

Polymorphism-aware phylogenetic models

Workshop, MIC-Phy 2021

Dominik Schrempf

February 16, 2021



Eötvös Loránd
University

Introduction

This workshop focuses on understanding and applying polymorphism-aware phylogenetic models (PoMo).

The goal is to 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 the usage information of commands.

```
1 less --help
```

Preparation - Installation of IQ-TREE2 I

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, 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
```

Option 3: Compile yourself (not shown).

Preparation - Installation of IQ-TREE2 II

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
Developed by Bui Quang Minh, James Barbetti, Nguyen Lam Tung,
Olga Chernomor, Heiko Schmidt, Dominik Schrempf, Michael Woodhams.

Preparation - Download of data

- IQ-TREE (install, try, how to get help).
- Test data (download, run normal mode, run PoMo).

Exercises

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.