

GeneMaths XT version 1.6: New Features

Easy wizard-driven import of raw data, a wide range of preprocessing and visualization tools, capability of analyzing and clustering over 500K genes per array in a single session, customization to specific needs using the powerful scripting language, interactivity with online databases. When it comes to performance and flexibility combined with ease of use, GeneMaths XT is the trustworthy solution for you.

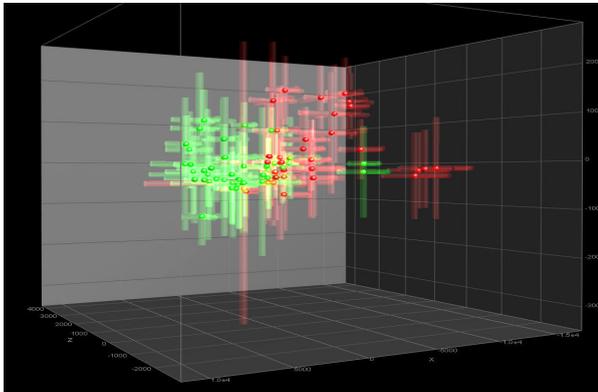


Figure 1. 3-D PCA view with error calculation.

Import wizard

In version 1.6, the ease of use for the import of raw data is facilitated by means of a intuitive import wizard and many predefined formats from all the major quantification programs. In addition GeneMaths XT can directly import Affymetrix CEL, CHP, the tab delimited GCOS and binary XDA-files. GeneMaths XT is also fully compliant with the GeneChip Command Console (GCCC; formerly project Calvin) specifications.

Because GeneMaths XT is MIAME-compliant, you can import/export data from or to EBI ArrayExpress. If you want to use data submitted to NCBI Gene Expression Omnibus (GEO), GeneMaths XT can be used for either the SOFT preprocessed data, the raw data, or the whole series data-sets.

Data preprocessing tools

GeneMaths XT offers a wide range of data preprocessing tools. Besides the standard normalization methods, GeneMaths XT offers the possibility to choose from a wide range

of methods to preprocess Affymetrix data including MAS5.0, dChip, RMA with many variants, the PLIER +16 method or to use a custom algorithm.

As an alternative to log-transformation, GeneMaths XT offers the possibility to apply Variance Stabilization to your expression data. The main advantage is that negative expression values that may occur after background correction can be dealt with.

Since GeneMaths XT is capable of calling BioConductor routines, you can use all your favourite R applications in a GeneMaths XT session.

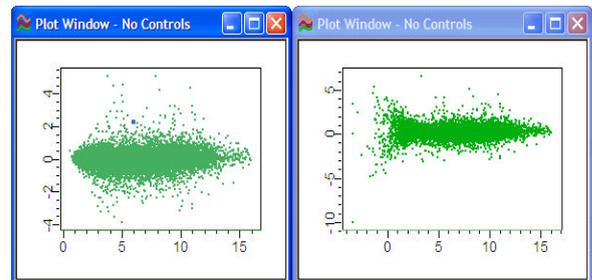


Figure 2. Variance stabilization (left) vs Log + Lowess (right).

Powerful display tools

GeneMaths XT offers wide range of visualization techniques that can be used on the raw data and the preprocessed expression values. To facilitate visual control of the data prior and after the preprocessing and analysis, GeneMaths XT version 1.6 provides display options in a tabular format and offers a number of new advanced graphical tools.

- Use the ANOVA report to find the major sources of the variance in the data. Statistically find out whether the normalization removed the undesired variation.
- Visually inspect the gene selections and compare the results of different statistical tests with the Venn-diagram option.
- Add links to the gene and/or array identifiers and additional information such as GO-information, or the whole KEGG-pathway, with one single mouse click.
- Show the layout of Loop-design experiments and perform the analysis.
- Using the Chromosome Map Viewer, you can locate e.g. the set of differentially expressed genes on the

chromosome, the data being dynamically linked to the Ensembl website.

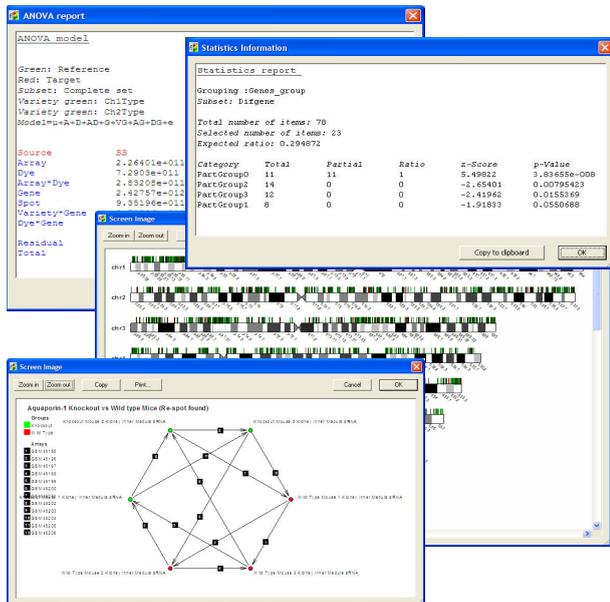


Figure 3. Visualisation tools and reports.

Querying and data mining

GeneMaths XT offers a range of new query tools, in particular Gene Set Enrichment Analysis. Rather than just looking at the expression of one single gene, it is also possible to look at a set of genes that belong to the same biological function or process. Based on a grouping from Gene Ontology identifiers, one can statistically check whether the group of genes itself is statistically expressed rather than a set of individual genes.

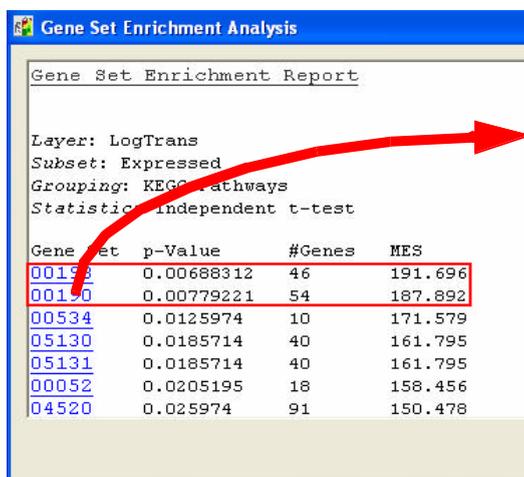
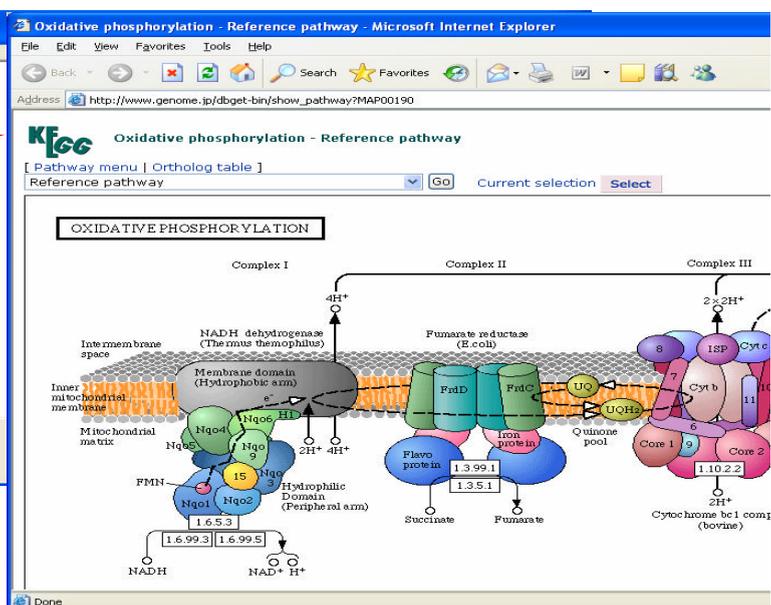


Figure 4. Gene set enrichment analysis.



Statistics and hypothesis testing

The impressive list of available statistics and clustering algorithms will offer you all the flexibility you need during your analysis. Recently added statistics include:

- Local Pooled Error
- LIMMA
- Z-score
- Two way ANOVA
- Ratio ANOVA for a generalized two color design.
- Polynomial fit for time-course analysis.
- q-value
- ...

Customization via scripts

The powerful GeneMaths XT script language offers numerous ways to speed up or enrich your daily analysis routine. Scripts can interact at any point in the preprocessing or analysis workflow. They can for example be used to automate (parts of) the workflow, but also to implement custom statistics or analysis tools, if not already provided by the software.

A rich database of script-based plugins and tools developed by Applied Maths is already available, and can be freely accessed or downloaded from our website by GeneMaths XT users.

Try it before you buy it

Browse to our website www.applied-maths.com to request your free evaluation copy of GeneMaths XT. With the help of the very comprehensive tutorials and the support team at Applied Maths, you will master the software in little time.