



SIGENAE – BASE

Plug-ins presentation

Philippe Bardou

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The aim of this document is to provide a short description of all plug-ins available on the SIGENAE BASE (BioArray Software Environment) server. The table below contains three sections corresponding to three kind of plug-ins : Analysis – Transformation – Visualization.

More details about each one (description, parameters, ...) are available on the BASE SIGENAE website (“Analyse data” => “Plug-ins” => Plug-ins name).

For new plug-ins development please ask to the SIGENAE team at : sigenasupport@jouy.inra.fr

| TRANSFORMATION – Plug-ins name prefixed by “Transformation -” | | |
|---|----|---|
| Name | Ch | Description |
| Filter : log2ratio(M) | ≥2 | Filters on log2ratio(M) for spots (i.e. position-reporter pairs) across Assays in a BioAssaySet. |
| Filter : Rank | ≥2 | Sorts spots according to their ratio and to assign spots a rank value reflecting the sort order. The ranking can be done around the median ratio or in a increasing or decreasing ratio order. To be able to use the rank in other plugins there is a function that stores the rank as the M value for each spot and there is also a built in rank filter that can filter out the top/bottom spots. |
| Filter : Ratio | ≥2 | Filters on ratio for spots (i.e. position-reporter pairs) across Assays in a BioAssaySet. |
| Filter - SIGENAE : Filter On Empty Spots | 1 | Filters datas using an arithmetic expression (using mean and/or median and/or standard deviation from the mean). |
| Filter - SIGENAE : Filter On Experience Percent | 1 | Filters datas. Spots are conserved if there are quantified values in at least x% of the experiences. |
| Filter - SIGENAE : Zero intensity | ≥1 | To zero intensity values. To describe which spot(s) will be zeroed, you can use three parameters "_" separated – Bioassay name – Reporter name – Block.Col.Row. |
| Filter : Spot (pos-rep) Presence | ≥2 | Filters for presence of spots (i.e. position-reporter pairs) across Assays in a BioAssaySet. |
| Merge bioassays Weighted | ≥2 | Merges together BioAssays by grouping them according to annotation types or syntactical differences in the name. The BioAssays are merged using a weight function defined by the user. |
| Norm. : Global median ratio | ≥2 | Scales the intensities in such a way that their geometric mean ($\sqrt{i1 * i2}$) is kept constant but the median of their ratios ($i1/i2$) is shifted to 1. |
| Norm. : Lowess | ≥2 | Provides intensity-based normalization. This is an efficient C++ implementation by Bjorn Samuelsson of the LOWESS algorithm. |
| Norm. : pin-based median ratio | ≥2 | Scales the intensities in such a way that their geometric mean ($\sqrt{i1 * i2}$) is kept constant but the median of their ratios ($i1/i2$) is shifted to 1. |
| Norm. : R Between Arrays(LIMMA+SMA) | ≥2 | Normalizes between arrays for 2ch experiments using R functions from Bioconductor (LIMMA) and SMA. |
| Norm. : R with Bioconductor(LIMMA) and SMA | ≥2 | Normalizes 2ch experiments using R functions from Bioconductor (LIMMA) and SMA. |
| Norm. - SIGENAE : Correction by vector | 1 | Transforms the datas by a normalization : correction vector. |
| Norm. - SIGENAE : Normalization (by block, mean, median...) | ≤2 | Transforms (global or by block) the datas by a normalization (mean, median, a value to define, the Nth higher value of the datas). |
| SIGENAE : Calculation of the log(value) | ≤2 | Calculates the log10 or the log base 2 of the intensities in a BioAssay. |

| VISUALIZATION – Plug-ins name prefixed by “Visualization -” | | |
|---|----|--|
| Name | Ch | Description |
| QC : Spoterror | 2 | Operates on one assay at a time. It makes a scatterplot of the spots' mean intensity (A) and deviation from the mean of M for all spots with the same reporter. It then fits a line to this plot using lowess, and then outputs for each spot a weighted mean of (the deviation from the reporter mean M and the fitted line). Hopefully this value can be used as an estimate of the measurement error for each spot. |
| R : Arrayplots | ≥2 | Constructs various plots for 2ch arrays : Imageplots, MA-plots with print-tip groups lowess curves, Boxplots, Density plots, Overall boxplots comparing arrays. |
| SIGENAE : Dotplot (ch1) | 1 | Dotplot all the BioAssays. |
| SIGENAE : Dotplot (ch2) | 2 | |
| SIGENAE : Summary Statistic | 1 | Calculates : max, nth max, mean, median, the nth min, min value for each BioAssay. A graph is plotted with this value. Moreover a correlation matrix and a covariance matrix are calculated according to a chosen method (pearson, kendall, or spearman method). |

| ANALYSIS – Plug-ins name prefixed by “Analysis -” | | |
|---|----|---|
| Name | Ch | Description |
| ADG1 ver 2 | 1 | Compares reporters in assays belonging to two different annotation types, e.g. ER Positive tumors and ER Negative tumors. The plugin groups the corresponding assays together according to annotations and then performs a t-test and a Mann-Whitney test to calculate the probability that there is a significant difference for that reporter between the two annotation groups. The plugin also calculates a noise weight for each reporter. |
| ADG2 ver 2 | 2 | |
| Correlation of A | ≥2 | Allows correlation studies between assays using Pearson and Spearman correlation. Output is a tab separated text file and a HTML report. |
| Correlation of M | | |
| Hierarchical clustering | 1 | Hierarchical clustering, bottom-up. The two closest points are merged and the new cluster is represented by an unweighted(median) or weighted(center of mass) average of the two points in gene expression space. |
| | ≥2 | |
| MDS | 1 | Multi-dimensional scaling (MDS) is a non-linear way to reduce the dimensionality of a data set. This implementation uses the Pearson correlations between assays as a distance metric. |
| | ≥2 | |
| MGH : avg-A | ≥2 | Computes "A" ($1/2 * \log_{10}(Ch1 * Ch2)$) per each reporter via mean/median/etc of spot A values. Can return A values as a reporterlist. Can plot histogram of A's. |
| MGH : avg channel intensity | 1 | Computes "average channel intensity" per reporter for a specified channel via mean/median/etc. Can return values as a reporterlist. Can plot histogram of average intensity. |
| | ≥2 | |
| MGH : fold ratio | ≥2 | Computes "fold ratio" for each reporter via mean/median/etc of spot intensity ratios. Can return fold ratios as a reporterlist. Can plot histogram of fold ratios. |
| MGH : limit intensity | 1 | Enforces a minimum value for spot intensities. Replaces all intensities below the min value specified with that min value. |
| | ≥2 | |
| MGH : t-test | ≥2 | Computes p-values for reporters. Can return p-values as a reporterlist. Can plot histogram of p-values. |
| PCA | ≥2 | Calculates the PCA of the sample variance-covariance matrix of the data. |
| SIGENAE – R : Hierarchical clustering | 1 | Draws a hierarchical cluster for the genes and for the sample. You can define the number of classes. The plugin gives for each class : the mean - the number of members - the members. |