1014-14-1439   **Serkan Hosten*** (`serkan@math.sfsu.edu`), Department of Mathematics, 1600 Holloway Avenue, San Francisco, CA 94132. *Bounds for real solutions to likelihood equations of phylogenetic trees.* Preliminary report.

Commonly used Markov models for molecular evolution of DNA such as Jukes-Cantor and Kimura models are toric models. The estimation of parameters can be done by solving a maxiumum likelihood problem. The number of complex solutions for associated likelihood equations has been studied. In this work, we give bounds for the number of real critical solutions, in particular for the biologically meaningful ones. (Received September 28, 2005)