Robust biomarkers from network-based data integration

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**Network enrichment analysis of high-throughput data is both sensitive and robust**

We developed a method for finding sensitive and robust biomarkers at the pathway level. Samples (patients etc.) are described with scores from network enrichment analysis, which transforms the original space of altered genes into a lower-dimensional space of pathways. The network-based data interpretation has the following strengths:
1) It naturally combines all major types of molecular interactions,
2) individual alterations of genomic sequence, gene methylation, transcription, and protein abundance are generalized at the pathway level, and
3) the pathway view enables low-dimensional statistical analysis and is transparent for biological interpretation.

These dimensions are then correlated with clinical or other phenotypes. The method was tested using in vitro drug screen data and then on clinical data of The Cancer Genome Atlas. It proved superior to the original single-gene analysis in terms of 1) level of correlation with drug sensitivity in cancer cell lines, 2) consistency of the discovered correlates when applied to an independent drug screen, 3) ability to explain differential survival of patients, and 4) relevance of the in vitro correlates to survival of patients who received the same drug.

**Consistency in differential expression analysis**

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

**Analysis pipeline**

R package NEArender: https://cran.r-project.org/

**Samples in the pathway space**

**Agreement between sensitivity to anti-cancer drugs in vitro and in the clinic**


From: Jeggari A. and Alexeyenko A.

From: Franco M. et al. Drug screen in vitro (Basu et al., 2013)

From: Franco M. et al.