

GenEx 5.0.1 A powerful tool for qPCR data analysis

GenEx is a popular software for qPCR data processing and analysis. Built in a modular fashion GenEx provides a multitude of functionalities for the qPCR community, ranging from basic data editing and management to advanced cutting-edge data analysis.

Basic data editing and management

Arguably the most important part of qPCR experiments is to pre-process the raw data into shape for subsequent statistical analyses. The pre-processing steps need to be performed consistently in correct order and with confidence. GenEx Standard's streamlined and user-friendly interface ensures mistake-free data handling. Intuitive and powerful presentation tools allow professional illustrations of even the most complex experimental designs.

Advanced cutting-edge data analysis

When you need more advanced analyses GenEx Enterprise is the product for you. Powerful enough to demonstrate feasibility it often proves sufficient for most users demands. Current features include parametric and non-parametric statistical tests, Principal Component Analysis, and Artificial Neural Networks. New features are continuously added to GenEx with close attention to customers' needs.

New features

Sample handling and samples individual biology often contribute to confounding experimental variability. By using the new nested ANOVA feature in version 5.0.1. of GenEx a user will be able to evaluate variance contributions from each step in the experimental procedure. With a good knowledge of the variance contributions, an appropriate distribution of experimental replicates can be selected to minimize confounding variance and maximize the power of the experimental design! For experiments with complex features, such as for example multifactorial diseases, analytical relationships and classifications may not readily be available. The support vector machine feature in the new version of GenEx is so easy to use that it will make this advanced supervised classification method easily available to novice users, while providing access to advanced parameters for experts.

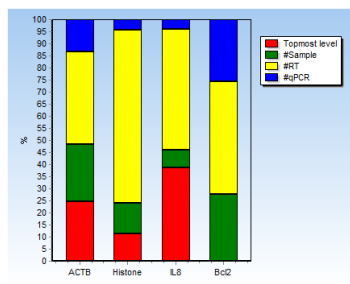
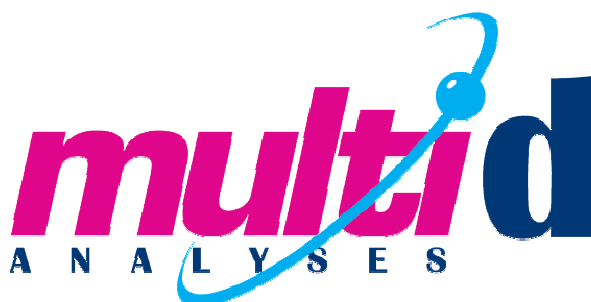
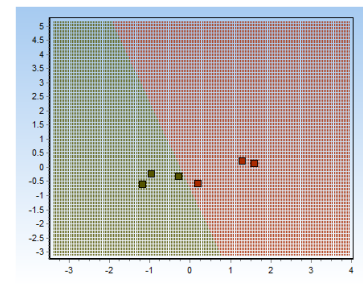


Figure 1 (left): A nested ANOVA evaluation of the variance contributions to the total experimental variability of four genes. In this particular case the largest variance contribution can be attributed to the RT step, indicating that more replicates at this stage will improve experimental power.

Figure 2 (right): A two-group classification of a large complex training data set (data not shown) by the support vector machine feature in GenEx. The plot shows the successful classification of six unknown samples.



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