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Qlucore Omics Explorer & Genevestigator Use Cases

The amount of gene expression data being produced in labs around the globe is exploding, particularly the use of RNA-Sequencing. The decreased experimental costs have made the technology accessible to the broader research society. However, the data is complex and bioinformaticians are sparse.

Qlucore Omics Explorer provides easy-to-use statistical tools and state of the art visualizations, empowering biologists to analyze their own data and achieve high quality results and conclusions.

There is a tremendous amount of expression data available in public repositories that could bring valuable and diverse biological insights, but are rather heterogenous and difficult to analyze. Genevestigator brings structure to public expression data and can be used to view gene lists in a biological context, get insight to their expression patterns and help design the next experiment.

Genevestigator provides the user with a large database of highly curated gene expression studies, together with flexible tools designed for meta-analyses. Qlucore Omics Explorer (QOE) focuses on dataset driven exploration and analysis.

Qlucore Omics Explorer and Genevestigator are two complementary tools/services, which when used together provides the end user with increased value and analysis options. The combination enables the user to start with their data set in QOE and then benefit from biological insights generated in the context of a large expression data compendium in Genevestigator.

Together we present three use cases on how the combination can be beneficial.

USE CASE A

INVESTIGATE THE BIOLOGICAL CONTEXT OF A LIST OF GENES (QOE TO GENEVESTIGATOR)

Description

By analyzing experiments using QOE, lists of genes that are regulated in a certain condition can be identified. These lists of genes can be further characterized by being compared to gene sets from publicly available gene ontologies. With the GSEA Workbench in QOE it is possible to directly investigate how the ranking of the genes in a data set matches different pathways or gene sets.

Another option is to export the gene list to Genevestigator and use various compendium-wide search tools to learn more about the gene list in a broader biological context.

- Condition search tools: Analyze the expression and regulation of gene lists across conditions (tissues, cell lines, diseases, etc.)
- Hierarchical clustering tool: Group genes according to their expression across various conditions.
- Biclustering tool: Identify groups of genes, which have a similar expression within a subset of conditions
- Signature tool: Identify conditions with similar gene expression signatures.
- Data Selection: Identify studies of interest, according to research area, study design or study type.

Preconditions

- Data in QOE must be gene-level data.
- The organism must match one of the organisms and array platforms (if probset ID) within Genevestigator

Basic Flow

1. Perform analysis in QOE. Output is a list.
2. Copy the variable list to the clipboard
3. Open the Gene Selection dialogue in Genevestigator and paste the gene list
4. Select the datasets to work with in Data Selection
5. The gene list is available in Genevestigator and can be analyzed further using the tools described above.

Qlucore Omics Explorer → Gene list → GENEVESTIGATOR
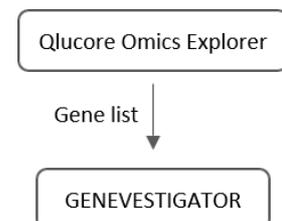
USE CASE (B):

GENERATE GENE-OF-INTEREST LIST (GENEVESTIGATOR TO QOE)
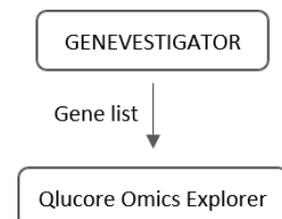
Description

In Genevestigator the user can produce lists of interesting genes termed genes-of-interest or GOI, using the various compendium-wide tools. Here, the user creates GOIs in Genevestigator and export them to QOE to study their behavior in more detail within a dataset.

Preconditions

- Same preconditions as listed in USE CASE (A)
- Data already loaded in QOE.

Basic Flow

1. Select the datasets to work with in Genevestigator.
2. Perform analyses of interest and generate gene lists from the results using "New Genes".
3. Right-click on the new gene list in the Gene Selection panel and copy them.
4. Paste the list of IDs into QOE.
5. The variable list is available in QOE and can be used in a number of ways
   a. Limit the data set to only these genes
   b. Color plots based on the content of the list
   c. Create new lists using set tools
   d. Look for correlation between genes

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USE CASE (C):

IMPORT DATASET FROM GENEVESTIGATOR TO QOE

Description

In Genevestigator, not only GOIs can be identified, but also studies of interest. Once a study with a specific setup and an interesting content have been identified, it can be exported to QOE for advanced analysis of individual data sets.

Actors

For direct import from Genevestigator, the user needs the permission to export datasets, such as having an Enterprise license. Alternatively, the identification of a study of interest can be performed in Genevestigator, but the data import to QOE could be done directly from the public repository.

Basic Flow

1. Make a Data Selection in Genevestigator.
2. Perform analyses and further limit your data selections according to interest
3. Once the final data is selected, export data in CSV format under "Datasets", as normalized absolute or relative values.
4. A single experiment of interest can be exported in GSE-format.
5. Import data with the QOE – Wizard
   a. Data exported from Genevestigator is perfectly suited for import by the Wizard.
   NOTE: For perturbation data, make sure to import only the fold-change data and not the p-values using the wizard. This can be achieved by selecting every second column in the wizard.

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