1041-05-45   **Kord Eickmeyer**, Institut für Informatik, Humboldt-Universität zu Berlin, Berlin, Germany, and **Ruriko Yoshida*** (`ruriko.yoshida@uky.edu`), Department of Statistics, University of Kentucky, 805A Patterson Office Tower, Lexington, KY 40506. *Geometry of the Neighbor-Joining Algorithm for Small Trees.*

In 2007, Eickmeyer et al. showed that the tree topologies outputted by the Neighbor-Joining (NJ) algorithm and the balanced minimum evolution (BME) method for phylogenetic reconstruction are each determined by a polyhedral subdivision of the space of dissimilarity maps $\mathbb{R}^{\binom{n}{2}}$, where n is the number of taxa. In this talk, we will present the behavior of the Neighbor-Joining algorithm on five and six taxa and study geometry and combinatorics of the polyhedral subdivision of the space of dissimilarity maps for six taxa as well as hyperplane representations of each polyhedral subdivision. We will also present some simulation results for one of the questions stated by Eickmeyer et al., that is, the robustness of the NJ algorithm to small perturbations of tree metrics, with tree models which are known to be hard to be reconstructed via the NJ algorithm.

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