ABSTRACT:
Alternative splicing and other processes that allow for different transcripts to be derived from the same gene are significant forces in the eukaryotic cell. RNA-Seq is a promising technology for analyzing alternative transcripts, as it does not require prior knowledge of transcript structures or genome sequences. However, analysis of RNA-Seq data in the presence of genes with large numbers of alternative transcripts is currently challenging due to efficiency, identifiability, and representation issues. We present RNA-Seq models and associated inference algorithms based on the concept of probabilistic splice graphs, which alleviate these issues. We prove that our models are often identifiable and demonstrate that our inference methods for quantification and differential splicing detection are efficient and accurate.

TITLE:
Inference of Alternative Splicing from RNA-Seq Data with Probabilistic Splice Graphs

SPEAKER:
Professor Colin Dewey
Dept. of BMI – Genome Center
UW-Madison

TIME & PLACE:
Wednesday, October 3, 2012
Room 140 Bardeen
4:00-5:00p

Cookies & Coffee @ 3:30 in Rm 1210 MSC