

# Combining 3D image analysis and omics science to better understand and foster the diversity of trout migration types

## Requérant principal UNIL

Claus Wedekind, Faculté de biologie et de médecine

## Requérant principal Université Laval

Louis Bernatchez, Faculté des sciences et génie

## Thématique

Use of 3D image analysis and omics science to better understand the diversity of trout (*salmo trutta*) migration types

## Activités

Analyzing fish through photography, 3D scanning and geometric morphometrics; tissue sampling; bioinformatic processing and analysis of data; organizing a workshop

## Descriptif

Conceptual background: Migration is a complex phenotype whose frequency and timing vary between and within populations. Migrating and non-migrating animals usually differ in behavior, morphology, and physiology. These differences need to be understood to better predict, for example, the demographic and evolutionary consequences of different management options. Many migration-related phenotypic traits seem to have genetic bases (Hess et al., 2016). Yet, this genetic control is often partial and migration appears to be plastic, i.e. dependent on environmental or social conditions. The interplay between the genetic background and epigenetic factors is still poorly understood.

In this project, using 3D image analysis and omics approaches, we will examine how gene expression and DNA methylation determine alternative migration morphotypes in a fish, the brown trout (*Salmo trutta*). This species is an excellent candidate to address this issue as it displays a remarkable diversity of migration strategies (Ferguson et al., 2019), is socio-economically and scientifically important in both Switzerland and Canada, and has become an important model in ecology and evolution.

Central role of digital technologies: Our project requires recognition of migration-related morphotypes via digital analysis of body shape and skin patterns and colorations, a technology that has considerable future application in the management of brown trout and other species with subtle morphotype variation. Identification of distinct morphotypes and subsequent classification of individuals will be conducted with multivariate geometric morphometrics of both 2D and 3D digital images, produced by the Wedekind group's 3D scanner (VR-5200 profilometer, Keyence International), and will require the use of high-dimensional data-analysis methods. This will then allow the development of machine learning algorithms for classification of fish based on images, for example, to aid species management and conservation.

High-throughput DNA sequencing technologies have made omics science (i.e., genomics, epigenomics, and transcriptomics) a big data discipline where large-scale molecular information can be obtained and compared between individuals. Such massive amount of (epi-)genomic data often necessitates the development of new tools and analysis pipelines. In our project, we will develop pipelines that allow us to

perform missing data imputation and generate pair-wise distance matrices calculated over millions of CpG sites to perform partial redundancy analyses.

Material and methods: (...) About 1000 of these 1+ brown trout will be studied morphometrically, and genotyping of tissue samples will be used to sex the fish and assign them to their half-sib families. Forty-eight individuals showing distinct migration-related morphotypes will then be selected from few half-sib families (to control for potential family effects). We will aim for a balanced sex ratio and include fish produced with cryopreserved and non-cryopreserved sperm. The sample size then allows testing for transcriptomic and epigenetic differences between up to 5 distinct migration-related morphotypes (Baerwald et al., 2016).

The use of transcriptomic methods will allow us to first assess gene expression differences between the migration strategies. If such differences are found, epigenomic methods will reveal whether they are driven by genetic or epigenetic changes.

### **Calendrier**

- Mid 2020 : analysis of 1000 fish and selection of 48 fish showing typical phenotypes
- Autumn/Winter 2020: sequencing and data processing
- Spring/Summer 2021: data analysis; UNIL PhD student to visit Laval lab
- Autumn 2021/Summer 2022: paper submitted for publication; organization of the workshop