Inadmissibility conjectures

March 15, 2006

Consider a finite-state Markov process on a phylogenetic tree T which generates an i.i.d. sequence X of k sites (specifically, consider the symmetric Poisson process, a.k.a. the Jukes-Cantor model, when there are just four states). Given a method M for reconstructing phylogenetic trees from sequences let $P(M(X) = T|T, \lambda)$ denote the probability that M correctly returns the tree T when X is generated by the Markov process on T with branch lengths λ.

Following decision-theoretic terminology, we say that a method M is *inadmissible* if there exists another method M' for which

$$P(M'(X) = T|T, \lambda) \geq P(M(X) = T|T, \lambda)$$

for all fully resolved phylogenetic trees T and choice of (strictly positive, but finite) branch lengths λ, and for at least one such pair (T, λ) we have strict inequality.

Prove (or disprove) the following conjectures.

- Maximum Parsimony is inadmissible

- Maximum Likelihood is inadmissible

Note that ML is known to be admissible in case there is a fixed known value of λ for each tree, and ML is performed subject to this constraint.