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A Digital Northern tool for assessment of Citrus differentially expressed genes



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Short Abstract: We present a web-based tool for the in silico assessment of differentially expressed genes. It allows the comparison between the results of the most important measuring methods for gene abundance, and also performs comparison of the gene with public protein repositories, and automatic functional classification.

Long Abstract:

In this work we present a web-based tool for the in silico assessment of differentially expressed genes (often called digital northern, or in silico hybridization). There are in the literature methods to measure the abundance of gene transcripts in cDNA libraries. However, there is no available tool that allows the comparison between the results of the most important methods, neither at the same time performs automatic data analysis. Therefore there was a need for the development of a new tool for the Citrus Biotechnology Laboratory (CBL). Although this tool was designed for the CBL Citrus cDNA libraries, it can be easily adapted to any kind of cDNA library data.

The pipeline of our tool includes: the choice of two or more cDNA libraries; automatic generation of tentative consensus sequences (TCS); for each individual TCSs, the computing of several different statistical analyses, namely the statistical test P-Value (Audic et al., 1997), the entropy (R-Value) among cDNA libraries (Stekel et al., 2000), the relative abundance for TCS composing reads, and the Fischer Exact Test. Automatic comparisons between the TCS and public protein repositories (e.g. GenBank, UniProt, KEGG, MIPS) are generated as well. It prints the results onto a HTML table, one TCS per row, performing automatic functional categorization (based on MIPS functional categories), showing the results of the comparison with the public databases, and creating pictures illustrating graphically the differential expression among the libraries, and the data distribution used for the entropy statistics.

This tool was successfully used by the CBL researchers to perform the analysis of differentially expressed genes in the Citrus EST Project (CitEST). A total of twenty comparisons were made, using eight Citrus and one Poncirus species; for each comparison, the number of evaluated libraries varied from two to six. Currently, we are preparing the manuscripts on the probable differentially expressed genes assigned by our tool.

References

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