

1035-B1-740

**Pam J Ryan\*** (pjryan@truman.edu), 100 E Normal St, Dept of Mathematics and Computer Science, Truman State University, Kirksville, MO 63501. *An Extension of Tajima's D Statistic by a Student-Faculty Cross-Interdisciplinary Team*. Preliminary report.

Through an NSF grant, Truman State has been able to fund cross-interdisciplinary teams of faculty and undergraduates to do mathematical biology research. My team is composed of one math and one biology professor, one math student, and two biology students. Our question relates to Fumio Tajima's 1989 paper, in which he introduced a new statistic (commonly called Tajima's D) to analyze evolutionary trends of genetic data. The statistic is used to determine if a population is increasing or decreasing in genetic diversity. However, it doesn't distinguish between genetic drift (random fluctuations in allele percentages) and selection. Anton Weisstein (the biology professor on our team), in his dissertation, introduced the idea of applying Tajima's D statistic to synonymous and nonsynonymous mutations separately to answer this question. A synonymous mutation results in a change to an amino acid in a protein; a nonsynonymous mutation does not change the amino acids in a protein. Our team is writing computer software to simulate different types of evolutionary processes and will then analyze samples of data to determine the type of selection pressure an organism is under. I will talk both about our research program in general and our specific project. (Received September 14, 2007)