ComBat Documentation

Module name:	ComBat
Description:	Performs batch correction on a dataset containing multiple batches
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Summary: This module runs the ComBat(Combining Batches) R script on a microarray dataset. The ComBat R script uses an Empirical Bayes method to adjust for potential batch effects in the dataset.

References:

- Johnson, WE, Rabinovic, A, and Li, C (2007). Adjusting batch effects in microarray expression data using Empirical Bayes methods. Biostatistics 8(1):118-127.

Parameters:

Name	Description
Input file:	input file – res, gct
sample info file:	A file containing information about the samples. The first three columns in the sample info file must be Array, Sample, and Batch.
covariate columns:	The covariate columns to use in analysis. This is a list specifying additional columns from sample info file to use in analysis (i.e, 4, 5, 7, …).
absent calls filter:	The filter to apply to genes with absent calls. Filters genes with absent calls in 1 - (filter absent calls) of the samples. This value must be between 0 and 1. A value of 1 implies no genes should be filtered. Ignored if input file is not a .res file.
create prior plots:	Whether to generate prior probability distribution plots
prior method:	Empirical Bayes priors distribution estimation method to use. Either a parametric or non-parametric method can be applied. If unsure of which method to use try the parametric method first since it is faster.
output.file:	Name of batch adjusted output file

Return Value:

1. <output.file>.<res, gct> , A file containing the batch effect adjusted dataset in the same file format as the input file

If "create prior plots" is yes:
2. <output.file>.plot.<pdf, jpeg>, A file containing the prior plots in either jpeg format (Windows only) or pdf format (all non-Windows platforms)

Platform dependencies:

Task type: Preprocess & Utility
CPU type: any
OS: any
Language: R (v. 2.5.0)