Exact likelihood evaluation for phylogenetic trees
with lateral trait transfer

Geoff Nicholls[1], Luke Kelly[1]

[1]Department of Statistics, University of Oxford, UK

Bayesian methods provide useful quantitative tools for phylogenetic analysis. In recent years they have been used for statistical models of language diversification. One approach, such as that of Gray and Atkinson (2003), has been to treat languages as collections of homologous traits evolving along a phylogenetic tree. However, there is to date no likelihood-based inference for models incorporating the lateral transfer of traits between branches of the tree. We address the problem of exact likelihood evaluation for Bayesian inference for a tree with L leaves.

Nicholls and Gray (2008) give a model for trait evolution incorporating lateral transfer of traits. Data is coded as a set of binary traits indicating the presence or absence of a trait in a given homology class. We write down a system of 2^L-1 linear differential equations determining the evolution of the mean frequencies for all site patterns of traits at the L leaves in this model. The system is tractable for small numbers of leaves only. Using a Green's Functions approach, we show how symmetries in the patterns can be used to reduce the system dimension to $O(L^3)$ and this supports a likelihood-based MCMC procedure for phylogenetic inference.

Keywords:
Statistical phylogenetics; likelihood evaluation; language diversification.