Postdoctoral Research Position: Evolutionary Bioinformatics
Dept. of Ecology & Evolutionary Biology
University of Tennessee Knoxville

Outstanding, motivated candidates are being sought for a post-doctoral position in the Gilchrist lab in the Department of Ecology & Evolutionary Biology at the University of Tennessee, Knoxville. The successful candidate will be supported by a three year NSF grant whose goal is to develop, integrate and test mathematical models of protein translation and sequence evolution using available genomic sequence and expression level datasets. Publications directly related to this work include Gilchrist. M.A. 2007, Molec. Bio. & Evol. (http://www.tinyurl/shahgilchrist11) and Shah, P. and M.A. Gilchrist 2011, PNAS (http://www.tinyurl/gilchrist07a).

The emphasis of the laboratory is focused on using biologically motivated models to analyze complex, heterogeneous datasets to answer biologically motivated questions. The research associated with this position draws upon a wide range of scientific disciplines including: cellular biology, evolutionary theory, statistical physics, protein folding, differential equations, and probability. Consequently, the ideal candidate would have a Ph.D. in either biology, mathematics, physics, computer science, engineering, or statistics with a background and interest in at least one of the other areas.

The researcher will collaborate closely with the PIs (Drs. Michael Gilchrist and Russell Zaretzki) on this project but potentiall have time to collaborate on other research projects with the PIs. In addition, the researcher will have opportunties to interact with other faculty members in the Division of Biology as well as researchers at the National Institute for Mathematical and Biological Synthesis (http://www.nimbios.org).

Review of applications begins immediately and will continue until the position is filled. To apply, please submit curriculum vitae including three references, a brief statement of research background and interests, and 1-3 relevant manuscripts to *mikeg[at]utk[dot]edu*.

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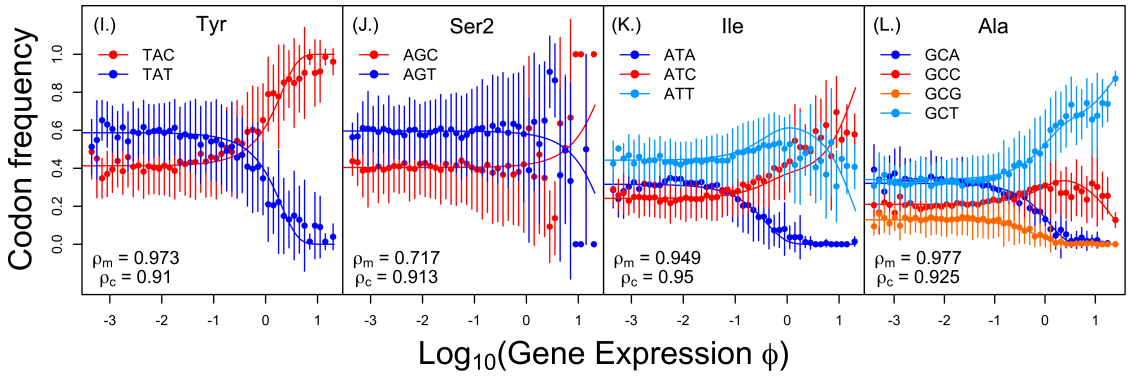

Comparison between predicted and observed codon usage vs. gene expression level in yeast based on a model of ribosome overhead costs and population genetics. Taken from Shah and Gilchrist 2011