

# DERIVING EQUATIONS FOR EQUIVARIANT PHYLOGENETIC VARIETIES

**Marta Casanellas**

Universitat Politècnica de Catalunya, Spain

marta.casanellas@upc.edu

Phylogenetics studies the evolutionary relationships among species using their molecular sequences. These relationships are represented on a phylogenetic tree or network. Modeling nucleotide or amino acid substitution along a phylogenetic tree is one of the most common approaches in phylogenetic reconstruction. One can use a general Markov model or one of its submodels given by certain substitution symmetries. If these symmetries are governed by the action of a permutation group  $G$  on the rows and columns of a transition matrix, we speak of  $G$ -equivariant models. A Markov process on a phylogenetic tree or network parametrizes a dense subset of an algebraic variety, the so-called phylogenetic variety.

During the last decade algebraic geometry has been used in phylogenetics for phylogenetic reconstruction and to establish the identifiability of parameters of complex evolutionary models (and thus guarantee model consistency). Since  $G$ -equivariant models have fewer parameters than a general Markov model, their phylogenetic varieties are defined by more equations and these are usually hard to find. We will see that we can easily derive equations for  $G$ -equivariant models from the equations of a phylogenetic variety evolving under a general Markov model. As a consequence, we will discuss the identifiability of networks evolving under  $G$ -equivariant models.

*Joint work with Jesús Fernández-Sánchez (Universitat Politècnica de Catalunya, Spain).*