TCGA MultiOmics Data Analysis

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Retrieval

- TCGA normalized level 3 datasets for RNASeq and RPPA
- For tumor types breast cancer and ovary cancer

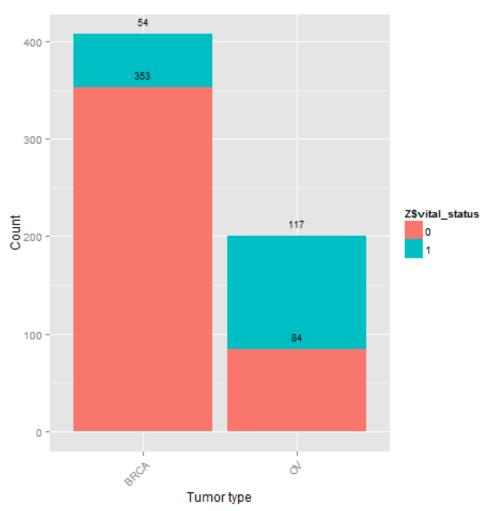
```
library("RTCGAToolbox")
firehose_datasets = getFirehoseDatasets()
firehose_dates= getFirehoseRunningDates()
BRCA.dataset = getFirehoseData (dataset="BRCA", runDate=firehose
OV.dataset = getFirehoseData (dataset="OV", runDate=firehose_dataset="OV")
```

Preprocessing

- Removed samples not having data for RNASeq and RPPA
- Removed variables for genes not matching with HGNC gene names
- Removed RPPA variables for antibodies matching the same gene, only the antibody with the maximum absolute average expression was conserved
- Scaling
- Removed variables with zero or near zero variance
- Removed variables with missing values
- Removed variables with correlation over 0.7

Samples

407 BRCA + 201 ovary cancer samples

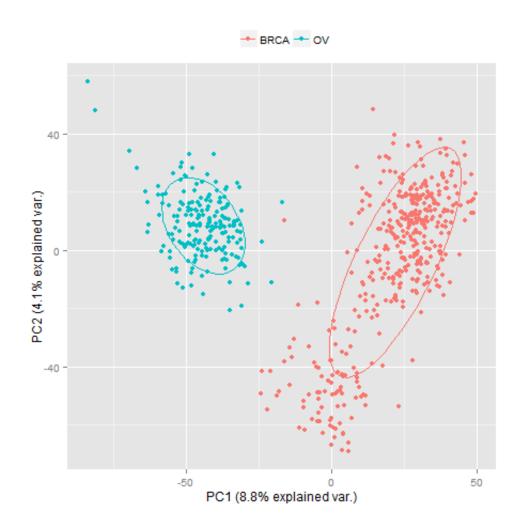


Variables

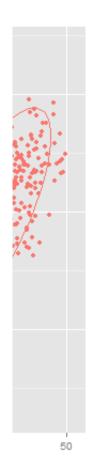
12880 gene expression + 55 protein expression variables are far too many to plot...

Principal component Analysis

Gene expression



ıt Analysis



8/18

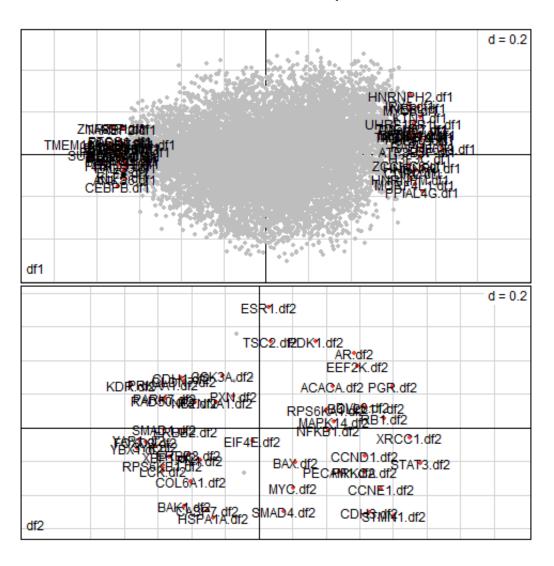
Multiple Co-Inertia Analysis (MCIA)

The 2 first PCs explain 34.05% and 11.55% of the variance



Multiple Co-Inertia Analysis (MCIA)

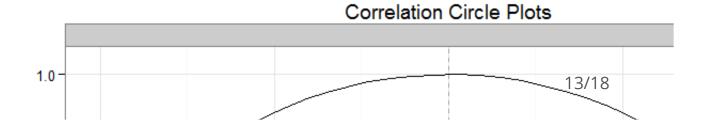
Labeled items are the top 100 variables



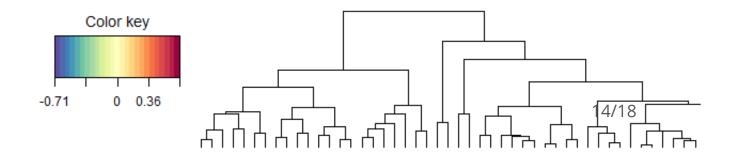
Samples

	plotindiv	
	Block: X	
BROABRCA BROARCA BR	ÇĄ	12/18

Variables



Heatmap



Network



Results

Matches between MCIA and sPLS top 100 and known oncogenes and tumor supressor genes

Results

Matches between MCIA and sPLS enriched pathways in Reactome

MCIA 17/18 sPLS

Other methods to study

- Canonical Correlation Analysis
- Regularized Generalized CCA (error with dataset)
- Regularized CCA (long computation)
- CCA with Elastic Net (did not found implementation)
- Procrustes (pending)