

STATISTICS COLLOQUIUM

MONDAY, MARCH 05, 2012

TALK: 4:00 P.M. — SCIENCE CENTER RM. 309

RECEPTION: 5:15 PM — SCIENCE CENTER, 7TH FLOOR

“Gene genealogies within a fixed pedigree, and the robustness of Kingman's coalescent”

**John Wakeley
Harvard University**

ABSTRACT

I will discuss a conceptual flaw in the backward-time approach to population genetics called coalescent theory as it is applied to diploid bi-parental organisms. Specifically, the way random models of reproduction are used in coalescent theory is not justified. Instead, the population pedigree for diploid organisms---that is, the set of all family relationships among members of the population---although unknown, should be treated as a fixed parameter, not as a random quantity. Gene genealogical models should describe the outcome of the percolation of genetic lineages through the population pedigree according to Mendelian inheritance. Using simulated pedigrees, some of which are based on family data from 19th century Sweden, I will show that in many cases the (conceptually wrong) standard coalescent model is difficult to reject statistically, and in this sense may provide a surprisingly accurate description of gene genealogies on a fixed pedigree. I will further illustrate the differences between the fixed-pedigree coalescent and the standard coalescent with analytical and simulation results. Differences are apparent in recent past generations, roughly $< \log_2(N)$ generations, but then disappear as genetics lineages are traced into the more distant past.