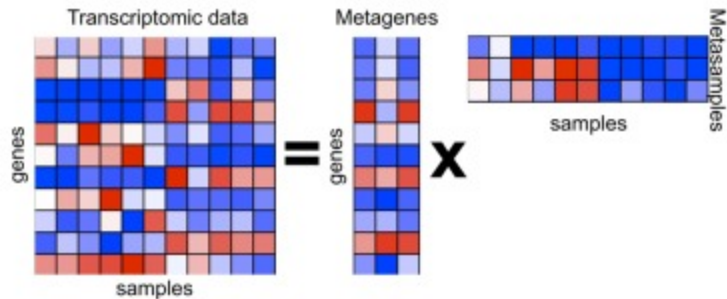
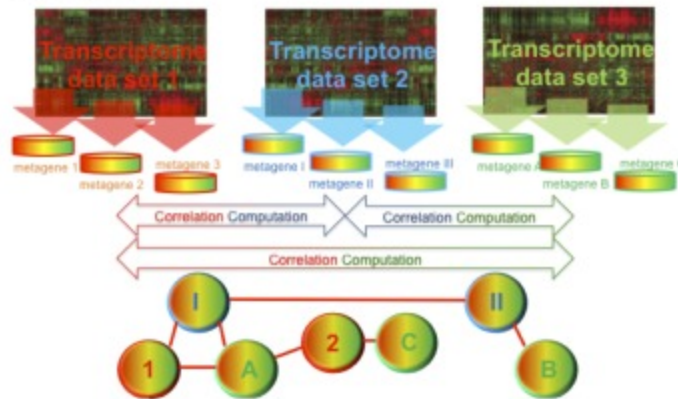


Step1. Decomposition of each dataset



Step2. Construction of the RBH network



Step3. Community detection



Step4. Community annotation

- Construction of weighted metagenes
- Characterization of weighted metagenes using driver genes, gene set enrichment analysis
- Characterization of metasamples using clinical information