In this practical, we will be using R, along with other web-service tools, to identify gene co-expression modules from human brain developmental transcriptome expression data. We will be using publicly available gene expression data from the BrianSpan Atlas, creating the networks with Weighted Gene Co-Expression Network Analysis in R, and characterizing these modules with ENRICHR.

Steps:

Download the expression data

Create a Summarized Experiment object with the data and metadata

Filter out low expressed genes (80% TPM == 0)

Calculate soft-thresholding values

Adjacency matrix to topological overlap matrix

Create network

Functional annotations