ABSTRACT:
Recent advances in DNA sequencing technology have led to new mathematical challenges in the analysis of the massive datasets produced in current evolutionary studies. In particular, much progress has been made in the design and analysis of computationally efficient algorithms for assembling the Tree of Life from present-day molecular sequences. In the first half of the talk, I will briefly review some of the mathematical techniques that have led to our current understanding of large-scale tree-building algorithms. Prior theoretical results, however, often rely on statistical models of molecular evolution that are too simplistic. In the second half, I will discuss recent work on the probabilistic modeling and analysis of more complex settings, including insertion-deletion events and lateral genetic transfer. No biology background will be assumed.

TITLE:
Assembling the Tree of Life: Theory Beyond the Substitution-Only Model of Sequence Evolution

SPEAKER:
Professor Sebastien Roch
Dept. of Mathematics
UW-Madison

TIME & PLACE:
Wednesday, January 30, 2013
Room 140 Bardeen
4:00-5:00p

Cookies & Coffee @ 3:30 in Rm 1210 MSC