Clustering Analysis
Babelomics 5.0
Exercises

Cankut ÇUBUK
March 9th, 2017

GDA
International Course on
Genomic Data Analysis

PRINCIPE FELIPE
CENTRO DE INVESTIGACION

Babelomics 5.0

http://babelomics.bioinfo.cipf.es/

http://courses.babelomics.org/

Exercises

1) Go to http://bioinfo.cipf.es/gda17/doku.php/program

2) Download GDA17_TCGA_265_mod_gene_BRCA_subtype_HER_Basal_Normal.txt (Prediction_clustering_exercises.zip)

   Data description: RNA-Seq data of 30 Breast Invasive Carcinoma (BRCA) samples taken from The Cancer Genome Atlas (TCGA) data portal. Contains 10 normal samples, 20 tumor samples with 2 subtypes (Basal-like and Her2-enriched).

3) Upload your file to Babelomics 5.0.

   Go to section Expression>Clustering

4) Cluster samples with given paramaters.

   UPGMA + Euclidean (square)

   UPGMA + Correlation coeff. (Spearman)

   Which distance parameter is better for proper clustering?

Exercises

5) Repat the analysis using the same distance parameters and SOTA method.

SOTA + Euclidean (square)

SOTA + Correlation coeff. (Spearman)

Do the results change based on the method or the distance parameter?

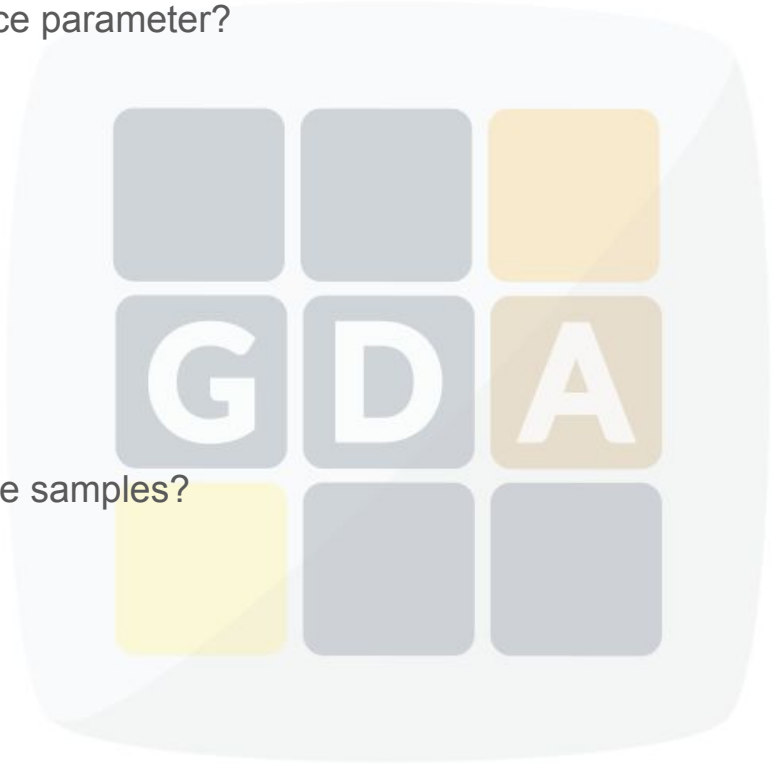
6) Try to cluster your samples with K-means.

Set k-value 6 and use Correlation coeff. (Spearman)

Check the results of K-means.

Are the results acceptable?

Is the dendrogram representing any hierarchy between the samples?



Exercises

7) Repeat the step 6 with k-value 3.

Did your result same as previous one?

8)) Try to cluster your samples with K-means.

Set k-value 2 and use Correlation coeff. (Spearman).

Can we say that K-means is good to distinguish tumor from normal?

Supervised Classification Analysis
Babelomics 5.0
Exercises

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Exercises

1) Go to http://bioinfo.cipf.es/gda17/doku.php/program

2) Download GDA17_TCGA_265_mod_gene_LUSC_train.txt (Prediction_clustering_exercises.zip)

Data description: RNA-Seq data of Lung squamous cell carcinoma (LUSC) samples taken from The Cancer Genome Atlas (TCGA) data portal.

Contains 11 Normal and 150 Tumor samples.

NOTE: It is always recommended to use balanced sample size to avoid biased training.

3) Download GDA17_TCGA_265_mod_gene_LUSC_test.txt (Prediction_clustering_exercises.zip)

Data description: RNA-Seq data of Lung squamous cell carcinoma (LUSC) samples taken from The Cancer Genome Atlas (TCGA) data portal.

Contains 6 Normal and 75 Tumor samples.

4) Upload your files to Babelomics 5.0.

   Go to section Expression>Class Prediction

Exercises

5) Select SVM, KNN and Random Forest

   Select Leave-one-out for error estimation

   Select Correlation-based Feature Selection (CFS)

6) Download test_result.txt

Which supervised classification method(s) works better?

How many genes were used for the prediction?

Are the selected genes same for all methods?