Polymorphism-aware phylogenetic models
Workshop, MIC-Phy 2021

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Introduction

This workshop is available on GitHub.

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 how commands are used.

```
1  less --help
```

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, 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

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

- Test data (download, run normal mode, run PoMo).

Exercises

- How to get help (IQ-TREE).
- Run normal model.
- Run PoMo.

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.

📄 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 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.