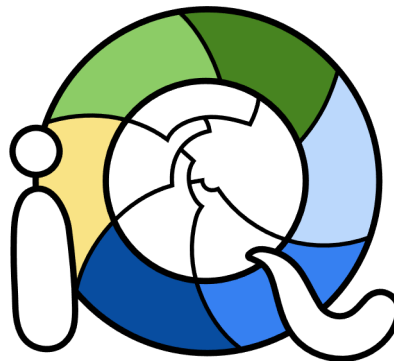


Wednesday 27 – Friday 29 July 2022

Workshop overview

- Interpreting phylogenetic trees
- Phylogenetic methods
- Bayesian phylogenetic analysis
- Molecular dating
- Phylogenomics



Contributors

MOLECULAR ECOLOGY, EVOLUTION, & PHYLOGENETICS LABORATORY



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Programme – Day 1

- | | |
|---------------|--------------------------------------------------------------------------------------|
| 11.00 – 11.10 | Welcome |
| 11.10 – 11.50 | Lecture 1.1: Introduction to molecular phylogenetics |
| 12.00 – 12.45 | Lecture 1.2: Evolutionary models |
| 13.00 – 13.45 | Lecture 1.3: Phylogenetic data |
| 14.00 – 14.45 | Lecture 1.4: Phylogenetic methods |
| 15.00 – 17.00 | Practical 1.1: Sequence alignment and phylogenetic analysis using <i>MEGA</i> |

Programme – Day 2

- 11.00 – 12.00 **Lecture 2.1:** Phylogenetic analysis with *IQ-TREE*
- 12.15 – 14.15 **Practical 2.1:** *IQ-TREE* workshop tutorial
- 14.30 – 15.15 **Lecture 2.2:** Bayesian phylogenetics 1
- 15.30 – 16.00 **Lecture 2.3:** Bayesian phylogenetics 2

Programme – Day 3

11.00 – 12.00 **Lecture 3.1:** Molecular dating

12.15 – 14.15 **Practical 3.1:** Bayesian analysis and molecular dating using *BEAST*

14.30 – 15.15 **Lecture 3.2:** Phylogenomics

15.15 – 16.00 Additional time for questions

Post-workshop **Practical 3.2:** Phylogenomic analysis using *ASTRAL*

Lecture materials

- Lecture slides available on Github
github.com/simon-ho/SydneyPhyloWorkshop
- Recordings of talks will be available on Dropbox after the workshop

Zoom webinar format

- Submit questions during webinar
 - Q&A function (questions not visible to attendees)
 - Chat function
- Answer to questions:
 - Typed responses during or after talks
 - Verbal responses after talks

Practical exercises

- Install software on your own computer
- Data files available on Github
- Teaching assistants will be available to answer questions

Practical 1.1 Sequence alignment and phylogenetic analysis using *MEGA*

Practical 2.1 *IQ-TREE* workshop tutorial

Practical 3.1 Bayesian analysis and molecular dating using *BEAST*

Practical 3.2 Phylogenomic analysis using *ASTRAL*