

The Development of Parsing Tools for Motif Detection Methods

**Kathryn Dempsey
(UNO Bioinformatics Major; NE-INBRE Scholar)**

Abstract:

Currently the Motif Tool Assessment Platform works with approximately 12 motif detection programs to analyze and format their results into an assessment that is useful to the scientific community. However, it does not currently incorporate motif detection algorithms that make use of phylogeny in their implementation. The objective of this independent study, then, would require that the student familiarize myself with several popular phylogenetic motif detection algorithms and incorporate them into the MTAP. This involves several steps: collect background information, build a test suite for each algorithm, plan and implement a robust way to run and parse the results of each program, and create the benchmarks required to validate our results. The algorithms that have been proposed are PhyME, PhyloGibbs, WeederH, EmenEM, Wgibbs, and MEME*.