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**Mateusz Michałek**. *Complete intersections for equivariant models.*

Evolutionary models are needed to study the evolution between nucleotide sequences. Some of the most usual models fit into the *equivariant* definition introduced in terms of the action of a permutation group in the set of nucleotides. *Phylogenetic invariants* are constraints satisfied by the joint probabilities of nucleotide patterns at the leaves of a phylogenetic tree evolving under a given evolutionary model. They have shown to be useful to characterize the model as well as to design methods for phylogenetic inference.

We study and construct phylogenetic invariants of some well-known equivariant phylogenetic models and the general Markov Model. These invariants allow us to describe a (Zariski open) neighbourhood of the no-evolution points in the model as a complete intersection. In other words, we provide a minimal possible number of explicitly constructed phylogenetic invariants that determine the model at biologically meaningful points. Our work is inspired by previous inductive constructions of phylogenetic invariants. It is motivated mostly by applications, as the number of phylogenetic invariants we construct is much lower than the number needed to generate the ideal of the corresponding variety. (Received August 08, 2015)