

Title and abstract submission for contributed talk
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Title: Phylogenetic reconstruction for time reversible models

Abstract: The main goal of Phylogenetics is to find evolutionary relations between biological entities. These relations are inferred from data and are encoded in a graph called a *phylogenetic tree*. The leaves of a phylogenetic tree represent the observed species, and each interior node corresponds to a common ancestor of the species descending from it.

Available data can come from DNA sequences or aminoacid sequences of different species, but once we have the data ¿How to determine which phylogenetic tree accurately represents the evolutionary relations hidden in the data? Generally there are two steps to solve this question: Model selection and phylogenetic reconstruction. On the first step the main goal is to decide how the transition of species occurs, and on the second step the goal is to build the phylogenetic tree. In this talk we focus on the second step in the case when the species evolve under a time reversible model, that is, we focus on the problem of phylogenetic reconstruction under the assumption that our species evolve under a time reversible model.

We start our talk by introducing the problem of phylogenetic reconstruction and defining the time reversible models, then we give an overview of how phylogenetic reconstruction has been done for popular evolutionary models for DNA sequences, and then explore how a toolset from Algebraic Geometry can help us create a general framework to study the phylogenetic reconstruction process for time reversible models. Our main example will be the Tamura Nei model for DNA, which is a continuous-time model with three parameters. We will present phylogenetic invariants that allow us to distinguish whether a tree fits the data. One of the main advantages of this new framework is that it can be used on a broader type of data other than DNA sequences.

This is joint work with Marta Casanellas and Roser Homs Pons.