

# Applications and pitfalls of multilocus amplicon sequencing with Oxford Nanopore technology

Martin Kapun / NHMW

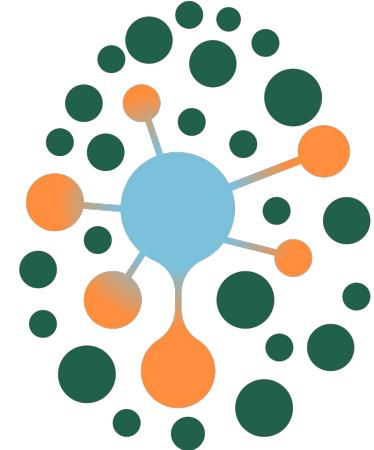
Sonja Steindl / NHMW

Astra Bertelli / UniPV, NHMW

NOBIS Meeting, Vienna, 28/11/2024



Disclaimer: Funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Research Executive Agency (REA). Neither the European Union nor the granting authority can be held responsible for them.



TETTRIs

nhm  
  
naturhistorisches museum wien

Wien 2024  
 NOBIS 18 AUSTRIA

# Welcome & Important Info

Duration: 13:00 - 16:00

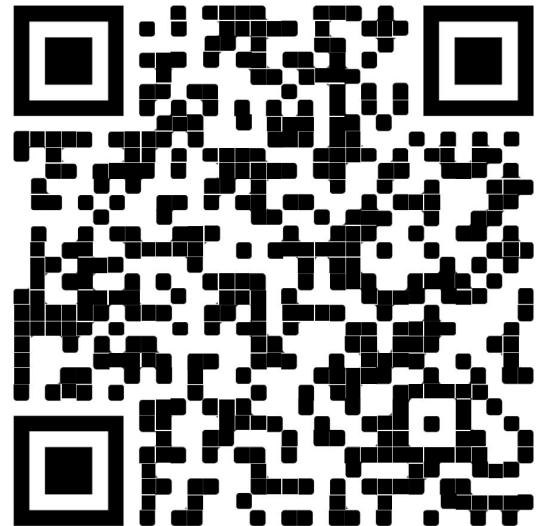
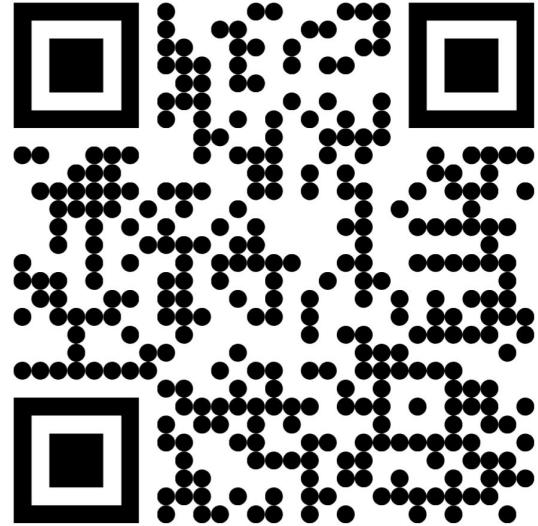
Wifi: NHM-Wien / KapLan

Password: jY5ixSuZnG / setudaki2664

Github repos:

<https://github.com/nhmvienna/AmpliPiper>

[https://github.com/nhmvienna/AmpliPiper\\_Workshop\\_2024](https://github.com/nhmvienna/AmpliPiper_Workshop_2024)



# Agenda of the day

**1h Part I - AmpliPiper:** Concepts and Modules

15' break

**45' Part II - Hands on:** Installation & data preparation

15' break

**45' Part III - Hands on II:** Advanced datasets, Limitations and Benchmarking

# Team NHMW

## Team: Collection



Helge  
Heimburg  
(LM Kärnten)



Nikola  
Szucsich



Oliver  
Macek

collecting; preserving;  
identification; ABOL  
database

# Team NHMW

## Team: Collection



Helge  
Heimburg  
(LM Kärnten)



Nikola  
Szucsich



Oliver  
Macek

collecting; preserving;  
identification; ABOL  
database

## Team: Laboratory



Luise  
Krucken-  
hauser



Paula  
Schwahofer



Sandra  
Kirchner



Elisabeth  
Haring



Johannes  
Süß

DNA-extraction; QC;  
PCR; sequencing

# Team NHMW

## Team: Collection



Helge  
Heimburg  
(LM Kärnten)



Nikola  
Szucsich



Oliver  
Macek

collecting; preserving;  
identification; ABOL  
database

## Team: Laboratory



Luise  
Krucken-  
hauser



Paula  
Schwahofer



Astra  
Bertelli  
(Uni Pavia)



Sandra  
Kirchner



Elisabeth  
Haring



Johannes  
Süß

DNA-extraction; QC;  
PCR; sequencing

## Team: Bioinformatics



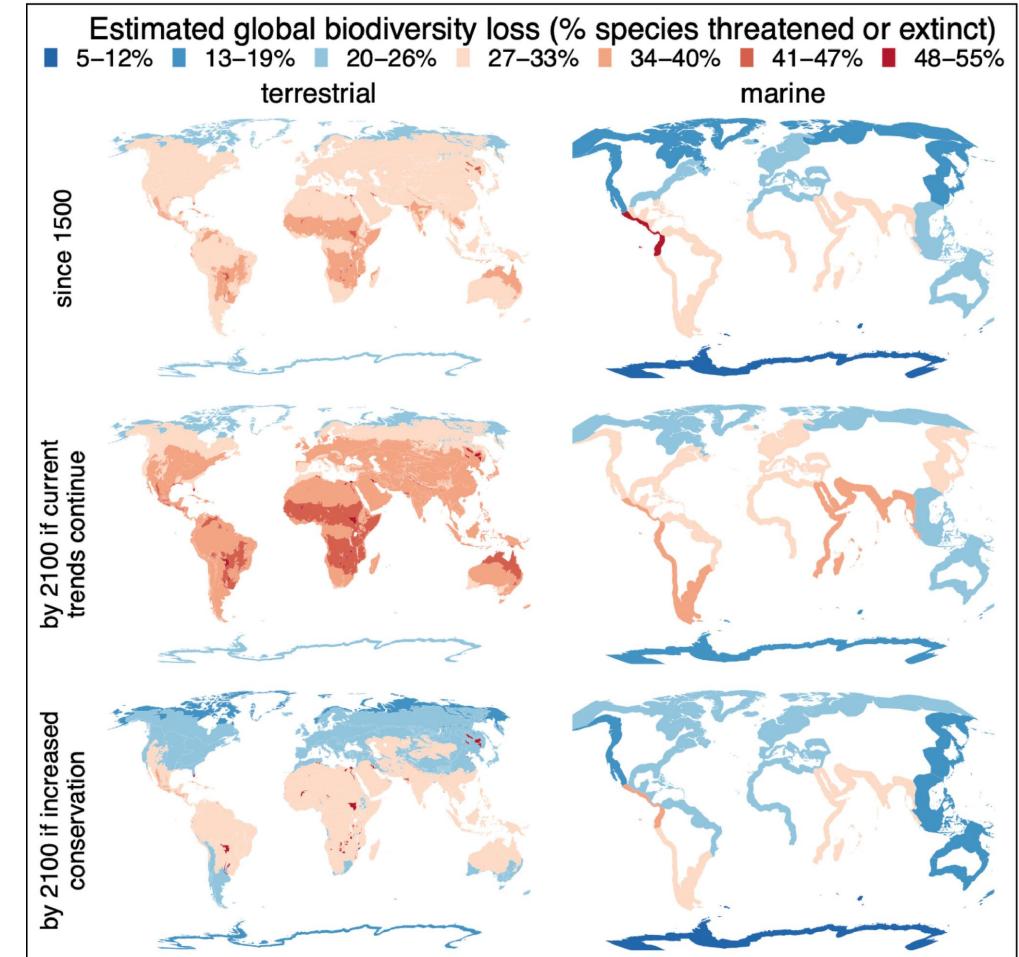
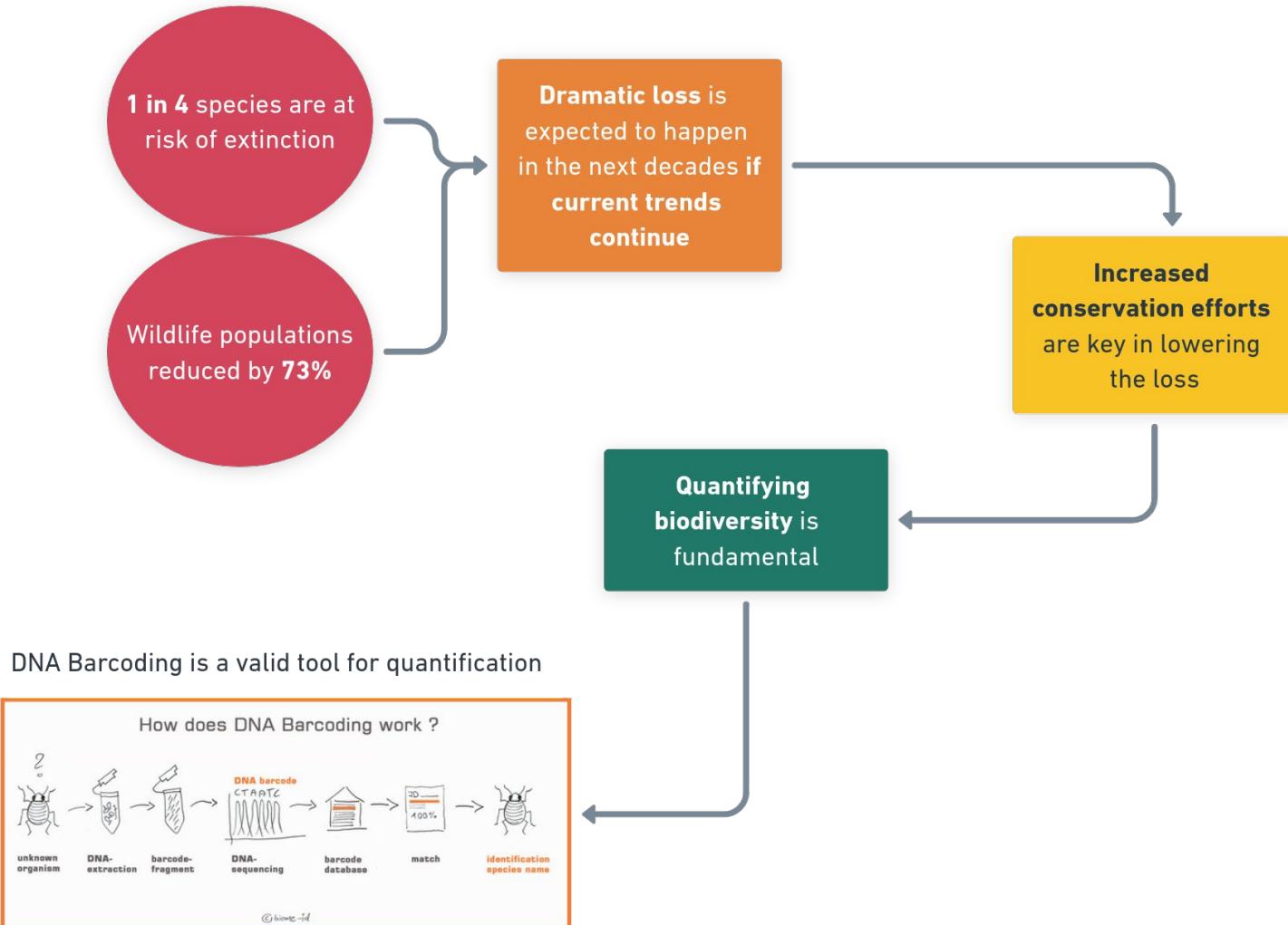
Sonja  
Steindl



Martin  
Kapun

basecalling; QC;  
Pipeline development

# Addressing the biodiversity crisis



Firest, I., et al. (2023) *Front Ecol Environ*

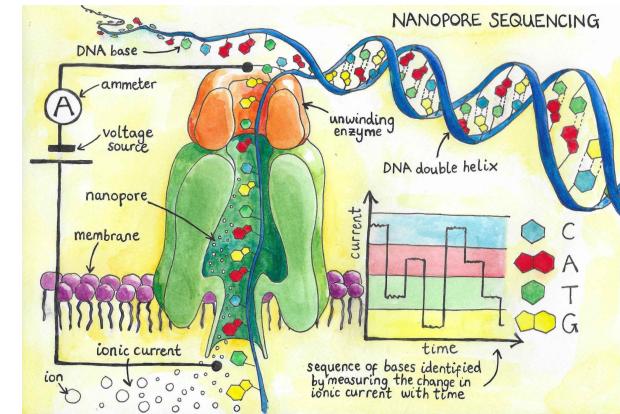
# From single to multilocus barcoding

Most barcoding approaches based on **single loci** (COI, ITS, etc.) with primers that **amplify a broad set of taxa**

- + **Well-established protocols mostly for haploid (mt) markers**
- + **Many databases** built for these markers (BOLD, etc.)
- **Detection of hybridization** not possible
- **Incomplete lineage sorting** may confound species delineation
- single gene trees often do not reflect the **genealogy of species**
- **Missing scalability** with classic SANGER sequencing

# ONT sequencing

- + allows **In-house sequencing**
- + Relatively **easy-to-use NGS technology**
- + **Cost-efficient** even with low sample throughput
- + **Fragment size of amplicons is not limited**
- + Growing set of **well-curated bioinformatic tools**
- **Error-prone**
- **Bioinformatics skills necessary**



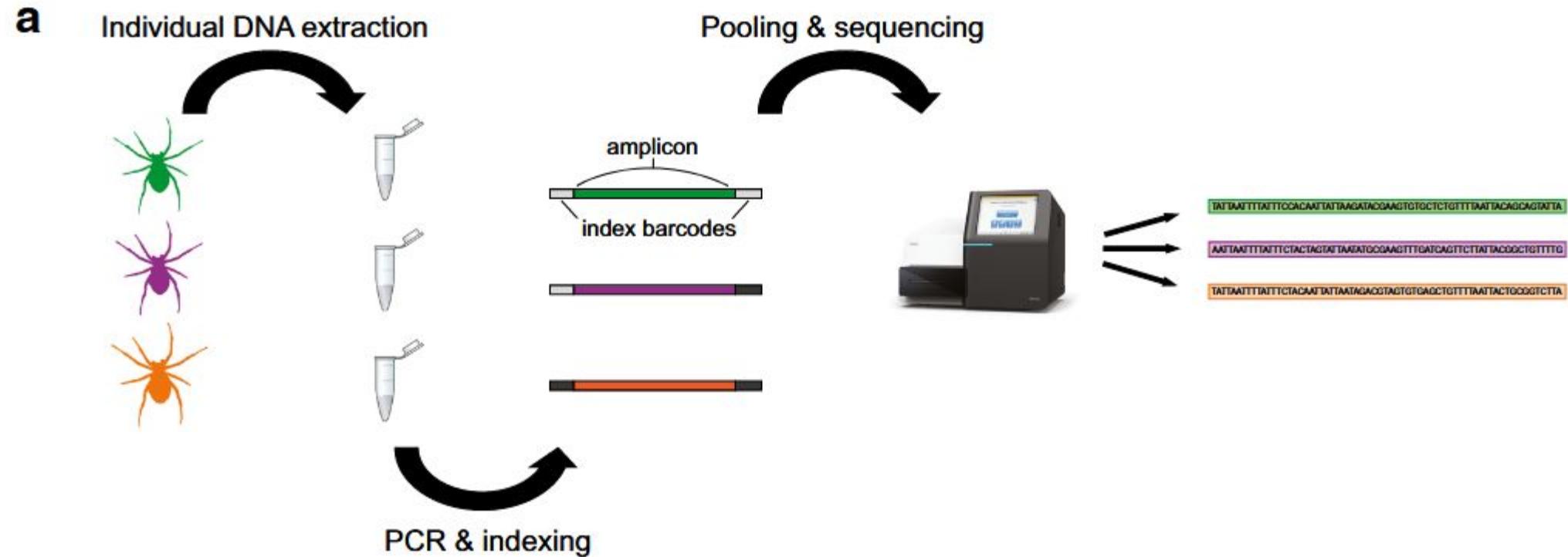
<https://oxsci.org/pore-over-these-advances-in-dna-sequencing/>



# Multilocus DNA barcoding with NGS technology

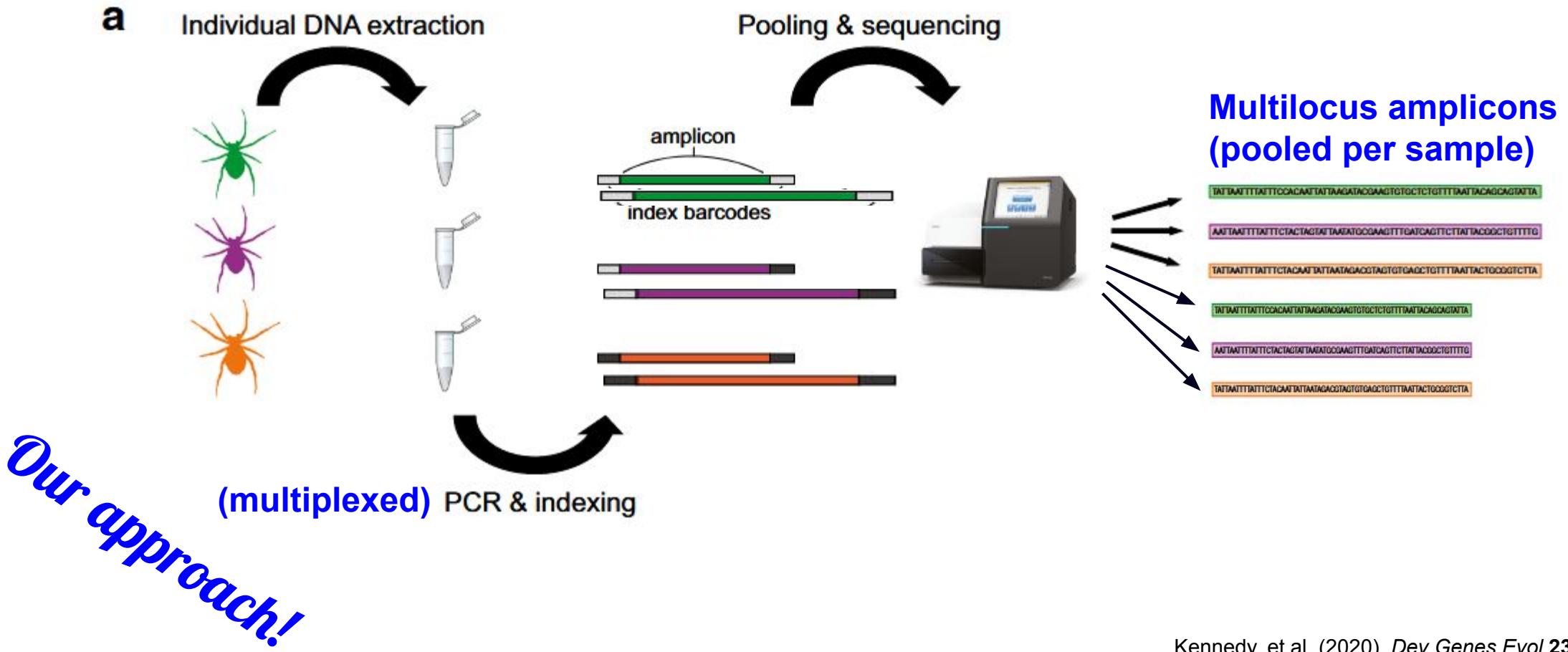
- + **Multiple** mitochondrial and nuclear **loci** can be jointly analyzed
- + Obtain information of **haplotypes** for di- and polyploid specimens
- + **Number** of examined specimens is **well scalable**
- + Compatibility and extensibility of available **databases** (BOLD, GenBank, etc.)
- + Benefit from **genomic resources**, e.g. BUSCO (Benchmarking Universal Single-Copy Orthologs)  
genes
- **High error rates**
- **Multiple Marker genes not (yet) well established**
- **not clear if single-copy**
- Pools of reads need to be **demultiplexed**

# From single locus pooled amplicon sequencing...



Kennedy, et al. (2020). *Dev Genes Evol* 230: 185–201.

# ... to multilocus pooled amplicon sequencing



Kennedy, et al. (2020). *Dev Genes Evol* 230: 185–201.

# Our Aim

- A simple yet powerful **combination of wet lab and bioinformatics protocols**
- Cost-efficiency through **multiplexed PCRs and pooled sequencing**
- **Easy-to-use bioinformatics pipeline** for
  - Demultiplexing of loci
  - Consensus sequence reconstruction
  - Species identification with BOLD
  - Basic Phylogenetic Analyses
  - (Species delimitation with ASAP)
  - Comprehensive and detailed logging, documentation and output
- **Use Case - hover flies (Syrphidae)**

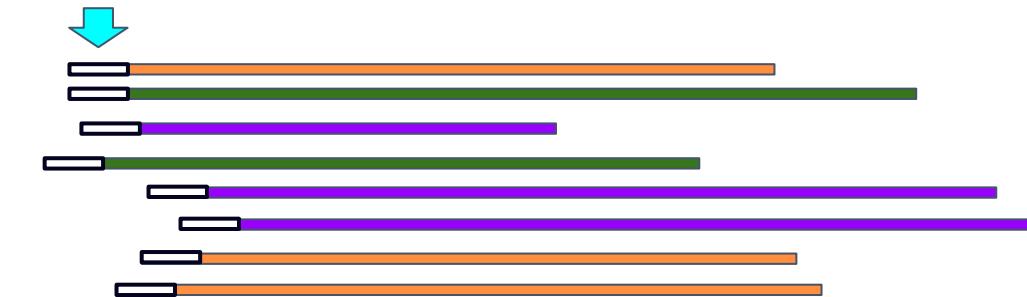
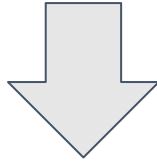
# AmpliPiper

- **Open Source**
- **Simple installation** of dependencies
- **Simple input file formats**
- **Comprehensive documentation**
- **Computational efficiency**
- **Versatile analyses**
- **Verbose logging**
- **Comprehensive output**

# Part I - AmpliPiper

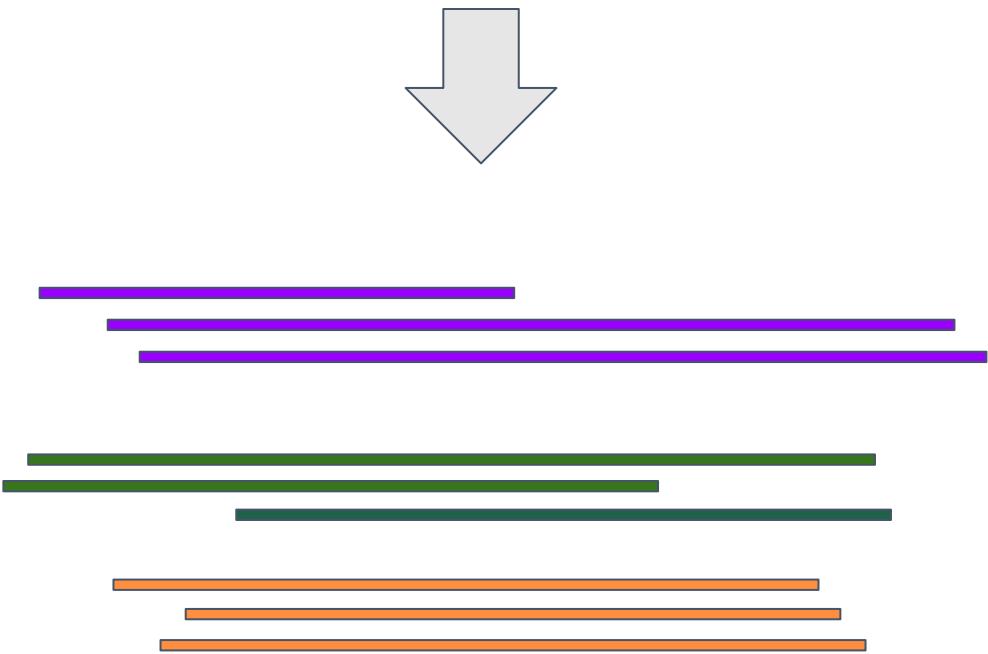
# Preparation of input NGS data

Raw multiplexed ONT sequencing data  
(tagged with ONT barcodes)



Basecalling with *GUPPY* (v.6.2.1 GPU)

- Super high accuracy mode (SUP)
- Demultiplexing by barcode (EXP-PBC096)
- Gzip compression of all files



# Preparation of input NGS data - [samples.csv](#)

## [samples.csv](#)

- **Comma-separated** file format
- Contains
  - sample **IDs**
  - paths to **demultiplexed gzipped** FASTQ files
- **One sample per line**
- **May contain header “ID,PATH”**

```
ID,PATH  
SAMPLE1,/PATH/TO/SAMPLE1.fastq.gz  
SAMPLE2,/PATH/TO/SAMPLE2.fastq.gz
```

# Preparation of input NGS data - primers.csv

## primers.csv

- **Comma-separated** file format
- Contains
  - primer **IDs**,
  - **fwd** and **rev** primer **sequences**
  - Expected **ploidy**
  - Expected **fragment size**
- **One sample per line**
- **May contain header**

```
ID,FWD,REV,SIZE  
Locus1,AGAGGA,GTATTAGA,650  
Locus2,AGTATT,GAGGAA,800
```

# Preparing AmpliPiper

## Requirements:

- **Linux** ( tested on CentOS, Ubuntu)
- **(Ana)Conda and Mamba** installed and in path
- ***setup.sh*** will install all dependencies when the pipeline is started the first time.

# Running AmpliPiper

## Minimal commandline:

```
AmpliPiper.sh \
--samples /path/to/samples.csv \
--primers /path/to/primers.csv \
--output /path/to/output-folder
```

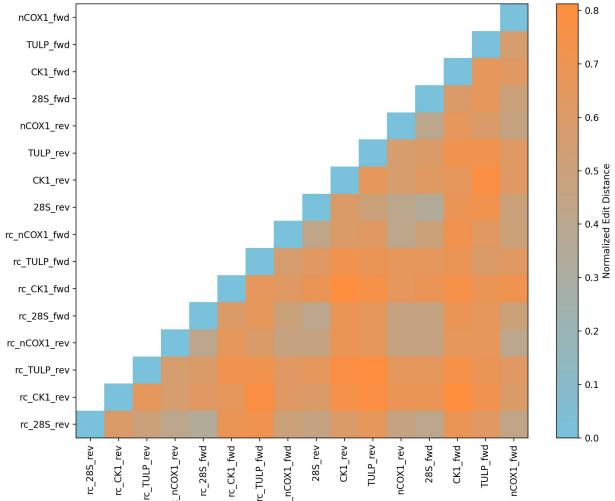
# AmpliPiper - optional arguments

## Optional Arguments

- `-b` or `--blast` : Enable BLAST search for species identification. When setting this parameter, you need to provide an email address (e.g., `--blast your@email.com`) for using NCBI entrez to retrieve taxonomic information for the BLAST hits (default: disabled).
- `-c` or `--similar_consensus` : Change the minimum similarity threshold (in percent) of amplicon\_sorter. If the similarity of two clusters are smaller or equal to the threshold, they are considered separately otherwise they are collapsed prior to consensus reconstruction (default: 96)
- `-e` or `--exclude` : Provide a text file with samples and loci to exclude from the analysis. Each row should contain the ID of a sample to be excluded. Names need to be identical to the IDs in `samples.csv`
- `-f` or `--force` : Force overwrite the output folder if it already exists (default: cowardly refusing to overwrite).
- `-i` or `--partition` : Use partition model for iqtree with combined dataset. △ may take very long △ (default: disabled)
- `-k` or `--kthreshold` : Define the threshold  $k$  for the maximum allowed proportion of mismatches for primer alignment during demultiplexing (default: 0.05).
- `-m` or `--minreads` : Set the minimum number of reads required for consensus sequence reconstruction (default: 100).
- `-n` or `--nreads` : Provide the absolute number or percentage of top-quality reads to consider for consensus sequence generation and variant calling (default: 500).
- `-q` or `--quality` : Specify the minimum PHRED quality score for read filtering (default: 10).
- `-r` or `--sizerange` : Define the allowed size buffer in basepairs around the expected locus length (default: 100).
- `-t` or `--threads` : Specify the number of threads to be used for parallel processing (default: 10).
- `-w` or `--nowatermark` : Remove the watermark from the tree figures
- `-y` or `--freqthreshold` : Retain consensus sequences for further analyses which are supported by raw reads, whose frequency in the total pool of reads is larger or equal to this threshold (default: 0.1).

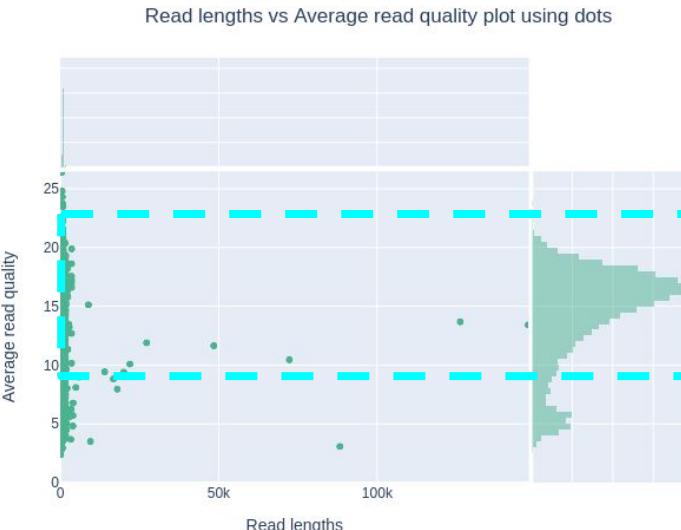
# Running AmpliPiper

Testing sequence  
similarity among primers



Custom python script  
edlib distances

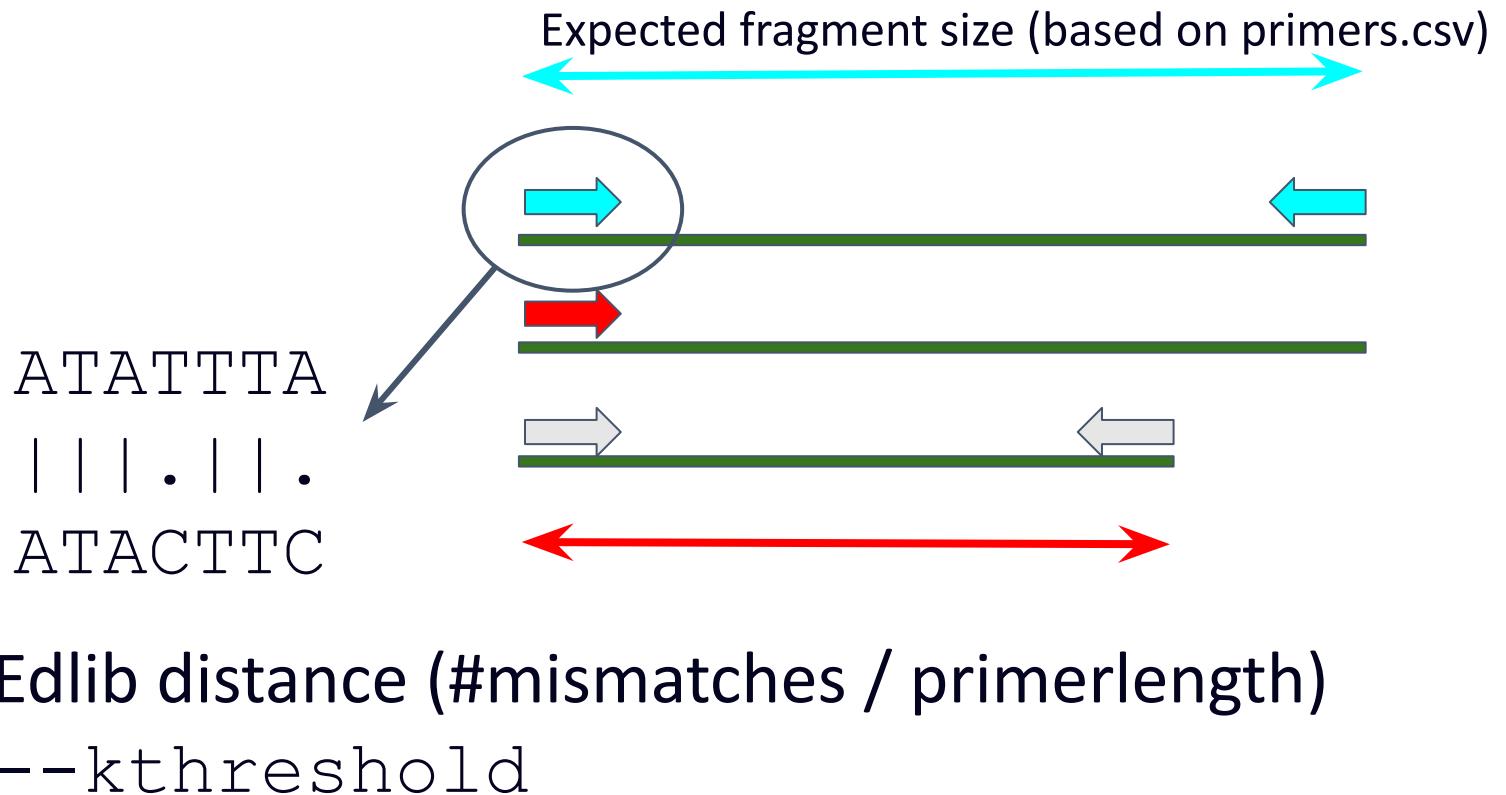
Filtering raw FASTQ by  
min PHRED quality



Chopper  
--quality 10

# Running AmpliPiper

## Demultiplexing by locus (custom script)



Locus 1 / sample 1

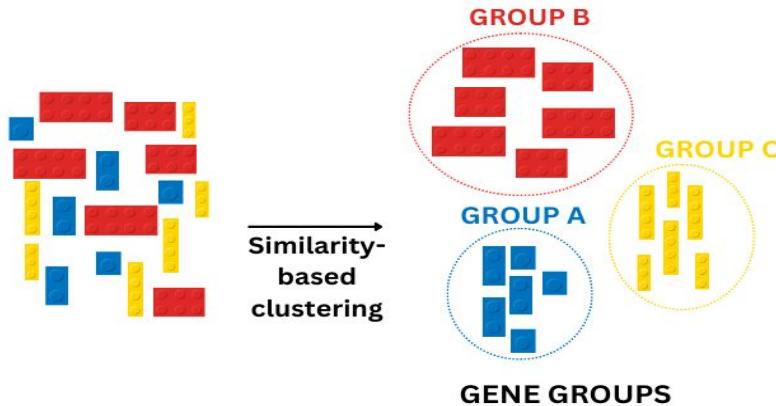
Locus 1 / sample 2

Locus 2 / sample 1

Locus 2 / sample 2

# Running AmpliPiper

## Consensus sequence reconstruction (amplicon\_sorter)

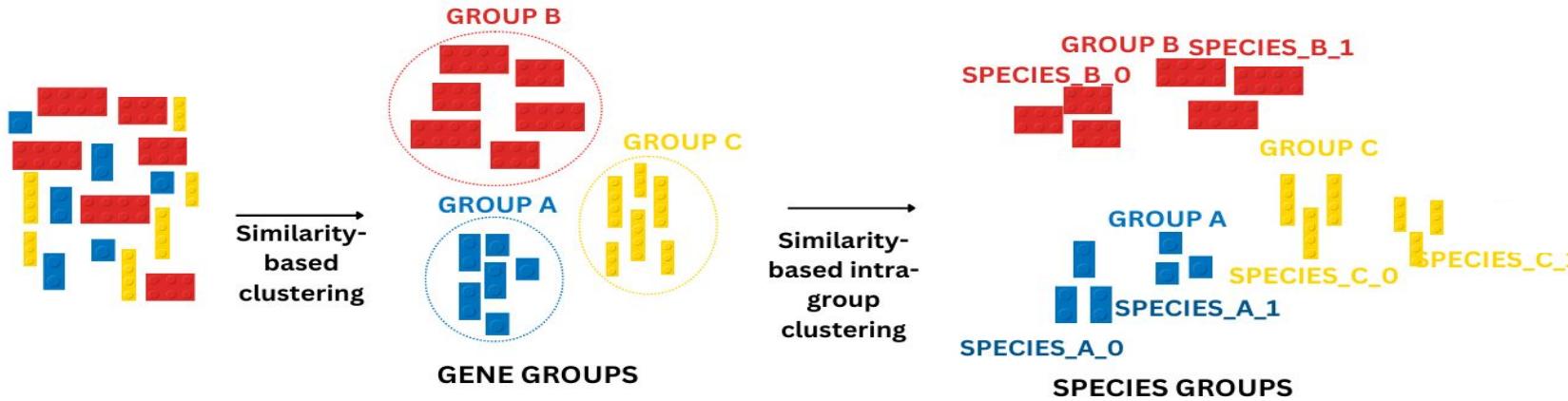


### AmpliconSorter

- Step 1: Similarity-based clustering (group your legos by color)

# Running AmpliPiper

## Consensus sequence reconstruction (amplicon\_sorter)

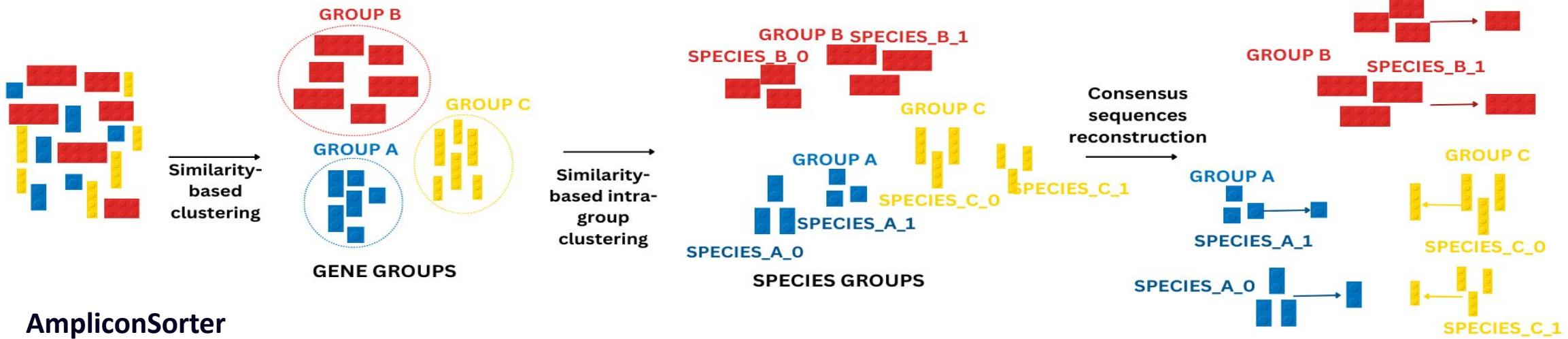


### AmpliconSorter

- Step 1: Similarity-based clustering (group your legos by color)
- Step 2: Similarity-based intra-group clustering (group same-color legos by size)

# Running AmpliPiper

## Consensus sequence reconstruction (amplicon\_sorter)

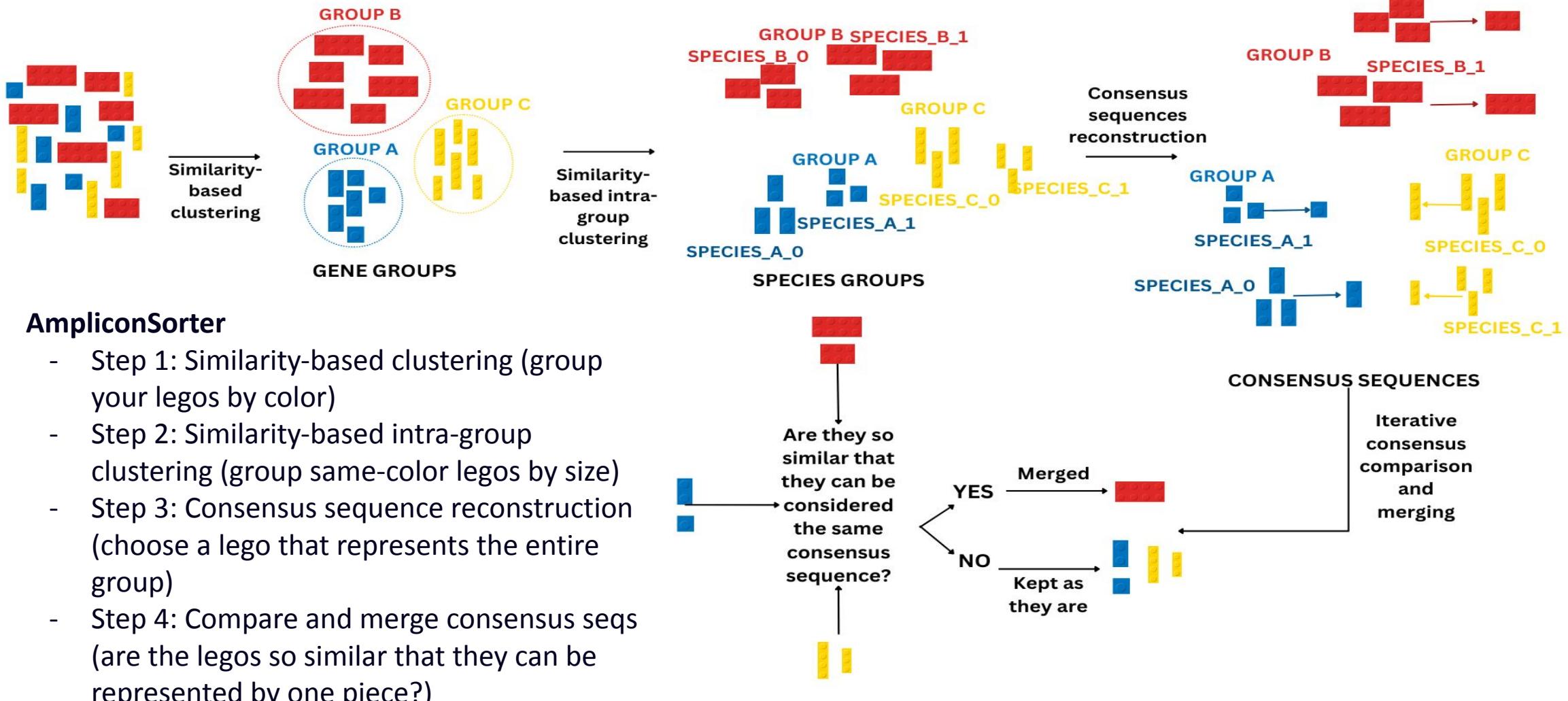


### AmpliconSorter

- Step 1: Similarity-based clustering (group your legos by color)
- Step 2: Similarity-based intra-group clustering (group same-color legos by size)
- Step 3: Consensus sequence reconstruction (choose a lego that represents the entire group)

# Running AmpliPiper

## Consensus sequence reconstruction (amplicon\_sorter)



# Running AmpliPiper

Modeling Ploidy ([custom script](#))

**Observed:**

Hap1: **264** reads -> 26%

Hap2: **734** reads -> 74%

# Running AmpliPiper

## Modeling Ploidy ([custom script](#))

### Observed:

Hap1: **264** reads -> 26%  
Hap2: **734** reads -> 74%

### Expectations:

```
TEST = {2:  
    {1: [np.array([0.0, 1.0])],  
     2: [np.array([1/2, 1/2])],  
     3: [np.array([1/3, 2/3])],  
     4: [np.array([1/2, 1/2]), np.array([1/4, 3/4])]},  
 3:  
    {1: [np.array([0.0, 0.0, 1.0])],  
     2: [np.array([0.0, 1/2, 1/2])],  
     3: [np.array([1/3, 1/3, 1/3])],  
     4: [np.array([1/4, 1/4, 1/2])]},  
 4: {1: [np.array([0.0, 0.0, 0.0, 1.0])],  
     2: [np.array([0.0, 0.0, 1/2, 1/2])],  
     3: [np.array([0, 1/3, 1/3, 1/3])],  
     4: [np.array([1/4, 1/4, 1/4, 1/4])]}}
```

# Running AmpliPiper

## Modeling Ploidy (custom script)

### Observed:

Hap1: 264 reads -> 26%

Hap2: 734 reads -> 74%

$$P(X = x) = \frac{n!}{x_1!x_2!\dots x_k!} \cdot p_1^{x_1} \cdot p_2^{x_2} \cdot \dots \cdot p_k^{x_k}$$

### Expectations:

```
TEST = {2:  
    {1: [np.array([0.0, 1.0])],  
     2: [np.array([1/2, 1/2])],  
     3: [np.array([1/3, 2/3])],  
     4: [np.array([1/2, 1/2]), np.array([1/4, 3/4])]},  
  3:  
    {1: [np.array([0.0, 0.0, 1.0])],  
     2: [np.array([0.0, 1/2, 1/2])],  
     3: [np.array([1/3, 1/3, 1/3])],  
     4: [np.array([1/4, 1/4, 1/2])]},  
  4: {1: [np.array([0.0, 0.0, 0.0, 1.0])],  
     2: [np.array([0.0, 0.0, 1/2, 1/2])],  
     3: [np.array([0, 1/3, 1/3, 1/3])],  
     4: [np.array([1/4, 1/4, 1/4, 1/4])]}}
```

# Running AmpliPiper

## Modeling Ploidy (custom script)

### Observed:

Hap1: 264 reads -> 26%

Hap2: 734 reads -> 74%

Ploidy	Expectation	Likelihood
2	[0.5, 0.5]	2.7E-52
3	[0.33, 0.66]	4.5E-07
4	[0.5, 0.5]	2.7E-52
4	[0.25, 0.75]	0.016

$$P(X = x) = \frac{n!}{x_1!x_2!...x_k!} \cdot p_1^{x_1} \cdot p_2^{x_2} \cdot \dots \cdot p_k^{x_k}$$

### Expectations:

```
TEST = {2:  
    {1: [np.array([0.0, 1.0])],  
     2: [np.array([1/2, 1/2])],  
     3: [np.array([1/3, 2/3])],  
     4: [np.array([1/2, 1/2]), np.array([1/4, 3/4])]},  
3:  
    {1: [np.array([0.0, 0.0, 1.0])],  
     2: [np.array([0.0, 1/2, 1/2])],  
     3: [np.array([1/3, 1/3, 1/3])],  
     4: [np.array([1/4, 1/4, 1/2])]},  
4: {1: [np.array([0.0, 0.0, 0.0, 1.0])],  
    2: [np.array([0.0, 0.0, 1/2, 1/2])],  
    3: [np.array([0, 1/3, 1/3, 1/3])],  
    4: [np.array([1/4, 1/4, 1/4, 1/4])]}}
```

# Running AmpliPiper

## Modeling Ploidy (custom script)

### Observed:

Hap1: 264 reads -> 26%

Hap2: 734 reads -> 74%

Ploidy	Expectation	Likelihood
2	[0.5, 0.5]	2.7E-52
3	[0.33, 0.66]	4.5E-07
4	[0.5, 0.5]	2.7E-52
4	[0.25, 0.75]	0.016

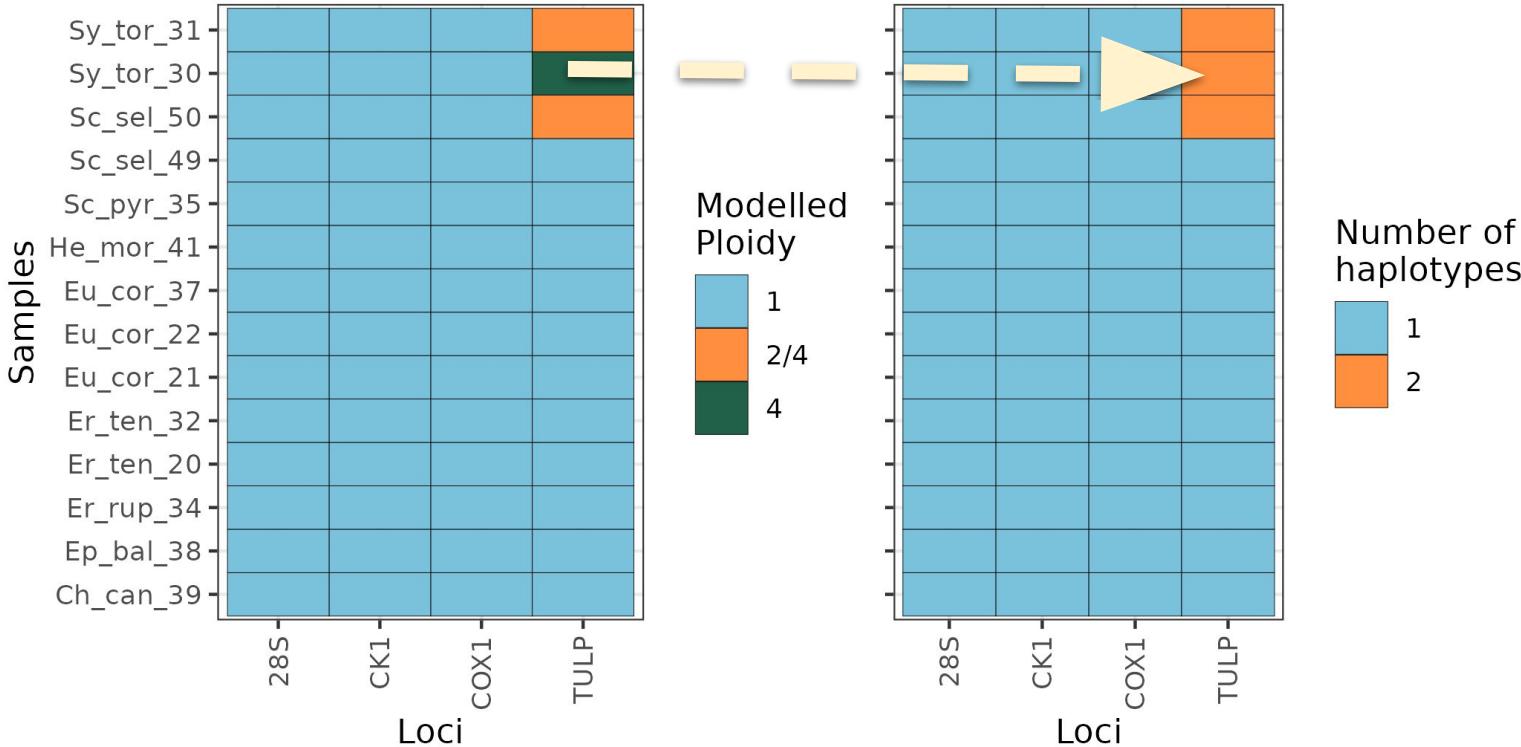
$$P(X = x) = \frac{n!}{x_1!x_2!...x_k!} \cdot p_1^{x_1} \cdot p_2^{x_2} \cdot \dots \cdot p_k^{x_k}$$

### Expectations:

```
TEST = {2:  
    {1: [np.array([0.0, 1.0])],  
     2: [np.array([1/2, 1/2])],  
     3: [np.array([1/3, 2/3])],  
     4: [np.array([1/2, 1/2]), np.array([1/4, 3/4])]},  
3:  
    {1: [np.array([0.0, 0.0, 1.0])],  
     2: [np.array([0.0, 1/2, 1/2])],  
     3: [np.array([1/3, 1/3, 1/3])],  
     4: [np.array([1/4, 1/4, 1/2])]},  
4: {1: [np.array([0.0, 0.0, 0.0, 1.0])],  
    2: [np.array([0.0, 0.0, 1/2, 1/2])],  
    3: [np.array([0, 1/3, 1/3, 1/3])],  
    4: [np.array([1/4, 1/4, 1/4, 1/4])]}}
```

# Running AmpliPiper

Modelled Ploidy and number of Haplotypes ([custom script](#))

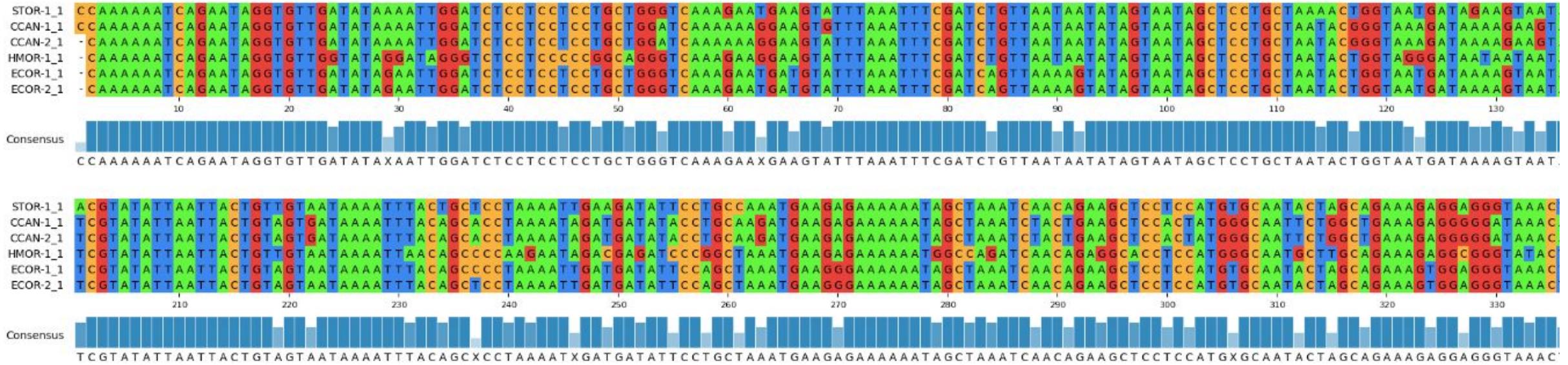


- By default: consensus sequences with < 10% frequencies are excluded
- `--freqthreshold 0.1`

Visualization with [ggplot](#)

# Running AmpliPiper

## Multiple Alignment (Mafft)



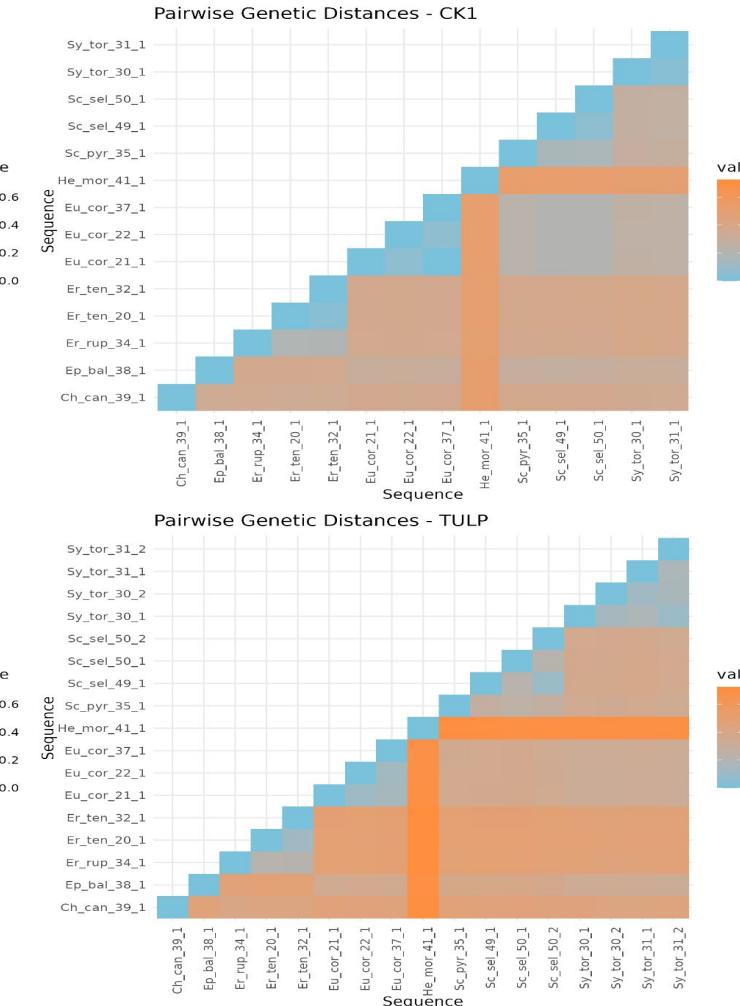
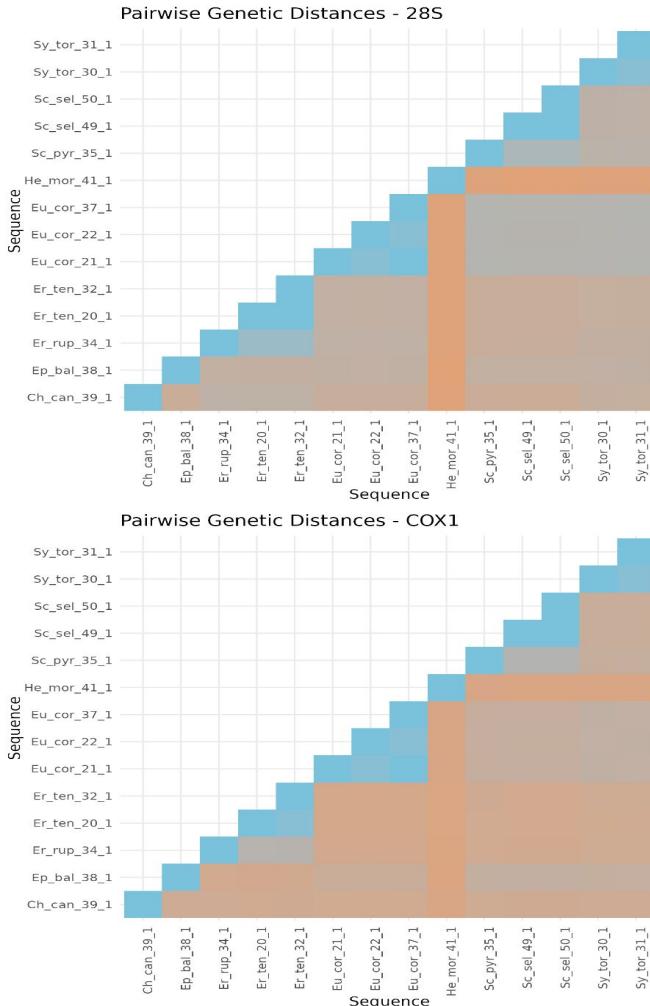
## Visualization with PyMSAviz

# Running AmpliPiper

## Genetic Distance

Dist=diff(S1,S2)/Length  
ape::dist.gene

## Visualization with ggplot::ggplot



# Running AmpliPiper

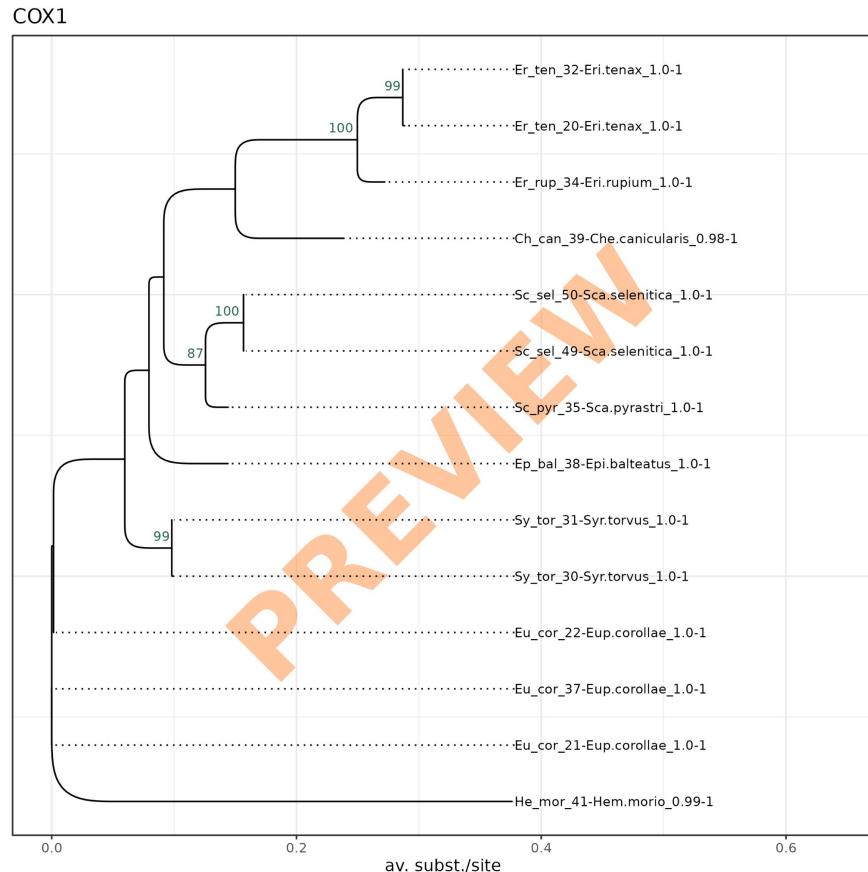
## Species Identification using the BOLD or BLAST API ([custom script](#))

SAMPLE	Taxon1 (sim%)	Taxon2 (sim%)	Taxon3 (sim%)	Taxon4 (sim%)	Taxon5 (sim%)	Taxon6 (sim%)
Ch_can_39_1	Cheilosia canicularis (97.99%); count = 3	Cheilosia oblonga (94.38%); count = 1	Cheilosia variabilis (94.37%); count = 4	Cheilosia vulpina (92.76%); count = 1	Cheilosia albitarsis (92.76%); count = 1	
Ep_bal_38_1	Episyphus balteatus (99.56%); count = 10					
Er_rup_34_1	Eristalis rupium (99.7%); count = 8	Eristalis hirta (99.09%); count = 1	Eristalis himalayensis (96.39%); count = 1			
Er_ten_20_1	Eristalis tenax (99.85%); count = 10					
Er_ten_32_1	Eristalis tenax (100.0%); count = 10					
Eu_cor_21_1	Eupeodes corollae (99.7%); count = 9	Eupeodes luniger (98.84%); count = 1				
Eu_cor_22_1	Eupeodes corollae (99.7%); count = 8	Eupeodes luniger (99.39%); count = 2				

- If locus name is COX1, ITS or MATK\_RBCL (Standard barcoding markers)

# Running AmpliPiper

Phylogenetic analyses based on loci-specific maximum likelihood ([iqtree](#))

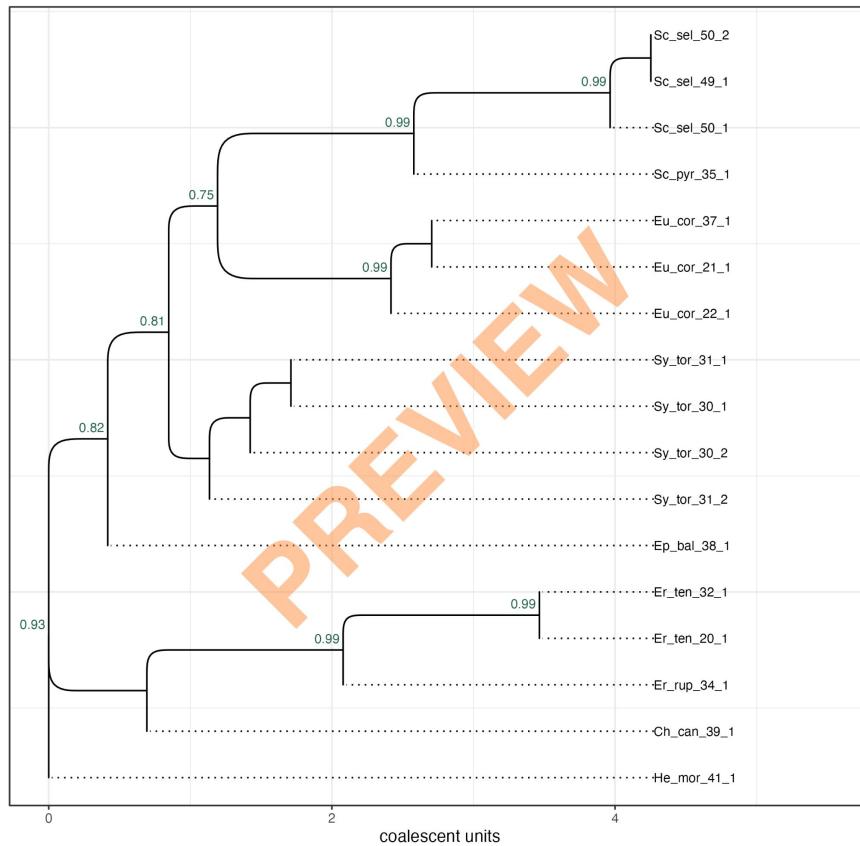


- If species ID successful, adjusted sample\_IDs in tree ([custom script](#))
- Tree plotting with [ggtree](#)
- Watermark to remind the necessity of integrating results with other taxonomical evidence

# Running AmpliPiper

Phylogenetic analyses based on (SUPER) trees - **integrating across all loci**

ASTRAL



## Concatenated dataset (iqtree)

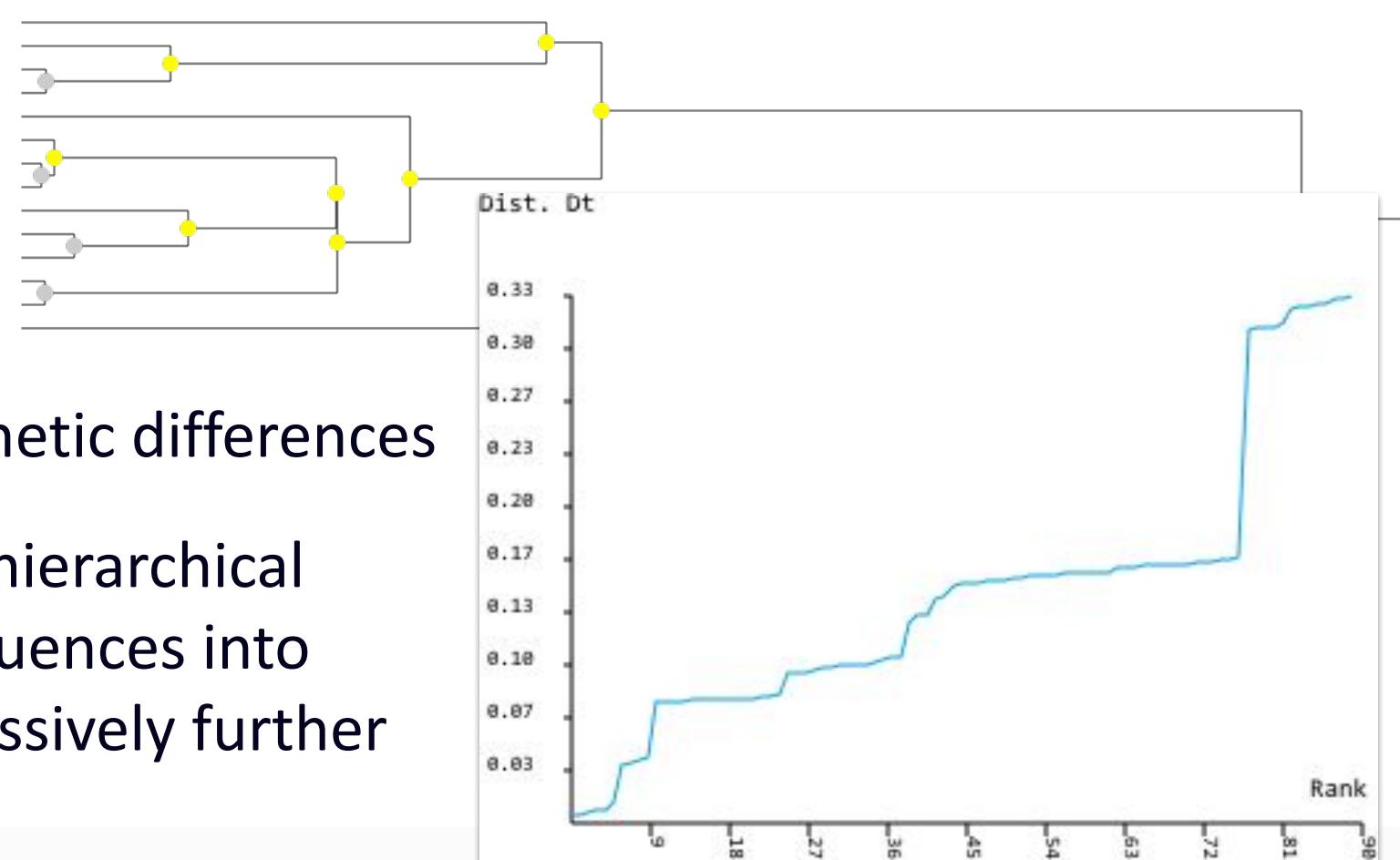
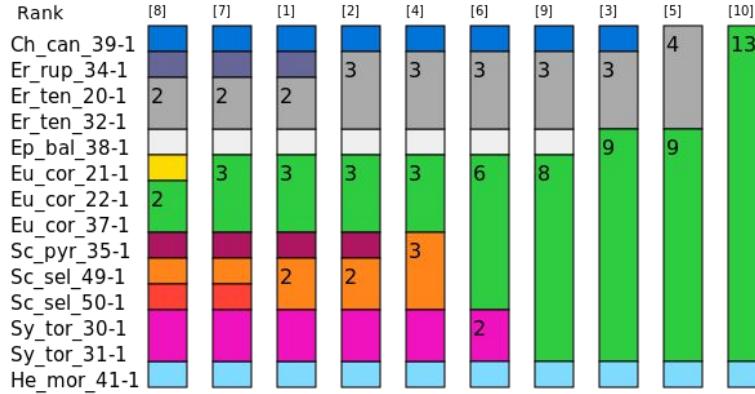
- **ML with (optional) separate substitution rates** for each locus in tree reconstruction
- Samples only included if < 30% gaps

## wASTRAL (aster)

- seeks the species tree that maximizes the number of shared quartets (unrooted fourtaxon subtrees) between gene trees and the species tree
- takes informations such as branch lengths and branch support into account

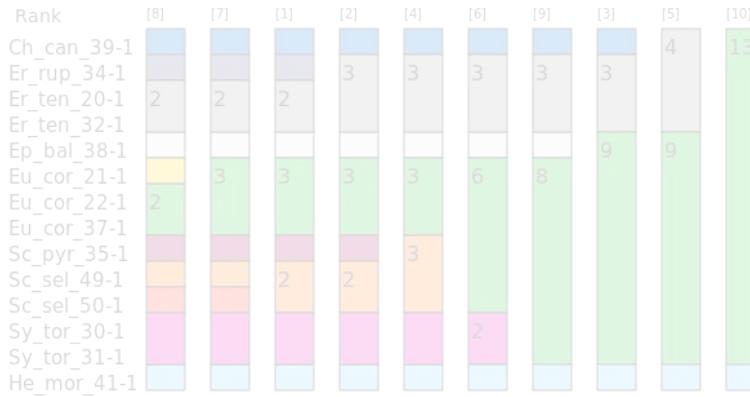
# Running AmpliPiper

## Species Delimitation (ASAP)

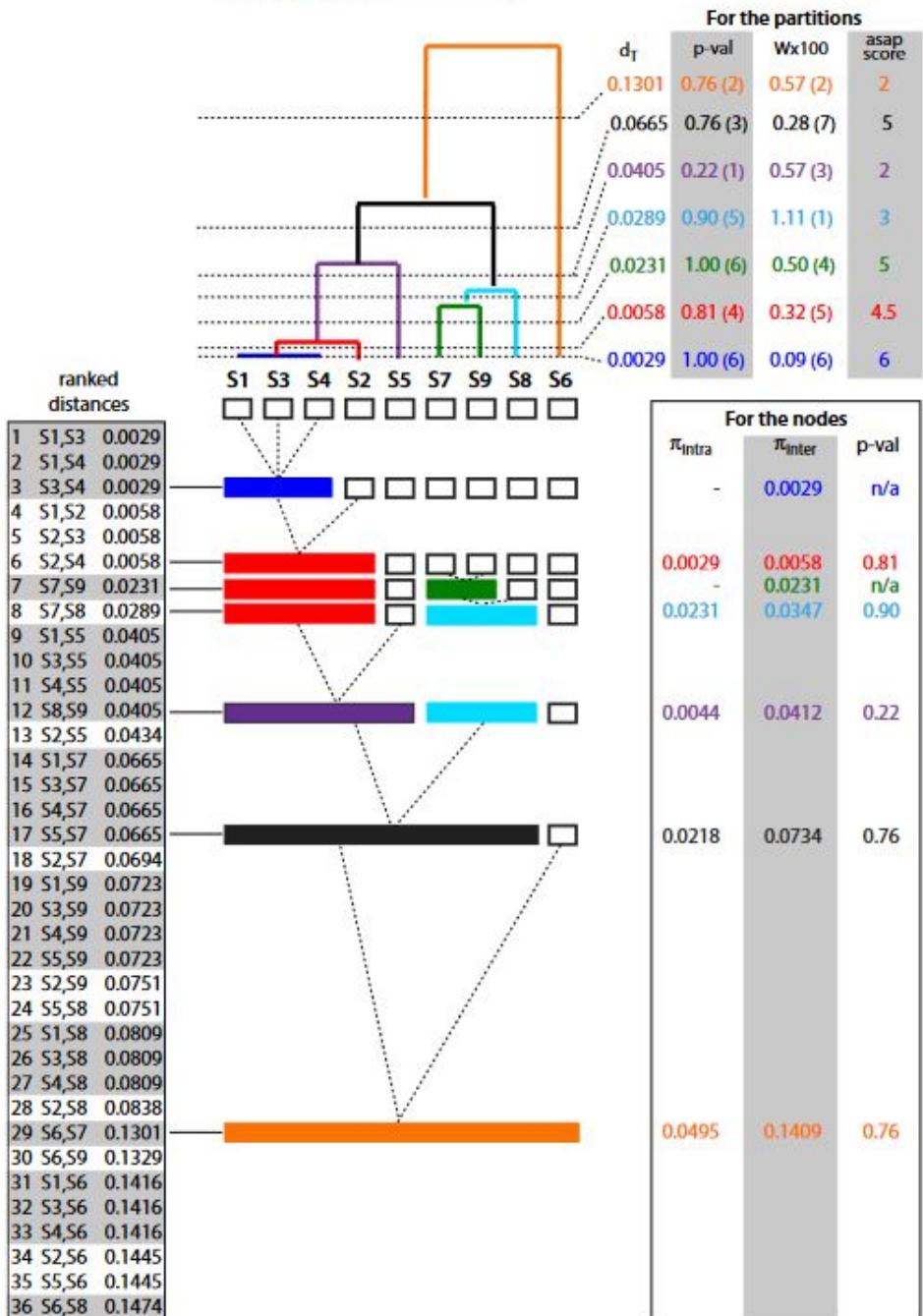


# Running AmpliPiper

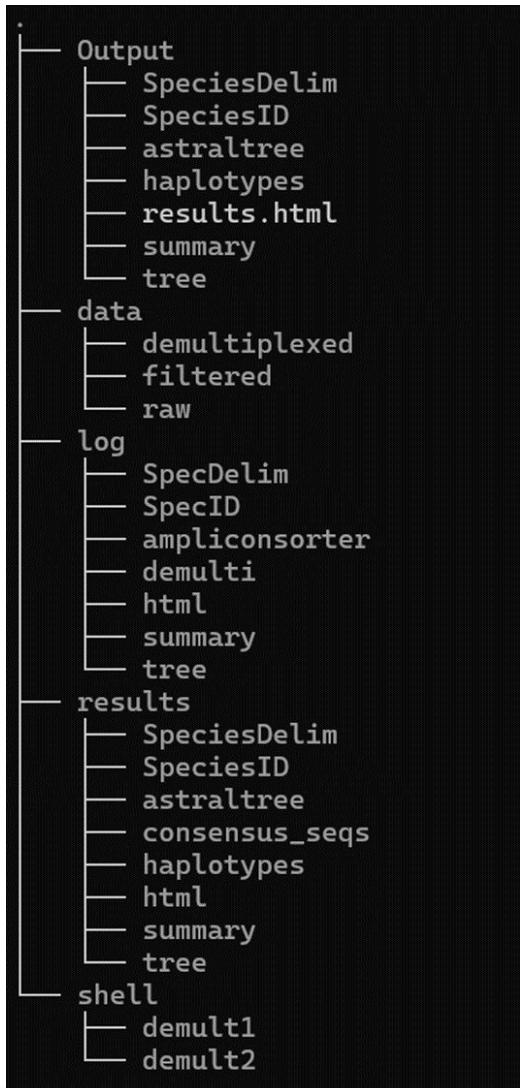
## Species Delimitation (ASAP)



- Ranking all pairwise genetic differences
- Subsequent ascending hierarchical clustering, merging sequences into “groups” that are successively further merged



# AmpliPiper - output



Final output folder with all the results on display in results.html

Folder with raw, quality/length-filtered and demultiplexed data

Folder with log outputs from every executed step inside the pipeline

Folder with intermediate and raw results file

Folder with shell scripts run in parallel during the pipeline execution

# AmpliPiper - output



Summary

Genetic Distances

Phylogenetic Trees

Consensus Alignment

Species Identification

Species Delimitation



Your analysis has finished.

Click on the tabs on the side to show the corresponding analysis results.

The following parameters were used for the analysis:

Parameters	Values
Quality threshold	10
Similar consensus threshold	97.5
Number of reads	200
Size range	100
Minimum reads required	50
Number of threads	200
K-threshold	0.05
Force Flag	yes
BLAST usage	capoony@gmail.com
Partition strategy	no
Outgroup Definition	He_mor_41

# AmpliPiper - output



Transforming European Taxonomy through Training, Research, and Innovations



Funded by  
the European Union

# AmpliPiper - output



Summary

Genetic Distances

Phylogenetic Trees

Consensus Alignment

CK1

28S

COX1

TULP

Species Identification

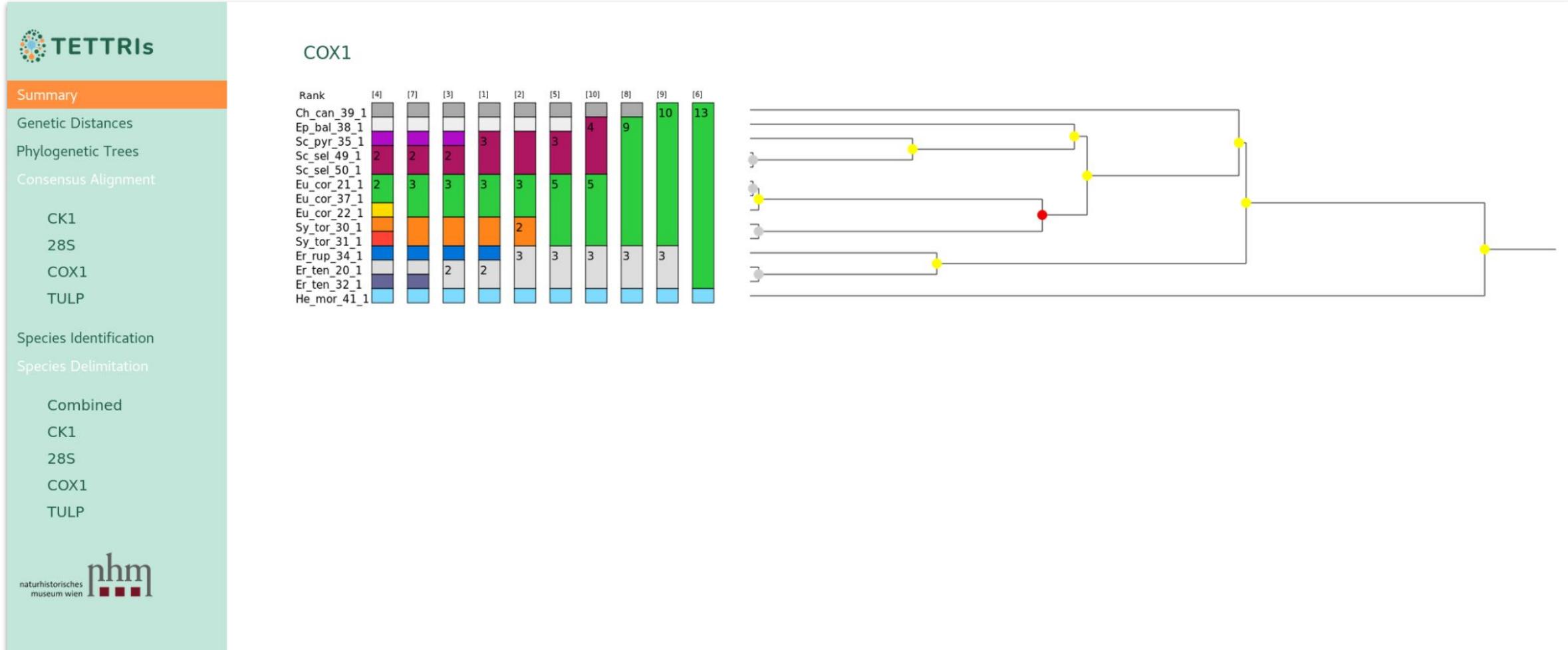
Species Delimitation

naturhistorisches  
museum wien

Summarized results for the Species Identification approach with BLAST.

SAMPLE	Taxon1 (sim%)	Taxon2 (sim%)	Taxon3 (sim%)	Taxon4 (sim%)	Taxon5 (sim%)	Taxon6 (sim%)
Ch_can_39_1	Cheilosia canicularis (97.99%); count = 3	Cheilosia oblonga (94.38%); count = 1	Cheilosia variabilis (94.37%); count = 4	Cheilosia vulpina (92.76%); count = 1	Cheilosia albifarsis (92.76%); count = 1	
Ep_bal_38_1	Episyphus balteatus (99.56%); count = 10					
Er_rup_34_1	Eristalis rupium (99.7%); count = 8	Eristalis hirta (99.09%); count = 1	Eristalis himalayensis (96.39%); count = 1			
Er_ten_20_1	Eristalis tenax (99.85%); count = 10					
Er_ten_32_1	Eristalis tenax (100.0%); count = 10					
Eu_cor_21_1	Eupeodes corollae (99.7%); count = 9	Eupeodes luniger (98.84%); count = 1				
Eu_cor_22_1	Eupeodes corollae (99.7%); count = 8	Eupeodes luniger (99.39%); count = 2				
Eu_cor_37_1	Eupeodes corollae (99.7%); count = 9	Eupeodes luniger (98.84%); count = 1				
He_mor_41_1	Hemipenthes morio (99.39%); count = 1	Bombyliidae sp. (89.35%); count = 9				
Sc_pyr_35_1	Scaeva pyrastri (99.7%); count = 10					
Sc_sel_49_1	Scaeva selenitica (100.0%); count = 4	Scaeva dignota (99.85%); count = 1	Scaeva komabensis (98.97%); count = 1	Scaeva mecoGRAMMA (98.38%); count = 2	Scaeva affinis (96.24%); count = 1	Scaeva pyrastri (95.66%); count = 1
Sc_sel_50_1	Scaeva selenitica (100.0%); count = 4	Scaeva dignota (99.85%); count = 1	Scaeva komabensis (98.97%); count = 1	Scaeva mecoGRAMMA (98.38%); count = 2	Scaeva affinis (96.24%); count = 1	Scaeva pyrastri (95.66%); count = 1
Sy_tor_30_1	Syrphus torvus (99.7%); count = 10					
Sy_tor_31_1	Syrphus torvus (99.7%); count = 10					

# AmpliPiper - output



# AmpliPiper - GitHub repository

[README](#) [GPL-3.0 license](#)

Language Bash Production status Beta Release v0.2.0 beta Requires Mamba and Conda Supported platforms linux



## AmpliPiper

This README provides a quickstart to the pipeline: if you want to dive deeper, check out the [complete documentation](#).

### Installation

The installation of dependencies requires [mamba](#) and [conda](#) to be already installed on your system.

To install the pipeline program:

1. Clone this repository:

```
git clone https://github.com/nhmvienna/AmpliPiper.git
```

2. Go to the cloned directory:

```
cd AmpliPiper
```

3. Run the setup script:

```
bash shell/setup.sh
```

### Input Data

**Primers**  
CSV-file with locus name, forward- and reverse primer sequences, expected fragment length and expected ploidy

**Samples**  
CSV-file with sample name and full file path to the sample-specific raw FASTQ-file

### Installation

**setup.sh**  
BASH script which serially installs third party software as conda environments locally within the AmpliPiper software folder

**Requirements**  
The package managers [conda](#) and [mamba](#) need to be preinstalled to download and install required third-party software

### 1. Haplotype reconstruction

#### Operation

#### Primer Alignment

Compare pairwise similarity among all primer sequences (including their reverse complements) with the edlib package

#### Program/Script

#### CompPrimers.py

#### Output file(s)

Distance matrix and heatmaps showing pairwise edit distances among primers

#### Data filtering

Based on PHRED-scaled basequality of raw ONT data in FASTQ format

#### NanoFilt

Filtered sequences in FASTQ format per sample

#### Demultiplexing

Locus-specific filtering of raw sequences based on amplicon length and similarity to primer sequences

#### DemultFastq.py

Filtered sequences in FASTQ format per sample and locus

#### Haplotype reconstruction

Reconstruction of one or more consensus sequences per locus and sample based on sequence similarity in the demultiplexed FASTQ reads

#### AmpliconSorter

Consensus FASTA sequence(s) per sample and locus. Tabular summary of AmpliconSorter output

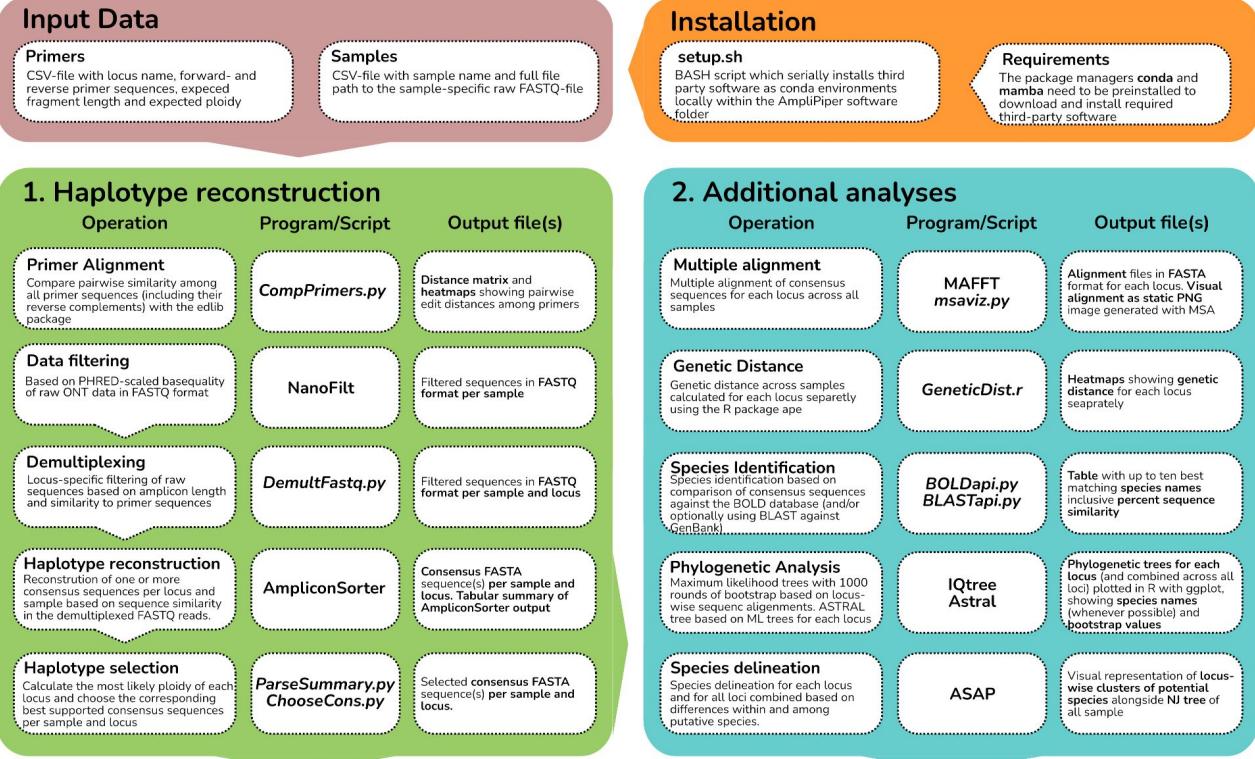
#### Haplotype selection

Calculate the most likely ploidy of each locus and choose the corresponding best supported consensus sequences per sample and locus

#### ParseSummary.py

ChooseCons.py

Selected consensus FASTA sequence(s) per sample and locus



<https://github.com/nhmvienna/AmpliPiper>

# AmpliPiper - documentation

AMPLIPIPER

Search AMPLIPIPER

AMPLIPIPER on GitHub

[Home](#)

[Installation](#)

[Prepare for the pipeline](#)

[Pipeline](#)

[Results](#)

[Troubleshooting](#)

[Authors, References and Citation](#)

[CHANGELOG](#)

## AmpliPiper

AmpliPiper is a comprehensive yet modular pipeline that is able to perform a wide variety of downstream tasks on raw, basecalled, Oxford Nanopore long reads.

[Get started now](#) [View it on GitHub](#)

Language: Bash | Production status: Beta | Release: v0.2.0 beta | Requires: Mamba and Conda  
Supported platforms: linux/macOS



AMPLIPIPER

Search AMPLIPIPER

AMPLIPIPER on GitHub

[Home](#)

[Installation](#)

[Prepare for the pipeline](#)

**Pipeline**

[Results](#)

[Troubleshooting](#)

[Authors, References and Citation](#)

[CHANGELOG](#)

### Pipeline workflow

TABLE OF CONTENTS

- Preprocessing
- Demultiplexing
- Consensus generation
- Haplotype reconstruction
- Genetic distance calculation
- Phylogenetic analysis
- Species Delimitation
- Species Identification
- HTML Summarization

### Preprocessing

The preprocessing step consists of two independent parts:

- Primers comparison:** primers are aligned, and their relative edit distance is calculated and represented as a heatmap. This serves as an informative step for the user, allowing them to adjust the k-threshold parameter based on the primers' distance.
- Quality filtering:** accomplished using NanoFilt, this step excludes reads that fall below the minimum quality threshold (set by passing the `--quality` option).

### Demultiplexing

Demultiplexing is a complex and delicate task for the pipeline, accomplished by a custom Python script, and is highly dependent on the parameters (especially k-threshold and size range) provided to the pipeline:

- First, the program reads the fastq file and the primers table.
- Next, the program iterates through each read in the fastq file, looking for a matching pattern for each primer. If the analyzed sequence aligns with both the forward and reverse primers, and the mismatches in these alignments are less than  $k * \text{len(primer)}$ , it gets demultiplexed with the primer taken into account.
- Once all reads have been demultiplexed, a quality selection takes place. If there are more reads than those specified with the `--nreads` option, only the top-quality ones are written to the final demultiplexed files. Otherwise, all reads are transcribed to the demultiplexed output file, but only if their number is higher than the one specified with `--nreads`.

This task is parallelized across multiple threads (when allowed).

<https://astrabert.github.io/AmpliPiper-docs/>

# Part II - Hands on

# AmpliPiper - Use Case

## *Syrphidae*



**14 samples**

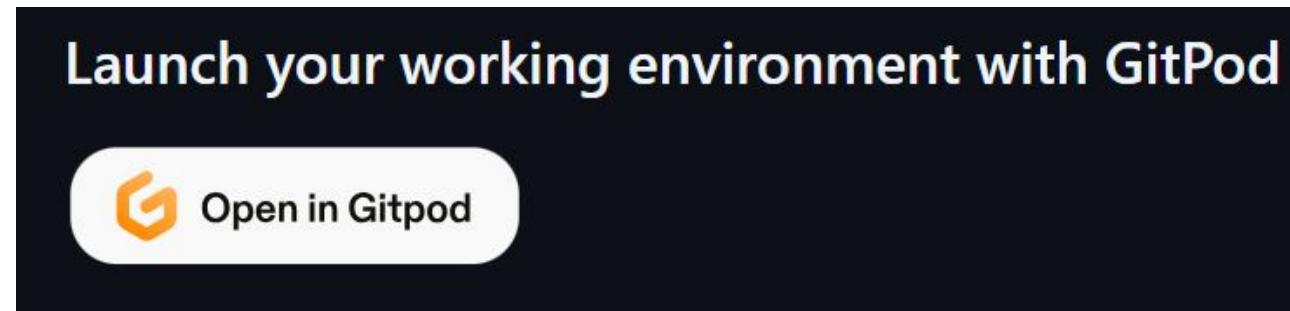
**4 loci**

(COX1, 28s, TULP, CK1)

- Biological System /Relevance (Pollinators)
  - Visitors of > 72% of global food crops
  - many larva important in biological pest control (predators of aphids)
- Taxonomy/Phylogeny
  - 2 of 4 subfamilies included (Eristalinae & Syrphinae)
- Where does the data come from?
  - Specimens sampled in the course of ABOL-BioBlitz
- 4 Loci (1 mt / 3 nuclear) from recent phylogenetic study (Moran et al. (2021))

# Let's test AmpliPiper

We prepared a virtual workspace where everyone can run AmpliPiper:



You will find it on the GitHub repository we shared with you!

# Let's test AmpliPiper

Choose the  
**Large** virtual  
machine  
instance!

## New Workspace

Create a new workspace in the Astra's Org organization.

 AmpliPiper\_Workshop\_2024  
github.com/nhmvienna/AmpliPiper\_Workshop\_2024

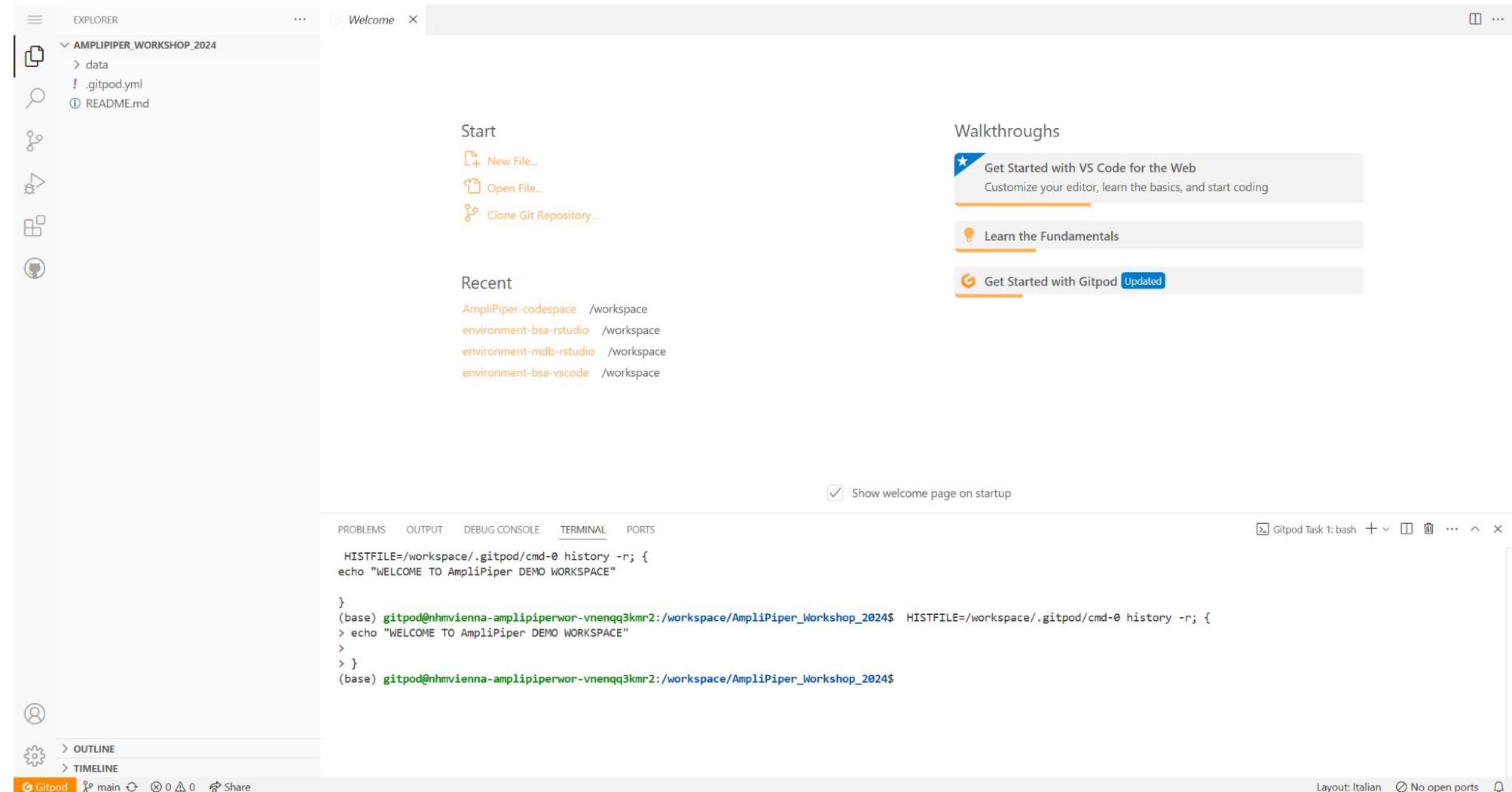
 VS Code · 1.95.3  
Editor · Browser

 Large  
Class · Up to 8 cores, 16GB RAM, 50GB storage

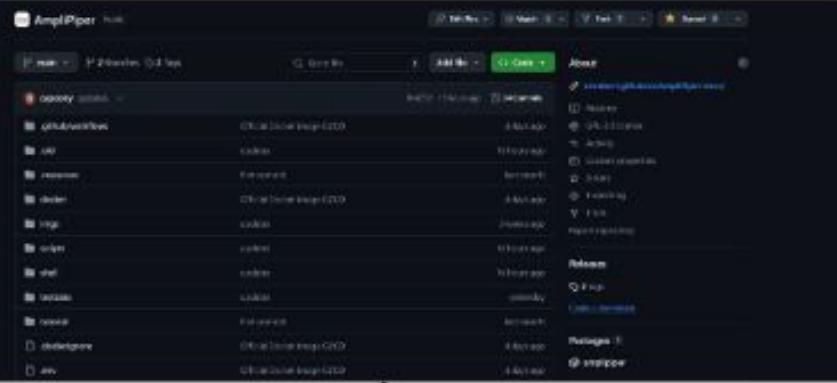
Continue (Ctrl + Enter)

# Let's test AmpliPiper

You will land  
on a **VSCode**  
based  
environment

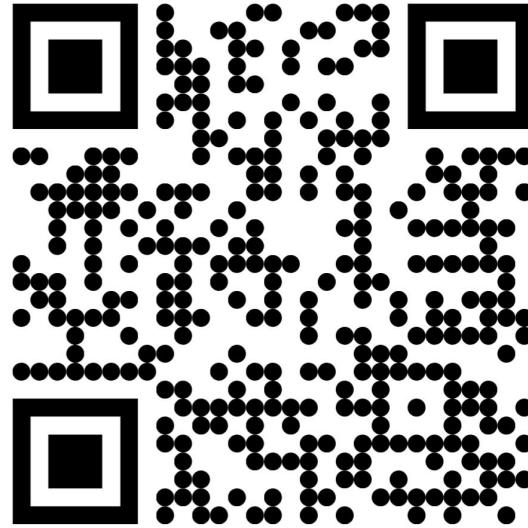


# Feeling fancy? Other ways to get AmpliPiper!

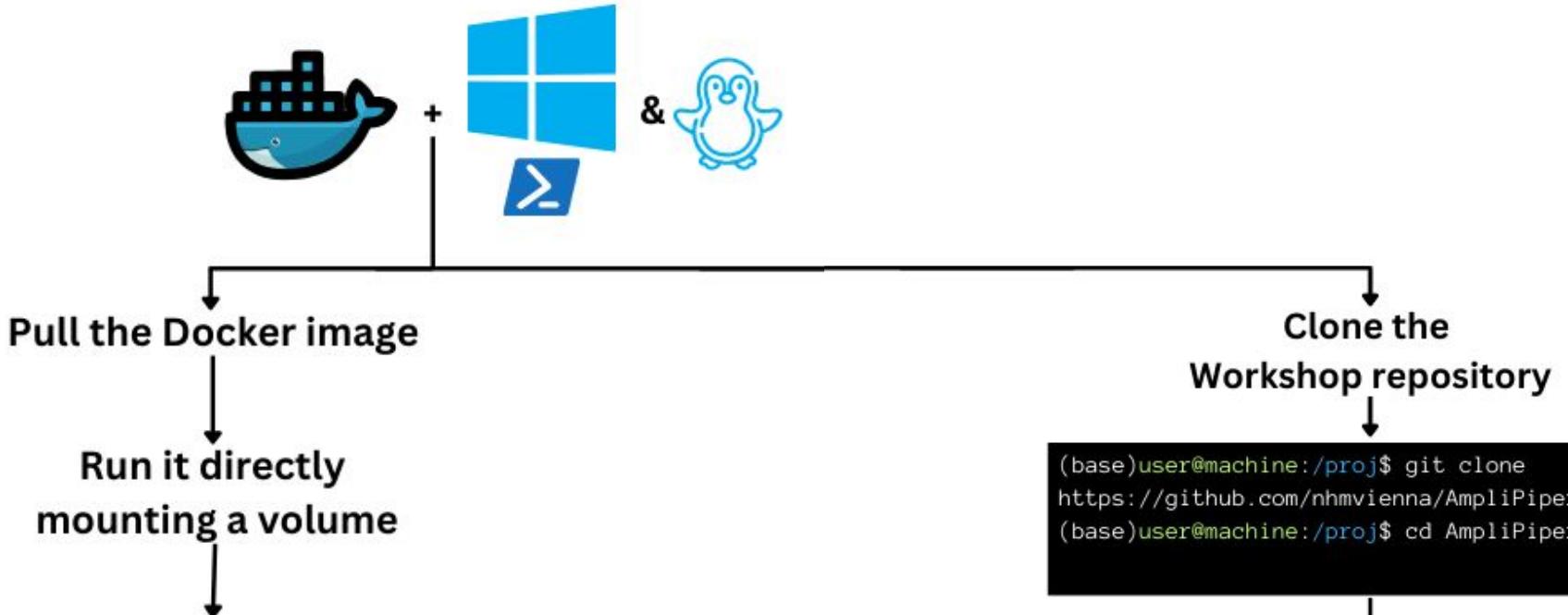


Clone the  
GitHub repository

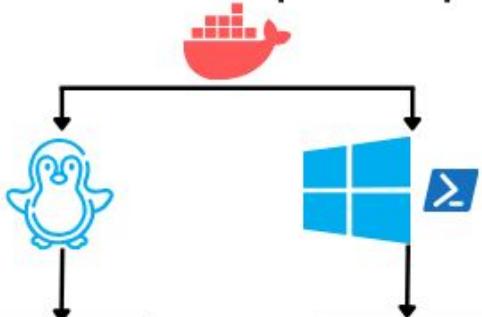
Execute the  
installation script



```
(base)user@machine:/proj$ git clone  
https://github.com/nhmvienna/AmpliPiper.git  
(base)user@machine:/proj$ cd AmpliPiper/  
(base)user@machine:/proj$ bash shell/setup.sh
```



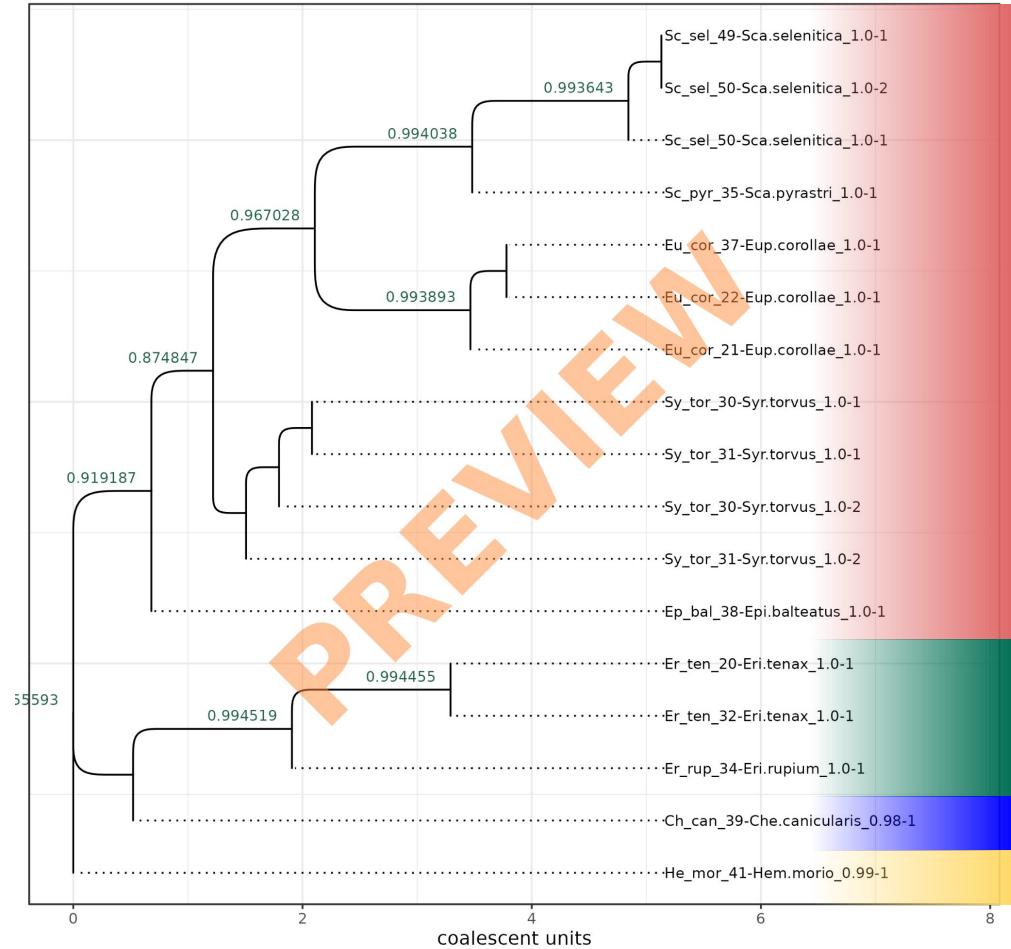
### Use Docker compose scripts



```
PS C:\Users\User\AmpliPiper_Workshop_2024>
.\compose.ps1
```

# Summary Syrphidae

ASTRAL



Syrphini



Eristalini



Rhingiini  
Bombyliidae

- Full agreement with morphological species identification
- Correct phylogenetic clustering
- High branch support
- Super/concatenated trees superior to individual loci

# Part III - Advanced Datasets, Benchmarking and Limitations

# AmpliPiper - optional arguments

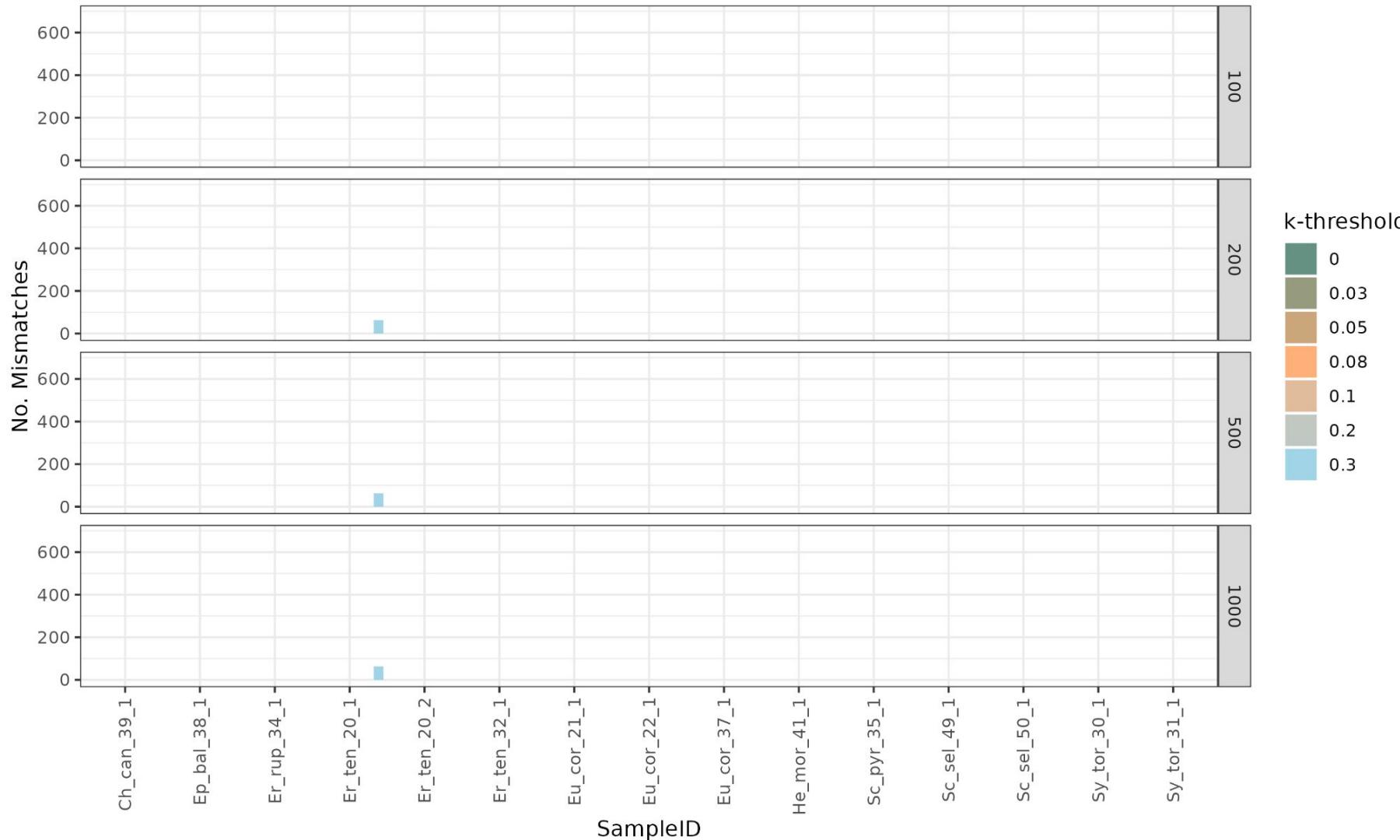
## Optional Arguments

- `-b` or `--blast` : Enable BLAST search for species identification. When setting this parameter, you need to provide an email address (e.g., `--blast your@email.com`) for using NCBI entrez to retrieve taxonomic information for the BLAST hits (default: disabled).
- `-c` or `--similar_consensus` : Change the minimum similarity threshold (in percent) of amplicon\_sorter. If the similarity of two clusters are smaller or equal to the threshold, they are considered separately otherwise they are collapsed prior to consensus reconstruction (default: 96)
- `-e` or `--exclude` : Provide a text file with samples and loci to exclude from the analysis. Each row should contain the ID of a sample to be excluded. Names need to be identical to the IDs in `samples.csv`.
- `-f` or `--force` : Force overwrite the output folder if it already exists (default: cowardly refusing to overwrite).
- `-i` or `--partition` : Use partition model for iqtree with combined dataset. △ may take very long △ (default: disabled)
- `-k` or `--kthreshold` : Define the threshold  $k$  for the maximum allowed proportion of mismatches for primer alignment during demultiplexing (default: 0.05).
- `-m` or `--minreads` : Set the minimum number of reads required for consensus sequence reconstruction (default: 100).
- `-n` or `--nreads` : Provide the absolute number or percentage of top-quality reads to consider for consensus sequence generation and variant calling (default: 500).
- `-q` or `--quality` : Specify the minimum PHRED quality score for read filtering (default: 10).
- `-r` or `--sizerange` : Define the allowed size buffer in basepairs around the expected locus length (default: 100).
- `-t` or `--threads` : Specify the number of threads to be used for parallel processing (default: 10).
- `-w` or `--nowatermark` : Remove the watermark from the tree figures
- `-y` or `--freqthreshold` : Retain consensus sequences for further analyses which are supported by raw reads, whose frequency in the total pool of reads is larger or equal to this threshold (default: 0.1).

# Benchmarking - comparison to Sanger sequences

- COX1: Pairwise alignment of Sanger sequences and consensus sequences from AmpliPiper with **edlib**
- Different combination of parameters
  - k-threshold (The maximum divergence allowed between primer sequences in primers file and read)
  - Minimum number of reads

# Benchmarking - comparison to Sanger sequences



- Sequences identical for almost all samples and parameter combinations
- 63 mismatches (~10%) only with k-threshold 30% in single sample!!

# Benchmarking - Simulations

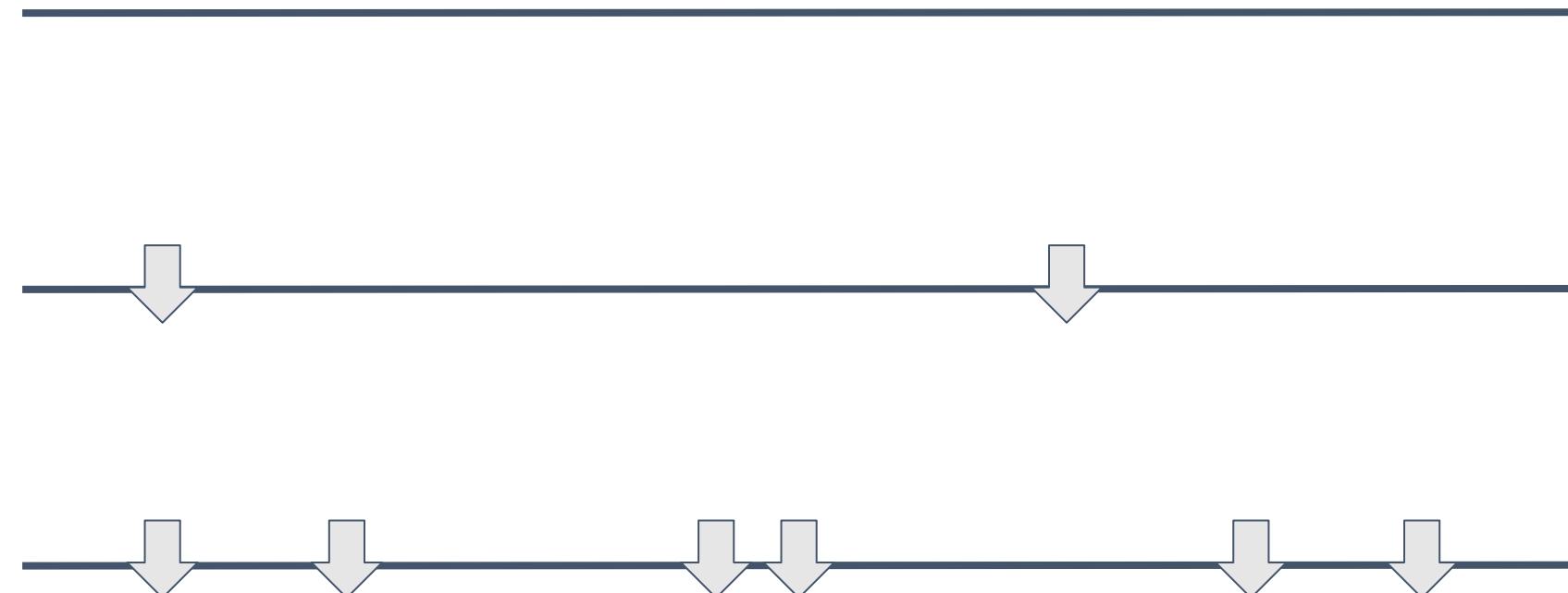
Sanger

COX1 - Stor\_1

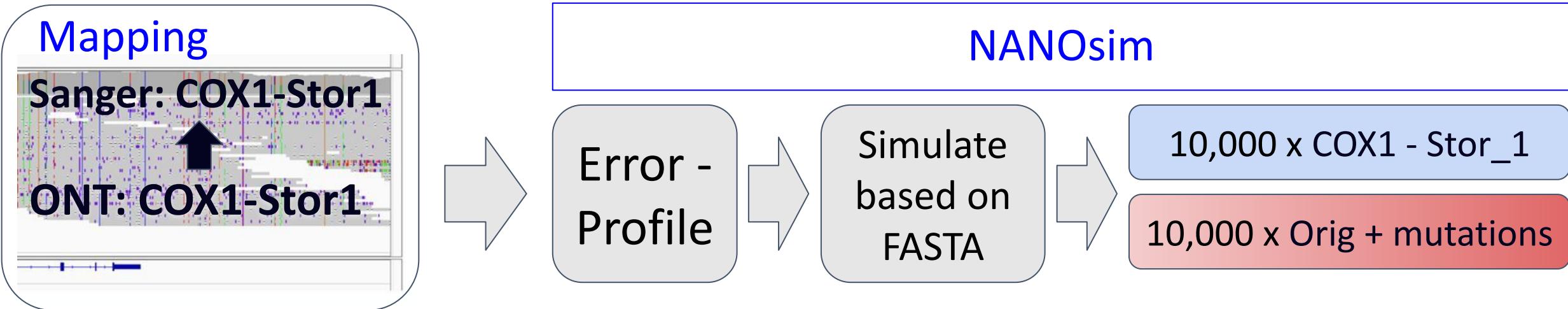
Rand. Mutations (1%)

•  
•  
•

Rand. Mutations (5%)



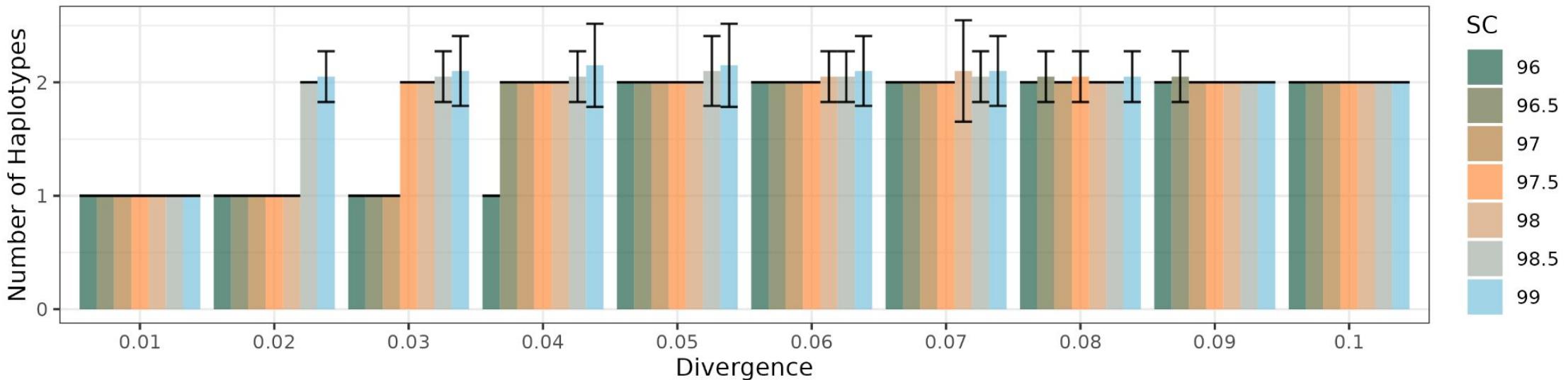
# Benchmarking - Simulations



- 20 x technical replication
- Pooling of simulated reads from original sequence and from mutated sequences (1% - 5% divergence)
- Benchmarking AmpliPiper (No. of Haplotypes, Mismatches)

# AmpliPiper - Benchmarking

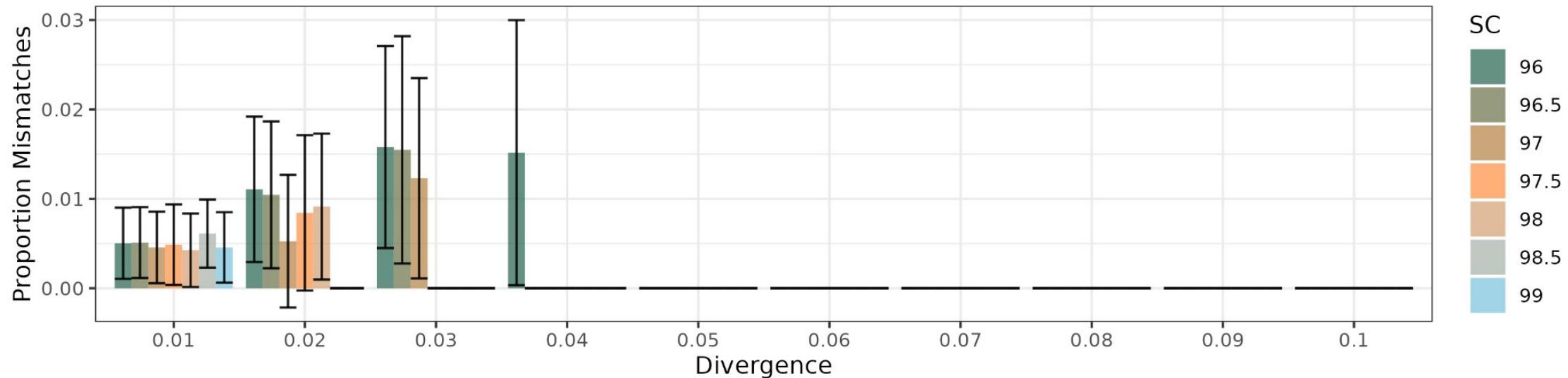
## Effects of consensus similarity threshold - Sensitivity



- 50:50 ratio of reads from original and mutated sequences
- **Number of reconstructed consensus sequences**

# AmpliPiper - Benchmarking

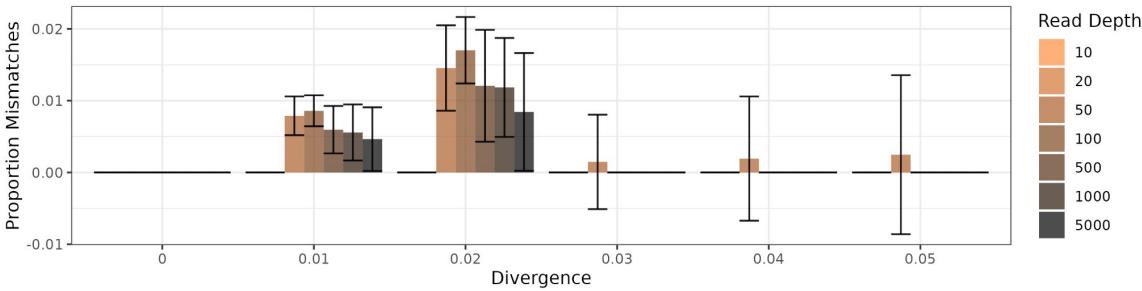
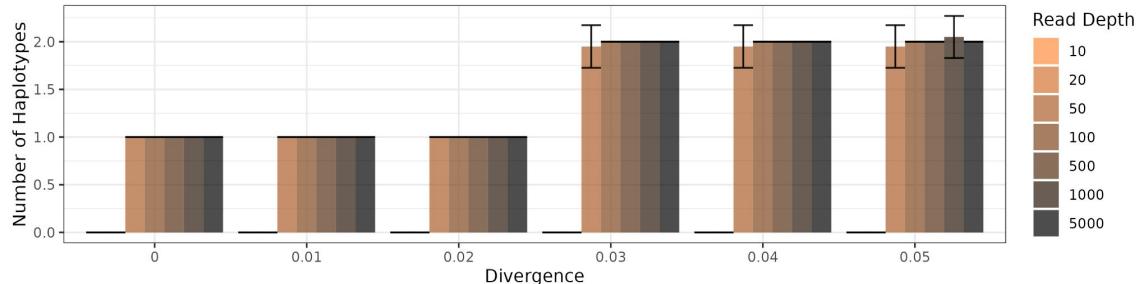
## Effects of consensus similarity threshold - Accuracy



- 50:50 ratio of reads from original and mutated sequences
- **Average proportion of mismatches to both original seq.**

# AmpliPiper - Benchmarking

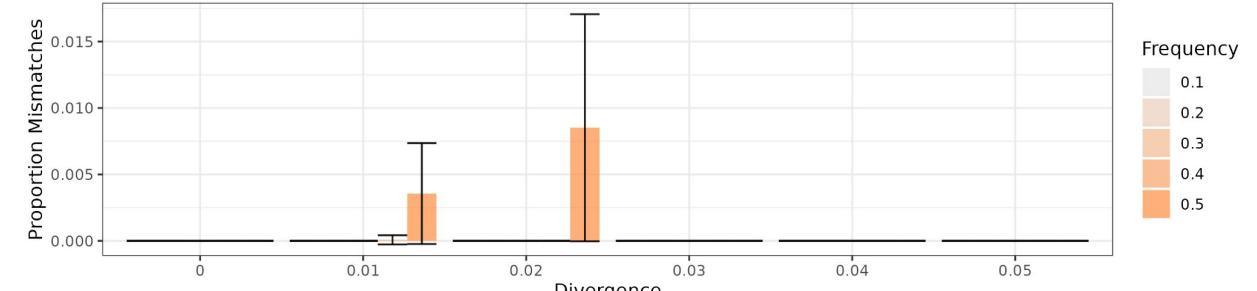
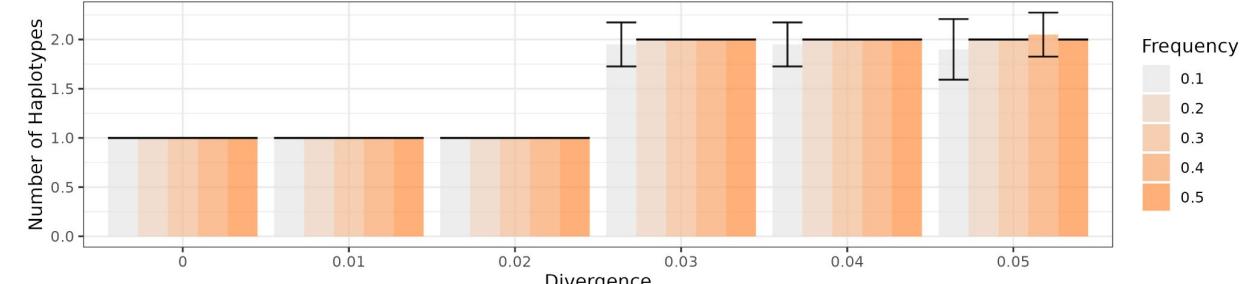
## Effect of read depth



**Locus reconstruction per sample:** unstable or null when using RD $\leq$ 50

**Mismatches with refseq:** irrespective of RD if divergence of the reconstructed sequences from the refseq  $\leq$ 2%

## Effects of haplotypes deviating from 1:1 ratio



**Locus reconstruction per sample:** production of chimeras if divergence of the reconstructed sequences from the refseq  $\leq$ 2%

**Mismatches with refseq:** found only with 40-60 and 50-50 ratios & only if the divergence of the reconstructed sequences from refseq  $\leq$ 2%

# Let's test some more complex datasets

## *Mercurialis*



8 out of 23 samples  
10 out of 28 loci

Gerchen, J.F., Veltsos, P., and Pannell, J.R.  
(2022). *Philos Trans R Soc Lond B Biol Sci* **377**: 20210224.

## *Opiliones*



8 samples  
COX1 locus

# Let's test some more complex datasets

Pick and prepare a dataset



Investigate results



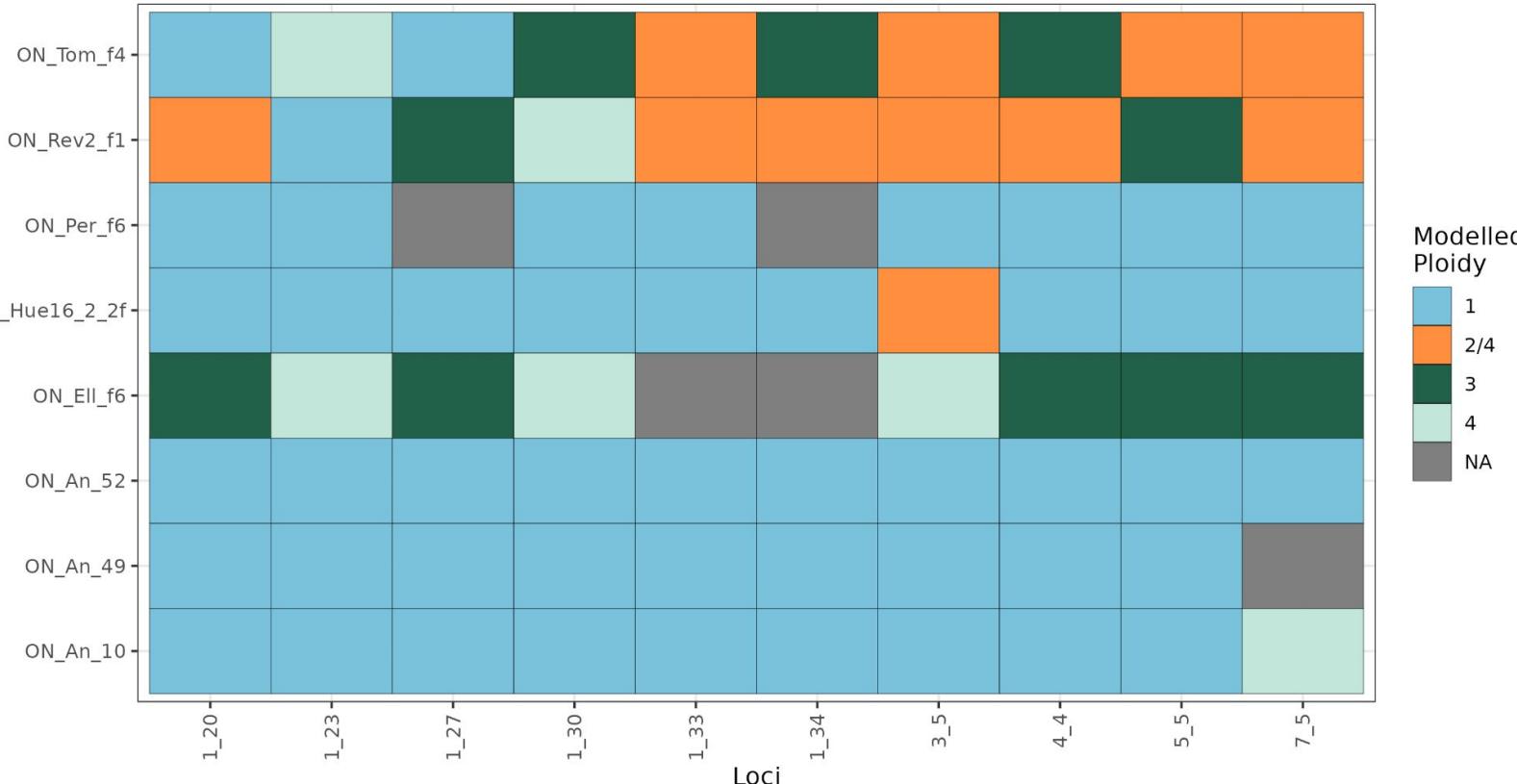
Parameters	Values
Quality threshold	10
Similar consensus threshold	97
Number of reads	1000
Size range	100
Minimum reads required	50
Number of threads	20
K-threshold	0.05
Force Flag	yes
BLAST usage	aastrabees@gmail.com
Partition strategy	no
Outgroup Definition	no



Repeat with different settings



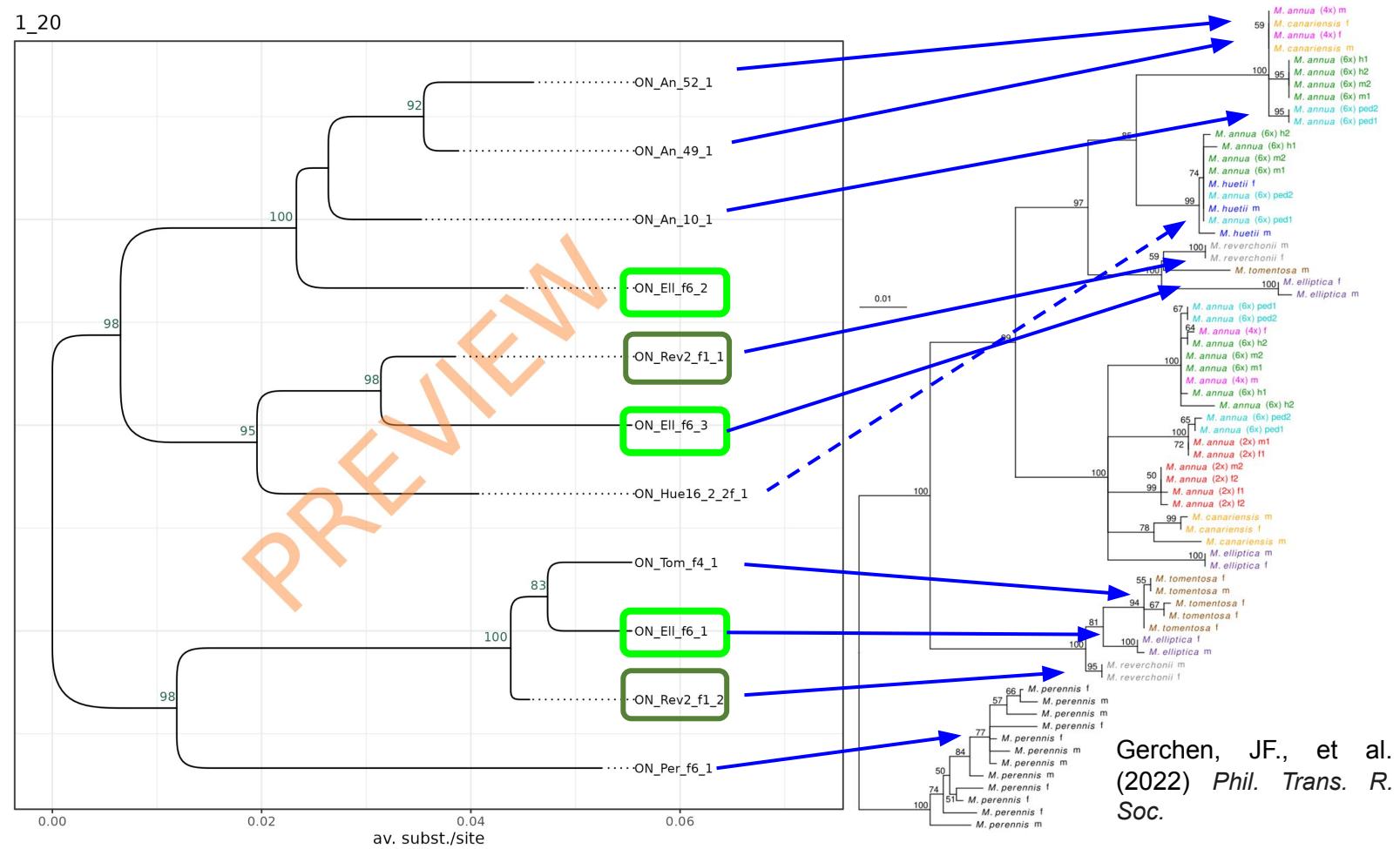
# Summary *Mercurialis*



- **Complex ploidy / inbreeding patterns**
  - Limited resolution (hexaploids!!)

# Summary *Mercurialis*

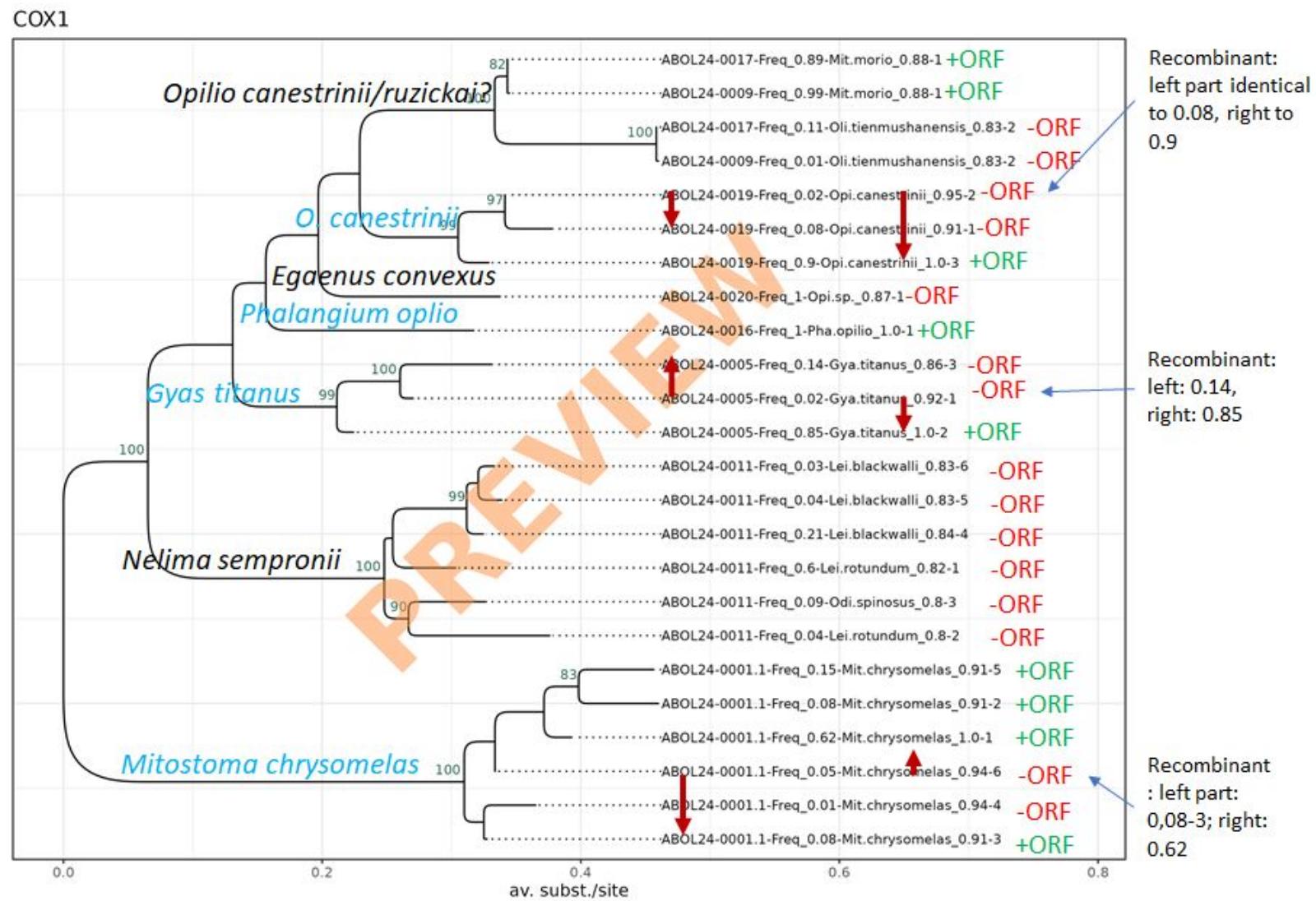
1\_20



- Complex ploidy / inbreeding patterns
  - Limited resolution (hexaploids!!)
- Allopolyploids
- Good congruence with published data (for some loci)

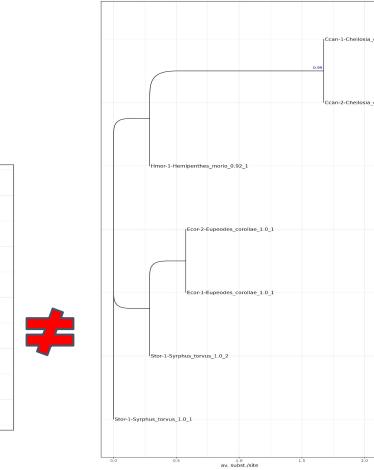
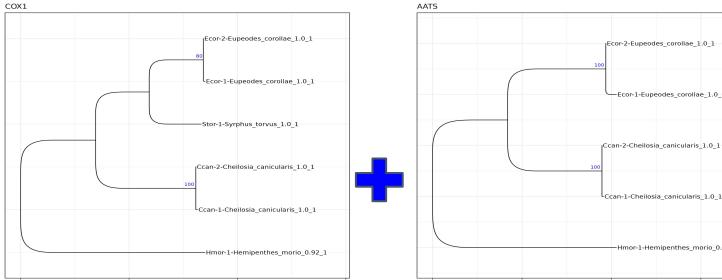
# Summary Opiliones

- Species ID not perfect  
(Database bias?)
- Massive amount of NUMTs
- Good agreement with SANGER sequences of clones
- Recombinants !!!
- Additional manual curation necessary (ORFs)

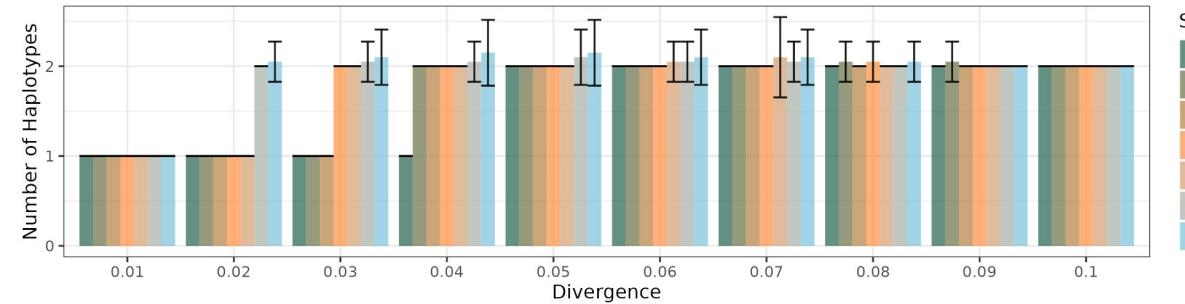


# Technical Limitations

## Phasing across loci



To distinguish highly similar haplotypes  
(>97%) within samples

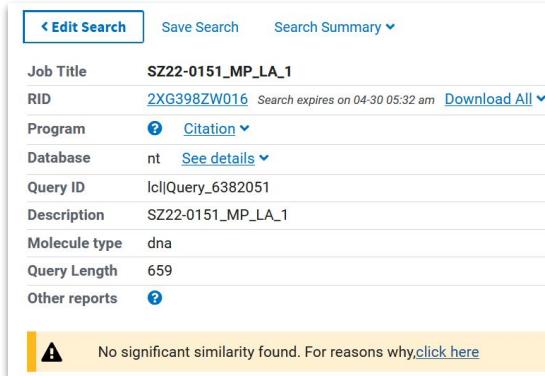
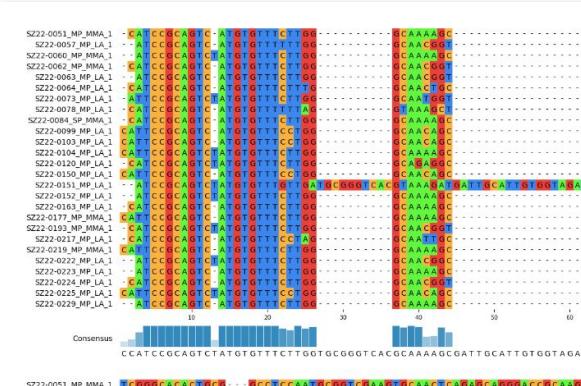


## Tricks & Tips

- Try tweaking `--similar_consensus`
- Remember that setting the parameter `>0.98` can result in an excess of haplotypes

# Technical Limitations

## PCR artefacts

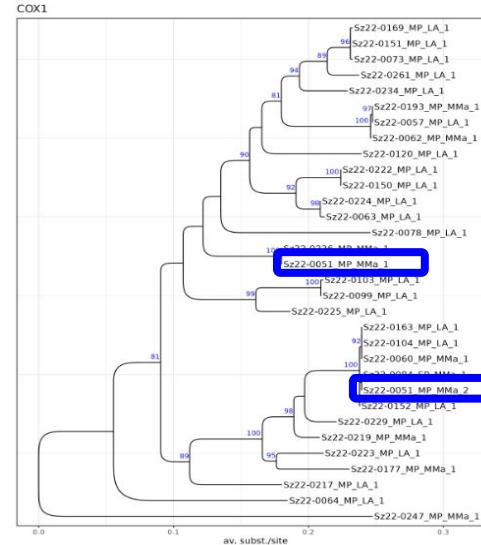


## Tricks & Tips

- Setting a strict --sizerange avoids chimeras
- Check species identification
- Exclude the sample(s)/locus(i) that show artefacts

## Contamination

SZ22-0051\_MP\_MMA\_1   TCGTATATTAAATAACTGTGT  
SZ22-0051\_MP\_MMA\_2   CCGTATATTAAATAATAAGTTGT

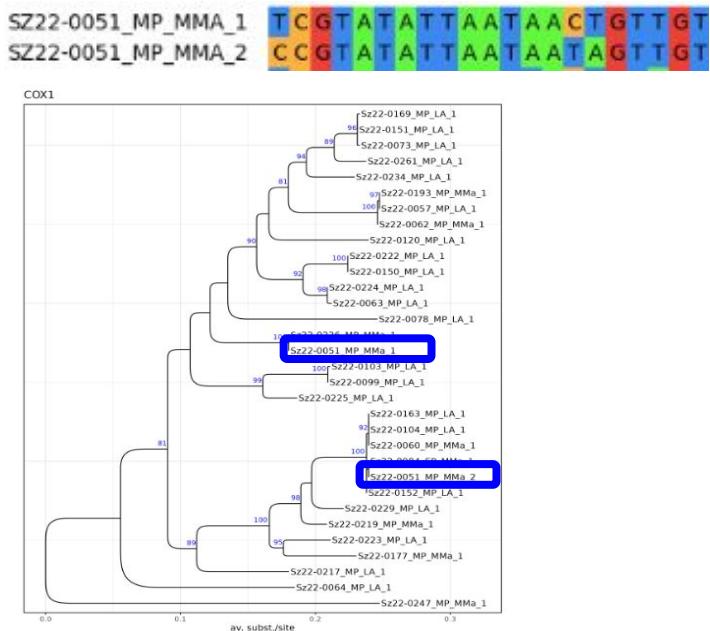


## Tricks & Tips

- First run with  
--freqthreshold  
0 to include all  
consensus sequences  
and test for  
inconsistencies

# Biological Limitations

## Numts/Duplications



## Polyplody/paralogues (multiple haplotypes)

Sample	Locus	#Haplotypes	Read Counts	Frequencies	Ploidy??
ON_A29_2	1_20	3	216/137/147	0.432/0.274/0.294	3
ON_A30_28	1_20	3	168/154/178	0.336/0.308/0.356	3
ON_A4_2h	1_20	2	274/226	0.548/0.452	2/4/6

## Tricks & Tips

- Inspect the frequencies of the consensus sequences
- Compare across multiple loci

## Tricks & Tips

- First run with `--freqthreshold 0` to include all consensus sequences and test for inconsistencies
- Check frequency of consensus and compare sequence similarity among consensus sequences

# Outlook

- Web interface + HTML I/O
- Markers based on BUSCO genes
- Modularity
- Integration with other databases and web services

# Thank you!