

Title: Improved methods for determining TF specificity

Author:

Gary D Stormo

Department of Genetics

Center for Genome Sciences and Systems Biology

Washington University School of Medicine

St Louis, MO USA 63110

Abstract

New high-throughput technologies offer unprecedented opportunities to determine the quantitative specificities of transcription factors (TFs). Optimizing the experimental details and the algorithms for data analysis can have large effects on the quality of the resulting motifs. Furthermore motifs can be simple, such as position weight matrices (PWMs) or more complicated, involving higher order interactions between positions and even combinations of multiple motifs for a single factor. This talk will cover our most recent work, on both the experimental and computational side, for determining optimal models for TF specificity. This can be further extended to develop recognition models for specific TF families where one predicts the specificity of a TF based only on its protein sequence. Our current work on this problem will also be described.