

FishEST: A TOOL THAT MINES EST LIBRARIES FOR GENES DIFFERENTIALLY EXPRESSED

Sales, R.M.O.B.; da Silva, F.R.

Embrapa Recursos Geneticos e Biotecnologia, Brasília, Distrito Federal, Brazil.

Cells can be characterized by its transcript composition: the amount of a protein, the final biochemical agent, is positively correlated with the abundance of its mRNA. Expressed Sequence Tags (ESTs), single pass reads from randomly selected cDNA clones, have proved to be a valuable resource for genome research and lead to the description of new genes. EST libraries can be associated to a tissue and/or developmental stage of an organism. However, the low number of clones on a single EST library (usually between 1,000 and 10,000) precludes it to faithfully represent the gene expression pattern. We present here a bioinformatics tool, FishEST, that allows rapid identification of up- or down-regulated genes on a previously clustered EST project. The tool allows one or more EST libraries to be treated as a single sample (a group), applies the Fisher's exact test on 2 given groups and lists the clusters showing significant differential expression. The use of this tool in EST projects ranging from ~6,000 ESTs from 6 libraries to ~155,000 ESTs from 49 libraries has shown its usefulness in correctly identifying differentially expressed genes.

<http://www.cenargen.embrapa.br/~felipes/>

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