Abstract Submitted
for the MAR15 Meeting of
The American Physical Society

Coalescent theory analysis of phylogenetic trees in a model of evolutionary dynamics[1] DAWN KING, SONYA BAHAR, University of Missouri at St. Louis — Phylogenetic trees and the hierarchal, biological levels of organization that exist within them are of great importance to evolutionary theory. With a neutral, agent-based model of evolutionary dynamics, we have investigated the conditions under which organisms form clusters, analogous to species. Previous work has shown phase transition behavior as a function of the maximum mutation size (μ) on a rugged landscape with assortative mating (Dees and Bahar, 2010), and, with the addition of bacterial fission, on a completely neutral landscape (Scott *et al.*, 2013). The bacterial version was then classified as belonging to the directed percolation universality class (Scott, 2014). Here, we further investigate the emergent property of speciation by analyzing the genealogical tree structures created by the forward-in-time reaction-diffusion dynamics of the three mating types – assortative, bacterial, and random – as a function of the random death percentage. Specifically, we will use Kingman's n-coalescent to investigate the distributions of the times to most recent common ancestor (TMRCA) and determine whether universal ratios exist.

[1] Supported by a "Studying Complex Systems" grant from the James S. McDonnell Foundation.

Dawn King
University of Missouri at St. Louis

Date submitted: 13 Nov 2014

Electronic form version 1.4