

GSTP

Seminar Series

University of Wisconsin–Madison
Genomic Sciences Training Program

*Fostering new paradigms for the
biological sciences*

Brad Anderson, PhD

GSTP Postdoctoral Fellow
Laboratory of Nicole Perna
Department of Animal Health and Biomedical Sciences and
Genome Center of Wisconsin
University of Wisconsin-Madison

Thursday, February 24th, 2005

5:00 p.m.

Room 1408, Genetics/Biotechnology Center, 425 Henry Mall

CGHScan: A Novel Algorithm for Establishing Deletion Boundaries Using Comparative Genomic Hybridization Data

Abstract:

Genome sequencing permits the design of high-density microarrays that can be used to perform many different kinds of functional genomics analyses. One such technique, comparative genomic hybridization (CGH), can rapidly identify the conserved and deleted/divergent regions between two organisms, especially for bacteria where chip density permits representation of the entire genome on a single microarray. We have developed an algorithm that analyzes normalized data to detect the boundaries of deleted or divergent regions in a genome independently of genome annotation. The program, CGHScan, uses an iterative random walk approach that integrates multi-layered significance testing to establish boundaries of differing regions between genomes from CGH data. The fact that CGHScan is independent of genome annotation permits higher resolution of such regions, which also more accurately reflects the biological events that causes regions to be deleted, which are also independent of genome annotation. An adaptation of the algorithm for the purpose of analyzing expression microarray data will also be presented.
