

Construct a co-methylation network for each of the 10 data sets and Corresponding robust similarity measures (Topological Overlap Matrices).

Rationale: make use of co-methylation patterns between CpGs



Define a consensus network and consensus modules by aggregating the 10 TOM measures

Rationale: find shared consensus modules in blood and brain tissue



Relate consensus modules to external information

Sample traits: age, gender

Gene Information: gene ontology (GO), cell markers (userListEnrichment)

Rationale: find aging related modules and understand their biological role



Study the preservation of the aging module across different data

Rationale:

- in similar data: check robustness of module definition
- dissimilar data: Illumina 450K data, pediatric population, cell types, MSC



Analysis of variance of module membership in the aging module

Sources of variation: Polycomb group target, CpG island, X-chromosome

Rationale: Understand relative contribution of factors