

Computation and **I**nformatics in **B**iology and **M**edicine
Training Program

Steve Goldstein, Ph.D.

CIBM Postdoctoral Fellow
Genetics/Biotechnology Center
Laboratory of Prof. David Schwartz
University of Wisconsin-Madison

***Sequences, maps, genomes
and graphs***

Optical mapping and sequencing are two systems capable of producing accurate, genome-wide descriptions of an organism's DNA, albeit at different scales. As the number of organisms mapped or sequenced grows, the analysis of these data is generating an increasingly rich set of biological questions and hypotheses. For example, a comparison of the sequences of two closely related organisms gives a wealth of information relating phenotype and genotype.

In this talk, I will present an algorithmic approach to genomic comparisons based on an abstraction known as the deBruijn graph. DeBruijn graphs provide an intuitive description of the data and have previously been used in whole-genome sequence assembly algorithms. I will describe a general method for efficiently representing data in a deBruijn graph and show how to apply the method to sequence- and map-based genomic comparisons and to sequence assembly base-calling error correction.

**Tuesday, March 11th
4:00 p.m.**

Room 1221
Computer Sciences / Statistics Building
1210 West Dayton Street