

Probability Seminar

Organizer: Tai Melcher & George Kordzakhia

Wednesday, 3:10–4:00pm, 330 Evans

May 10 **Erick Matsen**, Harvard

Uquity of synonymity: almost all large binary trees are not uniquely identified by their spectra or their immanantal polynomials

Phylogenetic tree shape statistics are numerical summaries of some aspect of the shape of a phylogenetic tree. Up to this time, most of the work on tree shape has been done using ad-hoc formulas which attempt to quantify some visible feature of tree shape. In this talk I will present some joint work with Steve Evans investigating a more mathematically natural approach based on matrix representations of the tree. The matrix representations we consider are the adjacency matrix, the Laplacian matrix (that is, the infinitesimal generator of the natural random walk), and the matrix of pairwise distances between leaves. We show for any of these choices of matrix that the fraction of binary trees with a unique spectrum goes to zero as the number of leaves goes to infinity.