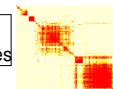# A. Single eigengene network analysis
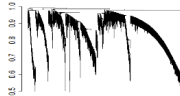
Construct network
Rationale: make use of interaction patterns between genes
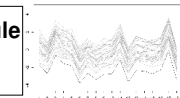

↓

Identify modules
Tools: Hierarchical clustering
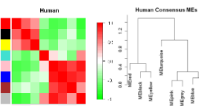Rationale: module- (pathway-) based analysis

↓

Find one representative for each module
Tools: eigengene (1st Principal Component)
Rationale: Condense each module into one profile

↓

Create network of representatives
Tools: Correlation of eigengenes
Rationale: Study relationships between pathways
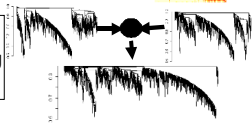

B. Differential analysis of eigengene networks.

Construct networks for each dataset
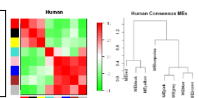Rationale: make use of interaction patterns between genes

↓

Identify consensus modules
Tools: consensus dissimilarity clustering
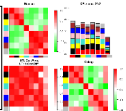Rationale: find preserved modules

↓

Construct eigengene networks in each dataset
Tools: eigengene as module representative
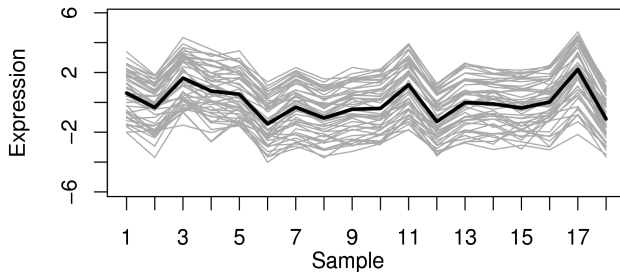Rationale: quantify relationships *between* pathways
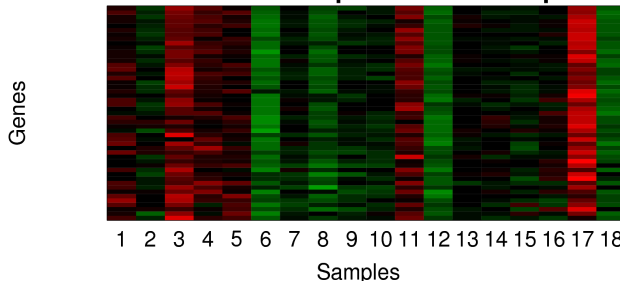

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Compare eigengene networks across sets
Tools: Measures of correlation preservation
Rationale: understand which biological conditions affect the relationships between modules

C. Expression levels of genes and eigengene

D. Module expression heatmap

E. Eigengene Expression