CRISPR, pigs, PCV2, host-virus interactions, genome-wide screen

Thomas Harvey
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Victor Boyartchuk
Email: victor.boyartchuk@nmbu.no

Task description:

Porcine circovirus type 2 (PCV2) is a pig pathogen that is associated with postweaning multisystemic wasting syndrome and other reproductive disorders. Our lab has developed a genome-wide CRISPR knockout (GeCKO) screening toolkit for use in pig cells. Applying this screen, we have identified two genes under negative selection when infected with PCV2. The next step in this work is to validate these genes by generating knockout cell lines and testing the effect on PCV2 susceptibility. This project will be heavily lab based. The main tasks include:

1. Develop a reproducible assay for infection of PK15 cells with PCV2 and monitor cytopathic effects.
2. Clone gRNAs targeting the genes of interest into lentiviral vectors and package lentivirus.
3. Transduce cells and test for knockout of the gene of interest in each cell line.
4. Determine the effect of knockout out the genes of interest on susceptibility to PCV2 by infecting knockout cell lines.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Enabling genome-wide CRISPR genome editing in salmon stem cells.

Key words: Crispr-Cas9, germline stem cells

Contact persons / supervisors:

Matthew Kent
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Victor Boyartchuk
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Task description:

Stem cells (SC) are a fascinating subset of cells that retain a potential to differentiate into several different, specialized cell types. Germline stem cells harvested from the testis of teleost fish, such as Atlantic salmon, can be cultivated in vitro and manipulated to generate sperm or, if desired, egg producing cells. This creates a unique opportunity to greatly accelerate introduction of a beneficial genetic variant into large populations. For example, many pathogenic viruses attach to host cells by recognizing a specific cell surface protein, if the identity of a gene encoding such a protein is known, we can modify it in cultured germline stem cells so that the protein is removed or modified. Stem cells can then be physically transplanted into sterile male embryos which will, at maturity, produce millions of sperm. Offspring from these will carry the modified protein and may show an improved resistance to viral infection.

To enable modification of germline stem cell we are deploying a CRISPR Cas9 genome editing toolkit that allows precise modifications of specific sites in genomic DNA. CRISPR based genome editing in teleost fish is still in its infancy and its efficient deployment requires characterisation of each component of CRISPR editing machinery for its suitability for use in fish. This Master project will focus on systematically testing of a range of existing reagents, such as Cas9 expression constructs in stem cell cultures, in order to identifying an optimal strategy to enable delivery of gene-editing machinery into salmon germline stem cells.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Single-cell RNA-Seq on wounded skin

Key words: Transcriptomics, single-cell, skin

Contact persons / supervisors:

Tomasz Podgorniak
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Gareth Gillard
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Task description:

As a part of LiceRESIST project framework, we will investigate transcriptome differences between healthy and wounded skin samples of salmonid species at a single-cell resolution, using 10x technology. Wound experiments will be done on live fish and/or on skin cell cultures. Depending on the candidate's wishes and project's goals, single-cell surface protein assays can be added to single-cell RNA-seq analysis.

Tasks:

- Wound experiment / fish handling
- Generation of high-quality single-cell suspensions from skin tissue
- Library preparation of scRNA-seq
- Bioinformatic analysis

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: How have immune genes evolved across the salmon family?

Key words: immune genes, copy number variation, evolution, whole genome duplication

Contact persons / supervisors:

Nicola Barson
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Task description:

Immune gene diversity is important for immune function and evolution. Adaptability of immune response is increasingly important both for aquaculture and wild fishes in the face of predicted expanded pathogen repertoire and abundance with climate change. However, immune genes typically include clusters of duplicated genes where the functional equivalence with genes in other species can be unclear. These clusters are formed by gene copy number expansion and contraction and have typically been difficult to sequence and annotate accurately. Recently we have generated multiple long read genome assemblies across the salmon family, providing an opportunity to understand the evolution of these genes using comparative genomics. In this project we will use these genomes to analyse the evolution of immune genes to gain insight into the evolution of the salmon immune repertoire. Immune gene evolution is heavily impacted by the salmon whole genome duplication event, understanding how this has impacted evolution of immune genes is especially important. The student will use computational methods to compare sequence diversity and copy number variation within and between species and relate this to selection on different classes of immune genes.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Genetic basis of age at maturity in wild Atlantic salmon

Key words: Atlantic salmon, GWAS, age at maturity

Contact persons / supervisors:

Nicola Barson
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Task description:

Age at maturity is a key trait for Atlantic salmon in both aquaculture and wild salmon. Genome wide association in wild Atlantic salmon discovered 2 large effect loci determining age at maturity, but the power to detect smaller effect loci was low because of the small sample size (n=1400). A larger scale GWAS in aquaculture salmon (n=11000) suggested an additional >100 small effect genes are involved in determining age at maturity. However, it is not clear if these loci also impact age at maturity in the wild because of the low sample size originally tested. By expanding the original wild data set to 4000 individuals we will test if smaller effect loci also contribute to age at maturity in wild salmon. This will allow us to test if the polygenic basis of age at maturity is conserved between wild and aquaculture environments.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Improve pipeline for assembling genomes from long-reads sequences.

Key words: assemble genomes, long-reads sequences, flye, canu, bioinformatics

Contact persons / supervisors:

Thu-Hien To

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Simen Rød Sandve

email: simen.sandve@nmbu.no

Task description:

Flye is the recommended tool to assemble draft genome from long-read sequences. It's in general fast and generates good assemblies. However, in some cases of highly duplication or highly heterozygous diploid genomes, its performance is unstable. We observed that in most of these cases, canu - another alternative tool that requires much more storage and computing resources - behaves better. But on the other hands, in some rare cases, flye produces better assemblies compared to canu. Beside of that, running flye with different overlap lengths would produce different assemblies and it's not always straight forward to select the best one. Some reconciling methods make the consensus assembly more contiguous but often makes the QV go down. Main tasks:

1) Understand what factors that conduct to flye's performance by looking closely at problematic fragments, so that we can possibility add some additional steps or find the good parameters to help flye overpasses this issue.
2) Design a way to use different assembly versions of flye to make a more contiguous one without dropping the quality.

We have data and draft assemblies from more than 20 fungi that student can use for this study. Student is desired to have bash/script competence and enjoy designing/testing methods.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Taxonomic classification from fish meal samples

Key words: fish meals, taxonomic classification, MetaCache, Kraken2, blast, k-mer

Contact persons / supervisors:

Thu-Hien To
email: thu-hien.to@nmbu.no

Task description:

We have sequencing data from lots of fish meal samples with different proportion of fishes. Using database of fish genomes, with different classification tools, we identify and quantify DNA of each fish in the samples. Tasks:

1) Study if it's possible to improve the problem of wrongly assignment to closely related species.
2) Study the impact of the qualities/repetitiveness of genome database to the results and how to normalize the database to reduce those impacts.

The student would be working on data analysis and running bioinformatic tools.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Fine mapping of chromosome regions underlying important exterior traits in pigs.

Key words: genomics, pigs

Contact persons / supervisors:

Dag Inge Maren van

email: daginge.vage@nmbu.no

email: maren.van.son@norsvin.no

Våge Son

Task description:

The aim of this study is to use available genotype and sequence data to fine map quantitative trait loci (QTL) regions affecting exterior traits like leg positions and motoric movement in pigs. The exterior of pigs is an important trait for overall robustness and animal welfare. Some of the identified genomic regions for exterior traits overlap QTL regions identified for traits related to growth. Fine mapping would clarify if the same mutations are involved in the different traits or if closely linked genes cause the overlapping QTL regions. Identification of causal mutations affecting these traits can help selecting the most robust animals for future breeding.

Genomic data is routinely used in pig breeding and it is also important to understand the biology underlying different traits in the breeding goal. Norsvin has genotype and whole genome sequence data available that can be used to identify genes and mutations which can have a large effect on different traits. Phenotypic data is also available for other traits like fertility, meat quality and slaughter quality, and we are happy to discuss and adapt the topic to the student's interest.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Coat color genetics/pattern recognition in Norwegian cattle

Summary The amount/extent of white patterns in cattle is a trait that is of some concern for the breeders. The phenotype varies from completely solid red/black animals to individuals that are almost white. The cattle breeding organization Geno have a large collection of images generated over many years. For these individuals, genotype data and in some cases DNA sequence, are also available. In this project, it is desirable to automate the recognition and quantification of white color patterns. There is different software for image analysis available that can be adapted to this task. The purpose is to get a better description of the phenotype than white/non-white. There are also identified 2 clear QTLs for this trait that might be fine mapped using DNA sequence.

Subject area (keywords)

Genetics, statistics, machine learning

Language thesis (Norwegian and/or English)

Norsk eller Engelsk

Bachelor or Master thesis

Master

Credits

60 ECTS

Project/company

Geno – Norwegian Association of Cattle Breeding

Please contact

Dag Inge Våge daginge.vage@nmbu.no Arne Gjuvsland arne.gjuvsland@nmbu.no

Master's project at Genome Biology

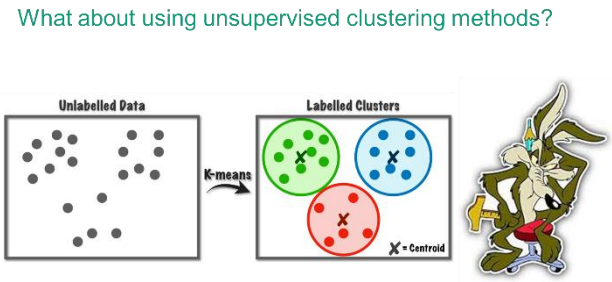
Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: MAGnificent: Implementation of clustering algorithms to improve Metagenomic Assembly Genomes (MAGs) recovery.

Key words: metagenomics, bioinformatics, clustering, High-Performance Computing, microbial communities

Contact persons / supervisors:

Arturo Vera-Ponce de León
Email: arturo.vera.ponce.de.leon@nmbu.no



Project description: Due to the high number of organisms and large complexity commonly observed in metagenomic data, recovery of single genomes has become a difficult task. To overcome this, MAGnificent project proposes the use of unsupervised cluster algorithms (e.g. k-means and hierarchical clustering) and taxonomical classification of the metagenomic reads to make more efficient and reduce the computational efforts to assembly, binning and recover Metagenome Assembled Genomes (MAGs).

Task:

- Test different cluster algorithms methods to reduce the number of input data (raw reads) in a metagenomic assembly.
- Generate a consensus meta-assembly of the clusters.
- By using different metagenomic binning tools (e.g Maxbin and Metabat2) generate a catalog of MAGs.
- Benchmark the algorithm with other MAGs recover tools.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: MetaONTeomics: Oxoford Nanopore Technologies for metagenomics

Key words: metagenomics, microbial communities, PromehtiON, bioinformatics

Contact persons / supervisors:

Arturo Vera-Ponce de León

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Phillip B. Pope

phil.pope@nmbu.no

Project description: Recently the use of long-reads sequencing technologies like Oxford Nanopore Technology (ONT) has revolutionized metagenomics. Nonetheless, there are only a few pipelines and workflows properly designed to use ONT data to generate assemblies, binning and annotation of metagenomic studies. The goal of this project is to design a complete workflow to analyze metagenomic data obtained by ONT and generate taxonomic and functional annotations of the microbial communities present in the samples

Task:

- Design an automated pipeline to process, assemble, binning and annotate metagenomes obtained by ONT sequencing technologies.
- Benchmark the tools with other pipelines publicly available

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Characterization of extracellular vesicles in fish mucus

Tomasz Podgorniak
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Prof. Hanne Cecilie Winther-Larsen
h.c.winther-larsen@farmasi.uio.no

Extracellular vesicles (EV) such as exosomes and microvesicles are small particles secreted by cells and packaged with proteins, lipids and nucleic acid. Due to their high mobility, they greatly contribute to communication between cells, are involved in immune system, tissue injury such as skin wounds and could also represent an unconventional mechanism of protein secretion into extracellular space. Most of the EV research is done specifically on exosomes and from plasma. However, extracellular vesicles exist also in fish mucus and have potential of being used as biomarkers of infection or tissue damage.
The role of MSc student is extraction and characterization of extracellular vesicles from mucus of salmonid fish and if possible, comparison of EV's miRNA between healthy and wounded skin. Moreover, characterization of EV population in mucus by Flow Cytometry can be also added to student's tasks.

Tasks:

- Isolation and characterization of EV from fish mucus
- Comparison of EV's miRNA secreted from wounded VS healthy skin in Atlantic salmon
- Surface marker identification of EV by Flow cytometry

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Mechanisms and evolution of genome regulation using salmon functional genomic data

Key words: gene regulation, multi-omics, functional annotation, genome evolution

Contact persons / supervisors:

Gareth Gillard
email: gareth.gillard@nmbu.no

Task description:

The EU Horizon project AQUA-FAANG has generated large amounts of mult-omic functional genomic data (RNA-seq, ChIP-seq, ATAC-seq, Hi-C, etc) on key fish species in aquaculture, with the goal to improve understanding of genome function and genotype-to-phenotype prediction. The data on the salmonid species Atlantic salmon and rainbow trout has been used to annotate regulatory regions of the genome, such as promoter and enhancer regions. How these regions are linked to regulating the expression of genes is a next big step in analysis of the data. A student interested in using bioinformatics methods on multi-omic sequencing and regulatory annotation data may analyze the relationship between gene expression and cis-regulatory elements in salmonid embryonic stages and across adult tissues, and investigate how regulatory elements have evolved following the salmonid whole genome duplication event.

Master's project at Genome Biology

Faculty of Biosciences, Department of Animal and Aquacultural Sciences (IHA)

Title: Decoding gene regulation with deep neural networks

Key words: Gene regulation, machine learning, deep neural networks, comparative genomics

Contact persons / supervisors:

Lars Grønvold
email: lars.gronvold@nmbu.no

Task description:

The student shall explore the use of deep neural networks (DNNs) to learn regulatory logic from genomic sequences. DNNs have successfully been applied to predict transcription factor binding, chromatin state (e.g. ATAC-seq) and even gene expression patterns. Most existing methods are limited to humans but we are interested in how it can be applied across species and studying the differences. Requires some out of the box thinking.

The student is free to explore any novel methods of their choice using published data. Here are some examples to choose from:

- Applying existing models across species.
- Explore novel model architectures for single cell ATAC-seq.
- Develop a model that predict ATAC-seq from sequence and RNA-seq.
- Develop regulatory code simulator and use it to test model architectures.
- Simulate regulatory evolution using existing models to calculate fitness.
- Dissecting trained models to extract regulatory logic.
- Compare duplicated regulatory regions in salmonids.

Student must be comfortable with coding and have knowledge of deep learning methods.