

Invariants for Small Phylogenetic Trees

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Abstract:

Statistical models based on phylogenies, or evolutionary trees, are used to study and quantify differences between species. A phylogenetic invariant for a model of biological sequence evolution along a phylogenetic tree is a polynomial that vanishes on the expected frequencies of base patterns at the terminal taxa. These invariants have been used, for example, in phylogenetic tree reconstruction generalizing popular methods such as neighbor-joining. Nevertheless, explicitly constructing such invariants is still very challenging. Due to the recursive nature of many algorithms in phylogenetics, it is important to classify these invariants for small phylogenetic trees. This work began in 2004 as part of the book Algebraic Statistics for Computational Biology. Our contribution consists in developing efficient algorithms to compute these polynomial invariants for several models based on small trees. Our results will be recorded as part of a website associated to the book which is and will continue being used in ongoing research in the field of phylogenetics.