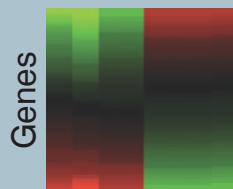


Input data

(a) Module repository

Modules from gene ontology and MSigDB

Samples



Expression profiles

Gene 1
Gene 2
Gene 3
Gene 4

Gene 5
Gene 3
Gene 1
Gene 7

Gene 2
Gene 3
Gene 5
Gene 8

Modules from high-throughput genomic experiments

Expression data repository

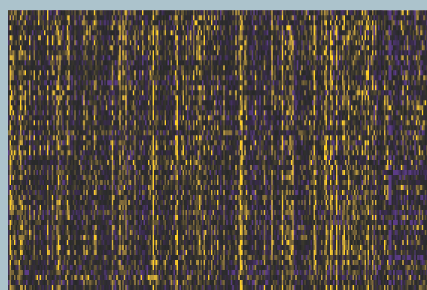
Tumors



p53 mutation
cancer subtype

Transcriptional profiling
of tumor samples with
clinical data and survival
information

Genes



Normalized expression profiles of tumors

(b) sample-level enrichment analysis (SLEA)



For each sample in expression
data set, perform EA

(c) Survival analysis (SA)

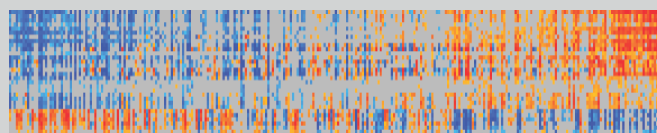
Stratify samples according to EA results



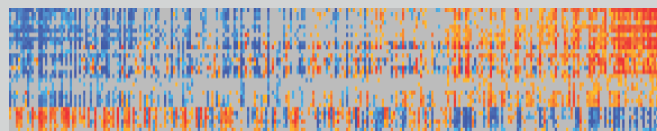
- Samples with positive z-score
and corrected p-value <0.05
- All the rest of the samples

(d) Enrichment profiles

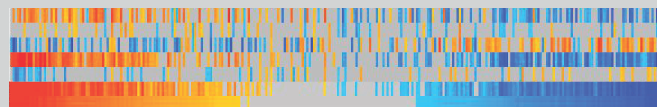
Tumors



GOBP
modules



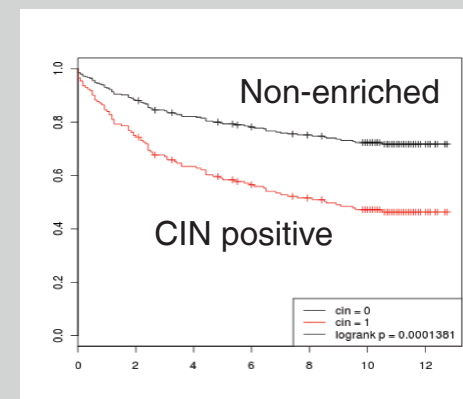
MSigDB
modules



Senescence
modules

(e) Relation to survival

For each data set,
Kaplan-Meier
curves of the two
groups



Results