



DetectipnP Documentation

Description: Compute detection p-values for gene-expression microarray data

Author: Kensuke Kojima, Yujin Hoshida, hoshida@broadinstitute.org

Summary

This module assesses whether a given signal intensity measured by microarray is significantly higher than background signal due to non-specific hybridization (so-called “present” signal). The background signal is modeled by using data of built-in negative control probes for the microarray. The significance for each signal is reported as a detection p-value. Furthermore, the module computes proportion of “present” probes in each sample (%P-call) based on a user-defined cut-off of detection p-value (default $p < 0.05$). It is recommended to use non-normalized data.

Parameters

Name	Description
input filename exp	Gene expression dataset (.gct)
input filename control	Expression of negative control probes (.gct)
perP threshold	Threshold of detection p-value for present signal, Default: 0.05

Input Files

1. input filename exp
Gene expression dataset in GCT file format without any normalization nor background correction.
2. input filename control
Expression dataset of negative control probes in GCT file format. Samples should be in the same order with the .gct file of gene expression dataset.

Output Files

1. <input filename exp>_detectionP.gct



Detection P values of each probe and sample in GCT file format.

2. <input filename exp>_percentP.txt
Sample list with %P-call. Tab-delimited text.

Example Data

“DetectionP_example_gene_expression_data.gct”: Gene expression dataset

“DetectionP_example_negative_control_data.gct”: Expression dataset of negative control probes

Platform Dependencies

Module type:	Preprocess & Utilities
CPU type:	Any
OS:	Any
Language:	R