

Seminari de Geometria Algebraica 2010/2011 (UB-UPC)

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Lie Markov models

Jeremy Sumner

University of Tasmania (Austràlia)

Recent work in theoretical phylogenetics has discussed the importance of “closure” of the associated probability models that describe the evolution of DNA sequences on trees. For most situations, closure of a phylogenetic model is assured by demanding that the Markov matrices arising from the model form a matrix semi-group. However, it is the case that the most popular models currently in use by practicing biologists does not give rise to a matrix semi-group. Hence, it is important to not only advertise this shortfall, but to also provide viable alternatives.

In this talk, I will discuss how powerful, but elementary, methods of Lie group theory can be applied to produce a complete list and classification of models that are closed. I will discuss how it is important to understand that most models satisfy certain symmetry relations under permutations of DNA nucleotides. I will review basic results of finite group actions and representations, and discuss how we exploit these methods, as well as general Lie theory, to define and construct “Lie Markov models”.

Joint work with Jesús Fernández Sánchez and Peter Jarvis (University of Tasmania).
