

Lecture 6

L6.2. Survival

Load library **survival**. Look for 2 datasets inside: *cancer* and *melanoma*. Investigate dataset with methods you have learned. Perform survival analysis and identify factors affection survival.

L6.3. Microarrays

Download and analyze time course miRNA data from <http://edu.sablab.net/data/gz/>

Affymetrix_miRNA2.txt – sample annotation

rma-sketch.summary.txt – result of APT import

Affymetrix_miRNA2.zip – data in tab-separated text

- a) Download, import and change the structure
- b) Keep only mature miRNA (annotated hsa-mir-.....)
- c) Visualize by PCA
- d) Detect differentially expressed miRNA by **limma** between 0h and 48h

L6.4. RNASeq

Load an extract of 60 samples of TCGA on lung squamous cell carcinoma from <http://edu.sablab.net/data/gz/>

LUSC60.RData – R binary (compressed) data file with raw count table and annotations

- a) Investigate the data
- b) Exclude genes which are never expressed (have 0 counts in all samples)
- c) Apply edgeR and DESeq2 to detect differentially expressed genes
- d) Compare results