

Seminario Aleatorio

Sesión 373

Speeding up Inference on genetic trees and graphs

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Abstract

Sequencing DNA samples has become cheaper and faster than ever, as a consequence there is an enormous amount of data available to analyse. Many models in genetics involve the coalescent tree, a mathematical construction that has both discrete and continuous features. Performing inference on these trees is very challenging due to their complex nature, however Bayesian Statistics and advanced Monte Carlo methods provide some solutions. For the first part of the talk I will be discussing sequential Monte Carlo methodology for exploring tree spaces, which has some clear computational advantages over Markov Chain Monte Carlo (MCMC). For the second part I will introduce the concept of recombination in bacteria that gives rise to Ancestral Recombination Graphs (ARGs), a generalisation of coalescent trees. Inference on ARGs is typically performed via a reversible-jump MCMC which may perform poorly; however, as presented here, recent developments in Bayesian computation provide ways to improve existing methods and code that may lead to faster inference.

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<https://itam.zoom.us/j/91443909666?pwd=c2JTNzVnSEJEN25lQXhqM1RVeEtXZz09>

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