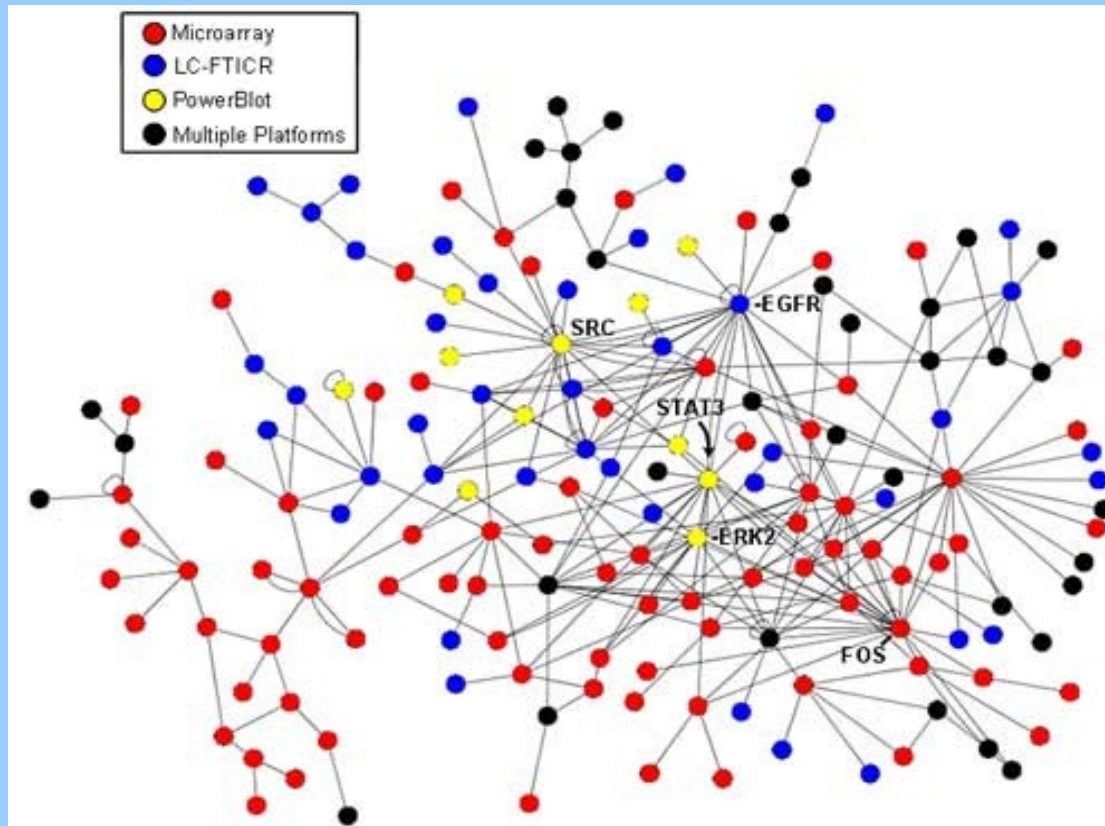


Network analysis

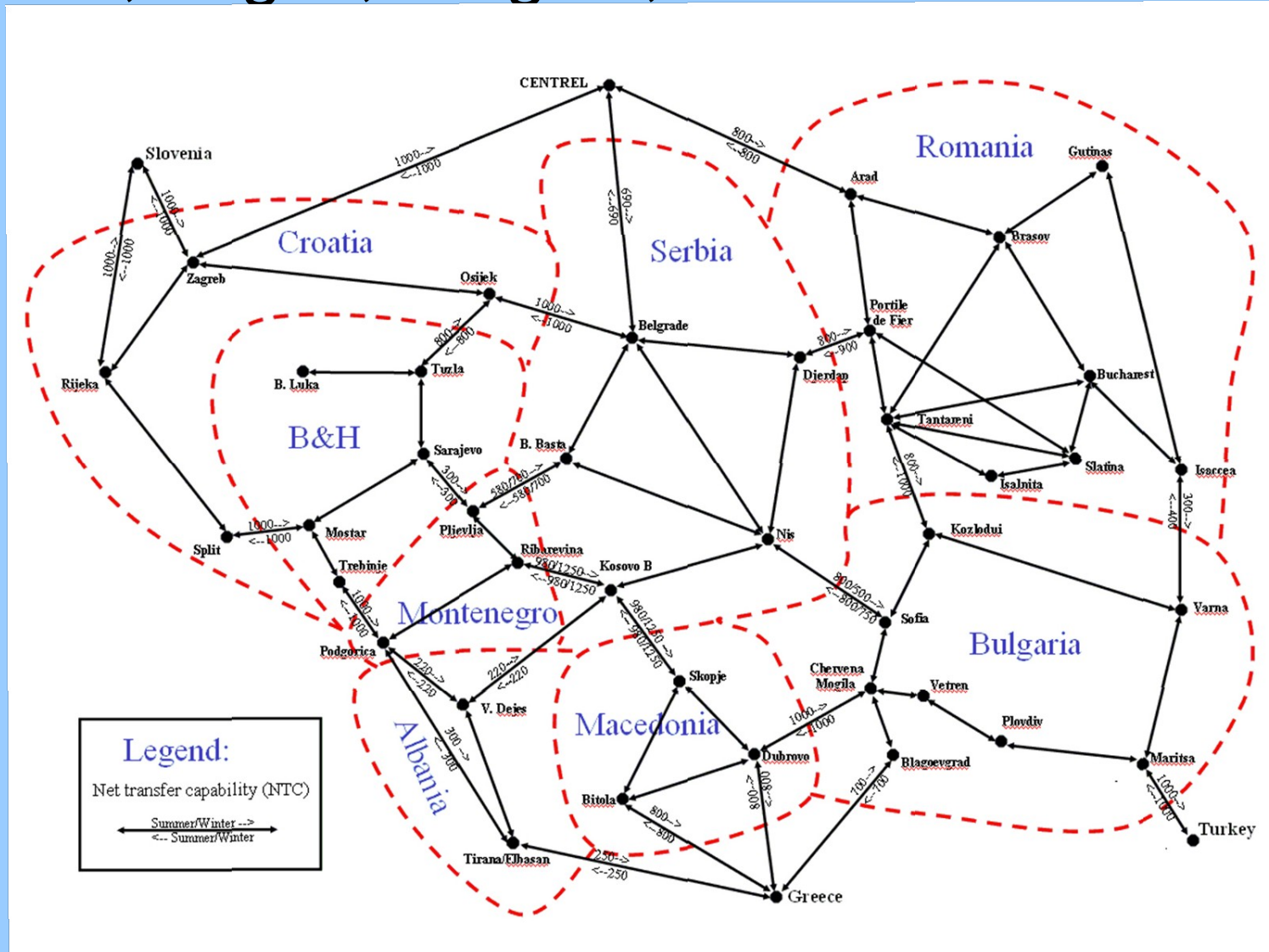


Cory Giles

RGCB/OMRF Cancer Informatics Workshop
January 16-18, 2013

Graph Review

- Nodes, edges, weights, directed/undirected



Popular biological networks

- KEGG
- Reactome
- NCI/Nature Pathway Interaction Database
- BioCarta
- Connectivity Map
- Gene Ontology

What do graphs model?

- Usually, nodes are genes/proteins and edges are physical or coexpression interaction
- But, other possibilities:
 - Drugbank (drug-drug and drug-gene)
 - Literature networks
 - Genetic interactions (LD, epistasis)
 - Ontologies can be viewed as graphs
 - Graphical models: Bayesian networks, Markov models (edges are conditional probabilities)

Coexpression network analysis

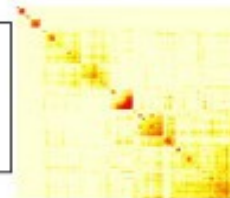
- Two ways to view gene-gene coexpression:
 - As network **modules**
 - best for network-centric analyses
 - As a graph with links between genes
 - best for gene-centric analyses
 - What are the N genes most coexpressed or anti-coexpressed with my gene of interest?
 - Can be used to predict functions for poorly-annotated genes

WGCNA can do many things for you

Construct a gene co-expression network

Rationale: make use of interaction patterns among genes

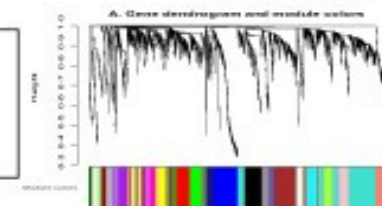
Tools: correlation as a measure of co-expression



Identify modules

Rationale: module (pathway) based analysis

Tools: hierarchical clustering, Dynamic Tree Cut

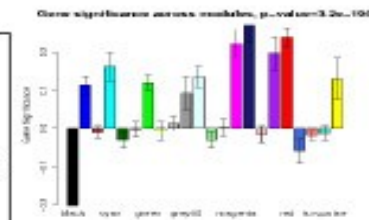


Relate modules to external information

Array Information: clinical data, SNPs, proteomics

Gene Information: ontology, functional enrichment

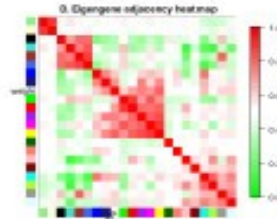
Rationale: find biologically interesting modules



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

