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Qlucore Omics Explorer makes RNA-seq analysis simple

RNAseq data can now be analyzed just as easily as microarray data

In recent years, transcriptomic profiling via next generation sequencing (RNA-seq) has emerged as both a technical and cost-effective alternative to arrays.

[Qlucore Omics Explorer](#) 3.0 supports direct import and normalization of [RNA-seq data](#) (aligned BAM files) which makes it easier to analyze digital gene expression data. With only a few mouse clicks the discriminating genes are identified and results are available in publication ready lists and plots, using Qlucore's next-generation bioinformatics software.

One of the most prominent advantages of RNA-seq compared to array-based techniques is that RNA-seq can be applied without extensive knowledge of the genomic sequence and the location of genes or other features of interest. Using Qlucore Omics Explorer, RNAseq data can now be analyzed just as easily as microarray data. These files can be directly imported and normalized and then functionality from heatmaps to statistical filters and PCA plots is available.

A key aspect of all functionality in Qlucore Omics Explorer is to make it as easy to use as possible. The purpose is to secure that scientists themselves can analyze and explore the experiment data. This enables new discoveries. With the support for RNA-seq data this option is now also available for the scientists. Additionally it was in the early days of RNA-seq analysis believed that count based statistical methods were required to receive stable results, but It is shown that statistical methods combining a variance-stabilizing transformation with t-test perform very well under many different conditions. They actually also seem to be more robust towards outliers. This means that all existing functionality in Qlucore Omics Explorer can be used directly and the scientist does not have to learn new stastical models but can focus on the biological results.

Key RNA-seq analysis and exploration functionality:

- Identify discriminating genes with a few mouse clicks
- Show results in the flexible and easy-to-use heatmap with hierarchical clustering
- Verify hypotheses using powerful statistics including ANOVA and different forms of regressions
- Compare with pathways and other biological information using the integrated and user friendly Gene Set Enrichment analysis (GSEA) Workbench

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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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