



SCHOOL OF INFORMATICS AND COMPUTING

Center for Bioinformatics Research Talk



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Indiana Memorial Union, Walnut Room

Thursday, March 30, 2017, 3:00 PM

Inferring natural selection on proteins from population- and network-scale models

Abstract: My group aims to understand how mutations and natural selection drive the evolution of the complex biomolecular networks that underlie life. To do so, we build detailed computational models to compare with genomic and experimental data. I'll first discuss recent "top-down" work in which we developed a novel diffusion approach to model the evolution of triallelic sites. Applying this model to fruitfly data, we for the first time inferred the correlation of selection strength between mutations at the same protein site. Remarkably, we found quantitative agreement between our genomic inference and direct biochemical experiments in other organisms. I will then discuss recent "bottom-up" work in which we used sensitivity analysis of biochemically-detailed network models to predict rates of protein evolution. Contrary to much recent work, our results suggest that natural selection on protein function is as important as selection on protein biophysics.

Biography: Ryan Gutenkunst received his Ph.D. in physics from Cornell University, where he worked with Jim Sethna on unveiling universal "sloppy" parameter sensitivities in systems biology models and on modeling their evolutionary implications. He then did a postdoc with Carlos Bustamante, where he developed $\partial a \partial i$, a powerful method for inferring population histories from genomic data. His second postdoc was with Byron Goldstein at Los Alamos National Lab, where Ryan modeled aspects of immune signaling in mast cells. Ryan joined the faculty in Molecular and Cellular Biology at the University of Arizona in Fall 2010. He is also a member of the BIO5 Institute, the Departments of Ecology and Evolutionary Biology and Epidemiology and Biostatistics, and the Graduate Programs in Applied Mathematics, Genetics, and Statistics. He continues to work on both systems biology and population genetics, with a focus on understanding the evolution of biomolecular networks.



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