



## ComBat Documentation

**Module name:** ComBat  
**Description:** Performs batch correction on a dataset containing multiple batches  
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**Date:** 05/5/2008  
**Release:** 1.0

**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	Choices
Input file:	input file – .res, .gct	
sample info file:	A file containing information about the samples. The sample info file must contain the three columns Array name, Sample name, 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, ...).	
filter absent calls:	The filter to apply to genes with absent calls. Filters genes with absent calls in 1-(filter absent calls) of the samples. 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:

output file

### Platform dependencies:

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

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