A post-doctoral research position is available in Dr. M.A. Gilchrist’s lab in the Dept. of Ecology & Evolutionary Biology at the University of Tennessee, Knoxville. The position is supported by a three year NSF focused on the development, integration and testing of multiple models of protein translation and sequence evolution using public genomic and gene expression datasets. More specifically, the goal is to understand the role of translation costs and errors and gene expression in the evolution of codon usage bias.

This research project is highly interdisciplinary drawing on concepts in cellular biology, evolutionary theory, statistics, and biophysics. Therefore, we are seeking candidates with a Ph.D. in biology, mathematics, physics, computer science, engineering, or statistics and some background at least one of the other areas. Research will involve using small and large scale clusters including those at the National Institute for Computational Sciences housed nearby at Oak Ridge National Laboratory (ORNL). Successful candidates will be able to work both independently and in collaboration with the PI, have good oral and written communication skills, proficient programming skills in higher level languages such as R or C, and have first-author publications in reputable journals.

In addition to working with the PI, the position provides opportunities for interactions with other faculty and researchers at the University of Tennessee, ORNL, and the National Institute for Mathematical and Biological Synthesis.

Application requirements:

- Current CV including three references
- Brief statement of research background and interests
- Copies of 1 to 3 relevant manuscripts

Application materials should be submitted in PDF format to bioinfo.postdoc@utk.edu. Review of applications is on going and will continue until the position is filled.

The Knoxville Metropolitan Area has a population of over half a million, a relatively low cost of living, and year round outdoor and cultural activities. The University of Tennessee is an equal opportunity employer.

Comparison between predicted and observed codon usage vs. gene expression level in yeast based on a model of ribosome overhead costs and population genetics. Taken from Shah and Gilchrist 2011