MICHIGAN STATE UNIVERSITY

Department of Statistics and Probability

COLLOQUIUM

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Inference of population history and natural selection from large samples of genomic data

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Abstract

Demographic inference refers to the problem of inferring past population events (migrations, admixture, expansions, etc.) from patterns of mutations found in sampled DNA. Apart from intrinsic appeal of understanding, for example, our origins and the peopling of our planet, this type of analysis is useful for forming a null model of human evolution, departures from which signal the presence of natural selection, population structure, and other interesting phenomena.

In this talk I will discuss recent statistical and computational innovations which enable us to infer demographies using modern data sets consisting of hundreds of whole-genome sequences obtained from populations all over the world. These include momi, a new software package for stable and rapid computation of the expected sample frequency spectrum (SFS) under complex demographic scenarios involving numerous diverged populations, as well as SMC++, a new probabilistic framework which couples the genealogical SMC++ process for a given individual with allele frequency information for a large panel of related samples. I will demonstrate how we are using these tools to learn about human expansion in the last 12,000 years, understand the mysterious origins of ancient DNA samples, and estimate when Europeans acquired lighter skin and the ability to digest lactose. Finally, I will discuss recent probabilistic results which enable us to control false discoveries in these procedures by reasoning about the distribution of pairwise shared ancestry that occurs under the neutral coalescent.

Portions of this work are joint with Jack Kamm, Pier Palamara, Dan Erdmann-Pham and Yun Song.

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