

1147-92-822

**Elizabeth Gross\*** (egross@hawaii.edu), Honolulu, HI 96822, and **Hector Banos** (hdbanoscervantes@alaska.edu), **Nathaniel Bushek** (bush0320@d.umn.edu), **Ruth Davidson** (redavid2@illinois.edu), **Pamela Harris** (pamela.e.harris@williams.edu), **Robert Krone** (rkrone@math.ucdavis.edu), **Colby Long** (long.1579@mbi.osu.edu), **Allen Stewart** (stewaral@seattleu.edu) and **Robert Walker**. *Dimensions of group-based phylogenetic mixtures.*

Identifiability results for 2-tree mixture models have relied on knowing the dimension of their corresponding join varieties, which raises the following question: When do the secants and joins of toric varieties corresponding to group-based phylogenetic tree models have the expected dimension? In 2011, Allman, Petrovic, Sullivant, and Rhodes showed that for the Jukes-Cantor model, the associated secant varieties of 2-tree mixtures have the expected dimension. In this talk, we extend this result and show that for the Kimura 2-parameter and Kimura 3-parameter models and any pair of trees (not necessarily binary), the corresponding join variety has the expected dimension. Additionally, we will discuss generalizations of this result to arbitrary group-based models and mixtures of an arbitrary number of trees. (Received January 29, 2019)