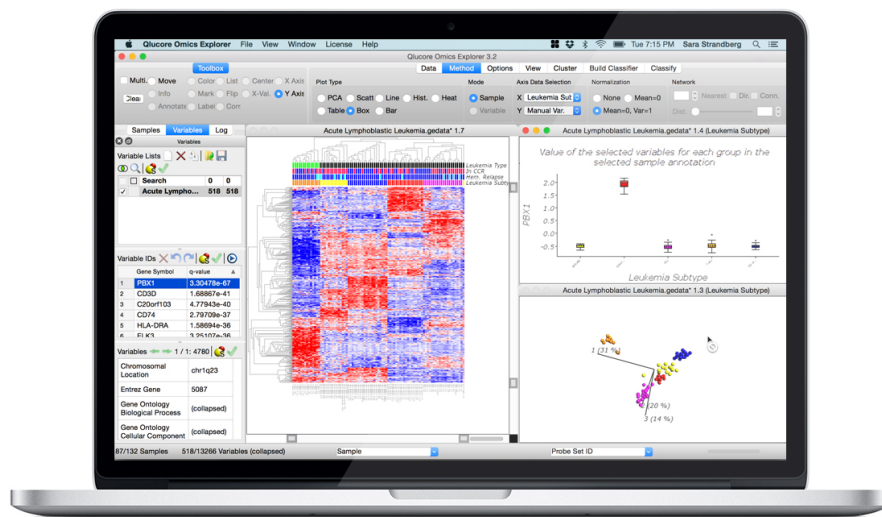


Qlucore Omics Explorer



Advanced Training

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Qlucore

Few tips

Preferences to configure: Qlucore - Preferences

Optimize the work space and toolbox at any time – double click on the main frame

Access **Dock windows**: right-click, or **View – Dock Windows**

Do not close the results/data unless instructed – we will be using them for a several exercises

Please follow the instructions/steps on the printed slides

Save results on your desktop, not in QOE data or Training folders

Follow **Extra** tasks if done before we move onto the next one!

1. Data import - Overview

- .txt files – open with Wizard (data, lists)
- Gedata files – Qlucore format – File/Open
- GEO data – File/Download
- Affymetrix CEL files – File/Open
- Agilent .txt files - File/Open
- Aligned RNA-seq BAM files: File/Open BAM files
- GSEA lists – integrated, "Export" button
- GO lists – integrated, "Export" button

8. Supervised Machine Learning: Classification and Prediction

1. **Build a classifier** for Leukemia subtype, choose from the following methods:

- kNN
- SVM
- Random Trees

2. Use this classifier to **predict subtypes** in another leukemia dataset.

Some uses:

- Predict a class or an outcome;
- Aid in identifying discriminating variables;
- Estimate the effect of covariates in the experiment;
- *make you algorithms smart... so you do not need to be!*

8. Classify and Predict - Steps

- Download dataset **GSE13425** from GEO (Qlucore – Download – GEO data – add accession number **GSE13425** and follow the wizard;
- Select the Tab **Classify**, and the following settings:

The screenshot shows the Qlucore software interface with the 'Classify' tab selected. The interface includes a top navigation bar with tabs: Data, Method, Options, View, Cluster, Build Classifier, and Classify. Below the tabs, there are two main sections: 'Classifier' and 'Normalization Mode'. The 'Classifier' section contains buttons for 'Load', 'Unload', and 'Show Report', along with a dropdown menu currently set to 'lass SVM no filter'. The 'Normalization Mode' section has two radio buttons: 'As Dataset' (unselected) and 'As Classifier' (selected). An 'Apply' button is located to the right of these settings. Below the settings, a status bar displays 'Data to test.gedata 1.1' and '2 (16 %)'.

- Select your classifier (Class KNN) and press **Apply**;
- Review the results: color the samples according to the new sample annotation **Predicted Leukemia Subtype**.
- Use other classifiers you built using SVM and Random Trees. Compare the results of all predictions working with new Predicted sample annotations.

8. Build a Classifier – Steps (no validation data)

1. Load the **Leukemia dataset** from the Help menu.
2. Select the tab **Build Classifier** and select the following settings:

Method	KNN	Ranking	Multi Group Comparison		Validation	no validation set	Settings
Key	Leukemia Subtype	Filter Value			Validation Key		Build

3. Press **Build** and Save the classifier on your desktop (call it Class KNN).
4. Review the **report**.

Extra: Build more with SVM and Random Trees, save them, compare Classification accuracy reports – **mean accuracy, individual class accuracy**. Build a classifier using gene symbols.

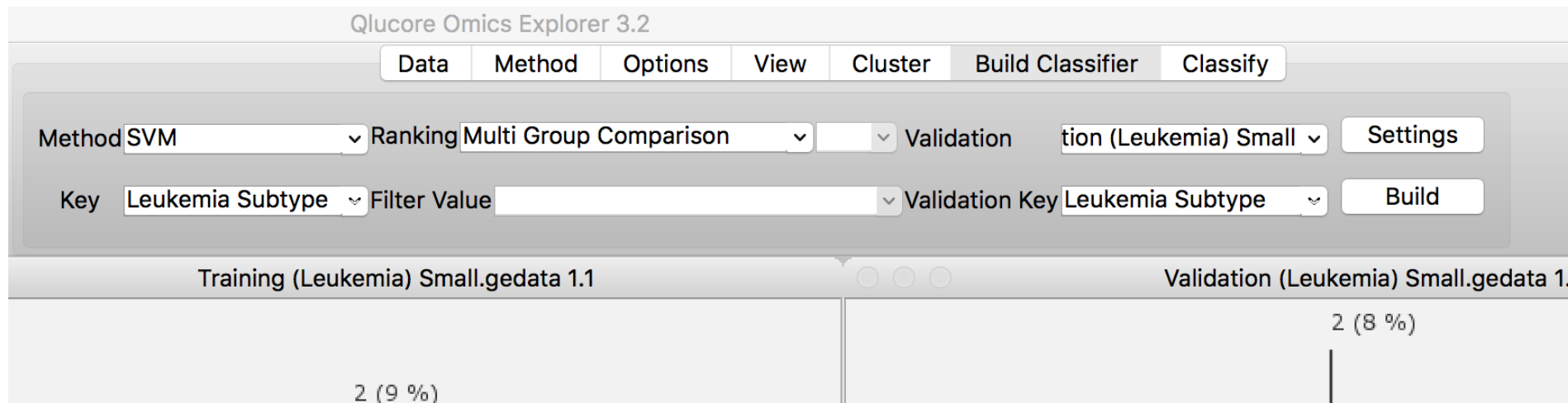
Variance Filtering before building can greatly improve accuracy!

Extra: Build a KNN classifier after filtering by variance to projection score = 0.39

8. Build a Classifier (with validation data)

Load your **Training data** (Classification folder: "Training (Leukemia)small.gedata", and **Validation data** named "Validation (Leukemia)small.gedata"

Select the tab/tool **Build Classifier**, and following settings:



The screenshot shows the 'Build Classifier' tab in the Glucore Omics Explorer 3.2 software. The interface includes a menu bar with 'Data', 'Method', 'Options', 'View', 'Cluster', 'Build Classifier', and 'Classify'. Below the menu, there are several configuration fields: 'Method' is set to 'SVM', 'Ranking' is set to 'Multi Group Comparison', 'Validation' is set to 'tion (Leukemia) Small', and 'Settings' is a button. Below these, 'Key' is set to 'Leukemia Subtype', 'Filter Value' is an empty field, 'Validation Key' is set to 'Leukemia Subtype', and 'Build' is a button. At the bottom, there are two data panels. The left panel is titled 'Training (Leukemia) Small.gedata 1.1' and shows '2 (9 %)'. The right panel is titled 'Validation (Leukemia) Small.gedata 1.1' and shows '2 (8 %)'.

The rest of the workflow is the same as in the previous exercise!

To classify use "To test.gedata". Find the new sample annotation in "To test" data with predicted leukemia subtypes.

Extra: Use data sets in your Classification folder: Extra_Classification with Validation (files - Training, Validation, To test). Try to exclude some sample groups and see whether it affects the accuracy.

More information on www.qlucore.com

- Qlucore Omics Explorer
 - Tutorial
 - Reference manual
- Homepage
 - Video workflows
 - How to documents
 - FAQ
- Monthly webinars
 - Qlucore.com

The screenshot shows the Qlucore Omics Explorer website. The header is blue with the QLUCORE logo and a quote: "Qlucore Omics Explorer is adding more creativity to our research than any other software I have used." - David Gisselsson Nord, MD, PhD, Associate Professor, Department of Clinical Genetics Lund University. Below the header is a navigation bar with links: HOME, COMPANY, PRODUCTS, CONTACT, SUPPORT, DOWNLOADS, and a LOGIN button with the email QLUCUST@QLUCORE.COM. A secondary navigation bar includes OVERVIEW, FEATURES, VERSION 2.3, Q&A, REFERENCES, and DOCUMENTATION. The main content area is titled "DOCUMENTATION" and contains a paragraph: "Below you will find various documents and video clips which will make it easier to use Qlucore Omics Explorer. All of these documents and films have deliberately been kept short to ensure greater clarity and focus." Below this is a section "MOVIES AND INTRODUCTIONS" with a list of items, each with a thumbnail, title, and file type icon (Video or .pdf). The items are: "Introduction To Qlucore Omics Explorer" (Video), "Introduction to 2D plots" (Video, Note: No sound.), "Qlucore Omics Explorer Features" (.pdf), "Qlucore Omics Explorer - a very brief introduction" (Video), "Working with fewer samples." (Video), "Work with subgroups and find discriminating variables. Generate lists with p- and q-values." (Video), and "Qlucore Omics Explorer Tutorial" (.pdf). On the right side, there are three blue buttons: "VERSION 2.3 NEWS", "HOW TO BUY", and "GET THE VISUALISATION GUIDE". Below these are sections for "DATA" (GENE EXPRESSION, PROTEIN ARRAY, MIRNA, DNA METHYLATION, PROTEOMICS), "DISEASE AREA" (CANCER, OBESITY, DIABETES), "PERFORMANCE" (with a bar chart), and "SCREENSHOTS" (with several small images).

QLUCORE "Qlucore Omics Explorer is adding more creativity to our research than any other software I have used." - David Gisselsson Nord, MD, PhD, Associate Professor, Department of Clinical Genetics Lund University

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OVERVIEW FEATURES VERSION 2.3 Q&A REFERENCES DOCUMENTATION

DOCUMENTATION

Below you will find various documents and video clips which will make it easier to use Qlucore Omics Explorer. All of these documents and films have deliberately been kept short to ensure greater clarity and focus.

MOVIES AND INTRODUCTIONS

Thumbnail	Title	File Type	Notes
	Introduction To Qlucore Omics Explorer	Video	
	Introduction to 2D plots	Video	Note: No sound.
	Qlucore Omics Explorer Features	.pdf	
	Qlucore Omics Explorer - a very brief introduction	Video	
	Working with fewer samples.	Video	
	Work with subgroups and find discriminating variables. Generate lists with p- and q-values.	Video	
	Qlucore Omics Explorer Tutorial	.pdf	

VERSION 2.3 NEWS

HOW TO BUY

GET THE VISUALISATION GUIDE

DATA

GENE EXPRESSION
PROTEIN ARRAY
MIRNA
DNA METHYLATION
PROTEOMICS

DISEASE AREA

CANCER
OBESITY
DIABETES

PERFORMANCE

SCREENSHOTS

Contact/support

support@glucore.com

yana.stackpole@glucore.com

Calendly link to [request a help session](#)