

# NON-INVASIVE BIOMARKER DISCOVERY IN FARMED FISH SPECIES: A MULTIOMICS APPROACH

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## Introduction

Biomarkers offer valuable insights into the fish's nutritional, physiological, and health status, aiding in early detection of imbalances, distress, and diseases. Identifying robust biomarker signatures would support the development of innovative prediction tools and non-invasive biosensors, advancing precision veterinary medicine for animal disease susceptibility, diagnosis, and treatment response in smart farming. However, available biomarkers to profile the immune and welfare status of farmed animals are still limited and generally require invasive procedures.

## Theoretical Framework

### Task 1. Data collection for model input.

Data is continuously gathered from different trials done within the IGNITION project. Focusing on three different species: Atlantic salmon (*Salmo salar*), rainbow trout (*Oncorhynchus mykiss*), and European seabass (*Dicentrarchus labrax*), water, skin, and epidermic mucus samples are being collected to generate transcriptomic, proteomic, and microbiome data. The data will be analysed and gathered into a centralized database, which, besides the data generated by the IGNITION project, also contains open-source data.

### Task 2. Novel biomarker discovery and prediction model development.

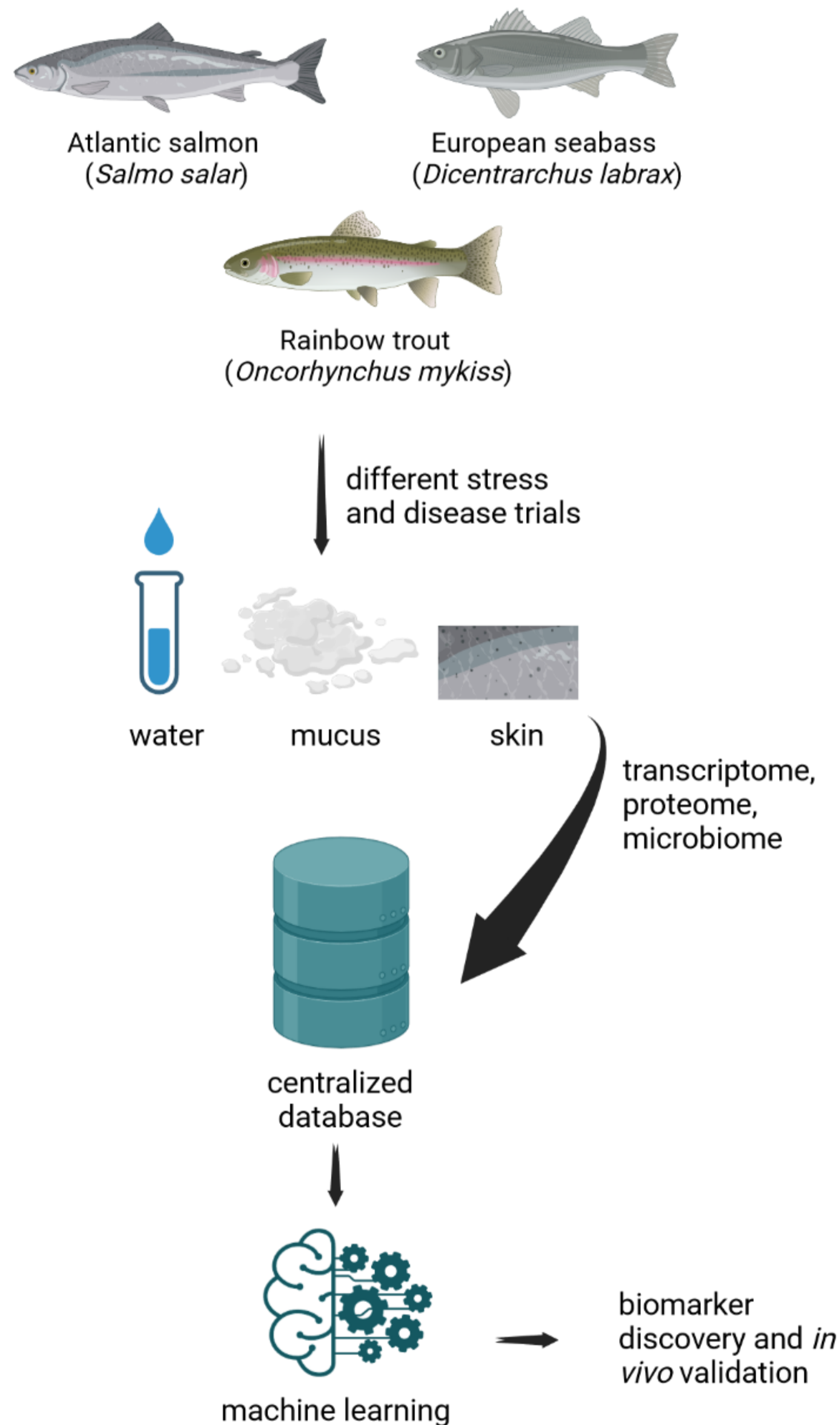
The collected data will be integrated using machine learning (ML) methods with the main goal of developing high-performance tools to predict disease resistance and animal robustness. Different machine learning techniques will be tested and stacked models will be potentially used to improve accuracy.

### Task 3. Field validation of biomarkers.

This task will validate the suitability of novel biomarkers from previous task in seabass, trout and salmon in collaboration with companies as partners in running projects. Trials will be carried out focusing on performance, health and survival.

## Aim

Discover and select biomarkers of stress and diseases among three target fish species. and perform validation trials for selected biomarkers under industrial conditions.



## Current Progress

Current focus is on transcriptomic data analysis and because the data is and will be generated from different institutions, to minimize the methodological variability, all transcriptomic data will be analyzed with the same pipeline. The quality of the raw data is assessed using the FASTQC (v0.12.1) and Multiqc (v1.19) and sequences trimmed using Cutadapt (v4.8) software. Transcripts are being quantified using the Nextflow nf-core/rnaseq (v3.14.0) pipeline for the mRNA gathered from the skin samples. The data is continuously being gathered into a centralized database.

## Acknowledgments

Work Co-funded by UKRI and by the European Union's Horizon Europe research and innovation programme (GA No. 101084651 - project IGNITION). TB received funds from FCT through grant 2023.04651.BDANA.

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Co-funded by the European Union

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