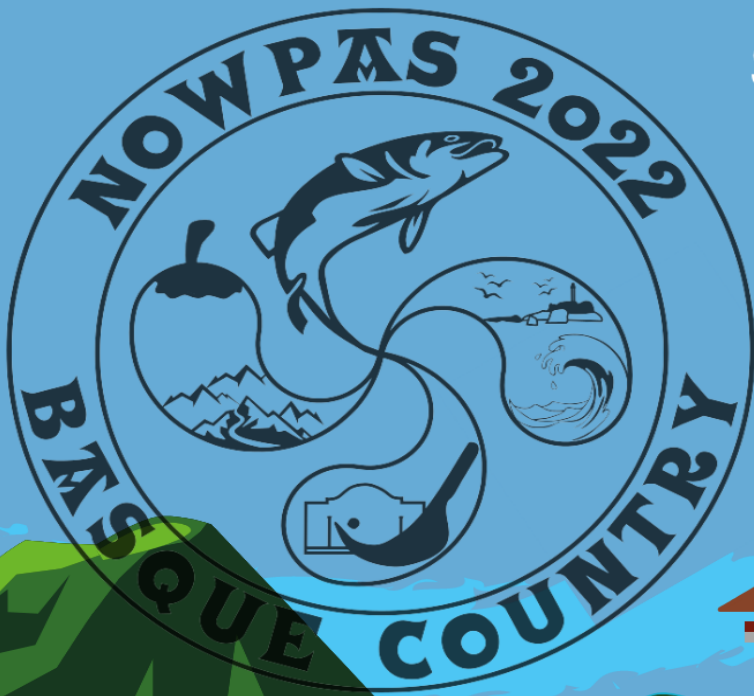


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Abstract Book

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Keynote Abstracts

The shrinking salmon of the River Eira

Geir Bolstad

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Abstract: The River Eira in Western Norway once held some of the world's largest Atlantic salmon: the historical average body mass of adult salmon returning to the river was 12 kg. After three episodes of river regulation in 1953, 1962 and 1975 the waterflow of the Eira was reduced to almost 1/3 of its historical value. This greatly impacted adult body mass, which today is about 4 kg on average. Using DNA from archived scale material, we document that this change has a genetic basis. The observed allele frequency changes at two loci associated with size at maturation, could predict over 80% of the decline in average body mass. By developing a model of the adaptive dynamics, using a quantitative genetics framework, we show how the average body size tracks its fluctuating optimum before catching up 5-7 salmon generations after the first waterflow reduction. The observed rate of adaptation, mediated by large effect loci, is astonishing and provide insight into the scope of evolutionary rescue following human disturbance.

Can we predict the fate of Atlantic salmon populations in the face of climate change?

Mathieu Buoro

UMR ECOBIOP, INRAE, Univ.Pau & Pays Adour, Saint-Pée s/ Nivelle, France

Abstract: Atlantic salmon *Salmo salar* is the subject of many management actions aiming at their conservation. There is a strong demand, expressed by a diversity of local to international bodies for assessing the consequences of climate change for this species relative to the conflicting objectives of both conservation and exploitation. However, our predictive ability is still limited by the complexity and uncertainty of current and future environments, complexity of the life cycle and especially by the challenges of teasing apart evolutionary change from more ‘plastic’ responses to environmental perturbation. I discuss the importance and complementarity of experimental research, long-term monitoring *in natura* and modeling approaches. Importantly, life cycle models provide a powerful tool for disentangling eco-evolutionary processes and investigating interactive, synergistic effects among multiple factors in order to better understand the eco-evolutionary responses of populations in the face of various scenarios of climate change. I will present a demo-genetic Individual-based model which is designed to investigate the demogenetic consequences of environmental change scenarios on an exploited population of Atlantic salmon. Without omitting its limits, I show how this approach allows to synthesize knowledge and to identify its gaps.

Tales of the Desolation Islands

Jacques Labonne

UMR ECOBIOP, INRAE, Univ.Pau & Pays Adour, Saint-Pée s/ Nivelle, France

Abstract: French southern archipelago of Kerguelen is one of the most remote places of the world. As biogeography would have it, these islands host a remarkable yet reduced biodiversity, long sheltered from human activities by distance. But as the “desolation” tag hints, the islands also harbour a rich history of failed ventures by people from many countries, which have left marks on the islands and their natural wealth. Part of these marks are the numerous willingly or non-willingly introduced taxa. Some of them thrived, often at the expense of the native species. The introduction of salmonid species led to various outcomes, since among 8 introduced taxa, 5 remain, and one of them is currently invading the whole archipelago.

The story that we will follow together tells about how and why were these fish introduced, what can explain their contrasted fates, and what our long-term monitoring has taught us so far. We will focus on some observed patterns, experiments and results, and the next questions in line. But we will also get a glimpse at how science is done in Kerguelen, at the everyday life in these wonderous landscapes, at our own failures and successes. All these little bits that make practicing science in the far corners of the map both a challenge and its own reward.

Tracking ghosts and rare phenotypes across the freshwater landscape

Anna M. Sturrock

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Abstract: Salmon exhibit unparalleled life history diversity, yet it is difficult to quantify the performance of different strategies given that we (a) typically only see the survivors and (b) are often hampered by data gaps that disproportionately impact the rarest phenotypes. In order to design management actions that boost salmon survival and resilience, we need to understand the plight of the ghosts and to support the phenological extremes, given that they could be the winners of tomorrow. Here, I will provide an overview of how using different sampling strategies, tissue types and chemical markers can provide novel insights into which traits are successful - and unsuccessful - under varying environmental conditions. In particular, I will demonstrate how otolith and eye lens isotope records and microstructure can be used in combination to reconstruct fine-scale movements and growth across the freshwater landscape, with a particular focus on Chinook salmon in California. When used in combination with strategic sampling across space and time, these approaches can provide new insights into movement patterns and trait selection that are simply unobtainable through traditional tagging approaches. In particular, these data have revealed the importance of early dispersers, nomadic wanderers, and late migrants across a range of climate scenarios. Importantly, the frequencies of different phenotypes varied among populations and years, suggesting the importance of maintaining a diverse life history portfolio, even in highly engineered systems. In a changing climate, there is a growing need to quantify and monitor processes that erode life history diversity in order to design management actions that promote viable and resilient salmon populations.

Impact of salmonids with rapid growth; from individuals to ecosystems

Line Elisabeth Sundt-Hansen (PhD)

Senior research scientist, Norwegian institute for Nature Research (NINA)

Abstract: What happens when we manipulate salmonids, so they grow faster? Or we manipulate other factors that impact growth? Why don't fish in nature obtain a larger body sizes faster? In this talk I will focus on how growth impacts salmonids at the individual and population level, and hopefully I end up at the ecosystem level.

Salmonids have an amazing ability to adapt to widely different environments and over thousands of years they have fine-tuned their life-history to a range of environmental parameters in their habitat. Growth rate is an important life-history trait that varies among individuals, families and populations. It is strongly associated with other traits that affect survival and fitness, and is the end-result of numerous biochemical, physiological and behavioural processes such as appetite and foraging behaviour, feed uptake efficiency, energy allocation and utilization and physical activity.

Humans have a long history in manipulating growth in animals for our advantage, through selective breeding for rapid growth in farmed salmon and developing genetically modified salmon reaching a larger size faster than wild fish. Breeding programs for many salmonids have focused on developing more extreme phenotypes (e.g. faster growth rate, and/or larger size at reproduction), which may disproportionately impact wild salmonids if they are released or escape into the wild.

In a series of experiments in semi-natural facilities at NINA's research station at Ims, we have tested how the rapid growth (potential) of farmed Atlantic salmon affects their behaviour and competition and interaction with wild Atlantic salmon. Further, we have tested how this competition is influenced by population density, food abundance and predation. From the individual approach, we then move up to an ecosystem approach and test how Atlantic salmon with a rapid growth potential impact the ecosystem and ecosystem functions, manipulating growth using growth hormone. Our results show that not only does rapid growth impact the individuals and other conspecifics, but also other organisms in the ecosystem and their functions.

Being a researcher is not rocket science, it's more complicated!

Eric Verspoor

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Abstract: Research represents an evolved cultural tradition. It involves collecting, organizing, synthesising and interpreting information, either at a personal or societal level, to advance understanding about perceived aspects of the world and why it is the way it is. By asking “why” and “what”, an evolved predisposition of man, and then doing research, individuals and humanity collectively can gain a more accurate picture of their own true nature and the world they are a part of. Some become career research scientists but they do not begin life as such. Rather each individual emerges out of the social context into which they are born and within which they grow up, a context which conditions whether they become researchers and, if they do, what they research and how their careers progress.

Becoming a researcher involves both a personal and professional journey, one of constantly learning, particularly about unknowns, and where the significance of events along the route travelled is only fully appreciated in retrospect. This becomes most apparent when reflecting on one's own career, as well as those fellow researchers. Here I consider these points with reference to my own career as a researcher in molecular population genetics and biodiversity conservation, in which I focused on salmonid fish and particularly the Atlantic salmon. I give my take on why I took a path leading to this career as well as how, despite the inevitable challenges, I have been able to realise a successful career – it is seldom if ever smooth sailing! Each person's journey will be different. However, it may be helpful, as it was for me when beginning my journey, to hear of how the careers of others came to be and evolved. For me there was always useful wisdom to be gained. From my own career probably the most helpful message I gained was the sage advice of the evolutionary biologist Theodosius Dobzhansky, echoed by many of his contemporaries, “Nothing in biology makes sense, except in the light of evolution”. I would suggest only a slight tweak to his words, and replace “biology” with “life”!

Delegate Abstracts

Nutrient remediation in spawning streams results in increased densities of juvenile Atlantic salmon

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Keywords: conservation, freshwater, fisheries management, nutrients

Abstract: Declining Atlantic salmon (*Salmo salar*) populations have resulted in a decreased import of marine-derived nutrients to spawning streams by returning adults. Restoration of nutrients to culturally oligotrophic streams has been shown to result in increased growth rate and biomass of juvenile salmon. Here the efficacy of nutrient restoration methods were tested, firstly through manipulating nutrient application method and secondly through manipulation of nutrient quantity. The application of pellets via scattering during winter resulted in significant increases in macroinvertebrate size and juvenile salmon biomass and density the following autumn, but with negative effects on individual salmon body size and condition. There were no significant effects of pellets applied in bags. The following year, the application of scattered pellets in winter and summer resulted in significant increases in juvenile salmon body size, condition, density and biomass. Scattered pellets may more effectively disperse a pulse of nutrients across a wider area, allowing for more even enrichment, but further research is required to understand the underlying processes.

On the edge of the abyss: Mathematical modelling of Atlantic salmon marine migration

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Keywords: Migration, modelling, survival, post-smolts, marine

Abstract: Recent declines in Atlantic salmon populations are largely attributed to decreasing marine survival rates. Survival probability of post-smolts during the months following marine entry is hypothesised as being low and variable, dependent upon body size and individual conditions experienced. Improving predictions of the migration pathways taken by post-smolts during this period could assist in characterising the local conditions experienced, helping to forecast fluctuations in marine survival. This project takes a modelling approach, with high specificity in its spatial and temporal scales, to challenge and develop current understanding of migratory routes of post-smolts from selected UK rivers during their first three months at sea. A Lagrangian particle tracking model will be developed to consider the movement of post-smolts from their point of sea entry to their convergence at an oceanographic feature on the continental shelf edge (Wyville Thomson Ridge) and subsequent potential path divergence. The model will use a high-resolution ocean model (Scottish Shelf Waters Reanalysis Service, SSW-RS) and will be run for each year of the 26-year SSW-RS period. It will consider multiple hypothesised swim behaviours of post-smolts including current following, directed swimming, and temperature or salinity gradient following behaviours. The plausibility and biological realism of these swim behaviours will be analysed, and the temporal variation of migratory routes will also be considered in relation to varying oceanographic conditions. These results will allow for a better understanding of the initial migration of Atlantic salmon from UK rivers, contributing to cooperative efforts in addressing research needs and informing conservation actions.

Novel Ex Vivo Mechanisms to Decode Sea Lice Mechanisms in Salmonid Fishes

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Keywords: Salmonids, sea lice, functional genomics, CRISPR

Abstract: Sea lice (*Lepeophtheirus salmonis*) represents the greatest economically important animal welfare problem in Norwegian aquaculture, threatening both sustainability and limiting overall production potential. Sea lice feed on the epidermal mucous and underlying tissues and blood of its host fish, resulting in lesions and secondary infections which may prove detrimental to fish health and viability. Currently, no effective treatment strategy exists which is able to combat the full scope of the sea lice threat. In nature, the heaviest sea lice burdens are found on Brown trout or Atlantic salmon as they display a particularly weak or entirely absent inflammatory response. Other species, such as Pink and Coho salmon display high levels of resistance to infection, with Coho displaying a both particularly rapid immune response and epithelial hyperplasia. As such, the goal is to discover and validate inflammatory responses and resistance mechanisms diverging in susceptible (Atlantic salmon) vs. resistant salmonids (Coho salmon). This will be conducted through characterisation of skin tissue in both Coho and Atlantic salmon using immunohistochemistry and in situ hybridization at different stages of lice infestation. In addition, establishment of novel cell lines will enable detailed studies of immune responses following exposure to sea lice excretions and homogenates. Finally, editing these cells with CRISPR could help to identify the underlying mechanisms causing differential resistance to sea lice infestation.

Stay cool: Effects of heat stress events and thermal refuge availability on Atlantic salmon (*Salmo salar*) juvenile growth, smolt condition and marine survival

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Keywords: behavioural thermoregulation, thermal refuge, temperature, freshwater

Abstract: The currently observed warming of rivers throughout Eastern Canada poses a threat to Atlantic salmon (*Salmo salar*) populations located at the southern edge of the species distribution where heat stress events are increasing in frequency and magnitude. Heat stress events should negatively affect growth and size-at-age of salmon parr due to increases in metabolic costs with temperature, and by the momentarily reduced feeding of juveniles during their use of thermal refuges. Yet, exploratory work showed that availability of thermal refuge in rivers could mitigate effects of heat stress events on growth of young of the year Atlantic salmon. Nonetheless, evidences of direct and longer-term impacts of heat stress events during the freshwater phase of Atlantic salmon are still scarce and there is a need to better document the mitigating role played by thermal refuges. This research program aims at elucidating the impact of heat stress events during the freshwater phase of Atlantic salmon life cycle. First, historical data will be analyzed to explore relationships between metrics of within river heat stress magnitude, duration, and frequency on smolt condition, age-at-smoltification, egg-to-smolt survival, and marine smolt survival. Second, field-based research will be conducted in Quebec and Maritimes rivers to determine the impact of heat stress events on juvenile salmon daily growth depending on thermal refuge availability and use. Investigating the linkages between salmon daily growth and heat stress events could lead to the development of important practical knowledge on the benefits associated with cold thermal refuge availability in rivers in the southern edge of Atlantic salmon distribution.

Impact of global changes on salmonids population : use of the Dynamic Energy Budget model

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Keywords: global change, salmonids, DEB theory, evolutionnary constraints

Abstract: During the last decades, it exists an increased interest in understanding the impacts of global change and anthropic disturbances on ecosystems. This global change impact freshwater ecosystem in several dimensions. One of them is the alteration of temperature cycle which directly affect poikilothermic species as salmonids. In addition, extreme events can interfere with river flows creating hypoxia events, and can result in reduced access to food resources and starvation for some species. To cope with the increase in energy expenditure and/or the decrease in food resources related to these disturbances, individuals will have to adopt strategies depending on their physiological limits or life-history traits. For example a salmonid will have to choose to allocate its energy for reproduction, at the expense of its life, or for survival, waiting for better conditions to breed. The Dynamic Energy Budget model is a good tool to understand how a fluctuant environment can interfere on the individual energy physiology, quantifying the energy with a simple system of equations. The first aim of my PhD research work is to develop an individual-based DEB model for *Daphnia magna*, and extend it to *Salmo trutta* in a second time. Then I will confront individuals to different scenarios: (1) ideal conditions, (2) temperature fluctuations, (3) starvation and (4) hypoxia. This model will help to understand the mechanisms used by an individual to adapt to global changes.

The influence of partial migration of Arctic charr (*Salvelinus alpinus*) on residents ecology and size structure

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Keywords: Partial migration, Arctic charr, freshwater stream ecosystems, life history

Abstract: Migration patterns are essential to understand as the temporal presence and absence of migratory individuals can have substantial impact on ecological dynamics of the different habitats that they inhabit. While some populations exhibit exclusively migratory or resident life histories, others show intra-population variation in migratory propensity, resulting in partially migratory populations. A major gap in our knowledge concerns the effects of partial migration on the ecology and structure of the resident individuals. Due to their relative simplicity and the high degree of replication, Greenlandic freshwater systems offer a unique possibility to study the evolution of migration versus residency. Numerous streams have been colonized by Arctic charr (*Salvelinus alpinus*), with subsequent establishment of resident populations inhabiting streams above waterfalls. These natural barriers prevent upstream movements from sections below that are occupied by partially migratory populations. Comparison of population structure, foraging strategies and annual growth between above and below resident individuals is necessary in order to assess the influence of migration in partially migratory populations. Population structure analyses in seven different drainages revealed a higher density of small juveniles below waterfalls. In the presence of migration juveniles show a limited growth likely due to competition with their conspecifics until they reach a certain size allowing them to feed on alternatives resources present in partially migratory systems (i.e. cannibalism of eggs, juveniles). Their subsequent high growth can lead to the emergence of giant resident individuals. Our results thus suggest that partial migration may shape population structure and influence the ecology of resident individuals.

The effect of hydropower on the behaviour and lake habitat use of sea trout in Aurland, western Norway

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Keywords: Sea trout, lakes, hydropower, behaviour, acoustic telemetry

Abstract: Lakes are abundant in Norwegian river systems and can offer important areas for refuge, energy conservation, and potential spawning grounds as sea trout migrate back during autumn for spawning and overwintering. Habitat alterations and fragmentation of rivers caused by hydropower related constructions are one of the main threats to migratory fish and impact the movement and behaviour of sea trout. Hydropower generates more than 90% of total electric energy produced in Norway, however, there is little information on how hydropower production affects the behaviour and lake habitat use of sea trout. To investigate, we conducted an acoustic telemetry study in Aurland, Norway, which contains Norway's third largest hydropower station and one of the best sea trout producing rivers in Norway. A total of 31 adult sea trout were captured by angling in river Aurlandselva and tagged with acoustic transmitters between July 20 and August 12, 2021. The tags contained temperature, acceleration, and depth sensors which provided information on movement patterns and lake use of sea trout. Preliminary results indicate that most individuals use the lake during the pre-spawning period.

Accelerometer-derived estimates of energy expenditure for lake-refuging trout suggest that lakes are potentially important areas for energy conservation in sea trout. The findings will have implications for hydropower production and stock assessment as a portion of spawners might inhabit the lake during annual population counts. Future research on regulated and unregulated watersheds is therefore needed to assess impact of hydropower on sea trout ecology and use of lakes throughout the year.

Running the gauntlet of Pathogens and Climate (PACE): impacts from infectious diseases on wild fish in the high north

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Keywords: salmon, sea trout, migration, disease, telemetry

Abstract: Little is known about the diversity and distribution of salmonid pathogens and their impacts on individual performance. A changing seascape due to anthropogenic activity and climate change means host-pathogen dynamics are likely to shift, necessitating an understanding of these processes for both fundamental and applied science. The PACE project will implement fish biopsy and tracking to model the diversity and distribution of viruses, bacteria, and parasites of Atlantic salmon (*Salmo salar*) and sea trout (*Salmo trutta*) along a latitudinal gradient in Norway and evaluate how these affect performance. Southern Norway is characterized by warmer temperatures and higher density of aquaculture and also more threatened stocks of salmon and sea trout. Northern regions are now exposed to relatively rapid warming and soon will encounter expansion of aquaculture activities. In three work packages we will use molecular genomics to reveal pathogen biogeography and with biotelemetry and bioenergetics modeling we will investigate how pathogens impact fish performance in terms of physiology, behaviour, and life history.

Evolutionary-driven management of brown trout (*Salmo trutta*. L) intraspecific diversity

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Keywords: Management, Intraspecific diversity, Eco-evolution, Modelling

Abstract: Human interventions have often led to the admixture of previously allopatric lineages, notably for salmonid species. In France, intensive stocking of Atlantic brown trout has led to a mosaic of outcomes regarding hybridization and introgression of Mediterranean alleles by Atlantic ones. To understand and predict this diversity dynamic, we developed an individual-based demo-genetic model, which implements identified reproductive isolation mechanisms – female preference and gene-by-environment embryonic survival – between both lineages. The model aims at representing the evolution of intraspecific diversity dynamics in various environmental contexts and under different management practices, by including eco-evolutionary mechanisms as well as their genetic basis. Simulations, considering pre- and post-zygotic isolation, indicate that evolutionary mechanisms help at predicting introgression dynamics, depending on the environmental context. Managers interested in native or intraspecific diversity conservation should therefore consider the role of both, reproductive isolation mechanisms and environmental factors in their decision-making regarding conservation action.

Unique viscoelastic properties of salmon ovarian fluid have biophysical implications for sperm-egg interactions

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Keywords: sexual selection, ovarian fluid, cryptic female choice, viscoelastic fluids

Abstract: The gamete level sexual selection of externally fertilising organisms is usually achieved by modifying sperm behaviour with mechanisms thought to rely on altering the chemical environment in which gametes perform. In fish this can be achieved through the ovarian fluid, a substance released with the eggs that has been found to have a pivotal role in modulating spermatozoa swimming behaviour and the reproductive outcome. While the effects of biochemical composition of this medium in relation to sperm energetics have been more frequently investigated, the influence of the physical environment in which spermatozoa swim and compete remain less explored in fish as in other external fertilizers. Our objective was therefore to gain insights on the physical structure of the ovarian fluid using a rheological approach, to understand its impact on reproduction. Through steady state and oscillatory viscosity measurements, we subjected salmon ovarian fluid from different females to variable shear stresses and angular frequencies the resembled the ones exerted by salmon spermatozoa swimming through the fluid to reach the egg. We show that the ovarian fluid, that in its relaxed state is a gel-like substance, under these frequencies behaves as a non-Newtonian viscoelastic and shear-thinning fluid, in which the viscosity decreases with increasing shear rates. We concurrently show that this fluid infringes the Cox-Merz rule above 7.6 Hz, showing a shear-thickening phase with a prevailing elastic response. This suggests the presence of a unique frequency-dependant structural network that can have relevant implications on sperm energetics and fertilisation dynamics.

Diversity in the internal functional feeding elements of Arctic charr, *Salvelinus alpinus*, morphs in Lake Thingvallavatn, Iceland

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Keywords: Morphology, Morphometric Evolution, Freshwater Ecology

Abstract: The diversity of functional anatomy related to feeding has been influenced by natural selection. This diversity is particularly impressive in fishes and correlates with ecological specialization and habitat choice. Differences between species originate as variation within species that selection acts upon. Arctic charr, *Salvelinus alpinus*, is a freshwater fish species known for its phenotypic variation and sympatric polymorphism throughout its distribution. In Lake Thingvallavatn, four different morphs of Arctic charr coexist: large benthivorous, small benthivorous, planktivorous and piscivorous charr, who differ in prey type and niche choice which is associated with differences in head shape and feeding morphology. It has been hypothesized that the internal functional feeding elements have also undergone adaptive evolution. One prior study found evidence of differences in specific structures. However, more knowledge of these traits is needed. The aim is to answer the following questions. 1) Which functional feeding elements vary among the morphs? 2) How independent/integrated are traits in different sections of the feeding apparatus? In this project adult fish from all four charr morphs in the lake were gathered. The heads of the fish were boiled to retrieve the bones and their structures examined using geometric morphometrics. The results will hopefully allow us to better understand how ecological divergence among Arctic charr ecomorphs manifests in internal feeding morphology.

Do all roads lead to home? Straying behavior of anadromous brown trout (*Salmo trutta*) over multiple spawning seasons

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Keywords: Sea trout, migration, natal homing, straying

Abstract: Natal homing, a strategy in which case individuals return to breed in the same river as to where they had hatched, is prevalent among salmonids. However, there is always a part of the population that do not return to their natal river, meaning they stray. To date, there is limited documentation on straying behavior and how it connects to different life-history characteristics especially over the course of the individual's life. In this study 21 538 out-migrating juvenile anadromous brown trout (*Salmo trutta* L.), also referred to as sea trout, were tagged over two years with passive integrated transponder tags (PIT) in order to follow their return to their natal and three non-natal rivers in a fjord system over multiple spawning seasons. Out of all the sea trout that returned to any of the rivers, 206 individuals were detected returning over multiple seasons, out of which 43% were strayers. A divergence in migratory strategies among strayers was documented, in which case a smaller proportion of strayers were only detected in non-natal rivers, while, the majority (67%) displayed high variability in their migratory routes by being detected in both their natal and non-natal river over multiple seasons. This study has documented high variation in migratory strategies that strayers in a sea trout population may display. Further, it is hypothesized that the strayers, that return to freshwater over multiple seasons may have significant effects to the overall genetic structure and population dynamics of both the donor and recipient populations.

Food availability for Atlantic salmon populations differs between rivers in Northeast Iceland

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Keywords: Atlantic salmon, food web, food availability, population dynamics, invertebrates

Abstract: Food availability is one of the main drivers of Atlantic salmon (*Salmo salar*) population dynamics, which impacts their growth and development. The trophic links between juvenile Atlantic salmon and invertebrates could vary along the river as well as between rivers, so food availability could impact the salmon's growth rate and density spatially. The aim of the study is to investigate whether food availability for Atlantic salmon populations differ spatially between the four rivers in Northeast Iceland. Electrofishing surveys were conducted and invertebrate samples (from surbers and drift nets) were taken along the rivers to collect information on the trophic links between salmonids and invertebrates in the system. Stomach samples from salmonids were also collected to quantify and identify the resources consumed by the fish. Species identification and size measurements were made for invertebrates and salmonids. Abundance and biomass data were then compared between sites and rivers. The results showed that the densities of some families of invertebrates differed between rivers. The number of stomach items found in salmon were different between the rivers and ages of salmon, with the abundance of Chironomidae larvae being the highest. Whereas juvenile salmon populations had similar densities between rivers. Therefore, prey choice may not be dependent on prey abundance in the river ecosystem, but further analysis will be needed as biomass data will still have to be included in analysis.

Fisheries management in spatially structured Atlantic salmon populations

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Keywords: dispersal, fisheries, management, modeling

Abstract: Despite extensive research on the causes and consequences of spatial dispersal, the implications of connectivity for conservation and management are poorly appreciated, especially for species for which dispersal rates are ignored or considered negligible such as salmonids. For such species, exploitation by fishing usually does not consider populations connectivity, and fisheries management rather focuses at population scale. To date, prior work already warned about the danger of ignoring spatial structure and connectivity of populations but a very few studies have explicitly compared different strategies of exploitation while also considering the spatial structure of populations. We use a spatially explicit demo-genetic agent-based model as a virtual laboratory to mimic a realistic Atlantic salmon populations network and compare several spatialized fishing strategies (e.g. fishing all populations, sink, or source only). We assess their consequences at the demographic, phenotypic and genotypic levels. We show different effects of spatialized exploitation strategies on metapopulation size, stability and synchrony, as well as life history strategies and genetic evolution of traits. Importantly, we show that the consequences of spatialized fishing strategies depend on the exploitation pressure acting on the local populations and on the metapopulation as a whole. Altogether, we argue that it is critical to account for metapopulation structure in defining fisheries management because spatialized exploitation of connected populations can lead to various demographic outcomes but also complex evolutionary trajectories.

Investigating environmental determinants of the smolt migration in a wild population of Atlantic salmon (*Salmo salar*)

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Keywords: phenology, state-space model, salmo salar, proximate factors

Abstract: Understanding the phenology of smolt migration, i.e. the timing of smolt leaving freshwater to enter the ocean, is important to better forecast the future of Atlantic salmon (*Salmo salar*) populations facing climate change. Smolting is a critical part of the life cycle of Atlantic salmon but it can be costly and hazardous. While migration to seawater can increase the fitness of individuals via higher growth conditions and fecundity, it comes with physiological costs and higher mortality risks. The phenology of migration is an adaptive process which can help to reduce the overall cost of migration by synchronizing favourable conditions in rivers and at sea.

Many studies investigated proximate factors influencing the timing of smolt migration and emphasized long term phenological change. However, interpreting phenological changes and investigating potential proximate factors influencing the timing of migration is challenging because our observations result from multiple dynamics processes (smoltification, migration decision, actual departure) and the observation process itself (capture/detection). Indeed, both biological and observation processes can be controlled by multiple and sometimes confounding factors (water discharge) that can affect our understanding of the observed changes in phenology.

My PhD project aims to explicitly disentangle these processes, identify the factors involved and explore the potential consequences of climate change and extreme climatic events on the phenology of migration. To do so, we will develop a model representing explicitly both the biological processes and the observation process in a unique framework using a long-term mark-recapture program of A. salmon juveniles in the Scorff river (France).

Assessing the effects of the new Atlantic salmon (*Salmo salar*) genome assembly on imputation accuracy

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Keywords: Aquaculture, Genome assembly, bioinformatics, genotype imputation, Atlantic salmon

Abstract: Integration of genomic information in aquaculture applications has vastly improved economically important traits in Atlantic salmon. However, producing whole-genome sequence information at population-wide level proves challenging. Genotype imputation is a cost-efficient method to infer missing genotypes for large cohorts using a smaller population as reference. Due to Atlantic salmon's genome complexity – resulting from recent whole-genome duplication - the first Atlantic salmon genome assembly constructed with short-read sequencing technology includes several errors (NCBI GeneBank reference: GCA_000233375.4). Majority of these errors involve duplicated regions and can affect assembly quality and inference accuracy. Here we present how the new Atlantic salmon genome reference (NCBI GeneBank accession GCA_905237065.2) of 90-fold improved contiguity impacts imputation performance. Using multiple imputation methods and genotype densities we explore the genomic landscape realized by the new assembly. We report physical extension for several chromosomes (35Kb - 27Mb) and complete intra- and inter-chromosome genomic rearrangement. Reposition of misplaced loci significantly increased average imputation accuracy in high genomic complexity regions (average R^2 from 0.27 to 0.67). However imputation accuracy is persistently lower for these regions compared to less complex loci. Accuracy heterogeneity can be attributed to unbalanced genetic marker distribution of currently available genotyping platforms. Furthermore, complex regions overlap several structural variation elements, a major genetic variation source that increases inference uncertainty, particularly in the Atlantic salmon genome. Overall, our study shows that the improved genome assembly significantly increases imputation accuracy. Our findings provide considerations for the design of future genotyping platforms, improving imputation accuracy and precision of downstream analyses.

DNA methylation differences during development distinguish sympatric morphs of Arctic charr (*Salvelinus alpinus*)

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Keywords: Bisulfite Sequencing, DNA Methylation, Molecular Evolution, Salmonid, RRBS

Abstract: Arctic charr (*Salvelinus alpinus*) is a polymorphic cold-water fish species belonging to the Salmonidæ family. In Iceland, *Salvelinus alpinus* is found in many places, but in Lake Thingvallavatn it displays remarkable morphological variation, in particular in terms of head and trophic apparatus development. The main focus of my PhD project was to look for DNA methylation differences during early development between the four sympatric morphs living in this lake using RRBS (Reduced Representation Bisulfite Sequencing). The data revealed strong methylome differences between the morphs, especially along the benthic-limnetic axis. These differences were located close to genes playing a role in interesting biological processes. Furthermore, repeat element sequences (such as small RNA sequences) were located in these regions. Next, we used qPCR to assess the expression of 14 genes showing varying methylation patterns and investigated correlations between methylation and gene expression in this model.

Identifying candidate adaptive loci and tracking their variation over the last 90 years in wild Baltic salmon

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Keywords: Genetic stock identification, population structure, genetic diversity, temporal genomics, management

Abstract: Atlantic salmon (*Salmo salar*) exhibit a broad range of diversity in key life history traits, such as maturation and migration timing. This variation has been found to have a genetic basis in multiple populations. Furthermore, anadromous salmon return to their natal location to spawn, which frequently results in strong geographical population structuring. Sustainable management of genetically distinct populations and their diversity is essential for maintaining the resilience of salmon stocks.

To study how human activities, in particular fishing, may influence the evolutionary trajectories of wild salmon populations, I use an almost century-old scale archive to investigate whether human impacts have altered the allele frequencies of genes relevant for the fisheries and ecology of the species in the northern Baltic. These include genes associated with maturation and migration timing. In addition, I use genetic stock identification to identify the origin of mixed salmon catches in the northern Baltic. I will present results from a genome-wide dataset of multiple Baltic salmon populations and hatchery broodstocks, including loci implicated in local adaptation in the largest Baltic salmon population. I will discuss using this type of genomic information as a basis of genetic monitoring that may improve our understanding of the effects of fishing on wild populations, and help preserve the biological diversity of the ecologically and economically important Baltic salmon.

Genetic and morphological variation of Atlantic salmon (*Salmo salar*, L.) in a recently repopulated river system

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Keywords: genetic structure, geometric morphometrics, migration, recolonisation

Abstract: Until the mid-1900s, the Yorkshire Ouse, England, used to be a nationally renowned salmon river supporting a fruitful fishery. In the second half of the 1900's, salmon in the river had undergone a drastic decline in numbers due to several factors possibly including heavy industry pollution, habitat degradation, a sequence of anomalously warm and dry years, and overfishing. For decades, no records of catch were reported suggesting a possible extinction of salmon in the river system. From the late '80s until present, following water quality improvement and habitat restoration, numbers of Atlantic salmon observed and caught in the catchment steadily increased year by year, and the Ouse now represents an interesting system in which to study recolonisation.

In this study, we aim to use genetic and phenotypic information to better understand the differentiation of salmon in the Yorkshire Ouse system. We will explore genetic substructuring within the river system, and investigate body shape differences of juvenile salmon between and within tributaries. The results of this study will increase our understanding of repopulation mechanisms of wild salmon in recovering rivers and will provide new, valuable insights to improve management and conservation of this iconic fish.

Growth of juvenile Atlantic salmon under future climate change scenarios

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Keywords: Climate-Change, Atlantic salmon, Machine-learning, Growing-degree-days, GCMs

Abstract: Native to the North Atlantic Ocean, Atlantic salmon populations are found in European rivers from the south of Spain to the north of Russia. Salmon populations have been in decline with climate change constituting a substantial threat to species viability with population outcomes associated with long-term resilience uncertain. Juvenile Atlantic salmon show considerable latitudinal patterns in rates of growth and development owing to geographical variation in water temperature and photoperiod. Here I present progress on efforts to model stream temperature using benchmark methods such as linear regressions and air2stream, but also machine learning methods (e.g. stepwise linear models, random forest, extreme gradient boosting, feedforward neural networks and recurrent neural networks). These models are subsequently coupled with downscaled General Circulation Models (GCMs) and Regional Climate Models (RCMs) to obtain projections of water temperature in a third order stream in the west of Ireland. The projections are then used to predict rates of juvenile Atlantic salmon growth specific to the river under different future climate warming scenarios. By having some mechanistic understanding of their action, the assessment of climate change impacts on the growth of juvenile Atlantic salmon should be a powerful aid for anticipating life history responses such as length of freshwater residency, the magnitude of any potential match-mismatch in smolt-migration windows, population turnover and many other aspects important in determining salmon population performance and fitness, which in turn will be important for designing strategies for their management.

An approach to induced pluripotency in Atlantic Salmon

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Keywords: Induced Pluripotency, Embryonic Development, Atlantic Salmon

Abstract: The most sought-after aspect of the induced Pluripotent Stem Cell (iPSC) research, regenerative medicine, may not be something for fish. However, other applications of iPSC like disease modelling, genetic engineering, and drug and toxicity testing are still significant. The lack of commercially available cell lines and information on the early development of the Atlantic Salmon compared to other model organisms make this research more challenging. Starting with a better understanding of the molecular mechanisms in embryonic development of the Atlantic Salmon, we wish to establish a method for iPSC culture for Atlantic Salmon.

As the initial step of the project, we have managed to establish a skin-fibroblast cell line and are currently characterizing it. Based on the knowledge we garnered from our work in early embryonic development, we will use this cell line for iPSC production using mRNA transfection. We believe it will be a valuable tool in furthering research in Salmonids. Especially in the understanding of host-pathogen interaction and how to prevent diseases.

Impacts of otter predation on adult Atlantic salmon (*Salmo salar*) in two rivers of Norway

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Keywords: radio-telemetry, Atlantic salmon, compensatory, additive, otter

Abstract: Atlantic salmon populations are declining throughout their distribution. Although predation may not be the proximate cause of declines, mammals that kill salmon in rivers before they spawn may have substantial impact on the breeder abundance, with consequences for effective population size. Predation can either occur prior to spawning and be additive or occur on post-spawners and be compensatory. Local concerns suggest otter predation inhibit recovery of some salmon populations by being additive. We tagged 45 adult Atlantic salmon in Aureelva 2020 and 30 salmon in Søre Vartdalselva 2021 with a radio transmitter/temperature logger package and tracked them September-January. Data were analysed to investigate whether predation was compensatory or additive. Otter predation was estimated by number of tags found on land and movement data, where the temperature logger provided date and time of predation. The findings will be crucial to addressing local human-wildlife conflicts around rivers where salmon are culturally and economically important and otters are protected as they continue to recover from overexploitation.

Inter and intraspecific variation in how anthropogenic impact correlates with near-shore fish movement

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Keywords: Multispecies, Fish Migration, Habitat Transitions, Ecological Niche, Fish Behaviour

Abstract: As anthropogenic impact continues to affect the aquatic world, fish movement is sensitive towards environmental changes, altering consumer nutrient energy distribution within food webs. The presented study is in its early stages to examine inter- and intraspecific variation in movement, behaviour, and temperature preferences of commercially important gadoid ((Atlantic cod (*Gadus morhua*), saithe (*Pollachius virens*)), and anadromous salmonid species (Arctic char (*Salvelinus alpinus*) and brown trout (*Salmo trutta*)). The aim is to understand how environmental stressors influence fish distribution in near-shore waters, early life habitat transitions, migration, and ecological niche, representing one of the first multispecies tracking studies in the Icelandic marine environment. The following question is addressed: Do environmental or anthropogenic drivers (temperature, sea cages, invasive species etc.) shape the distribution, and behaviour of these marine and anadromous fish species? Preliminary acoustic telemetry data on fish distribution in space and time with temperature and depth will be presented. The early results suggest species segregation by temperature and identify gadoid fish aggregations at sea-cages.

A mixed methods approach to understanding the diversity of chars (*Salvelinus* spp.) in the central Canadian Arctic

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Keywords: Arctic char, Dolly Varden, morphometrics, genetics, community-partnered research

Abstract: Arctic char (*Salvelinus alpinus*) are critically important for food security in the remote Canadian Arctic due to their abundance and availability for year-round harvest, and are vulnerable to climate-induced changes to aquatic ecosystems due to their life stage-specific dependency on multiple habitats. Despite their importance and vulnerability, the genetics, ecology, and demography of anadromous Arctic char are understudied, making it difficult to anticipate the effects of climate change on species persistence. Observations by subsistence fishers of physical variation in fish appearance, along with anecdotal scientific data, have suggested that the closely-related Dolly Varden (*S. malma*) may also be present in the central Arctic, hundreds of kilometers east of their purported range, as per the scientific literature. Using an 87K SNP array, morphometrics, meristics, and local knowledge, I am assessing the diversity of chars in multiple river systems across the Canadian Arctic. Preliminary results suggest that two rivers predominantly support Dolly Varden, with one also supporting Arctic char. Hybrid fish, while present, are exceedingly rare, suggesting that the two species retain largely distinct spawning times and/or habitats. Morphometric analyses show quantifiable variation in head shape and fin placement between fish that are genetically Arctic char and those that are genetically Dolly Varden, supporting the hypothesis that visual differences correlate with genetic variation on a species level. In collaboration with subsistence fishers, these data will help inform habitat restoration and management, thereby ensuring the viability of a critical subsistence fishery.

Local adaptation and demographic history shaped geographic patterns of Arctic charr after postglacial colonization in Iceland

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Keywords: Arctic charr, ddRADSeq, population genomics, demographic history, Iceland

Abstract: Understanding the contemporary geographic distribution of species with high intraspecific diversity requires a thorough investigation of genetic variations that reflect the interactions of historical process, local adaptation and selection. Arctic charr (*Salvelinus alpinus*) colonized Icelandic water systems following the retreat of the icecap around 10,000 years ago, and since then have diversified into multiple ecological forms. To explore how evolutionary forces and stochastic effects of demographic events have shaped the colonization pattern of Arctic charr in Iceland, we studied the genetic differentiation within and among charr occupying both sea-accessible and landlocked sites. By using ddRADSeq approach we genotyped 251 individuals from 18 sea-accessible sites (average sample size per location = 14) and 134 individuals from 6 landlocked sites in Iceland. Thirty four individuals from sites in Scotland and Greenland were also included for phylogenetic inference. Analyses of 17,946 single nucleotide polymorphisms (SNPs) reveal that Icelandic charr are genetically distinct from the Greenland and Scotland samples. While at finer spatial scales within Iceland, charr from sea-accessible sites had higher heterozygosity than from landlocked sites. Hierarchical genetic structures were observed for anadromous charr as neighboring hydrographic systems tend to harbor distinct populations grouped by regions. Compared with anadromous charr, landlocked charr were genetically highly differentiated, which may potentially due to high levels of genetic drift and/or historical bottlenecks. Demographic reconstruction identified evidence for reductions in effective population size shared by most of the anadromous populations during last glaciations, while more specific and stronger decline were observed for certain landlocked populations.