Press Release

Qlucore launches new version of Omics Explorer 3.1 for Mac users

[Qlucore](), a world leader in the development of bioinformatics software, has announced the launch of the Mac version of Qlucore Omics Explorer 3.1 data analysis software.

With a growing number of Mac users within the scientific and research community, and the consequent need for data analysis software suitable for Macs, Qlucore has responded to this demand with the launch of its Mac version of Omics Explorer 3.1 which will complement its long established Windows version.

"The beauty of the Qlucore Omics Explorer 3.1 and Macs are that they are both very user friendly, and so will work well together to give the user the full potential of visualization and optimization of their results," commented Carl-Johan Ivarsson, CEO Qlucore. "With the Mac user base expanding amongst more and more scientists and researchers, there was a gap in the market which Qlucore has been able to fill. The software is highly interactive, and can be easily understood, even if the user has had little or no previous knowledge of bioinformatics. Qlucore Mac Omics Explorer 3.1 will be able to deliver results faster than other vendor offerings".

The Mac Version 3.1 includes a wide range of functionalities, like its Windows cousin. The focus is on maximizing the outcome of research by making it easy to analyze experiment's data from a biological point of view. Three examples of this are; inbuilt Gene Ontology Browser, a very easy to use Gene Set Enrichment analysis function, and freedom to explore data using any variable identifier: variable collapse.

The inbuilt Gene Ontology (GO) Browser, and the fast, intuitive Gene Set Enrichment Analysis workbench (GSEA) 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 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.

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 unique Projection Score system developed by Qlucore provides the user with information on how well the visual representation actually represents the data. It helps determine the real signal from noise when working with PCA visualization. The projection score is presented as a "traffic light" in the statistics dialog showing when the visualization is including more information compared to if the data was random. Green means a good projection score.

One of the benefits of the new 3.1 version, is a well-defined open interface to R. The impact of this interface is that users can utilize a broader range of statistical tests, and there will be greater flexibility allowing users to use existing tests in R and write new ones. With an interface to R, the inbuilt statistical functions of Qlucore Omics Explorer will be extended to include the full suite of statistical methods available in R. Another big advantage is that the researcher will not have to be a skilled R user to use and access the scripts. Instead, bioinformaticians will be able to do script development and once the R scripts are in place, it will, for the researcher, be a case of selecting from a dropdown box in the statistics dialog in Qlucore Omics Explorer. The program will be shipped with two R scripts supporting tests based on Limma and Wilcoxon methods.

Version 3.1 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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