

1067-X1-1689

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Through an NSF grant, Truman State University has been able to fund cross-interdisciplinary teams of faculty and undergraduates to do mathematical biology research. Our team is considering an extension of Tajima's D statistic, which 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 doesn'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 data to determine the type of selection pressure an organism was under. I will talk both about our research program in general and our specific project. (Received September 21, 2010)