

James Dillon, University of Scranton, Scranton, PA and NIMBioS: National Institute for Mathematical and Biological Synthesis, Knoxville, TN, USA

Weijie Li, Luther College, Decorah, IA and NIMBioS, Knoxville, TN, USA

Andre Perez, University of Texas, El Paso, TX and NIMBioS, Knoxville, TN, USA

Juanjuan Chai, NIMBioS, Knoxville, TN, USA

Michael Gilchrist, Department of Ecology and Evolutionary Biology, University of Tennessee and NIMBioS, Knoxville, TN, USA

Modeling protein translation and genome evolution

Protein translation, an important step in gene expression that assembles the proteins used throughout the cell, is one of the most fundamental and conserved biological processes. Yet like all biological processes translation has intrinsic costs and processing errors. Due to redundancy inherent in the genetic code (e.g. codons GAA and GAG both code for glutamic acid), the evolution of coding sequences will be influenced by these costs and errors. The goal of this summer's research be to use mathematical models of the intra-ribosomal processes responsible for the costs and errors during protein translation in order to study the patterns found within the genomes of different organisms. The outcome of this work will be a better understanding of how the ribosome works and, in turn, our ability to extract information from genomic sequences.

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