

COLLOQUIUM

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Mitochondria, Aging, and Sequencing Errors

Tuesday, April 3, 2012

A405 Wells Hall

10:00 a.m. - 10:50 a.m.

Refreshments: 9:40 a.m.

PLEASE NOTE TIME CHANGE

Abstract

We all lose strength as we age, accelerating as we grow older. One hypothesis for this is that the muscle mitochondria, which are exposed to a large amount of oxidative stress, accumulate DNA errors over time. A local study to explore this has collected muscle biopsy tissue from multiple grandmother-mother-daughter sets, and sequenced their mitochondrial DNA with a high depth of coverage using the Illumina platform. Each read from this platform is tagged with a reliability score, and most analysis pipelines start by discarding all reads below some threshold and then taking the consensus of all the others; the underlying biological model is that there is a "true" answer at each base. Here we are interested in the true variability at each base (some locations may have high mutation rates, some low); we use all the data and explicitly incorporate the reliability values into the analysis. This talk will describe the analysis model along with some interesting aspects of the data found along the way, e.g. run to run variability and A/C/G/T specific biases.

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