What's New in BRB-ArrayTools Version 4.5.0

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Visualization Tools:

Added the Ward's linkage method in the "Dynamic Heatmap Viewer" and "Cluster Samples Only" tools.

Analysis Tools:

Added a new option to find differentially expressed genes by controlling the 'Local false discovery rate' (Efron, et al 2001) in the class comparison (between groups of arrays) tool.

Developed tools for differential expression analysis between two classes on RNA-Seq count data with "DESeq2" or "edgeR" packages.

Importing, Filtering, Normalization and Annotation:

Added an importer to import RNA-Seq count data.

Added an importer to import GSE data from GEO.

Modified code in the ST array importer to use the "oligo" package to allow importing of Affymetrix gene 1.0, 1.1, 2.0 and 2.1 ST arrays. The use of "aroma.affymetrix" package has been deprecated.

Added Arabidopsis array with the TAIRG version in the custom cdf option.