

PIPGES · WEBINARS

MAR · 19
2021

02:00 PM

SCALABLE COALESCENT INFERENCE BY SAMPLING TAJIMA'S TREES

The observed sequence variation at a locus informs about the evolutionary history of the sample and past population size dynamics. The standard Kingman coalescent model on genealogies – timed trees that represent the ancestry of the sample – is used in a generative model of molecular sequence variation to infer evolutionary parameters. However, it is computationally challenging to use this inference when sample size grows. We will discuss a lower-resolution coalescent model, called Tajima heterochronous n -coalescent, as a computationally efficient alternative to the Kingman coalescent. We will study how to quantify the size of the underlying state space, compute the likelihood, employ it in a Bayesian nonparametric model, and use it in applications.

The link will be available
on the day of the event at:

<https://tiny.one/pipges>

SPEAKER

Lorenzo Cappello

Stanford University

Interinstitutional Graduate Program in Statistics (PIPGES) of Federal University of São Carlos with University of São Paulo promotes seminars groups (temporarily webinars, due to pandemic issues) of researches involving Probability, Statistics, Machine Learning etc. Our interest, among other things, is to stimulate the sharing of knowledge, as well as the connection between members of the program and researchers in other institutions.

Organizer

Michel H. Montoril, Department of Statistics,
Federal University of São Carlos.

BIO

Lorenzo Cappello is a postdoctoral fellow since 2018 at School of Humanities & Sciences - Statistics, Stanford University, USA. He has a PhD in Statistics (2018) from Università Bocconi (Italy), with a sandwich period (2015- 2017) at Department of Statistics and Data Sciences, University of Texas (UT), Austin, USA. Among other things, Lorenzo Cappello is interested in Biostatistics and Bayesian nonparametric Statistics.

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