



UNIVERSITY of

NIMBioS Interdisciplinary Seminar

Dr. James Degnan Dept. of Mathematics and Statistics Univ. of Canterbury

3:30 p.m.*, April 10, 2012 NIMBioS, Blount Hall, 1534 White Ave, 4th floor

"Modeling hybridization: Gene trees in species networks"

Over the last few years, many methods have been developed to infer species relationships (species trees) from trees inferred from molecular data (gene trees). Several of these methods assume a particular model, called the multispecies coalescent, which typically assumes that all incongruence between gene trees and species trees is due to incomplete sorting, in which the most recent common ancestor of two gene copies is more ancient than their most recent ancestral population. As species tree methods mature, it is becoming possible to simultaneously model other sources of incongruence as well, such as hybridization and gene duplication. Although closely related species are likely to have incomplete lineage sorting as a source of incongruence, some groups, such as plants, fish, and insects, are particularly likely to experience hybridization as well. I will report on some recent efforts to model gene tree probabilities when species relationships are not tree-like due to hybridization and discuss some open problems in this area.

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*Join us for refreshments in the NIMBioS Lobby on the 4th floor at 3 p.m.

For more information about this and other NIMBioS Seminars, visit http://www.nimbios.org/seminars

The National Institute for Mathematical and Biological Synthesis (NIMBioS) brings together researchers from around the world to collaborate across disciplinary boundaries to investigate solutions to basic and applied problems in the life sciences. NIMBioS is sponsored by the National Science Foundation, the U.S. Department of Homeland Security, and the U.S. Department of Agriculture with additional support from The University of Tennessee, Knoxville.

