Research Experiences for Undergraduates (REU) 2012 Abstract

DILLON, J., LI, W., PEREZ, A., GILCHRIST, M., and J.J. CHAI. Modeling Protein Translation and Genome Evolution National Institute for Mathematical and Biological Synthesis, Knoxville, TN, University of Scranton, Scranton, PA, Luther College, Decorah, IA, University of Texas, El Paso, TX, University of Tennessee, Knoxville, TN.

In amino acids with multiple synonymous codons there is a redundant tendency to use certain codons over others. This tendency, referred to as codon usage bias (CUB), remains relatively unexplained. Our model assumes that this bias is related to the overhead cost of ribosome usage. Protein translation is an extremely expensive cellular process, so we assume selection for faster translation and thus a larger pool of free ribosomes. This seems sensible, as it appears this bias favors codons which stall the ribosome less and thus are translated quicker. A correlation of 0.67 was observed between MAP values of protein production rate attained from our model and empirically measured rates in *S.cerevisiae*. Because of experimental error in the measured rates, the variable nature of protein production, and the stochastic quality of evolution itself, we can't expect to achieve a 1-to-1 correlation. However, since our current model is based on ribosome pausing, a finite cellular energy budget, and principles of population genetics and probability,greater accuracy can be achievedby expanding our model to account for more biological phenomena. The significance of this model is that it allows us to leap from a genotype, or codon frequencies, to predicting a corresponding protein production rate. This has major implications for species whose protein production rates have not been empirically measured.