New version of Qlucore Omics Explorer brings researchers more freedom to focus on research insights and accelerate scientific breakthroughs

Qlucore Omics Explorer 2.3 will give scientists clearer, quicker analysis of bigger, more complex data sets – and better results

Qlucore, (www.qlucore.com) a world leader in the development of bioinformatics software, has today unveiled the latest version of its advanced data analysis software. Qlucore Omics Explorer 2.3 will provide researchers with instant and simultaneous access to an even larger set of multiple plots, enhanced and faster integration when sharing large sets of data, and more flexible options for ordering and visualizing larger heatmaps that use even less memory.

The latest version Qlucore Omics Explorer 2.3 has a number of completely new features such as new box plots, line plots and histogram plots. These have been developed to help researchers visualize, explore and analyze an even wider range of integrated high-dimensional data sets interactively and in real time.

In addition to these new features, Qlucore Omics Explorer 2.3 offers some significant upgrades including an easy data import and export facility from a wide range of devices and platforms, an enhanced heatmap plot facility allowing much easier detection of patterns and instant clustering ability of many thousands of variables.

> "Qlucore Omics Explorer 2.3 reduces analysis time, enhances results and improves everyday efficiency with easier data import and export, more plot functions and an enhanced heatmap for easier pattern recognition," says Carl-Johan Ivarsson, President, Qlucore. "All the latest enhancements target the same key objective: to make it simpler and faster for researchers, biologists and scientists to import, analyze and report on their own and other data instantly."

The data import functionality of Qlucore Omics Explorer 2.3 is enhanced significantly in two key areas. There is a new, flexible data import wizard enabling import of a wide range of data from various devices and platforms, plus it is possible to directly import Affymetrix CEL files.

Other upgraded features include new and improved data plotting options. Researchers can now generate greatly enhanced heatmaps with a wide range of ordering and configuration options which leads to more flexible analysis. The hierarchical clustering algorithm is faster and less memory consuming, facilitating instant clustering with several thousands of variables. There is also a more

flexible scatter plot function, allowing both variables and samples to be plotted freely as well as the completely new plot types box plot, line plot and histograms.

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Carl-Johan Ivarsson, MSc, is a co-founder and CEO of Qlucore. He has more than 15 years' experience in the international software and telecommunication industries, in both business management and sales, including two years as the head of Ericsson Mobile Platforms in China

About Qlucore

Qlucore started as a collaborative research project at Lund University, Sweden, supported by researchers at the Departments of Mathematics and Clinical Genetics, in order to address the vast amount of high-dimensional data generated with microarray gene expression analysis. As a result, it was recognized that an interactive scientific software tool was needed to conceptualize the ideas evolving from the research collaboration.

The basic concept behind the software is to provide a tool that can take full advantage of the most powerful pattern recognizer that exists - the human brain. The result is a fast, user friendly and powerful software program that lets the user handle and filter data and the same time instantly visualise it in 3D. The application areas span multiple fields with the common factor that large sets of numerical data need to be analyzed. Over the last five years major efforts have been made to optimize the early ideas and to develop a software program that is extremely fast, allowing the user to explore and analyze high-dimensional data sets with the use of a normal PC, interactively and in real time.

Qlucore was founded in early 2007 and the first product was released the same year. The latest version of this software, called Qlucore Omics Explorer, is a major step in providing researchers an easy to use and still powerful tool for analysis of large numerical datasets. The combination of best in class visualization, fantastic speed and advanced statistics support and user friendliness puts the user in focus and supports instant analysis and creativity. The visualization methods range from an innovative use of principal component analysis (PCA) to interactive heatmaps and flexible scatter plots. All user action is at most two mouse clicks away. The company's early customers are mainly from the Life-science and Biotech industries and they use Qlucore Omics Explorer on gene expression data, protein data, DNA methylated data, micro RNA data and other genomic data. Please read examples of our peer reviewed publications in scientific journals.

Press Contact:
Chaz Brooks / Alison Scarrott
Chaz Brooks Communications Ltd (CBC)
Tel: +44 (0)1483 537 890
Email: chaz@chazb.com
Web: www.chazb.com

Qlucore Contact:
http://www.qlucore.com
Phone: +46 46 286 3110