Gene set-based clustering of gene expression data

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- **Gene expression profiling** is a way of studying **activity** of genes of different organisms, organs or cell lines etc and what **molecular pathways** are active. Usually, it is performed using microarray or RNA sequencing technology.

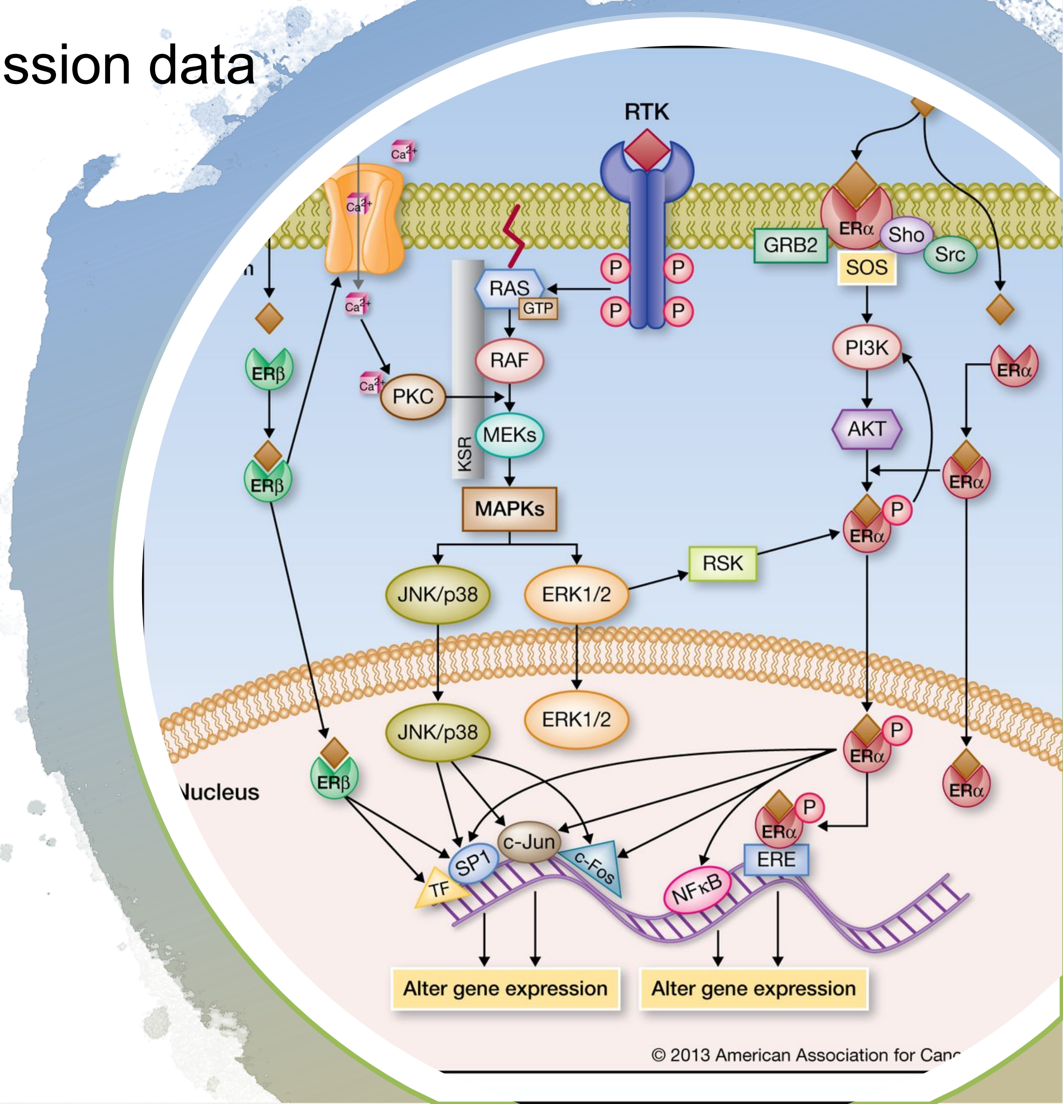
- **Clustering** of gene expression profiles is used to determine if there are any similar and diverse groups of samples.

- When clustering expression profiles **various similarity measures** can be considered, depending on the objective of the analysis. One interesting perspective is brought by the so-called **pathway activation scores**, or similar parameters, that try to capture the activity of a given pathway or gene set.

- However, when clustering samples (expression profiles) one needs a similarity score between the said samples. Here we propose to use a gene-set measure, e.g.

Similarity(x1, x2) = abs(Score(x1, gene_set) - Score(x2, gene set)),

- to produce groupings of samples relative to a reference gene set.



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Aims of the project:

The project will implement (in R) a package allowing such clustering with various activation scores (Z-score, Kolmogorov-Smirnoff, GSEA etc) and a number of alternative similarity functions (e.g. absolute difference, log-ratio etc). For testing purposes, MSigDB will be used for gene set selection and publicly available colon-cancer expression data sets.

- **Main steps:**
  - Study a tutorial on data clustering in R
  - Study some examples of R packages
  - Get familiar with data representation (within existing R packages)
  - Study some methods for gene set scoring (R packages)
  - Implement the new similarity function
  - Compare with correlation-based similarity
  - Test the package on publicly available colorectal cancer or breast cancer dataset (GEO database https://www.ncbi.nlm.nih.gov/gds) – preferably normalized microarray data