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AB Applied Biosystems

Real-Time StatMiner: Advanced Data Mining Software for Applied Biosystems RT-PCR Data Analysis.

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Abstract

Nowadays, real-time qPCR is the most accurate technique for relative gene expression quantification and it is expanding to other areas like miRNA profiling, biomarker discovery, diagnostics and Copy Number Analysis. The amount of data generated and complex experimental setups are demanding advanced bioinformatic tools that help researchers in the analysis and interpretation of raw data. Therefore, bioinformatics are the key complement to the instrumentation and reagents. Integromics and Applied Biosystems introduce a new high-performance software specifically designed for the new era of quantitative real-time PCR instrumentation. The software aims at providing accurate relative quantification by a powerful combination of interactive visualization, advanced statistics and data mining. The user is intuitively guided throughout the analysis process and gets to results within a few minutes. This facilitates the use of the tool by non-experts in biostatistics but does not limit its power as statisticians can add or manipulate the procedures contained in the software.

Real-time StatMiner

High-throughput performance from AB Instrumentation and Taqman Assays

Take advantage of the Applied Biosystems complete solution for Gene expression applications:

❑ TaqMan® Low Density Array for Gene signature analysis
❑ Applied Biosystems 7900HT Fast Real-Time PCR System
❑ >700.000 highly efficient, specific and sensitive TaqMan® Gene Expression Assays
❑ > 850 specific TaqMan® microRNA Assays
❑ Universal PCR cycling conditions
❑ New! TaqMan® Gene Expression Mastermix

Powerful statistical and data mining algorithms

State-of-the-art statistics are key to produce reliable and accurate relative quantification results. The software's computational module is implemented in the **R language** that benefits from the existing libraries in **Bioconductor** (www.bioconductor.org).

❑ Advanced filtering of outlier genes and samples.
❑ Automatic assesment of expression stability for endogenous genes by different methods (Normfinder, Genorm, etc).
❑ Differential expression by statistical tests reporting p-values and accurate foldChange measures.

Interactive Visualization

The software is implemented as a plugin of Spotfire Decisionsite©, a leading application for professional and interactive visualization of multidimensional data.

❑ Multiple visualizations: Profiles, ScatterPlots, Heatmaps, Barcharts, etc.
❑ Interactive and dynamic filtering.
❑ Advanced Clustering methods: (hierarchical, K-Means, PCA…)
❑ Automatic reporting.
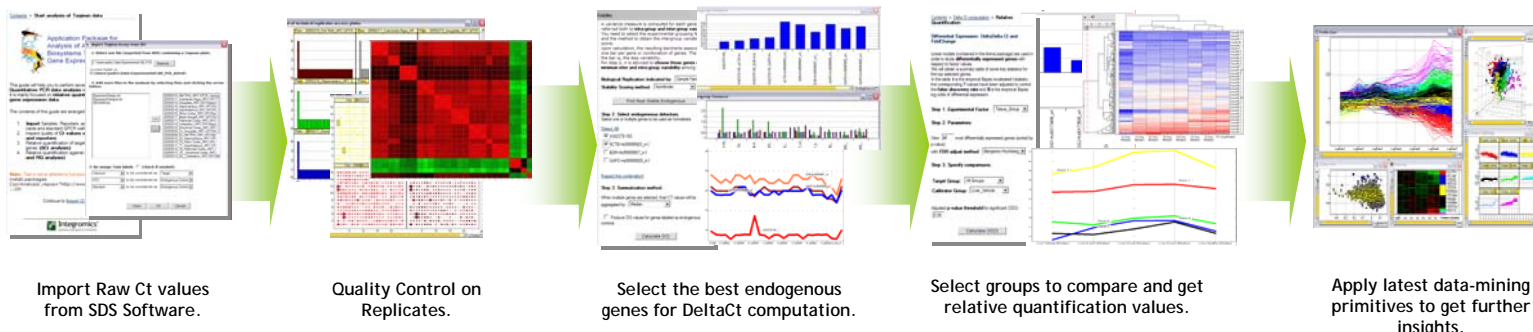❑ Management of gene lists

Functional Interpretation

Once the results from the analysis highlight the existence of characteristic expression profiles, the software provide means to enrich the numerical information with **functional annotations** provided by content repositories like the **Panther database** (www.pantherdb.org). Annotations can be further explored with Integromics ArrayUnlock©

Extensible Modular approach

The software implements *analytical workflows* that can be easily adapted to specific user needs, specific application areas or experimental settings. That means that the user interface, visualizations and the computational scripts can be easily expanded/modified. We provide customizations for specific areas like **microarray integration**, **miRNA profiling** and **CopyNumberAnalysis**.

Analytical Workflow

Import Raw Ct values from SDS Software.

Quality Control on Replicates.

Select the best endogenous genes for DeltaCt computation.

Select groups to compare and get relative quantification values.

Apply latest data-mining primitives to get further insights.

System Requirements: Microsoft Windows, Spotfire DecisionSite for Functional Genomics. R-Bioconductor

For more information or request a demo, please visit the Applied Biosystems booth or contact Integromics at www.integromics.com