

New version of Qlucore Omics Explorer launched

[Qlucore](#), a world leader in the development of bioinformatics software, announces Qlucore Omics Explorer 3.5 of its data analysis software.

Key features of the new version include the addition of Templates and an extensive upgrade of plot configuration and options giving improved visualizations.

Main developments

Templates for configured workflows

Templates, based on Python, is a new functionality in the program that makes it possible to create a script of commands that are executed by Qlucore Omics Explorer (QOE). The program provides a number of templates for basic functionality and demonstration purposes and allows the user to write new templates, with a user interface. The addition of Templates will add great value to organizations since they can create standardized analysis templates for standard analysis. The integration with Python also opens a whole new world of possibilities for customization.

The addition of Templates lets the user:

- Run exactly the same analysis many times
- Integrate QOE in existing work-flows and expand them
- Configure a favorite analysis for a quick start
- For new users: Get started with pre-configured templates for standard analysis
- For learning: Use templates to explore the program and get a feeling for functionality

Richer plot configurations

An extensive upgrade of 2D plots allows for more precise and elegant visualization and reporting. The more flexible plots will produce better outputs that can be configured to the user's exact presentation and desired content.

Projection Score

A more general implementation of Projection Score. Addition of an "Optimization" option to select the variance filter cut-off that maximizes the Projection Score.

Dimensionality estimation using Scree and Talus plots

Two new plot types to assist in estimating the data dimensionality (from an information perspective), the so called intrinsic dimension.

Significance levels and Tukey

Tukey based p-values in list export and option to filter on difference.

Upgraded NGS module

Includes presentation of HGVS descriptions of the amino acid changes caused by variants both in Genome Browser and report. If the variant is situated in a protein coding region of a gene, both nucleotide and amino acid descriptions are included on the protein level.

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About Qlucore

Qlucore (www.qlucore.com) is a leading provider of a new generation intuitive bioinformatics software. The Qlucore software combines powerful statistical methods with real time visualization. This shortens analysis time, adds more creativity to the research process, strengthens the path to new findings and facilitates easier and more fruitful collaboration between biologists and bioinformaticians.

The Qlucore Omics Explorer software makes it possible to interactively explore and analyse multivariate data sets, from small to very large as well as data generated with NGS technologies. The new NGS Module is an add on to Qlucore Omics Explorer, consisting of an interactive Genome browser and flexible and interactive filter options. One of the key features is to enable synchronization between the expression analysis of RNA-seq data and genomic information, making researchers even more productive.

Qlucore was founded in 2007 by leading researchers at the Departments of Mathematics and Clinical Genetics at Lund University, Sweden. Today Qlucore has customers in about 25 countries around the world, with sales offices in Europe and North America, and distribution in several countries in Asia. Many of the leading pharmaceutical companies use Qlucore in their research, as well as hospitals and universities around the world.

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