

5th Annual Joint Bioinformatics Workshop

July 19, 2005
2229 Seamans Center
University of Iowa

by

Michael Smith
University of Iowa

CLiPH: A System for Prioritizing Candidate Gene Lists

ABSTRACT

Genetic disease studies begin with a list of genes commonly referred to as a candidate list. This list serves as a schedule of work representing resources that a research lab will spend investigating a disease; screening the highest ranked genes first and progressing towards the bottom. Ranking the list is a key task since the ranks represent the order in which the genes will be investigated. Currently this is a manual task based upon an investigator's reading and interpreting scientific data, such as involvement in a pathway, along with non-scientific data, ranging from information in a journal article to ideas exchanged at a conference. Instead of making ranking decisions on a single data field, the Candidate List Prioritization Heuristic (CLiPH) application allows researchers to examine all available experimental data to create an automatically prioritized candidate list. CLiPH also allows users to quickly edit data thresholds to observe and visualize the effect on the current data and create additional prioritizations. By using all supporting evidence, CLiPH can generate a prioritized candidate list which may decrease the number of genes that need to be screened, and thus decrease the time required, before finding the cause of a disease.