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Seth Sullivant* (smsulli2@ncsu.edu). *Maximum agreement subtrees.*

Probability distributions on the set of trees are fundamental in evolutionary biology, as models for speciation processes. These probability models for random trees have interesting mathematical features and lead to difficult questions at the boundary of combinatorics and probability. This talk will be concerned with the question of how much two random trees have in common, where the measure of commonality is the size of the largest agreement subtree. The case of maximum agreement subtrees of pairs of random comb trees is equivalent to studying longest increasing subsequences of random permutations, and has connections to random matrices. This elementary talk will try to give a sense of what is known (not very much) and what is unknown (lots!) about this problem. (Received February 13, 2018)