NIMBioS

National Institute for Mathematical and Biological Synthesis

cordially invites you to an

Interdisciplinary Seminar

with

NIMBioS Postdoctoral Fellows Invited Distinguished Visitor

Dr. Ward Wheeler

on

"Improvements in tree and network alignment algorithms"

Tuesday, April 18, 2017
3:30-5 p.m.
Reception & refreshments at 3 p.m.

Hallam Auditorium, Room 206
1122 Volunteer Boulevard

Dr. Ward Wheeler is Curator-in-Charge of the American Museum of Natural History Science Computing Facility and professor of the Richard Guilder Graduate School. His research focuses on systematic theory and its application to the historical relationships among and within a number of metazoan lineages. He has developed theory and algorithms to interpret evolutionary patterns from multiple sources of phylogenetic information including anatomy, behavior, and a diversity of genomic information. His laboratory at the AMNH reconstructs evolutionary graphs to study how metazoan taxa and their anatomy and genomes have evolved over the past 500 million years. Wheeler develops software and hardware tools that are put to use in the museum's quest to link extinct lineages with the genomes, morphology, and behavior of species that survive today. Wheeler joined the Museum in 1989 and has authored over 150 scientific publications and books, including a general textbook of systematics. He has also authored software packages and has been awarded a US patent in DNA sequence analysis.

Abstract: Tree-Alignment (sensu Sankoff) has been known to be NP-hard for some time. Recent improvements in both the quality (in terms of optimality score) and time complexity of heuristic approaches to this problem are discussed in the context of soft-wired networks. The effectiveness of these approaches to both simulated and real data sets are discussed.

THE UNIVERSITY OF TENNESSEE KNOXVILLE

**The seminar will be live streamed. Visit
http://www.nimbios.org/videos/livestream.
Join the conversation on Twitter using #nimbios**

NSF