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BIOL 341- Applied Bioinformatics I

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lmFit() and eBayes()

The limma package contains the lmFit() and eBayes() functions, and is used to analyze microarray gene expression data. The expression data is normalized then the lmFit() function is applied to fit each gene/probeset in the expression data to a linear model. The data and design matrix are the arguments within the lmFit() function that is used to fit the data to the linear model. Once this is done, the eBayes() function is applied to adjust the standard errors then identify and rank genes that are differentially expressed through statistical analysis. The argument for the eBayes() function is the linear model fit data from the lmFit() function application.

Reference:

Pevsner, J. (2015). Bioinformatics and Functional Genomics (3rd ed.). West Sussex: John Wiley & Sons Inc.

Smyth, G., & McCarthy, D. (2020). ebayes: Empirical Bayes Statistics for Differential Expression. Retrieved 29 August 2021, from https://rdrr.io/bioc/limma/man/ebayes.html.