1014-92-1316   **Scott R. Herriott*** (`herriott@mum.edu`), 1000 N. Fourth St. #1070, Fairfield, IA 52557.
Modeling the Divergence of Two Genetic Lineages.

Nucleotide substitution data can be used to determine the time since two genetic lineages had a common ancestor. The simplest mathematical model of DNA change used for such dating is akin to carbon-14 dating. However, DNA substitution differs from atomic decay in that repeated substitutions at a site can reverse an earlier change and thus reduce the apparent difference between two lineages as they evolve separately. The more complex divergence models describe substitution among the four nucleotide base pairs as a 4x4 Markov process whose discrete events are Poisson in time. The modeling problem is to derive an equation for q(T), the expected number of nucleotide sites that will appear to be the same in two DNA sequences that have been evolving separately for T years. The data used are the Markov matrix and a vector of initial nucleotide frequencies. This paper derives a new and simple proof of the most elementary result in this field, the Jukes-Cantor equation, where the Markov probabilities and initial frequencies all 1/4. The paper then derives a formula for q(T) in the general case of any Markov matrix and any initial frequency vector, assuming first a common substitution rate across sites and generalizing to a substitution rate that varies according to a gamma distribution. (Received September 27, 2005)