Visualize and Explore

- QC (outliers, mislabeled samples)
- Make observations - identify structures, patterns
- Generate new hypotheses
- Browse the genome

Analysis

- t-test, ANOVA, Regressions, R scripts. Open API to R, Batch exec
- Variant calling
- Easy generation and export of reports, status, and plots
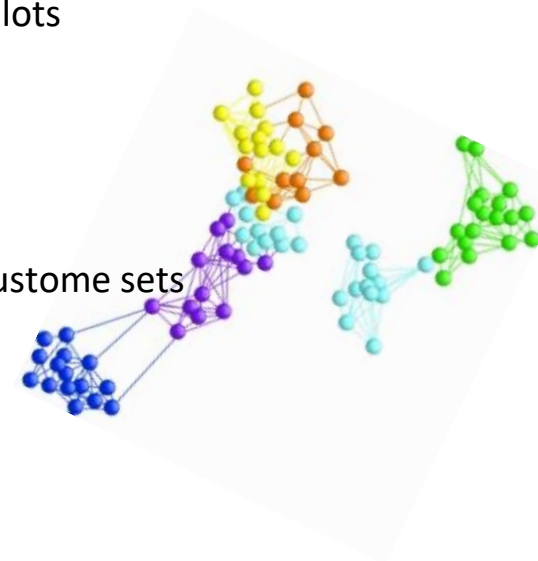- Save your session, share

Biological Insight

- Gene Set Enrichment using MSigDB, reactome, or custome sets
- Explore annotations
- GO Browser

Classify and Predict

- Build classifiers
- kNN, SVM, RT
- Predict sample class, outcome, etc.

Side by Side	Merged datasets
Results on separate plots	Results on the same plot
Statistical analysis – q calculated separately for each (cannot just combine)	Statistical analysis – q calculated for a combined variables set
Correlation possible for one type at a time	Correlation available for all data types
Manual annotation of one data with results from another	Easier to relate sample annotations interpreting results
PCA – signals are from one data type	PCA– Signals blend together, may mask each other if opposite
Limited to one data type at a time	Can zoom in on one data type at a time
No scale issue	May need to scale before merging matrices
ML – limited to one type	ML – advantage of considering both for the best performance

Two types of data for the same samples: Gene expression and Proteomics

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1			Sample id	1	2	3	4	5	6	7	8	9	10	11	
2			Treatment	Drug1	Drug1	Drug1	Drug3	Drug2	Drug2	Drug1	Drug2	Drug2	Drug3	Drug3	Drug1
3			CON__Q3SX14 abundance	16.521	16.259	16.571	16.394	-3.3219	16.043	16.545	16.131	16.04	16.252	-3.3219	-3
4	Gene /Protein	Type													
5	S100A11	Gene		5.331	4.995	5.13	6.368	6.438	5.252	5.508	5.334	5.724	6.069	6.441	
6	GPX1	Gene		9.91	10.396	9.857	10.361	8.816	9.149	10.066	8.731	9.045	8.98	10.178	
7	CTNNA1	Gene		7.568	7.8495	7.169	7.425	7.2435	6.931	7.492	7.003	7.276	7.1575	6.918	7
8	RPS15	Gene		11.636	11.594	11.58	11.826	11.105	10.855	11.598	11.132	10.732	11.584	11.64	1
9	sp|P15407|FOSL1_HUMA	Protein		16.177	15.954	16.064	15.75	16.059	16.321	16.133	16.246	16.155	15.917	15.764	1
10	sp|P16144-2|ITB4_HUMA	Protein		17.115	16.337	17.068	16.756	16.856	16.253	16.573	16.597	17.094	17.862	17.111	1
11	sp|P16278-3|BGAL_HUM/	Protein		16.382	15.459	16.036	17.248	16.097	15.508	15.747	16.267	15.851	16.356	17.116	1
12	sp|P16401|H15_HUMAN	Protein		19.844	18.746	19.206	17.415	18.894	18.947	19.409	19.159	20.105	17.004	17.485	1

Multi-omics data   Sheet1   +

Select destination and press ENTER or choose Paste   150%

Two+ types of data for the same samples mRNA and miRNA

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VARIABLE ID	CLASS mRNA or miRNA	BH-A0DO-01B-11 tumor	BH-A0DT-01A-21 tumor	BH-A18J-01A-11 tumor	BH-A18K-01A-11 tumor	BH-A18L-01A-32 tumor
SAMPLE ID / **STATUS**						
A1BG_mRNA	mRNA	-0.126167	0.3425	0.955333	-0.3585	0.888667
A2BP1_mRNA	mRNA	-1.8395	-2.62283	-0.892	-1.78083	-1.735
A2ML1_mRNA	mRNA	0.022	0.3075	-1.5205	0.7615	-1.2775
A2M_mRNA	mRNA	1.4965	0.99375	0.425	-0.668	-0.071
A4GALT_mRNA	mRNA	1.217	1.084	1.22883	-0.8405	0.773667
A4GNT_mRNA	mRNA	-0.134	-0.4485	-0.42	0.1745	0.1175
AAAS_mRNA	mRNA	-0.75725	-1.00375	-0.58375	-0.20775	-0.389

ML – predictive model on miRNA

Classifier Training Report

Type: Random Tree Classifier
Number of variables used by classifier: 245
Classifier name: random trees miRNA

Class Accuracy Number of Samples
normal   0.928571   14
tumor   1   14

Mean / Total 0.964286 28

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ML – predictive model on mRNA+miRNA

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Classifier Training Report

Type: Random Tree Classifier
Number of variables used by classifier: 24 (only mRNA selected)
Classifier name: **miRNA_mRNA** Boosted trees

Validation Score
Class Accuracy Number of Samples
normal 0.928571   14
tumor   1   14

Mean / Total 0.964286 28

QLUCORE

Next steps

1. Download and install the trial version ([Mac or Win version - links](#), you will need to register), and then update the license key in **Qlucore – License – Activation Key** with the key from us

2. Book a session with us – get help importing your data and setting up your analysis. Here is a link https://calendly.com/yana-stackpole/30min

3. Explore your data in a cool GUI in a way that makes sense to you!

Reach out any time Yana.Stackpole@Qlucore.com

System requirements
Base module

FOR WINDOWS

- Windows 7, Windows 8 or Windows 10
- 512 MB of RAM memory
- A graphical card with support of at least Open GL 2.1
- 5 GB of free hard disk space
- Qlucore Omics Explorer is available in both a 32-bit and 64-bit versions. The program takes full advantage of processors with multiple cores and computers with multiple processors.

FOR MAC

- Max OS X 10.15 or 10.14
- 512 MB of RAM memory
- A graphical card with support of at least Open GL 2.1
- 5 GB of free hard disk space