1014-92-468   **Elizabeth S. Allman** and **John A. Rhodes*** (`j.rhodes@uaf.edu`), Department of Mathematics and Statistics, University of Alaska Fairbanks, PO Box 756660, Fairbanks, AK 99775. *Identifiability of the covarion model of phylogenetics.*

The covarion model of molecular evolution extends more standard base-substitution models by incorporating a switching mechanism in which any site in a sequence may change back and forth between being free to mutate (on) and being held invariable (off) in different parts of the tree. When sequences are observed, however, the on-off state of sites is hidden. The covarion model is believed to increase biological realism in some situations, but identifiability results are needed to justify its use in inferring evolutionary trees from sequence data.

In particular, from a joint distribution of states at the leaves of the tree it is possible to identify the tree topology. Provided there are sufficiently many leaves on the tree, substitution probabilities describing mutations on internal edges of the tree are also identifiable. The key elements of the proof come from algebraic considerations of a more general model. (Received September 16, 2005)