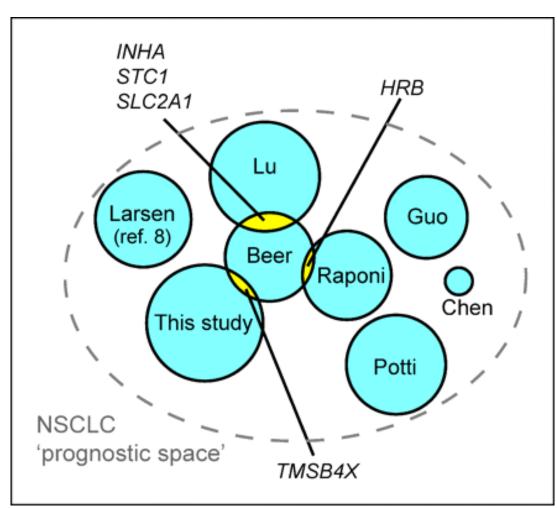
Andrey Alexeyenko







Poor overlap between published biomarkers and signatures of clinical phenotype



Major, "unavoidable" reasons:

- Molecular heterogeneity between patients;
- •N genes > N patients => Dimensionality curse;

Other reasons:

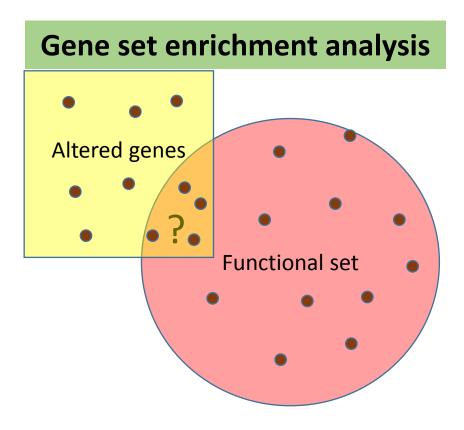
- Different sub-types of patient population;
- Different microarray platforms;
- •Technical noise.

Gene expression signatures of lung cancer relapse

From: Roepman et al., 2007



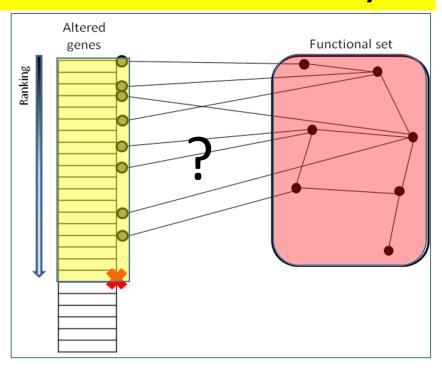
Enrichment analysis: characterization of novel gene sets



Huang da W, ... Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. Nature Protocols, 2009

https://david.ncifcrf.gov

Network enrichment analysis

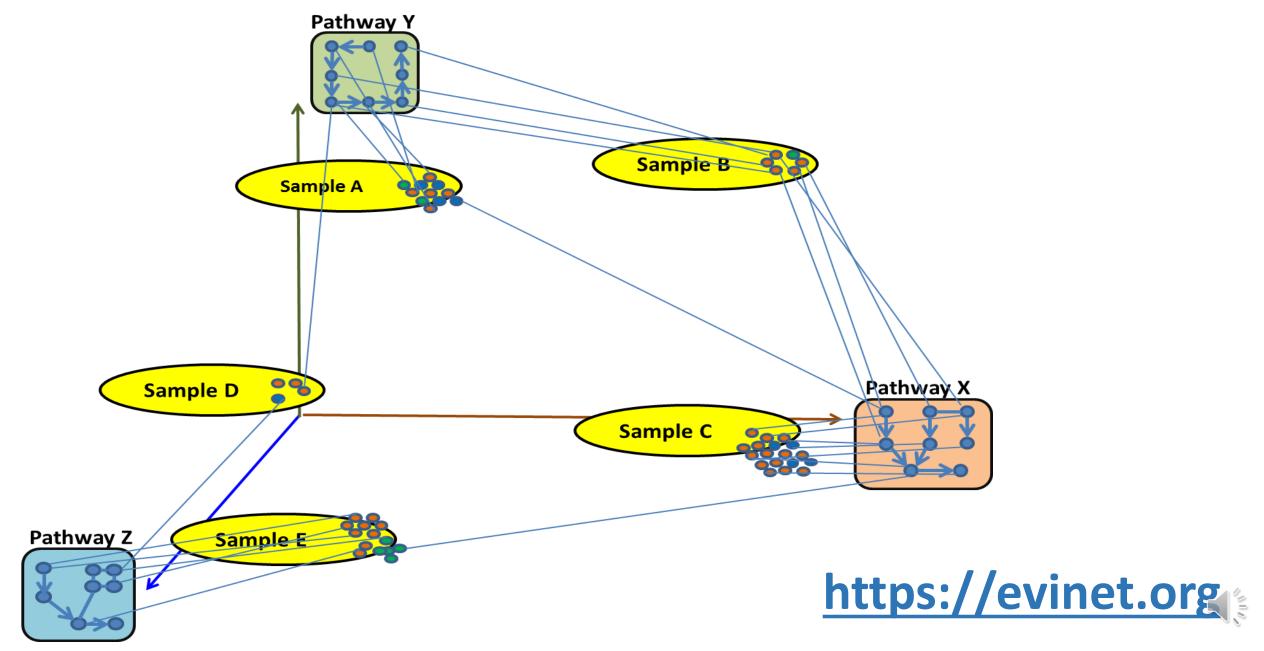


Alexeyenko A, Lee W, ... Pawitan Y. **Network enrichment analysis**: extension of gene-set enrichment analysis to gene networks. **BMC** Bioinformatics, 2012

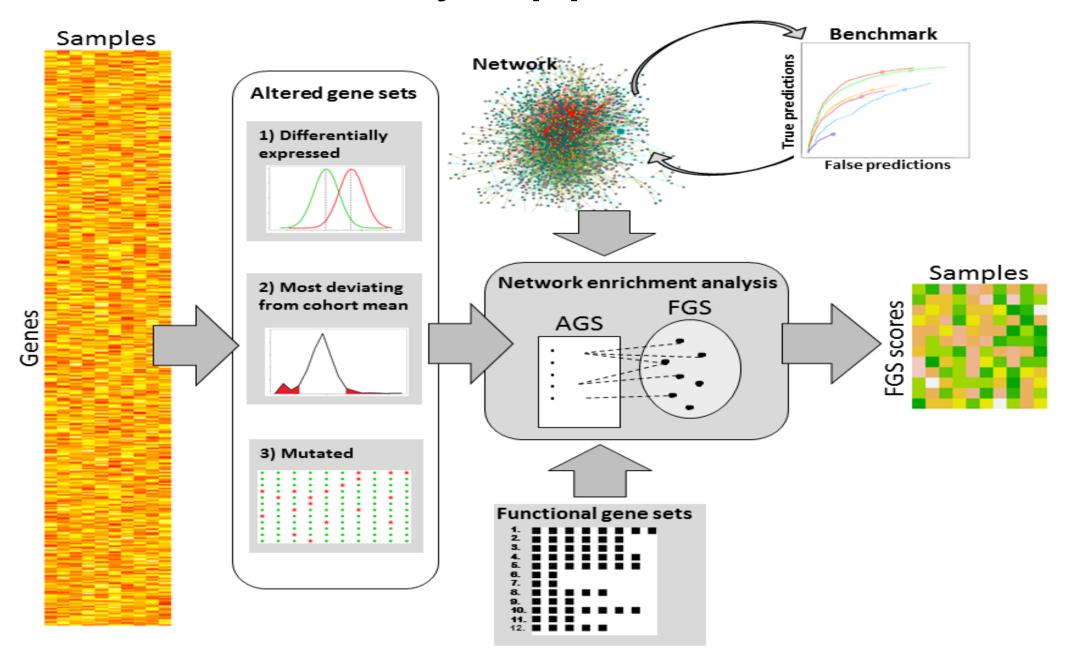
https://research.scilifelab.se/andrej_alexeyenko/HyperSet/



Samples in the pathway space

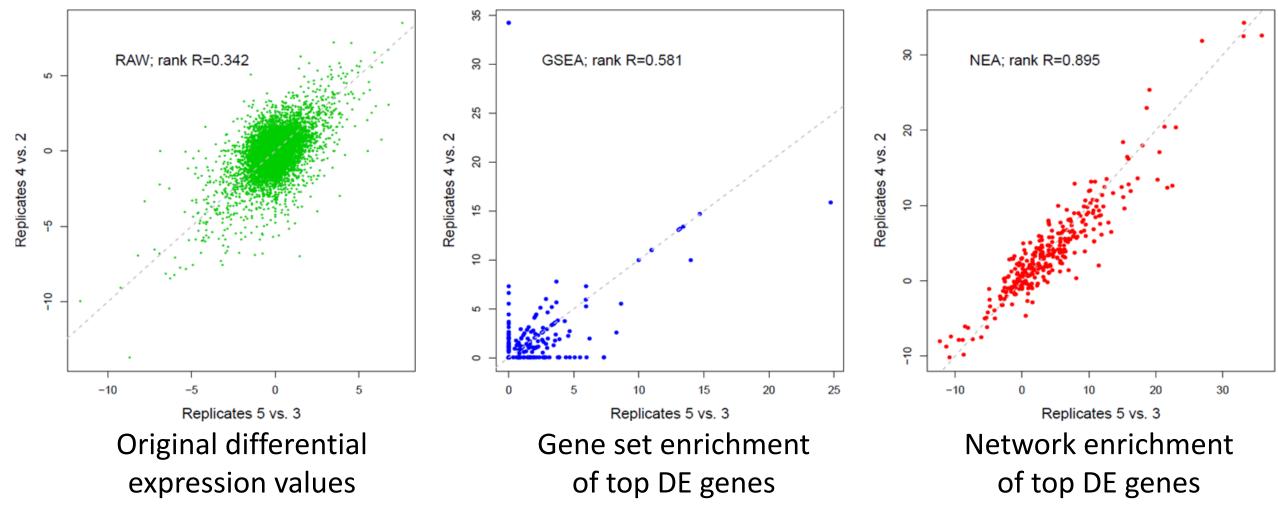


Analysis pipeline





Consistency in differential expression analysis

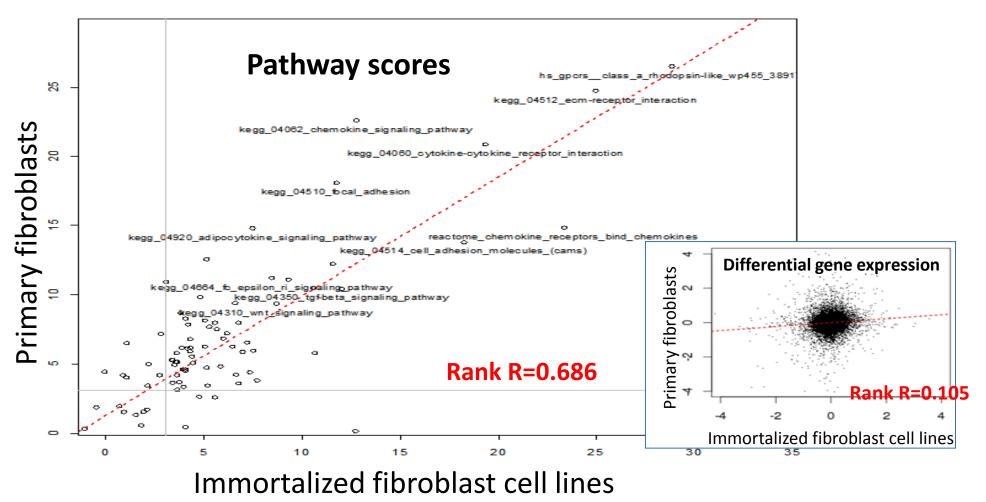


FANTOM5: gene expression in gingivial epithelial (GE) versus tenocyte cells (TC) using samples from two different donor pairs (GE: #4 and #5; TC: #2 and #3)

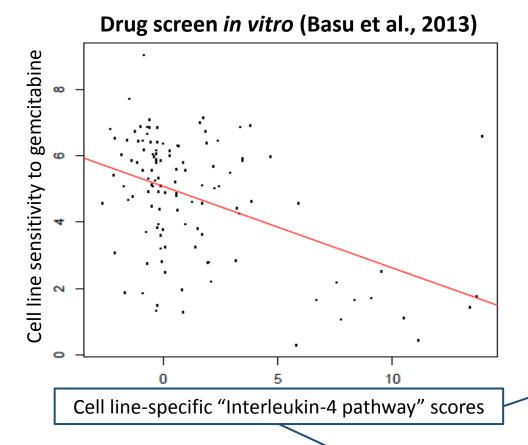
From: Jeggari A. and Alexeyenko A.



Two experimental models of tumor inhibition are similar at the pathway (and not gene) level

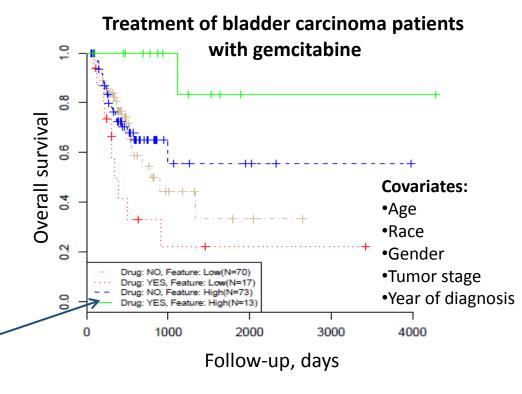


From: Alexeyenko A., Alkasalias T., ... and Klein G. Confrontation of fibroblasts with cancer cells in vitro: gene network analysis of transcriptome... J Exp Clin Cancer Res. 2015

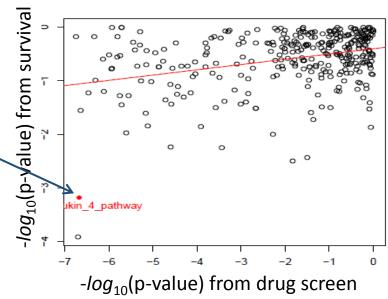


Drug-pathway associations hold when followed from *in vitro* to the clinic

From: Franco M. et al.



Performance in vitro and in the clinic, all pathways

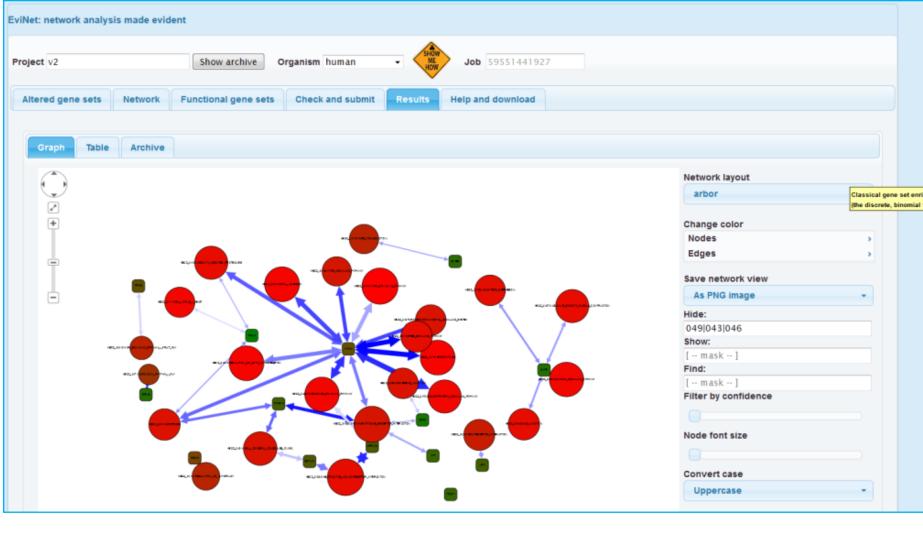




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https://evinet.org

