



# NIMBioS

National Institute for Mathematical  
and Biological Synthesis



## **NIMBioS Interdisciplinary Seminar** **Dr. Juanjuan “JJ” Chai** **NIMBioS Postdoctoral Fellow**

**3:30 p.m.\*, November 8, 2011**  
**NIMBioS, Blount Hall, 1534 White Ave, 4<sup>th</sup> floor**

### **“On the number of binary characters needed to recover a phylogeny using maximum parsimony”**

In phylogenetics it is known that for a given set of characters, under maximum parsimony, there could be more than one phylogeny with the most parsimonious score. In a special case where each character only changes its state once, the most parsimonious tree is unique. This case is called homoplasy-free and the number of characters required is on the same order of the number of taxa in the phylogeny. Steel and Penny conjectured that given  $C \cdot \log N$  binary characters, one can recover the unique maximum parsimonious tree with  $N$  taxa. We give an explicit construction to show that this is true. Biologically, this means that some patterns of homoplasy are phylogenetically informative and can exponentially reduce the amount of data needed to resolve a phylogeny.

*\*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.*