

# 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.

```
1 less --help
```

# Preparation - Download workshop and data

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

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

Option 2: Manually download the archive.

```
1 wget https://github.com/pomo-dev/micphy-workshop/archive/master.zip
2 unzip master.zip
3 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).

# Preparation - Installation of IQ-TREE2

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.

```
1 iqtree2 --version
2 /path/to/iqtree2 --version
3 ./relative/path/to/iqtree2 --version
```

# Preparation - Installation of IQ-TREE2

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 - Test IQ-TREE2 version

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

```
1 iqtree2 --version
2 # /path/to/iqtree2 --version
3 # ./relative/path/to/iqtree2 --version
```

IQ-TREE multicore version 2.1.2 COVID-edition for Linux 64-bit built Jan 1 1980  
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Olga Chernomor, Heiko Schmidt, Dominik Schrempf, Michael Woodhams.

## Exercise - How to get help

- How to get help (IQ-TREE).



## Exercise - Run a DNA substitution model

- Run normal model.

## Exercise - Run PoMo

- Run PoMo.
- Find best N.
- Compare different DNA substitution models.
- Use gamma rate heterogeneity.
- Probably perform model test?

# 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](https://doi.org/10.1093/sysbio/syv048).
-  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](https://doi.org/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](https://doi.org/10.1016/j.jtbi.2016.07.042).

## Bibliography II

-  Schrempf, Dominik and Asger Hobolth (2017). “An alternative derivation of the stationary distribution of the multivariate neutral Wright–Fisher model for low mutation rates with a view to mutation rate estimation from site frequency data.” In: *Theoretical Population Biology* 114, pp. 88–94. DOI: 10.1016/j.tpb.2016.12.001.
-  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.