

1137-92-300

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Distinguishing phylogenetic networks.

Phylogenetic networks are increasingly becoming popular in phylogenetics since they have the ability to describe a wider range of evolutionary events than their tree counterparts. In this talk, we discuss Markov models on phylogenetic networks, i.e. directed acyclic graphs, and their associated algebra and geometry. In particular, assuming the Jukes-Cantor model of evolution and restricting to one reticulation vertex, using tools from commutative algebra, we show that the semi-directed network topology of large-cycle networks is generically identifiable. (Received February 06, 2018)