Development of a QIIME2-Based Pipeline for Phylogenetic Placement of COI-5P Sequences Using Hidden Markov Models and Reference Trees

J.D.M. Wesseling
Onder begeleiding van: Dr. R.A. Vos

Naturalis Biodiversity Center

Radboud Universiteit

Introduction

- Overview of biodiversity assessment and the role of metabarcoding.

- QIIME2 and value of integrating reference trees

- Aim: Integrating external phylogenetic reference trees into QIIME 2 for improved PD metrics.

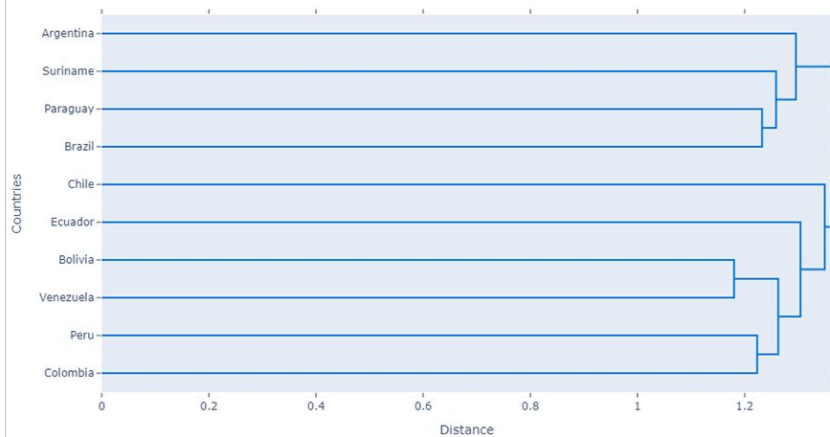# Suggested workflow

- Demultiplexing and denoising
  - QIIME2
- Create reference database
  - BOLD
  - BLAST
- Alignment
  - HMMer
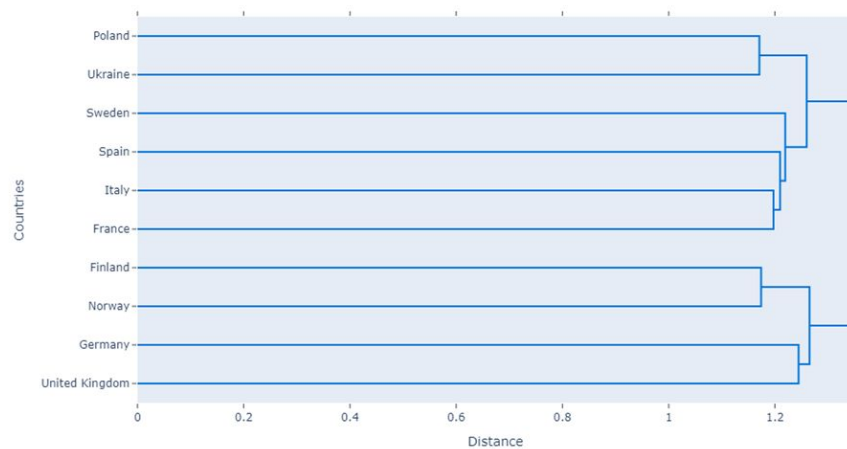- Phylogenetic placement
  - RAxML
  - pplacer
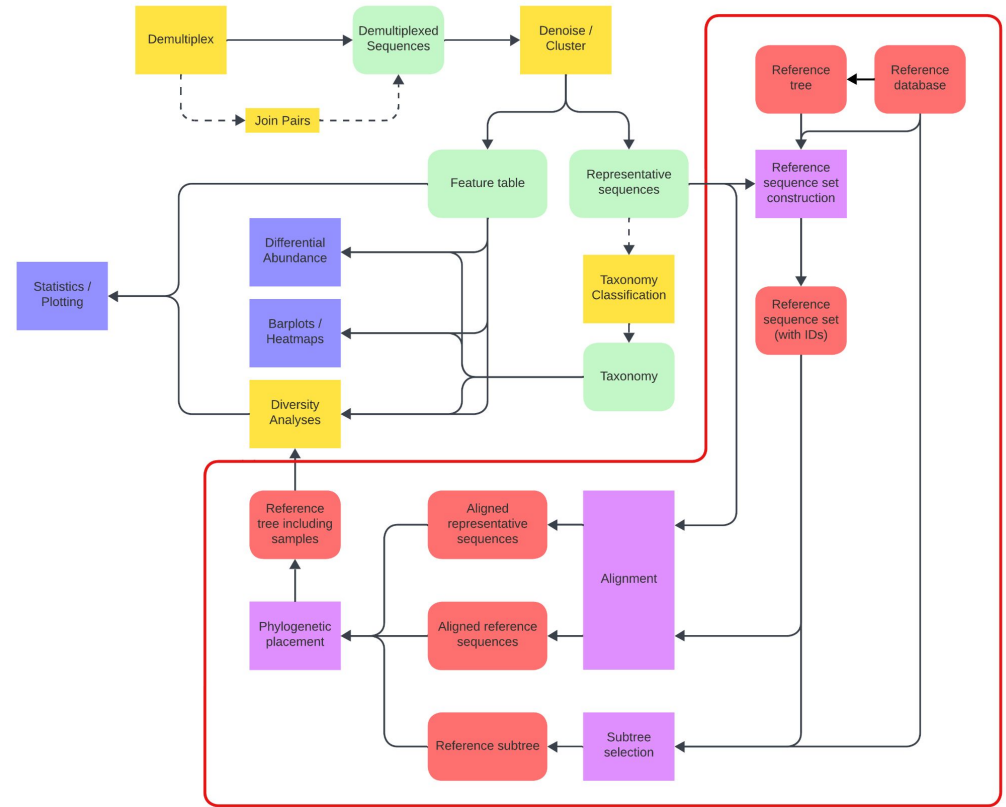
Results

- A reference tree with grafted samples

- PD metrics obtained from this tree

- Geographical sample
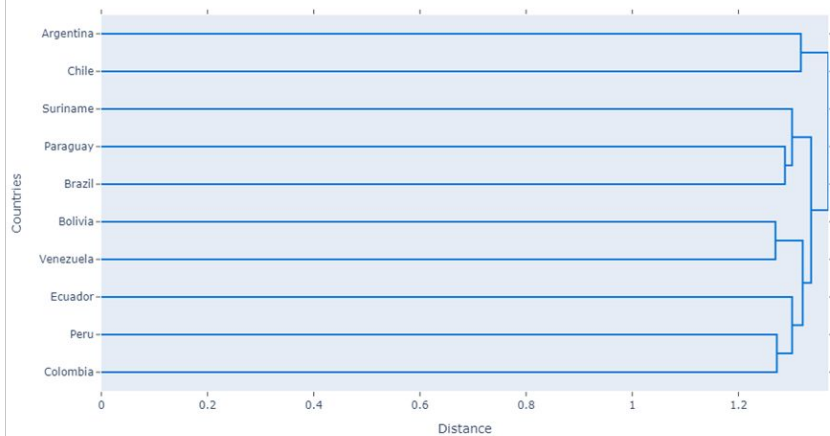 - South America
  - Europe

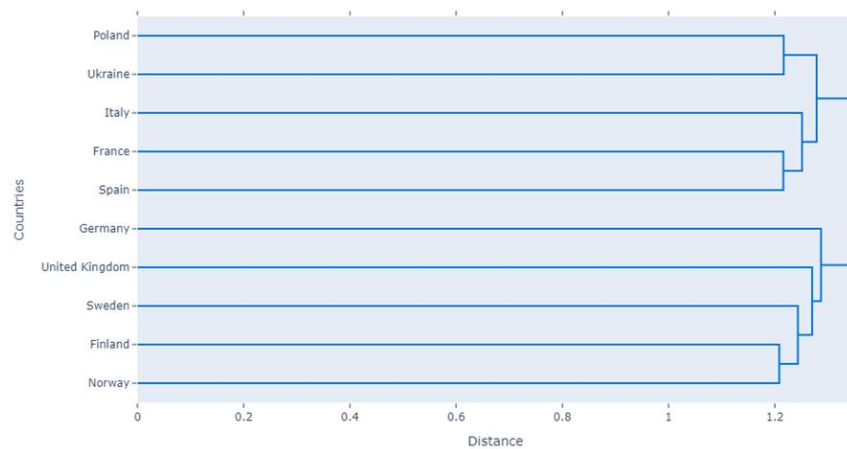**A** Dendrogram of unweighted UniFrac distance matrix (SA de novo tree)

B Dendrogram of unweighted UniFrac distance matrix (EU de novo tree)

C Dendrogram of unweighted UniFrac distance matrix (SA grafted on reference tree)

D Dendrogram of unweighted UniFrac distance matrix (EU grafted on reference tree)

Discussion & future goals

- Need for benchmarking different alignment and placement tools for use with larger datasets

- Future development: Streamlining workflow for easier integration in biodiversity studies.

- Expanding beyond COI-5P to other barcode markers for broader applicability.