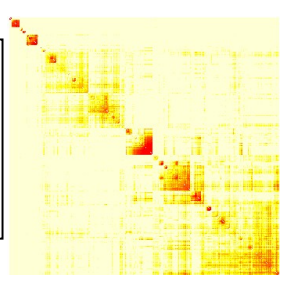


Construct a gene co-expression network

Rationale: make use of interaction patterns among genes

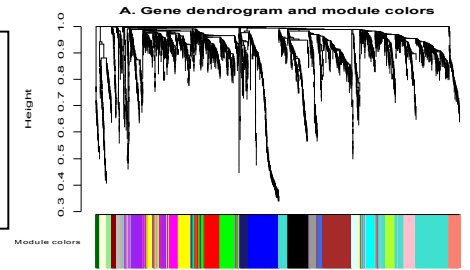
Tools: correlation as a measure of co-expression



Identify modules

Rationale: module (pathway) based analysis

Tools: hierarchical clustering, Dynamic Tree Cut

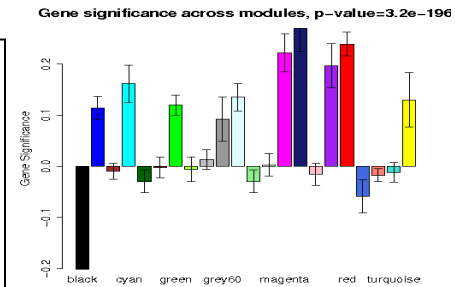


Relate modules to external information

Array Information: clinical data, SNPs, proteomics

Gene Information: ontology, functional enrichment

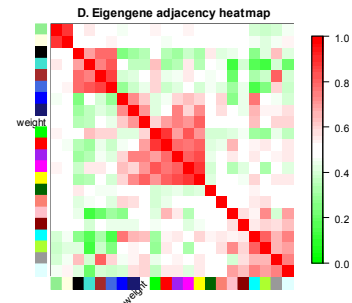
Rationale: find biologically interesting modules



Study module relationships

Rationale: biological data reduction, systems-level view

Tools: Eigengene Networks



Find the key drivers in *interesting* modules

Rationale: experimental validation, biomarkers

Tools: intramodular connectivity, causality testing

