

BI-CO MATHEMATICS COLLOQUIUM

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“Using exact ascertainment and joint spectra to learn human genetic history”

Friday, March 23, 2012

Talk at 4:30 – KINSC H109
Tea at 4:15 – KINSC Math Lounge, H208

Abstract: We begin with a brief description of the nature of the data that modern technology is now making available in genetics. We review ‘f-statistics’, a useful methodology for learning about genetic phylogeny. We give some examples that we found to be surprising. We motivate the definition of the ‘allelic spectrum’, and then show how algebraic methods can be used to calculate it exactly given a specific demography. We describe some remarkable data that we have generated, explain why ancient alleles (such as from the Neandertal genome) are useful for the analysis, and show implications for the genetic history of Africa.

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