



www.applied-maths.com

GeneMaths XT version 2.0 Upgrade - Release Note

28 January 2008

- **Aspect & scopes**

Aspects and *Scopes* add a whole new dimension to data processing in GeneMaths XT. While subsets provided you with the ability to flexibly filter out sets of entries for subsequent analysis, sometimes a completely different way of looking at a set of entries is needed. For example while preprocessing your data, you might want to do a background correction. At this point you need data of individual spots and individual arrays. Once preprocessing is done though you want to focus on the biology. So now samples and genes are important, while spots and arrays are no longer relevant.

This is exactly what **aspects** do. *Spots* might be an example of an aspect you have right after import. Once you want to zoom in to genes, you can collapse the individual spots to genes by using the contents of a text field. GeneMaths averages over the individual spots and presents you with a new root subset. The same can be done with arrays to collapse them to biological samples. Naturally each aspect has its own groups, annotation text fields and selection, but each of these can be manually transferred from one aspect to another.

A view of a microarray data matrix consists of two aspects: e.g. spots x arrays. This is what we call a **scope** of the data.

Derived aspects can be generated in different ways:

- By collapsing identical entries in a text field.
- By collapsing (possibly overlapping) groups: e.g. collapse all the genes which have the same GO entry. One gene may influence several GO entries.
- Especially for complicated color designs a dedicated *Collapse by contrast* exists: this transforms the values of the individual arrays to the corresponding values of the samples by full design matrix calculations.

- **Similarities & Data filters**

Cluster analysis, Partitioning and SOM have two common steps in setting up a calculation:

- Data filter: optionally transforms the data matrix. If there are many arrays, the amount of noise in the data often disturbs the creation of well-defined clusters. An analysis on the first N components of a PCA (unsupervised) can now be done, or the average over known groups (supervised) can be taken.
- Similarity: the range of similarity coefficients has been extended.

These options can easily be installed (e.g. by automatic update).

- Set up and visualize the preprocessing strategy, integrates seamlessly with undo functionality and dynamic calculations.



www.applied-maths.com

- **Extended classifier functionality**
 - Intuitive classifier wizard.
 - 4 new classifiers have been added: Naive Bayes, Logistics Regression, PredictionAnalysis for Microarrays (PAM) and Classification by Nearest Centroid (ClANC).
 - Extended validation technology by *leave-one-out* algorithm.

- **Interface**
 - Group Window: view groups and the selected items in them, select all members of a group with one click.
 - Zoomsliders in main view, plot view and PCA view (Control + mouse wheel zoom in at current point).
 - Fully compliant with Vista's User Access Control features.
 - Completely revised automatic update feature, fully compliant with Windows Vista.
 - Vastly extended script language.
 - More intuitive menu structure.
 - Better support for complicated two color designs: e.g. improved LIMMA, improved design visualization.
 - Improved integration with R.