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Decoding ancient genomes: Genomics approaches and innovative species recognition pipeline for diadromous fish

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ABSTRACT

Understanding the evolution of wild species is crucial for developing effective population management strategies and predicting their future trajectories. In my doctoral research, we opted for genomics approaches to explore the demographic history of two iconic diadromous fishes: *Anguilla anguilla* (European eel) and *Salmo salar* (Atlantic salmon). We aim to elucidate their adaptive responses to environmental changes. Setting this project apart is the sequencing and genotyping of both archaeological (aDNA) and modern DNAs samples. Our study encompasses archaeological samples from various locations across Europe, spanning a temporal range of 17,000 years – from the Paleolithic to the modern era. To accurately assign species to each sample, we developed DeFiS (*Detect Fish Species*), a pipeline relying on reference genomes and samples to analyze k-mers: fixed-size nucleotide sub-strings. The list of k-mers and their occurrences from specific dictionaries for both reference genomes and samples. By comparing the dictionaries of the samples with those of the references, we could assign each sample to a specific species. We are currently validating the pipeline using freely available modern samples of all European diadromous fish species found in public databases (NCBI, Essembl, and scientific paper). The aim is to provide a valuable resource for biological scientists. Our method offers a significant advancement in the species identification process for aDNA research. By accelerating and refining this crucial step we aim to contribute to future aDNA-based investigations by facilitating the work of biologists studying wild species evolutions.

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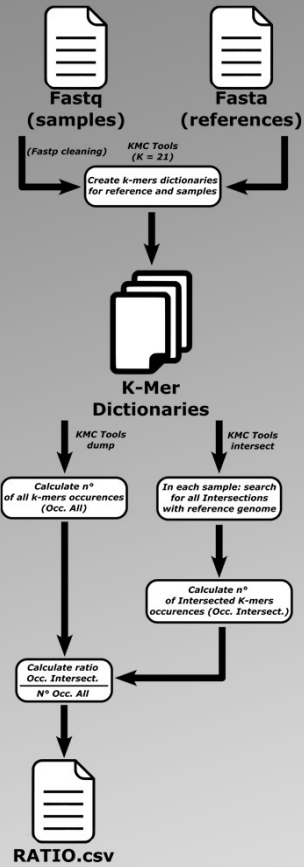
Patrick Jacques^{1*}, Sarah Maman^{2*}, Régis Debruyne³, Brice Ephrem⁴, Aurélie Manicki¹, Christophe Klopp⁵, Myriam Sternberg⁶, Gaston Rognon⁷, Léonard Ransan⁷, Chloé Bellanger⁷, Joelle Chat¹, Philippe Béarez³, Natacha Nikolic^{1,8}

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Introduction and study context

Understanding the evolution of wild species is crucial for developing effective population management strategies and predicting their future trajectories. Ancient DNA (aDNA), DNA collected from archeological samples, has the potential to serve as a window into the demographic history of species. But **Ancient DNA suffers from three major issues** : it is fragmented, degraded, and contaminated.

Taxonomic assignment of aDNA samples is thus a complex affair. To meet this challenge, we are developing **DeFiS**, a pipeline for aDNA taxonomic assignment based on **K-mers** : fixed-size nucleotide sub-strings.



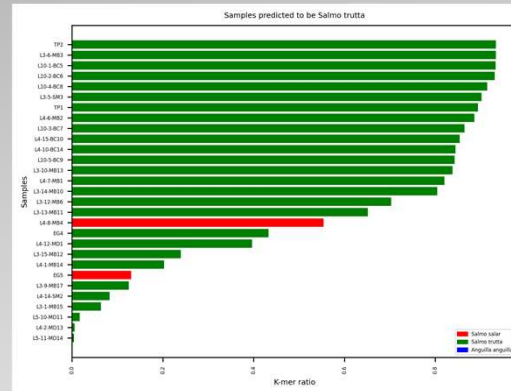
Method

A dictionary is a list of **k-mers occurrences** found in a genome. We can link a reference genome to our sample thanks to the **DeFiS pipeline** which can determine samples' species with a **k-mers ratio**:

$$\frac{Nb_{Occ} \text{ Kmers Intersect}^\circ}{Nb_{Occ} \text{ Kmers total}}$$

The highest ratio shows the sample' species.

At the end, the tool will enable the **determination of the taxonomy** of an ancient or modern DNA sequence by comparing it with the dictionary of reference databases



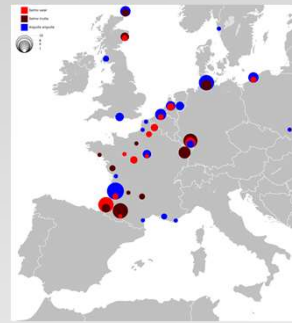
Results

Our method offers a significant advancement in the species identification process for aDNA research on **diadromous fishes**. By accelerating and refining this crucial step we aim to contribute to future aDNA-based investigations by facilitating the work of biologists studying wild species evolutions.

We are currently validating the pipeline using freely available modern samples of all European diadromous fish species found in public databases (NCBI, Essembl, and scientific paper). The aim is to provide a **valuable resource for biological scientists**.

On left: one example of results regarding the identification of presumed diadromous fish species by archeoichthyologists, such as Atlantic salmon, brown trout, or European eel.

Our results first demonstrate that archeoichthyologists make few errors, and secondly, that we assign the species correctly for the majority of samples.



Map of samples used to test the pipeline on aDNA.

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