

Poster K-5

Title: SAM as a plugin for BASE



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Short Abstract: This poster describes the implementation of Significance Analysis of Microarrays (SAM) as a plugin for BASE, a opensource system for the analysis of microarray experiments

Long Abstract:

In order to gain some insights about the metabolic pathways that are contributing to a disease or to a stress response, a current approach is to search for differentially expressed genes using DNA microarray experiments. The tracking of which parameters were used in the various steps analysis of microarray data can be very hard to perform, specially when the tools are not fully integrated within a system. Therefore the usage of a system like BioArray Software Environment (BASE - <http://base.thep.lu.se/>) plays a very important role in the retrieval of the data as well as in the interpretation of the results. In order to be able to perform the complete analysis in a single system, it must have all the required tools. To select differentially expressed genes, one would usually run a t-test, an Anova or Significance Analysis of Microarrays (SAM - <http://www-stat.stanford.edu/~tibs/SAM/>) among others. Within this context, the development of an open source plugin for BASE would increase the adherence to a microarray analysis platform, mainly if such plugin runs SAM. This method was originally implemented as plugin for Excel, a proprietary software. More recently it became also available in R (www.r-project.org), a statistics open source platform, which usage requires programming skills. We have implemented a plugin in Perl that requires R to enable the usage of SAM with BASE. Our plugin allows the search for differentially expressed spots using two-class unpaired analysis and multiclass analysis. It also allows the user to see the R code in use to load the data in R and execute SAM. Therefore, if the user decides to run the script manually, the script is already there. Additionally, the script runs standalone, as long as it receives a BaseFile format through the standard input.

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