

Package Content Description

btm_annotation_table.xls

MS Excel spreadsheet file, containing BTM module titles, member genes, annotation categories and levels, web links, top matched pathways, transcription factors, gene ontologies, etc. Intended for data reuse.

BTM_application_tutorial.pdf

The application tutorial of BTM in pdf format.

BTM_for_GSEA_20131008.gmt

The file to use BTMs as gene sets in GSEA program.

monocytes_vs_bcells.txt

Example microarray data, 3 monocyte samples and 3 B cell samples, in Affymetrix probesets. Tab delimited, UNIX text file.

gene_ab_correlation.rnk

A pre-ranked example file for GSEA, where genes are ranked by their Pearson correlation to antibody response.

btm_tool.py

Our Python program to demonstrate how to convert gene expression to module activity, to do enrichment test on a gene list and to do antibody correlation analysis.

btm_example_data.py

Data file for **btm_tool.py** . Do not edit.

MCV4_D3v0_probesets.txt

Example microarray data, in Affymetrix probesets. Tab delimited, UNIX text file.