

Center for Bioinformatics Research Talk

Antonis Rokas

Thursday, October 23, 2014

4:00pm

Oak Room, IMU

Harnessing Genomics for Phylogenetic Insights

Abstract: A fully resolved tree of life remains one of evolutionary biology's holy grails. Historically, the greatest hindrance to attaining this goal has been that the amounts of linear sequence data available were too few to generate a fully resolved phylogeny of all life. The ever-increasing availability of new genome sequences coupled with the emergence of powerful new DNA sequencing technologies have led to the generation of unprecedented amounts of data from an abundance of organisms, us into the era of phylogenomics, and obliterated sequence data collection as a limiting factor. However, even with data from hundreds or thousands of genes, fully resolved phylogenies are rarely attained due to the presence of conflict between different gene trees, a phenomenon known as incongruence. My talk will present recent work from my group on the problem of incongruence.



Short Bio: I am an Associate Professor of Biological Sciences and Biomedical Informatics at Vanderbilt University and the holder of the Cornelius Vanderbilt Chair in Biological Sciences. I received my Ph.D. in 2001 from Edinburgh University for research on the evolutionary ecology of oak-feeding gallwasps. Before my joining Vanderbilt, I worked at the Broad Institute of MIT and Harvard as a Research Scientist (2005-2007), and at the University of Wisconsin-Madison as a postdoctoral fellow (2002-2005). Research in my lab combines computational and experimental

approaches to investigate the factors influencing phylogenetic accuracy and their usefulness in obtaining more robust phylogenies, the molecular origins of human pregnancy, and the molecular foundations of the fungal lifestyle. Further information is available at as.vanderbilt.edu/rokaslab



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