# Polymorphism-aware phylogenetic models Workshop, MIC-Phy 2021

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#### Introduction

This workshop is available on GitHub.

Our goal is to understand polymorphism-aware phylogenetic models (PoMo) and learn how to apply PoMo to phylogenetic data.

In the course of this workshop, we will infer a phylogenetic tree from a test data set using IQ-TREE2.

If you need help, please interrupt me anytime!

## Preparation - Command line shell

Basic knowledge of the command line shell of your choice is assumed.

- If you do not know basic commands such as cd, ls, or less, just follow the presentation.
- Otherwise, try to complete the workshop yourself.

In case you are lost:

• Have a look at the manual pages, if they exist.

```
1 man less
```

• Read how commands are used.

```
less --help
```

# Preparation - Download workshop and data

#### Option 1: If you have git installed, use it.

```
git clone https://github.com/pomo-dev/micphy-workshop.git
cd micphy-workshop
```

#### Option 2: Manually download the archive.

```
wget https://github.com/pomo-dev/micphy-workshop/archive/master.zip
unzip master.zip
cd micphy-workshop-master
```

#### The advantage of Option 1 is that you can:

- update your working tree using git pull (if I have to change something during the workshop);
- reset to the initial state in case you mess something up with git reset --hard HEAD (be careful, this erases all uncommitted changes made by you).

## Preparation - IQ-TREE2: Installation

Option 1: Repository of your Linux distribution. For example, using Arch Linux and the Arch User Repository.

```
1 yay -S iqtree
2 aura -A iqtree
```

Option 2: Download the binary executable from the IQ-TREE2 homepage. Make sure that you have permission to execute the file (chmod +x), and that the executable is either in your PATH, or that you give the path during execution.

```
iqtree2 --version
/path/to/iqtree2 --version
./relative/path/to/iqtree2 --version
```

### Preparation - IQ-TREE2: Installation

Option 3: Compile yourself (not shown).

Option 4 for script kiddies or experienced users: Use nix-shell and the shell.nix expression provided in the base directory of the repository.

1 nix-shell

Welcome to the MIC-Phy PoMo workshop.

The following version of IQ-TREE2 is available:

IQ-TREE multicore version 2.1.2 COVID-edition for Linux 64-bit built Jan 1 1980 Developed by Bui Quang Minh, James Barbetti, Nguyen Lam Tung, Olga Chernomor, Heiko Schmidt, Dominik Schrempf, Michael Woodhams.

## Preparation - IQ-TREE2: Test version

Depending on how you installed IQ-TREE2, please check that the version agrees with the one I am using.

```
iqtree2 --version

// /path/to/iqtree2 --version
// /relative/path/to/iqtree2 --version
```

IQ-TREE multicore version 2.1.2 COVID-edition for Linux 64-bit built Jan 1 1980 Developed by Bui Quang Minh, James Barbetti, Nguyen Lam Tung, Olga Chernomor, Heiko Schmidt, Dominik Schrempf, Michael Woodhams.

# Exercise - IQ-TREE2: Access help

• How to get help (IQ-TREE).

### Exercise - Run a DNA substitution model

• Run normal model.

### Fruit fly data

Data from PopFly<sup>1</sup>. 9 populations with an average number of samples per population of approximately 19, and an estimated heterozygosity of 0.0109:

```
NTH Netherlands
```

EG Egypt

FR France

**GA** Gabon

**GU** Guinea

EF Ethiopia

KN Kenyia

SB South Africa (Barkly East)

SP South Africa (Phalaborwa)

Why is it important to check the heterozygosity?

<sup>&</sup>lt;sup>1</sup>Hervas et al. (2017).

#### Exercise - Run PoMo

```
iqtree2 -nt 4 -redo -s data/fruit_flies_1000.cf -m HKY+P+N9 -pre fruit_flies_1000.cf.N9
```

- Run PoMo.
- Find best N.
- Compare different DNA substitution models.
- Use gamma rate heterogeneity.
- Probably perform model test?
- Bootstrapping.
- Compare branch lengths for different N values.
- Compare to using normal DNA substitution models.
- Probably provide results for the 10k alignment (different N, different G, with bootstrapping?).

#### Literature

```
PoMo De Maio et al. (2015).
```

Reversible PoMo Schrempf et al. (2016) and Schrempf and Hobolth (2017).

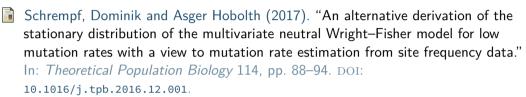
Advanced models with PoMo Schrempf et al. (2019).

IQ-TREE2 Minh et al. (2020).

# Bibliography I

- De Maio, Nicola, Dominik Schrempf, and Carolin Kosiol (2015). "PoMo: An Allele Frequency-Based Approach for Species Tree Estimation." In: *Systematic Biology* 64.6, pp. 1018–1031. DOI: 10.1093/sysbio/syv048.
- Hervas, Sergi, Esteve Sanz, Sònia Casillas, John E Pool, and Antonio Barbadilla (2017). "Popfly: the Drosophila Population Genomics Browser." In: *Bioinformatics* 33.17, pp. 2779–2780. DOI: 10.1093/bioinformatics/btx301.
- Minh, Bui Quang, Heiko A Schmidt, Olga Chernomor, Dominik Schrempf, Michael D Woodhams, Arndt von Haeseler, and Robert Lanfear (2020). "IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era." In: *Molecular Biology and Evolution* 37.5. Ed. by Emma Teeling, pp. 1530–1534. DOI: 10.1093/molbev/msaa015.
- Schrempf, Dominik, Bui Quang Minh, Nicola De Maio, Arndt von Haeseler, and Carolin Kosiol (2016). "Reversible polymorphism-aware phylogenetic models and their application to tree inference." In: *Journal of Theoretical Biology* 407, pp. 362–370. DOI: 10.1016/j.jtbi.2016.07.042.

# Bibliography II



Schrempf, Dominik, Bui Quang Minh, Arndt von Haeseler, and Carolin Kosiol (2019). "Polymorphism-Aware Species Trees with Advanced Mutation Models, Bootstrap, and Rate Heterogeneity." In: Molecular Biology and Evolution 36.6. Ed. by Naruya Saitou, pp. 1294–1301. DOI: 10.1093/molbev/msz043.