ExpressionFileCreator Documentation

Module name: ExpressionFileCreator
Description: Creates a RES or GCT file from a set of Affymetrix CEL files
Author: Joshua Gould, gp-help@broad.mit.edu

Summary
The ExpressionFileCreator module creates an expression dataset from a set of individual Affymetrix CEL files. The conversion is done using the standard Affymetrix probe modeling algorithm MAS5, the RMA algorithm, the GCRMA algorithm, or the dChip algorithm. The result is a matrix containing one intensity value per probe set, in the GCT or RES file format described at http://www.broad.mit.edu/cancer/software/genepattern/tutorial/gp_fileformats.html.

Samples can be annotated by specifying a clm file. A clm file allows you to change the name of the samples in the expression matrix, reorder the columns, select a subset of the scans in the input zip file, and create a class label file in the cls format, also described on the web page above.

By default, sample names are taken from the CEL file names contained in the zip file. A clm file allows you to specify the sample names explicitly. Additionally, the columns in the expression matrix are reordered so that they are in the same order as the scan names appear in the clm file. For example, the input zip file contains the files scan1.cel, scan2.cel, and scan3.cel. The clm file could contain the following text:

scan3   sample3   tumor
scan1   sample1   tumor
scan2   sample2   normal

The column names in the expression matrix would be: sample3, sample1, sample2. Additionally, only scan names in the clm file will be used to construct the GCT or RES file; scans not present in the clm file will be ignored.

Notes:
- The results obtained from running MAS5 and dChip differ slightly from the official implementations of these algorithms.
- The input file can be a zip of CEL files or a zip of gzipped CEL files.

References:
1. Affymetrix. Affymetrix Microarray Suite User Guide. Affymetrix, Santa Clara, CA, version 5 edition, 2001.
2. Rafael A. Irizarry, Bridget Hobbs, Francois Collin, Yasmin D. Beazer-Barclay, Kristen J. Antonellis, Uwe Scherf, and Terence P. Speed. Exploration, normalization, and summaries of high density oligonucleotide array probe level data. Biostatistics, 2003b. To appear.
3. Li, C. and Wong, W.H. (2001) Genome Biology 2, 1–11.
4. Li, C. and Wong, W.H. (2001) Proc. Natl. Acad. Sci USA 98, 31–36.

Parameters:

Name	Description	Options
input filename	A zip file containing CEL files or	

	gzipped CEL files	
method	The method to use	GCRMA;RMA;MAS5;dChip
quantile normalization	(GCRMA and RMA only) Whether to normalize data using quantile normalization	yes;no
background correct	(RMA only) Whether to background correct using RMA background correction	yes;no
compute present absent calls	Whether to compute Present/Absent calls	yes=yes (create res file);no=no (create gct file)
normalization method	(MAS5 only) The normalization method to apply after expression values are computed. The median column is used as a reference.	linear fit;mean scaling;median scaling;none;quantile normalization
clm.filename	tab-delimited text file containing one scan name, sample name, and class name per line	
output file	The base name of the output file	

Return Value:

1. gct or res file
2. cls file if clm.filename is supplied

Platform dependencies:

Task type:	Preprocess & Utility
CPU type:	any
OS:	any
Language:	R