Title: Statistical inference from the tree of life
Speaker: Dr. Claudia Solis-Lemus, University of Wisconsin-Madison
Date: Tuesday, January 24th
Time and Location: 12:05-12:50pm in 3-1637

Abstract: Phylogenetics studies the evolutionary relationships between different organisms, and its main goal is the inference of the tree of life. Usual statistical inference techniques like maximum likelihood and bayesian inference through Markov chain Monte Carlo (MCMC) have been widely used, but their performance declines as the datasets increase (in number of genes or number of species). I will present two new approaches suitable for big data: one, importance sampling technique for bayesian inference of phylogenetic trees, and two, a pseudolikelihood method for inference of phylogenetic networks. The proposed methods will allow scientists to include more species into the tree of life, and thus complete a broader picture of evolution.