ABS24: BAYESIAN PHYLOGENETICS AND INFECTIOUS DISEASES

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Villa del Grumello, Via per Cernobbio 11, Como,

26-30 August 2024

Monday August 26th

13.00-14.00	Registration
14.00-16.00	Lecture: Introduction to phylogenetics, phylodynamics and phylogeography
16.00-16.30	Coffee break
16.30-18.30	Lecture: Continuous-time Markov chain (CTMC) models on trees

Tuesday August 27th

9.00-10.30	Lecture: Bayesian phylogenetics
10.30-11.00	Coffee break
11.00-13.00	Practical: Estimating rates and dates in yellow fever
13.00-14.30	Lunch
14.30-16.30	Lecture: Coalescent and birth-death-sampling processes
16.30-17.00	Coffee break
17.00-18.30	Participants' talks

Wednesday August 28th

9.00-11.00	Practical: Phylodynamic inference of respiratory viruses
11.00-11.30	Coffee break
11.30-13.00	Lecture: Scalable gradients in phylogenetics

Thursday August 29th

9.00-10.30	Lecture: Modern CTMCs and phylogeography
10.30-11.00	Coffee break
11.00-13.00	Practical: Phylogeography diffusion in discrete space
13.00-14.30	Lunch
14.30-16.00	Lecture: Approximations and surrogate sampling
16.00-16.30	Coffee break
16.30-18.00	Students' choice lecture
19.00-22.00	Social dinner

Friday August 30th

9.00-11.00	Lecture: Brownian diffusions on trees
11.00-11.30	Coffee break
11.30-13.00	Practical: Phylogeographic diffusion in continuous space

IMPORTANT NOTE

It is important to have your own PC for the practical lessons. Remember to take it with you before leaving.

Please install the following software on your PC in advance to start your lessons smoothly:

- ❖ BEAST X (v10.5.0-beta3) -- download and installation instructions: http://beast.community/installing
- ❖ BEAGLE (v4.0.0) -- download and installation instructions: http://beast.community/beagle
- ❖ FigTree (v1.4.4) -- download and installation instructions: http://tree.bio.ed.ac.uk/software/figtree/
- ❖ Java (>= v9)
- ❖ R (>= 4.0)

REFERENCES

1. Data Integration in Bayesian Phylogenetics (2023) Annual Review of Statistics and Its Application, https://doi.org/10.1146/annurev-statistics-033021-112532

2. Virus genomes reveal factors that spread and sustained the Ebola epidemic (2017) Nature, https://doi.org/10.1038/nature22040