

FlexArray stand alone R based statistical analysis of microarray data

Contributed by Administrator

FlexArray is a Microsoft Windows software package for statistical analysis of microarray data. Currently, the analysis of Affymetrix GeneChip® and Illumina BeadChip® expression arrays is supported.

The main strong points of this software are

- Runs on Microsoft Windows
- Support for Affymetrix GeneChip® arrays and support for Illumina BeadChip® expression arrays
- Easy to use data import
- Intuitive visual representation of the data analysis process in the form of an "analysis pipeline"
- Comprehensive collection of statistical data processing algorithms, built on the framework of Bioconductor:
 - Preprocessing and normalization: MAS 5, RMA, PLIER, GC-RMA, dChip, and Custom for Affymetrix, lumi for Illumina
 - Statistical testing: t-test, ANOVA, LPE, SAM, Empirical Bayes, Bayes T, cyber-T
 - Fold-change and group statistics calculations
 - False discovery rate: FDR (Benjamini Hochberg and Benjamini Yekutieli), FWER (Holm, Hochberg, Sidak Single Step, Sidak Step Down, and Bonferroni)
- Description of every algorithm and every parameter
- If an algorithm is not available in a particular context, FlexArray will provide a detailed description of the reason why.
- Plug-in architecture for algorithms: end-users can easily integrate new analysis methods into the software
- A wide variety of plots applicable to every level of the analysis:
 - Quality Control plots for raw data, including spot intensity maps, QQ-plots, scatter plots, histograms, and box plots
 - Plots for normalized data and for sample means, including scatter plots, QQ plots, MvA plots, and histograms
 - PCA plots for quick assessment of the experiment
 - Plots for statistical test results, including Volcano plots, and histograms
 - A number of innovative plots, e.g. the shiv plot combining a box plot with a signal intensity histogram and a data variance curve
 - A number of plots specifically designed to facilitate comparisons between various analysis methods, e.g. the CAT plot, or the overabundance plot
 - Venn diagrams to compare gene lists
- Description of every plot
- Plots can be zoomed in, panned, and exported to a number of formats, including EPS
- Plug-in architecture for plots: it is quite easy to add a new plot to the program
- Context-sensitive data table with such features as sorting, filtering, search, export, column resizing and reordering, etc.
- Flexible annotation import
- Gene list generation, management, and visualization
- Tools to compare outputs of multiple analysis methods
- Full analysis history, including the values of all parameters used in algorithms, full execution log, and remembering the exact form of the R script used
- Re-usable analysis protocols: create an analysis schema once and then re-use it for your subsequent experiments, or pass it on to your colleagues