## RUTGERS UNIVERSITY DEPARTMENT OF STATISTICS AND BIOSTATISTICS HILL CENTER #501, BUSCH CAMPUS, PISCATAWAY

## www.stat.rutgers.edu

## Seminar

**Speaker:** Paul Edlefsen, Harvard University

**Title:** Profile HMMs for DNA sequence families: the Conditional Baum-Welch and

Dynamic Model-Surgery algorithms

**Date:** Thursday January 21, 2010

**Time:** 12:00 Noon

Place: 552 Hill Center

## **Abstract**

Profile hidden Markov Models (Profile HMMs) are widely used for protein sequence family modeling, but are rarely used for modeling DNA sequence families because the Baum-Welch EM algorithm used to parameterize Profile HMMs performs particularly poorly in the DNA context. I will report the results of a simulation study comparing the Baum-Welch algorithm to two new approaches, Conditional Baum-Welch and Dynamic Model Surgery, showing that these provide a great improvement over Baum-Welch in both the protein and DNA domains. I will also compare these methods in the context of the transposon (interspersed repeat) modeling problem that originally inspired the research.