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Sivan Rottenstreich* (sr286@georgetown.edu), Georgetown University, Mathematics
Department, St. Mary's Hall, 3rd Floor, Washington, DC 20057. *A Coalescent Theory Analysis of
a Population Structure Statistic.*

Populations are often divided into subpopulations or demes. An individual in a given deme tends to mate with other individuals in that same deme. This preferential mating pattern leads to the evolutionary phenomenon of inbreeding. F_{st} is a statistic that biologists use to estimate inbreeding levels. Inbreeding levels are correlated with levels of migration and population subdivision. Biologists use F_{st} to estimate migration rates and perform hypothesis tests for the existence of population subdivision.

In this talk we introduce a stochastic model of evolution in a subdivided population. We then use coalescent theory to analyze the distribution of F_{st} . We prove rigorous results describing the distribution of F_{st} under different mutation rates. We show that under certain scaling limits, F_{st} will converge to a deterministic value while under other scaling limits F_{st} converges to a random variable with large variance. We show that the key quantity in determining the variance of F_{st} is the product of mutation rate and population size. Finally, we comment on the implication of our results to biological applications. (Received January 21, 2008)