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