RRE & ClAW: two new java tools for microarray data mining - (session: Other)

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The availability of highthroughput technology as microarrays rises up the need for biologists of new computational tools to investigate the functional implications related to the presence of transcriptional differential expressions.

For this reason, last year, we have finished the developed MedMOLE a prototype tool to categorize and simplify the tedious work of getting over the literature related to coregulated genes.

This time we present two tools written in java:

RRE (Regulative Region Extractor) and ClAW (Clustering Analyser Wrapper).

RRE is a tool allowing the extraction of all potential regulative regions from genomic data files. In particular, it uses the GBS or GBK files to identify the gene/CDS annotations and extracts gene upstream regions (default 2000 kb), 5'UTRs, introns, 3'UTRS, gene downstream region (default 1000 bp) from the corresponding FA files.

The tool extracts in fasta format the previously described regions from NCBI human/mouse/drosophila genomes data in 2-4 hours depending on the available hardware.

RRE can be linked to an automatic data downloader based on CURL and it allows the rebuild of the data set any time an update is available at NCBI.

We found this tool very useful to generate the data sets needed to perform genome-wide analysis on transcriptional signals present in regulative regions.

Furthermore, in april it will be available at www.bioinformatica.unito.it a web interface to the data generated by RRE (Human/Mouse/Drosophila) based on SPITFIRE and accessible upon registration.

ClAW instead is a graphical interface to the clustering suite CLUTO, which allows gene clustering on the basis of GO Biological process annotation.

The tool uses locusLink GO annotation to assign the GO terms to a list of LL Ids given by the user, making simpler the use of CLUTO via a graphical interface and producing graphical and textual outputs of the clustering results.

User can also request to integrate the set of GO terms used for the clustering with those available for the orthologous genes.The possibility to integrate in the clustering also the GO terms of orthologous organisms is helpful to fit into clusters poorly annotated genes. We found ClAW particularly useful to functionally associate differentially expressed genes derived by microarray experiments.