Press Release
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Latest release of Qlucore software helps researchers reach beyond the current experiment

Omics Explorer 3.0 features new integrated tools which combine measured data with system biology to enable easier, faster and more creative analysis

Qlucore, a world leader in the development of bioinformatics software, has today unveiled Qlucore Omics Explorer 3.0, the latest version of its advanced and easy to use data analysis software. Upgraded functionalities include two new integrated tools that focus on facilitating the analysis of data by comparing how the experiment corresponds to published(public) information and results – a system biology approach. The most important advances in version 3.0 include the new inbuilt Gene Ontology (GO) Browser, and a fast, intuitive Gene Set Enrichment Analysis workbench (GSEA) that will provide a complete set of results for large data sets (132 x 50000) with three mouse clicks, and in less than 30 seconds.

The new GO browser will allow fast and convenient search in any ontology. After finding interesting results the matching genes can be exported to the Variable window and used as a normal variable list. Both GO and GSEA will allow the scientist to easily generate extensive lists of domain specific information. Visualization will become easier as the new functionality will allow scientists to view all elements of a specific list in a dedicated color in all open plots. This aids the scientist in interpreting the combination of their own experiment against publically available information.

Commenting on the new Omics Explorer 3.0, Carl-Johan Ivarsson, CEO said, "Omics Explorer 3.0 is our most advanced and intuitive version to date, and the new integrated tools enable users to access and compare results extremely quickly and easily with previous findings and published research. For the first time researchers will have a level of freedom that allows them to easily undertake creative analysis in their research."

In the past many scientists have had to overcome the problem of working with identifiers for variables in public data being different from those used in their own experiments. This has made their work complicated and tedious when comparing information. The new Qlucore Omics Explorer 3.0 has solved this problem by the introduction the variable collapse function.

The variable collapse function is essential for data sets with multiple measurements for the same variable. A typical example is for gene expression microarrays where you measure several probes or

features that match to one gene. Using the variable collapse you can either study your data on Gene level or probe/feature level.

In addition, the introduction of the unique Projection Score system developed by Qlucore provides the user with information on how well the visual representation actually represents the data. The Projection Score measures the informativeness of a low-dimensional representation obtained by PCA, and allows explicit comparison of representations corresponding to different variable subsets.

Version 3.0 has also been developed with a focus on data content. The new file import functionality for aligned RNA-seq (BAM files) will make it easier for users who want to analyze digital gene expression data as once the files are imported everything else is done automatically, with easy access to all Qlucore Omics Explorer analysis functionality. These include; heatmap with hierarchical clustering, PCA plots, fold change filtering, GSEA analysis, ANOVA analysis.

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About Qlucore

Qlucore was founded in 2007 as a collaborative research project at Sweden's Lund University. The firm was supported by researchers from the Departments of Mathematics and Clinical Genetics to address the vast amount of high-dimensional data generated with microarray gene expression analysis. It was recognized that an interactive software tool based on visualization was needed to conceptualize the ideas evolving from research collaboration.

The basic concept behind the software is to provide a tool that can take full advantage of the most powerful pattern recognition system that exists - the human brain. The result is an extremely fast core software engine which enables the user to handle and filter high dimensional data (big data) and instantly visualize it in 3D. This assists the user in identifying hidden structures and patterns.

The latest version of the software, Qlucore Omics Explorer, is used by scientists in more than 20 countries and is a key tool among other biologists and medical doctors to creatively analyze their experiment data. The Company's customers are mainly from the Life-science and Biotech areas.

One of the key methods used by Qlucore Omics Explorer to visualize data is dynamic principal component analysis (PCA), an innovative way of combining PCA analysis with immediate user interaction. PCA analysis works by projecting high dimensional data down to lower dimensions. The specific projections of the high-dimensional data are chosen in order to maintain as much variance as possible in the projected data set. With Qlucore Omics Explorer, data is projected and plotted on the two dimensional computer screen and then rotated manually or automatically.

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