

Undergraduate Colloquium in Mathematics
Wednesday, February 28th, 3:00 PM – 4:00 PM
Center for the Visual Arts, Room 149

**Distinguishing Between Genetic Drift
and
Selection Using a Modification of Tajima's D Statistic**

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Abstract:

Many statistical measures have been applied to genetic sequences to discern evolutionary history. One commonly used statistic, Tajima's D statistic, is used to analyze evolutionary trends of genetic data; in particular, is it used to determine if a population is increasing or decreasing in genetic diversity. However, it can't distinguish between genetic drift (random fluctuations in allele percentages) and selection. We applied Tajima's D statistic to synonymous (non protein-changing) and nonsynonymous (protein-changing) mutations separately to answer this question. Our team wrote computer software to simulate different types of evolutionary processes and then analyzed a sample of HIV data to determine the type of selection pressure an organism was under. Our results suggest that the modified version of Tajima's test can distinguish among several major evolutionary models but it has limited power.



