



The University of Chicago
Department of Statistics

Mini-seminars for First Year Ph.D. Students

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Maximum Likelihood Methods for Phylogenetic Trees

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110 Eckhart Hall, 5734 S. University Avenue

ABSTRACT

The Brownian motion model for the evolution of characters of species will be used to derive the likelihood of evolutionary tree topologies, given observed mean characters for a set of species. Some examples will be given to illustrate various techniques used in dealing with the likelihood and how to find the ‘most likely’ evolutionary tree. Computational issues will also be briefly discussed. We will follow closely the methods due to Felsenstein (1973, 1981).