# DeFIS - Detection pipeline with k-mers analysis to identify species

Sarah Maman, Gaston Rognon, Chloé Bellanger, Léonard Ransan, Patrick Jacques, Christophe Klopp, Régis Debruyne, Brice Ephrem, Myriam Sternberg, Aurélie Manicki, et al.

# DEFIS - DETECTION PIPELINE WITH K-MERS ANALYSIS TO IDENTIFY SPECIES.

DeFIS « Detection of Fauna and flora: Identification of Species ».

## CONTEXT

- DNA highly degraded.
- Quick identification focuses on repeated zones.
- Conventional mapping tools inadequate.

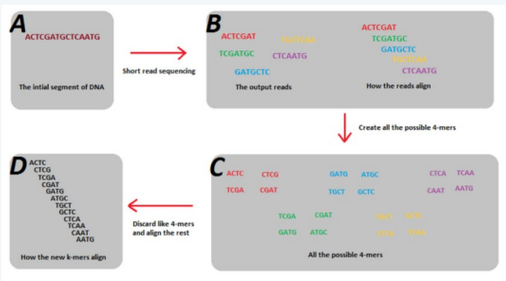
For:

- Modern and ancient DNA.
- Tested on several species and on genomes of different sizes.

## K-MERS DEFINITION

A k-mer is a subsequence of length k nucleotides extracted from a longer sequence.

Source: https://en.wikipedia.org/wiki/K-mer




## DETECTION PIPELINE PRINCIPE

Identifies species by comparing k-mers dictionaries between:

- a chosen reference genome,
- and the studied samples.

## PIPELINE STEPS & RESULTS

This pipeline includes :

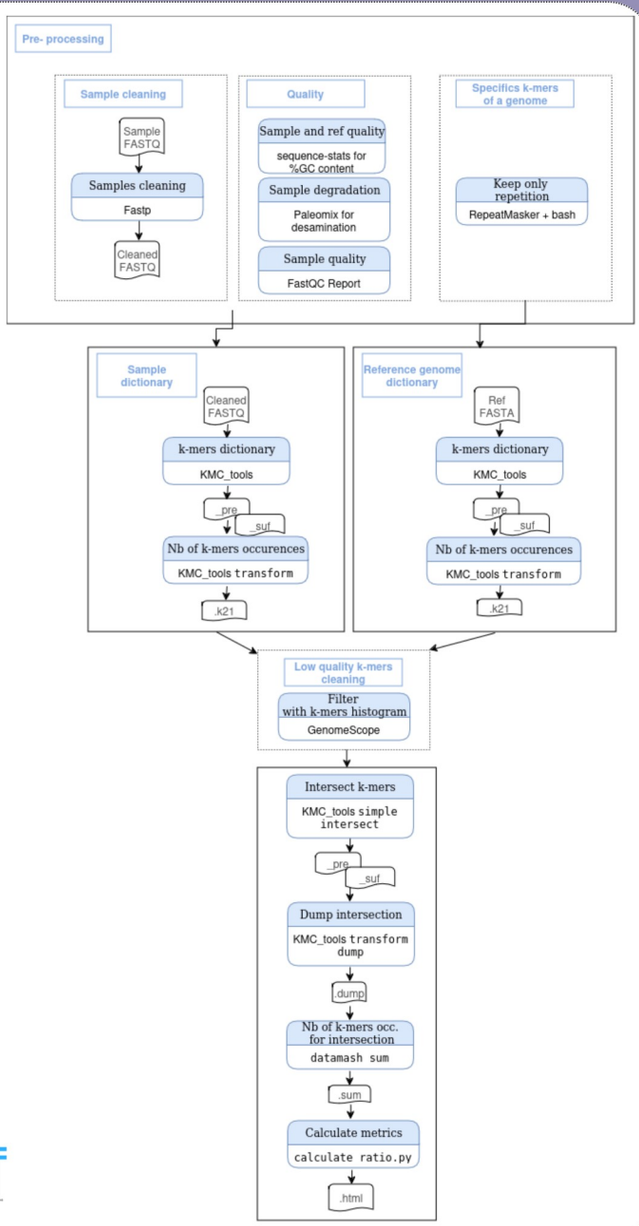
- Pre-process to clean and analyse quality as %GC content or degradation.
- KMC_tools [1] to generate k-mers dictionaries for reference genome(s) ans sample(s).
- Intersect these dictionaries.
- Calculate metrics as Jaccard similarity/dissimilarity indices [2], ratio.
- Determine the closest species.
- HTML report to display results.

This pipeline is being improved to save processing time and computing resources:

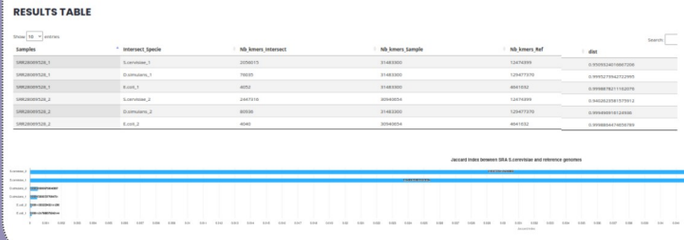
- Study the works of Camila Duitama (akmerbroom & decom) [3] [4]
- To minimize dictionaries sizes: filter out low-quality k-mers, erroneous k-mers.
- To focus on repeated zone:
  - Specific of a genome.
  - Provide an indication of resistance to DNA degradation.
  - Provide some precomputed sets of k-mers.

This potential impact of repeated zones is being studied by comparing small dictionaries, representing those most commonly found within a species.

This pipeline has already been employed with success to taxonomically identify fish archaeological remains, the oldest ones dating from the paleolithic period [5].




**RESULTS TABLE**



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