

# Community Structure in “Multislice” Networks

Exploring networks which vary across time, tie type, and community scale

Support: NSF (PJM, TR, KM), JSMF (MAP), Fulbright (JPO)

KITP Colloquium

## REPORTS

### Community Structure in Time-Dependent, Multiscale, and Multiplex Networks

Peter J. Mucha,<sup>1,2,3</sup> Thomas Richardson,<sup>1,2</sup> Kevin Macon,<sup>1</sup> Mason A. Porter,<sup>4,5</sup> Jukka-Pekka Onnela<sup>4,7</sup>

Network science is an interdisciplinary endeavor, with methods and applications drawn from across the natural, social, and information sciences. A prominent problem in network science is the algorithmic detection of tightly connected groups of nodes known as communities. We developed a generalized framework of network quality functions that allowed us to study the community structure of arbitrary multislice networks, which are combinations of individual networks coupled through links that connect each node in one network slice to itself in other slices. This framework allows studies of community structure in a general setting encompassing networks that evolve over time, have multiple types of links (multiplexity), and have multiple scales.

The study of graphs, or networks, has a long tradition in fields such as sociology and mathematics, and it is now ubiquitous in academic and everyday settings. An important tool in network analysis is the detection of mesoscopic structures known as communities (or cohesive groups), which are defined intuitively as groups of nodes that are more tightly connected to each other than they are to the rest of the network (1–3). One way to quantify communities is by a quality function that compares the number of intracommunity edges to what one would expect at random. Given the network adjacency matrix  $A$ , where the element  $A_{ij}$  denotes a direct connection between nodes  $i$  and  $j$ , one can construct a quality function  $Q(A, S)$  for the partitioning of nodes into communities as  $Q = \sum_{i,j} (A_{ij} - P_{ij})\delta(g_i, g_j)$ , where  $\delta(g_i, g_j) = 1$  if the community assignments  $g_i$  and  $g_j$  of nodes  $i$  and  $j$  are the same and 0 otherwise, and  $P_{ij}$  is the expected weight of the edge between  $i$  and  $j$  under a specified null model.

The choice of null model is a crucial consideration in studying network community structure (2). After selecting a null model appropriate to the network and application at hand, one can use a variety of computational heuristics to assign nodes to communities to optimize the quality  $Q$  (2, 3). However, such null models have not been available for time-dependent networks; analyses have instead depended on ad hoc methods to

piece together the structures obtained at different times (6–9) or have abandoned quality functions in favor of such alternatives as the Minimum Description Length principle (10). Although tensor decompositions (11) have been used to cluster network data with different types of connections, no quality-function method has been developed for such multiplex networks.

We developed a methodology to remove these limits, generalizing the determination of community structure via quality functions to multislice networks that are defined by coupling multiple adjacency matrices (Fig. 1). The connections encoded by the network slices are flexible; they can represent variations across time, variations across different types of connections, or even community detection of the same network at different scales. However, the usual procedure for establishing a quality function as a direct cost of the intracommunity edge weight minus that

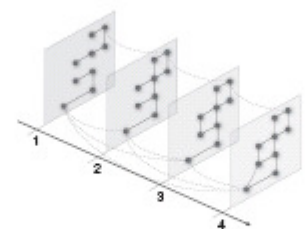


Fig. 1. Schematic of a multislice network. Four slices  $s = \{1, 2, 3, 4\}$  represented by adjacency matrices  $A_s$  encode intraslice connections (solid lines). Interslice connections (dashed lines) are encoded by  $C_{rs}$ , specifying the coupling of node  $j$  to itself between slices  $r$  and  $s$ . For clarity, interslice couplings are shown for only two nodes and depict two different types of couplings: (i) coupling between neighboring slices, appropriate for ordered slices; and (ii) all-to-all interslice coupling, appropriate for categorical slices.

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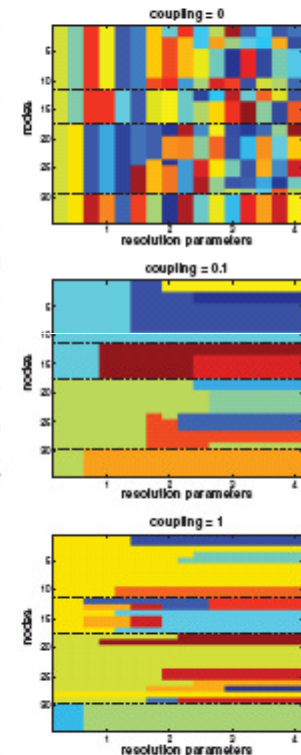


Fig. 2. Multislice community detection of the Zachary Karate Club network (22) across multiple resolutions. Colors depict community assignments of the 34 nodes (renumbered vertically to group similarly assigned nodes) in each of the 36 slices (with resolution parameters  $\gamma_s = \{0.25, 0.5, \dots, 4\}$ ) for  $\omega = 0$  (top),  $\omega = 0.1$  (middle), and  $\omega = 1$  (bottom). Dashed lines bound the communities obtained using the default resolution ( $\gamma = 1$ ).

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# Community Structure in “Multislice” Networks

1. Community Detection
  - Modularity
  - Applications
2. Multislice Framework
  - Laplacian Dynamics
  - Examples

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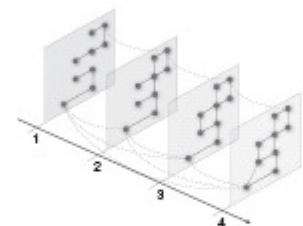


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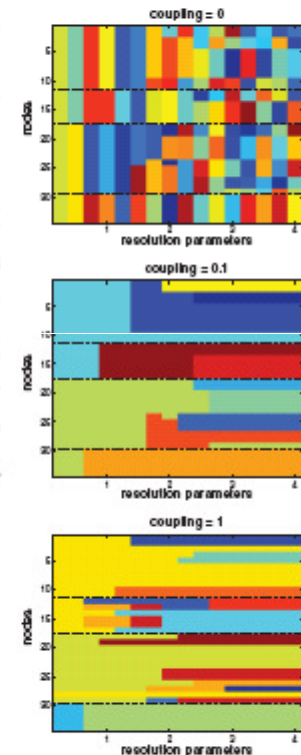
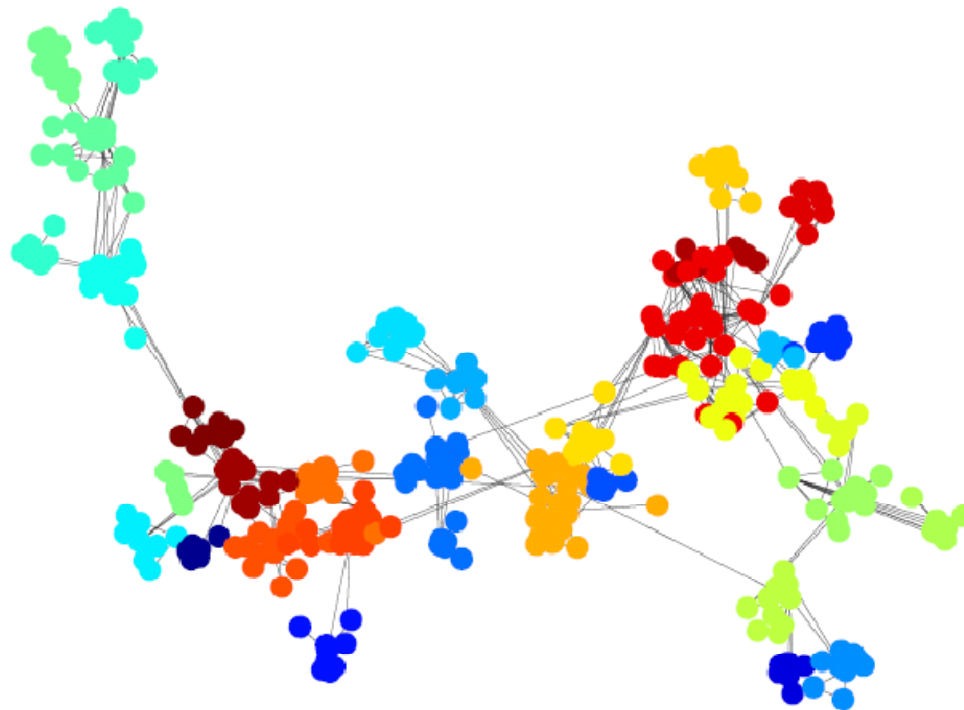


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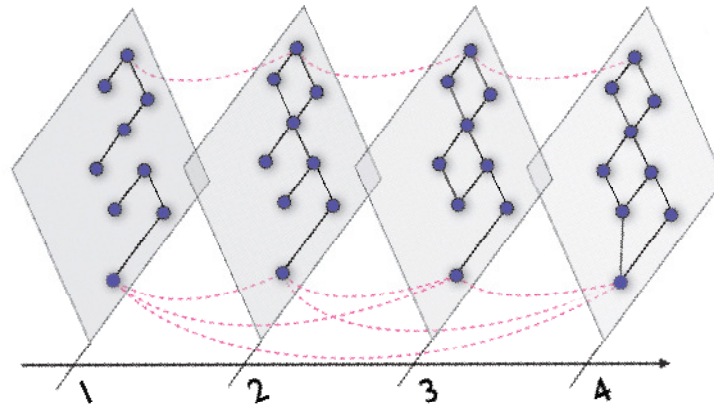
# Philosophical Disclaimer

- Jim Moody (paraphrased): “I’ve been accused of turning everything into a network.”
- PJM (in response): “I’m accused of turning everything into a network **and** a graph partitioning problem.”
- *“Structure  $\leftrightarrow$  Function” but we’ve only had tools for identifying structures in limited settings*



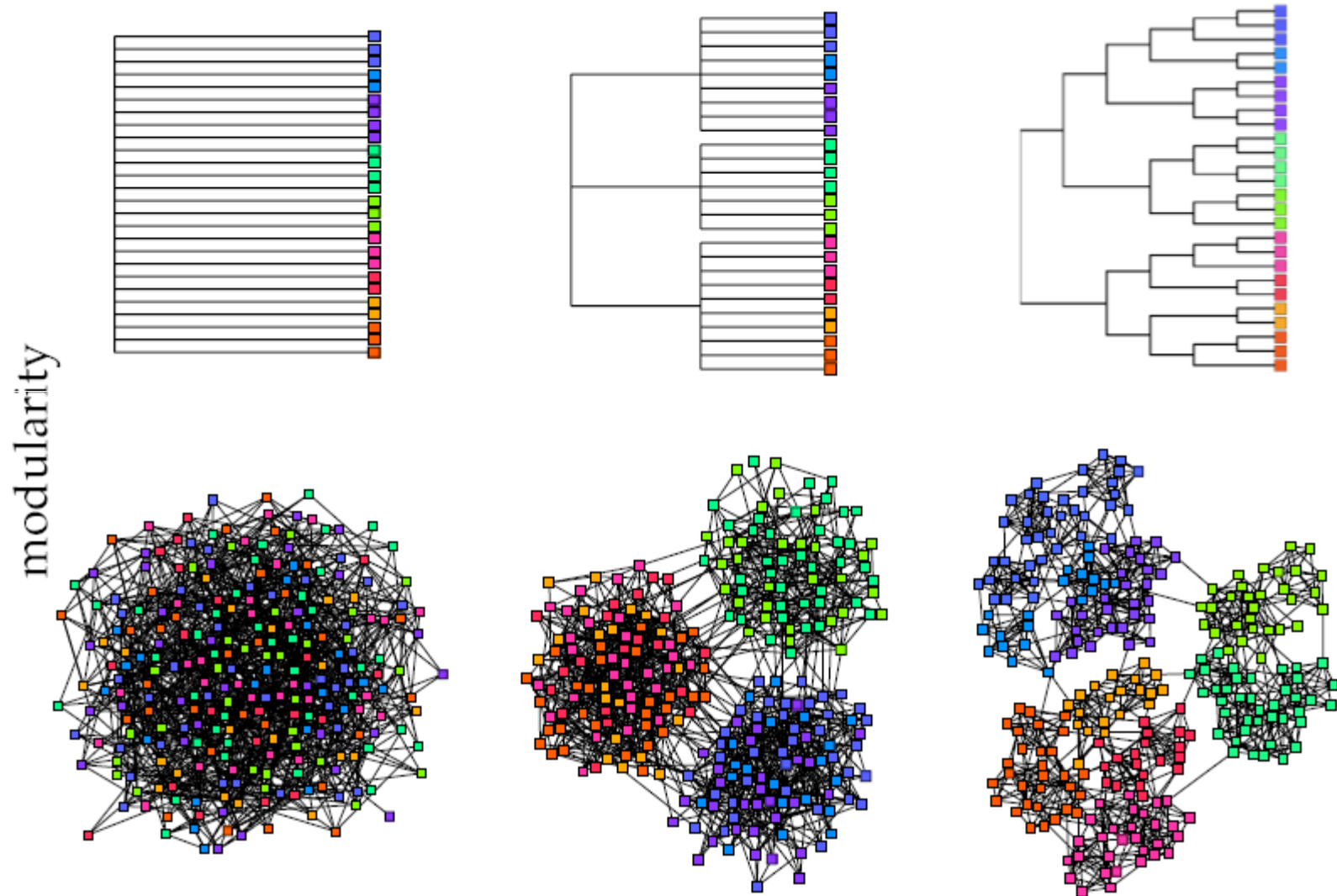
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***How to extend the notion of modularity in networks to multiple networks between the same actors/units, i.e. how to properly use identity in modularity?***

# “Structure $\leftrightarrow$ Function/Process”



Images by Aaron Clauset

# Community Detection Preliminaries

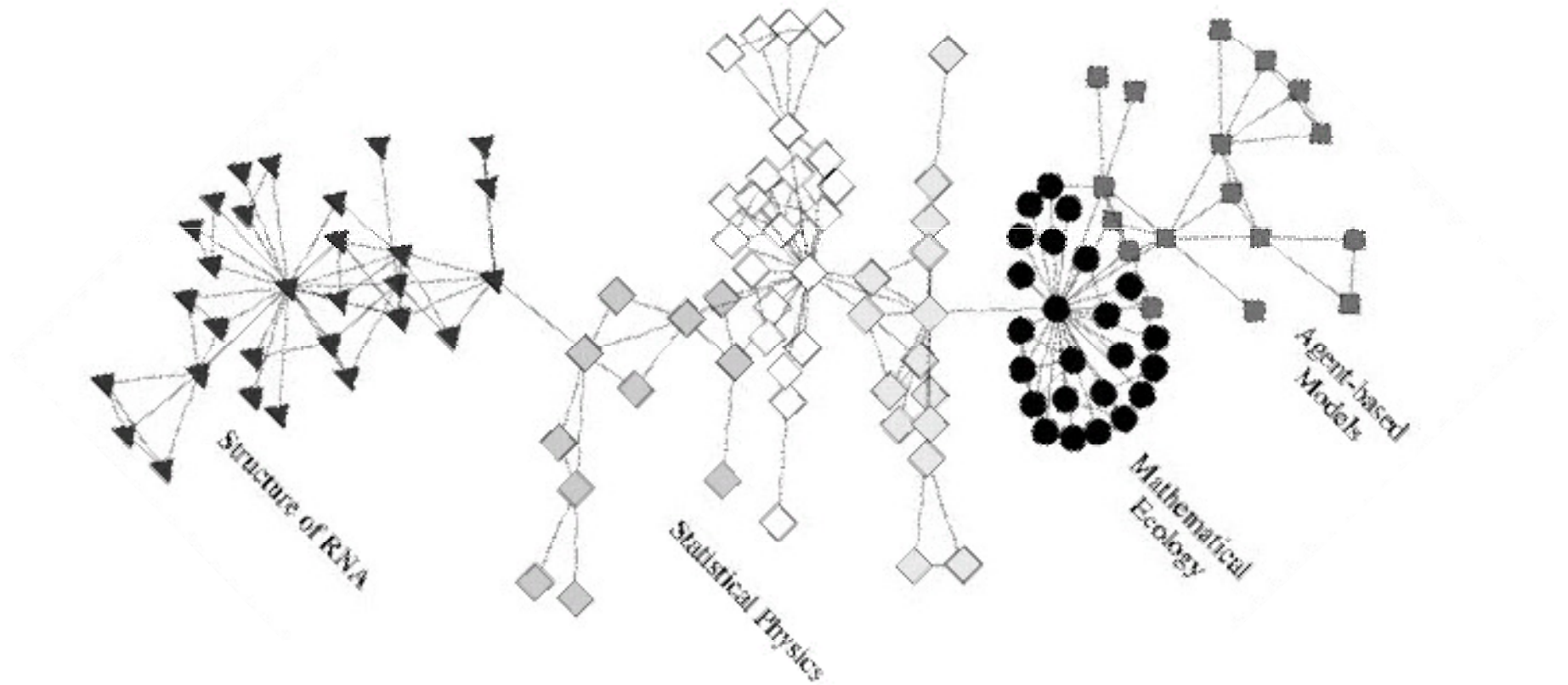
- Computational sledgehammer for large data
- “Hard/rigid” v. “soft/overlapping” clusters
- A community should describe a “cohesive group,” and there are varying formulations and algorithms
  - Linkage clustering (average, single), local clustering coefficients, betweenness (geodesic, random walk), spectral, conductance,...
- Classic approach in CS: Spectral Graph Partitioning
  - Need to specify number of communities sought
- Modularity: a good partition has more intra-community edges than one would expect at random
- *But what does “at random” mean?!?*
- ***Definitional identity arcs are fully expected***

“Communities in Networks,” Porter, Onnela & Mucha,

*Notices of the American Mathematical Society* **56**, 1082-97 & 1164-6 (2009).

“Community Detection in Graphs,” S. Fortunato, *Physics Reports* **486**, 75-174 (2010).

- Girvan & Newman (2002): “Community Structure”
  - Building from biology, computer science, and sociology: spectral graph partitioning, hierarchical clustering, and cohesive social groups



# Community Detection: Null Model & Computational Heuristics

$$Q = \frac{1}{2W} \sum_{i,j} B_{ij} \delta(C_i, C_j), \quad B_{ij} = A_{ij} - P_{ij}$$

- **GOAL:** Assign nodes to communities to maximize modularity (*however, typically there may be **many** near-optimal configurations* [Good, de Montjoye & Clauset])
- Cannot guarantee optimal modularity without full enumeration of possible partitions
  - *NP-complete problem*
- **Numerous packages developed/developing**
  - e.g. igraph library (R, python)
  - ***Need to pick null model appropriate to problem***



# Modularity (Newman-Girvan)

- Independent edges, constrained to expected degree sequence same as observed.
- Requires  $P_{ij} = f(k_i)f(k_j)$ , then quickly yields

$$P_{ij} = \gamma \frac{k_i k_j}{2W}$$

- $\gamma$  resolution parameter ad hoc (default = 1)  
(*Reichardt & Bornholdt, Lambiotte et al.*)
- *Modularity problems [that we will table for today]:*  
*Resolution limit (Fortunato & Barthelemy),*  
*Degenerate landscape (Good, de Montjoye & Clauset)*

# Community Detection: Other Models

$$Q = \frac{1}{2W} \sum_{i,j} B_{ij} \delta(C_i, C_j), \quad B_{ij} = A_{ij} - P_{ij}$$

- Erdos-Renyi (Bernoulli)

$$P_{ij} = p$$

- Newman-Girvan\*

$$P_{ij} = \gamma \frac{k_i k_j}{2W}$$

- Leicht-Newman\* (directed)

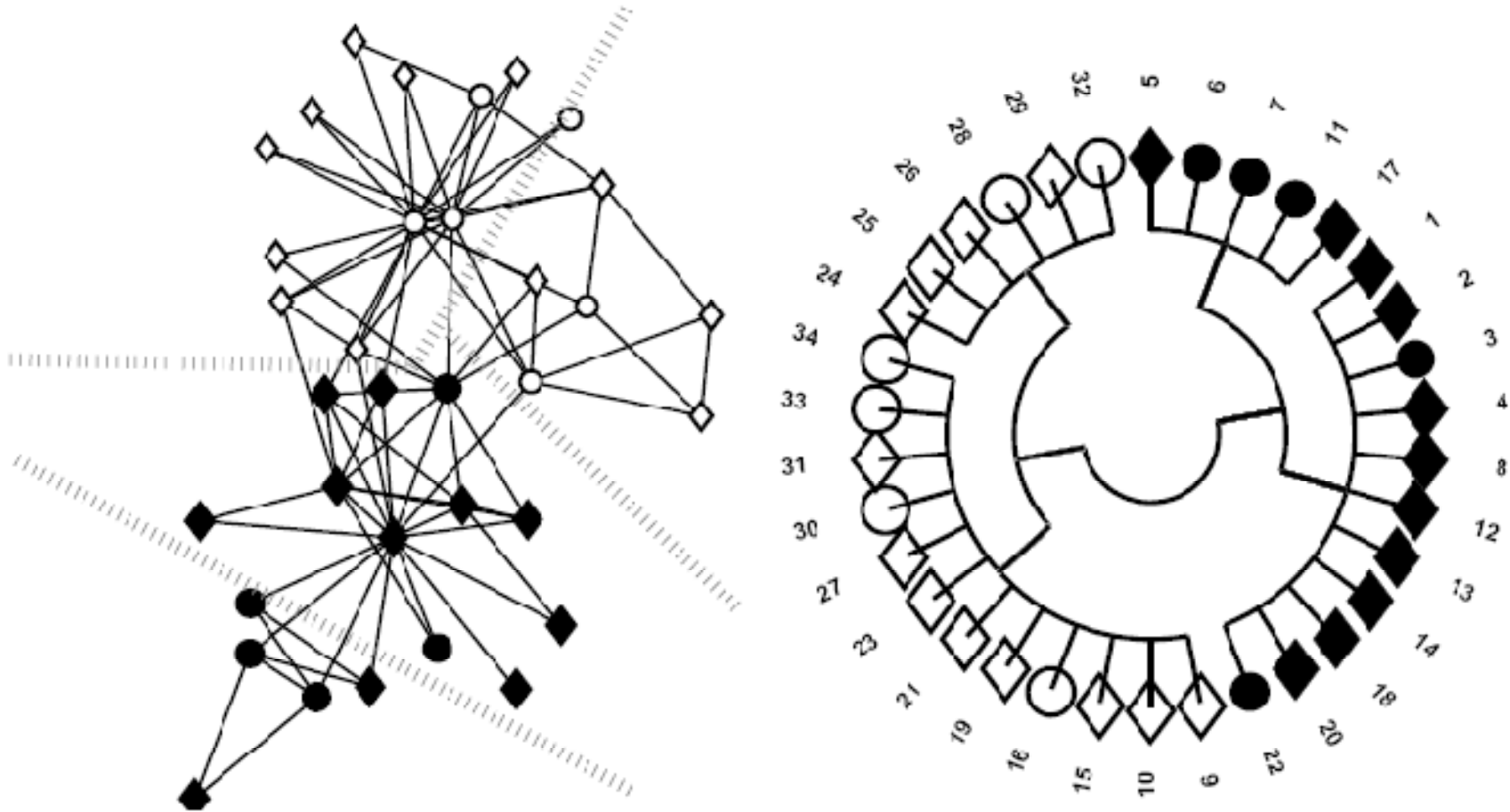
$$P_{ij} = \gamma \frac{k_i^{in} k_j^{out}}{W}$$

- Barber\* (bipartite)

$$P_{ij} = \begin{cases} \gamma \frac{k_i d_j}{W} \\ 0 \end{cases}$$

*Similar back-of-envelope calculation with identity arcs fails because they are definitional*

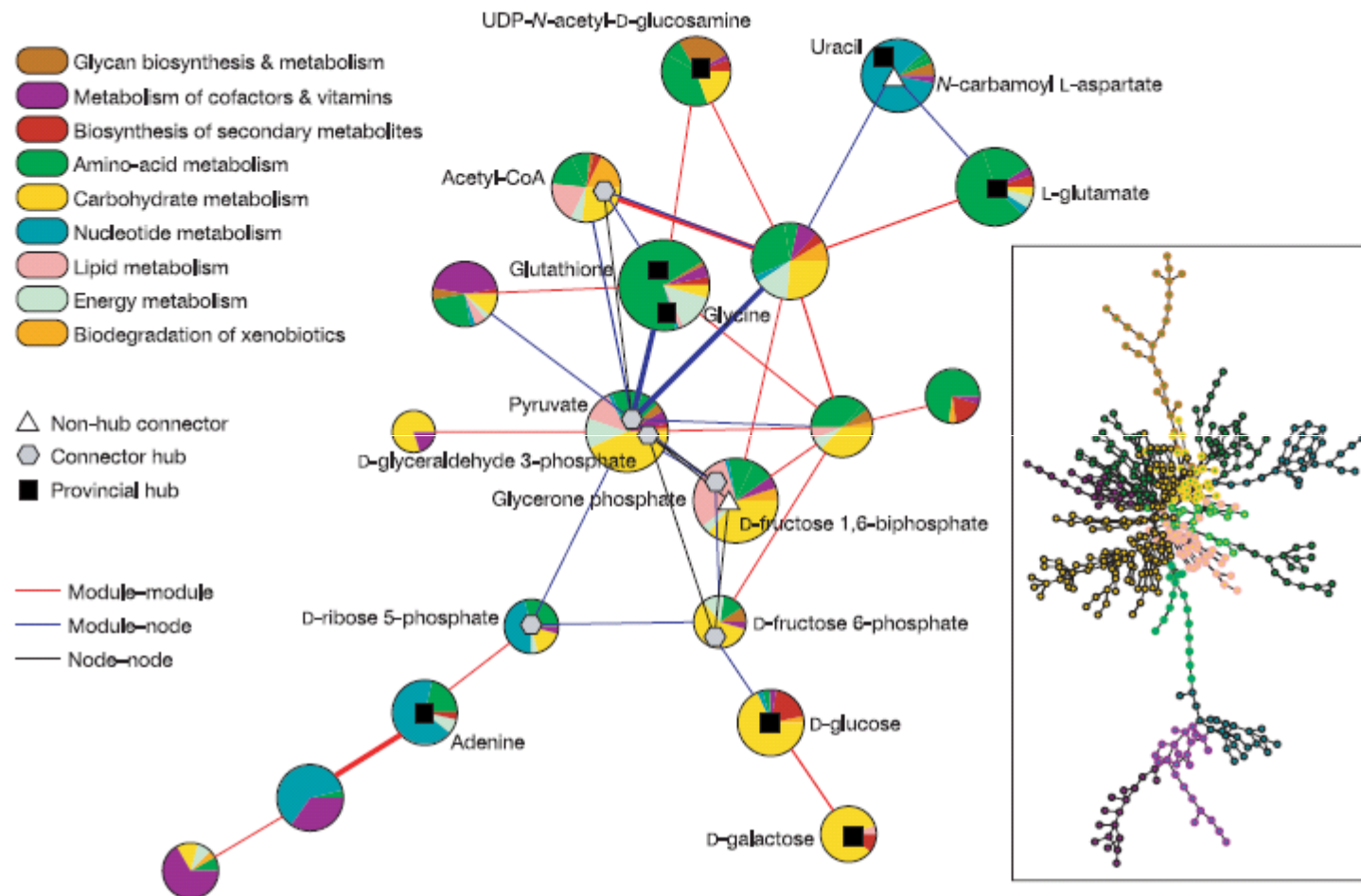
# Zachary Karate Club



The partition optimizes *modularity*, which measures the number of intra-community ties (relative to randomness)

# Metabolic Networks

(Guimera & Amaral, Nature 2005)

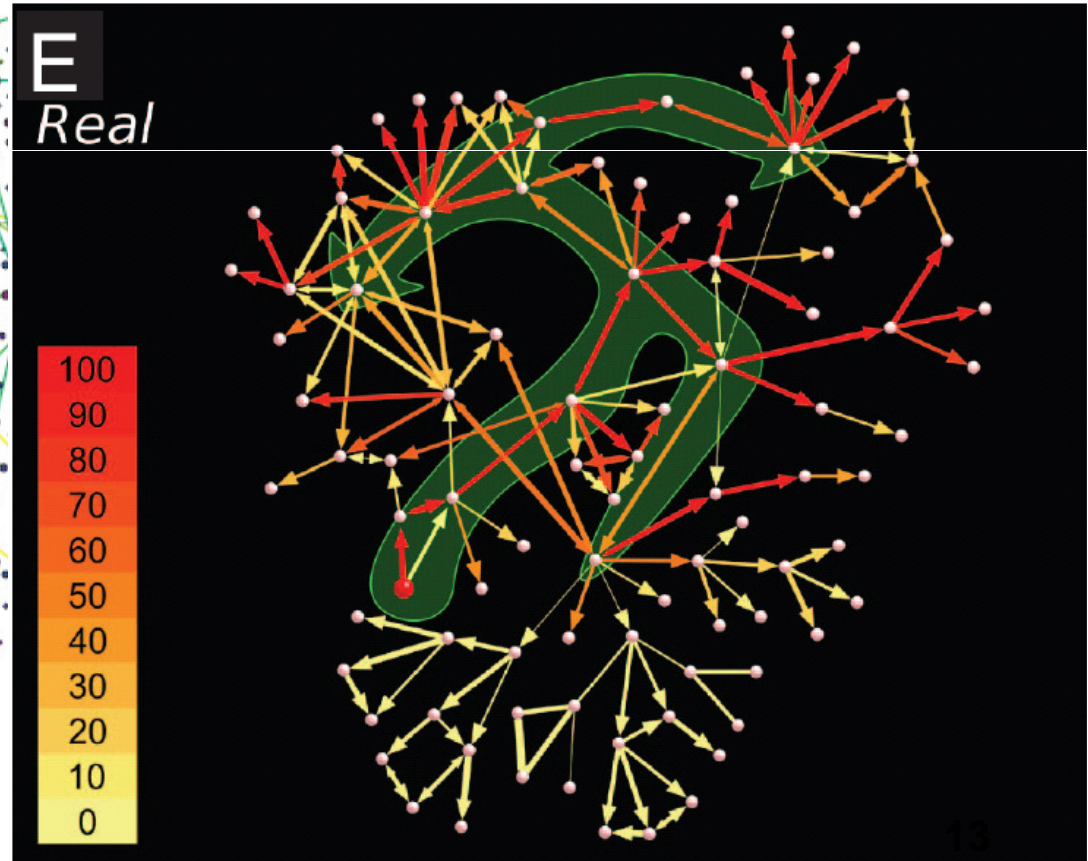
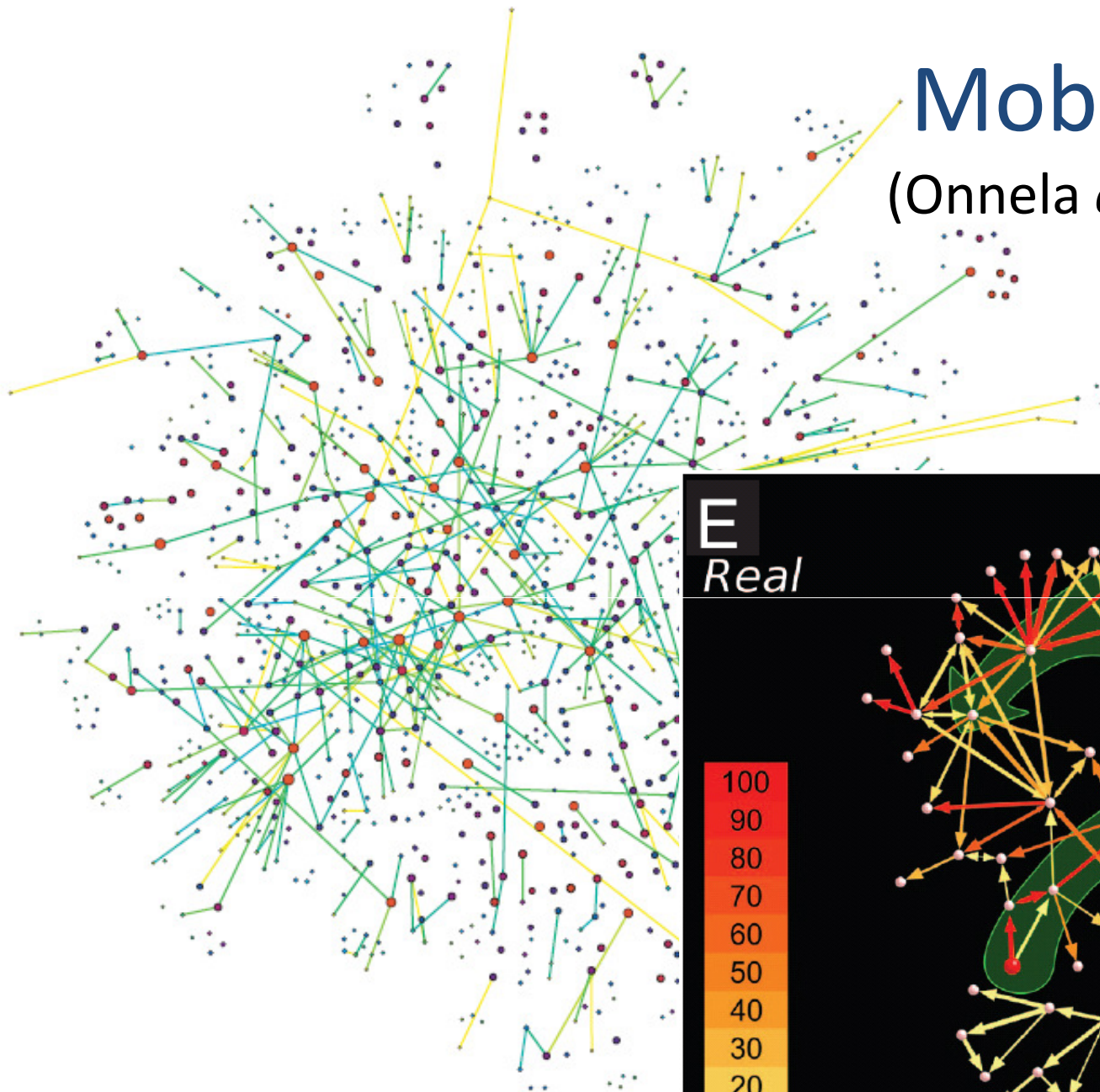


**Figure 3** Cartographic representation of the metabolic network of *E. coli*. Each circle represents a module and is coloured according to the KEGG pathway classification of the metabolites it contains. Certain important nodes are depicted as triangles (non-hub connectors), hexagons (connector hubs) and squares (provincial hubs). Interactions between modules and nodes are depicted using lines, with thickness proportional to the

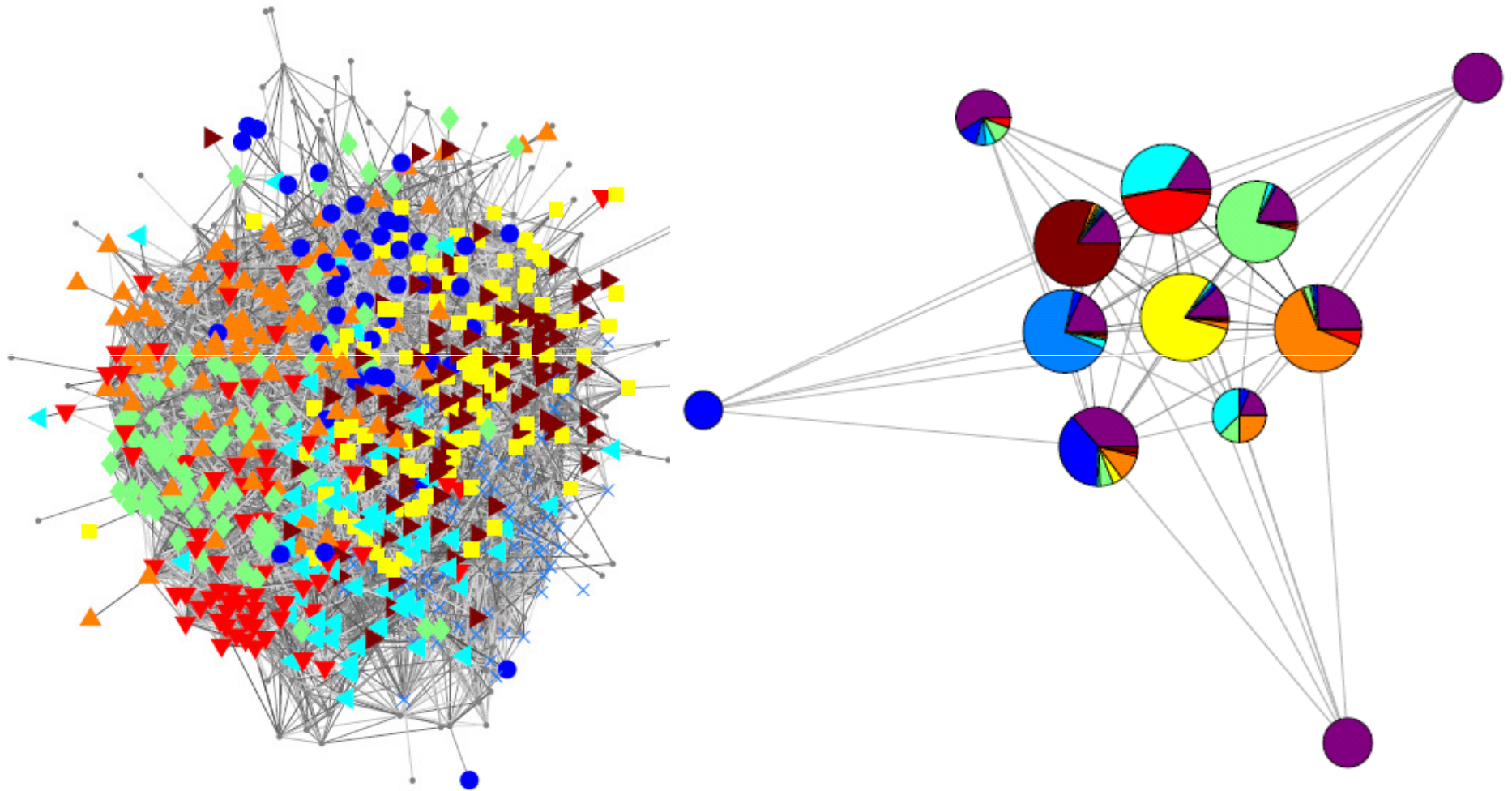
number of actual links. Inset: metabolic network of *E. coli*, which contains 473 metabolites and 574 links. This representation was obtained using the program Pajek. Each node is coloured according to the 'main' colour of its module, as obtained from the cartographic representation.

# Mobile Phones

(Onnela *et al.*, PNAS 2007)

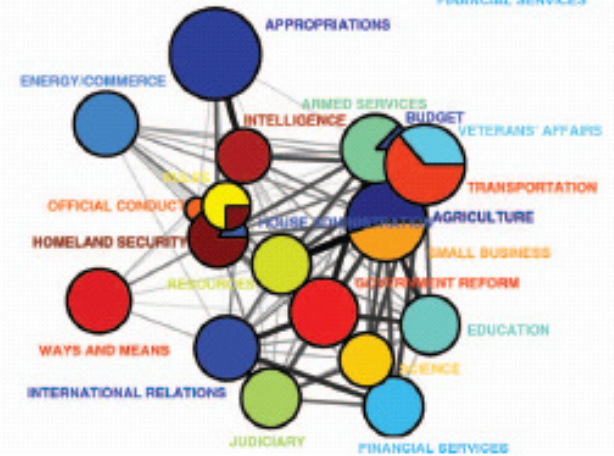
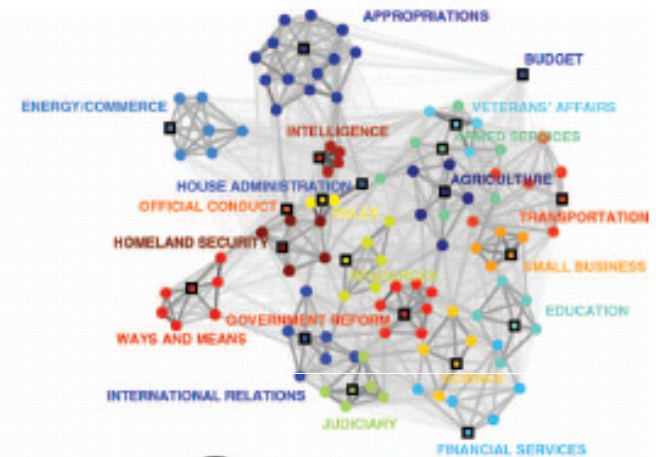


# Facebook (Traud, Kelsic, PJM & MAP [arXiv])



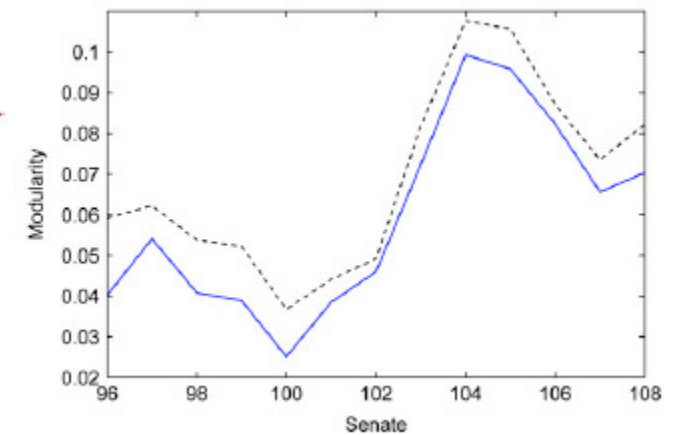
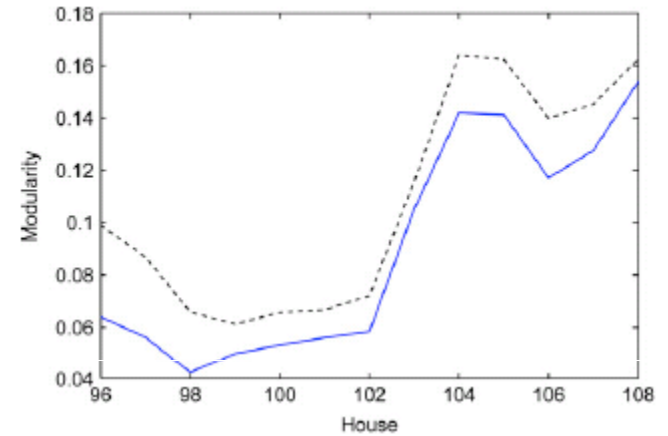
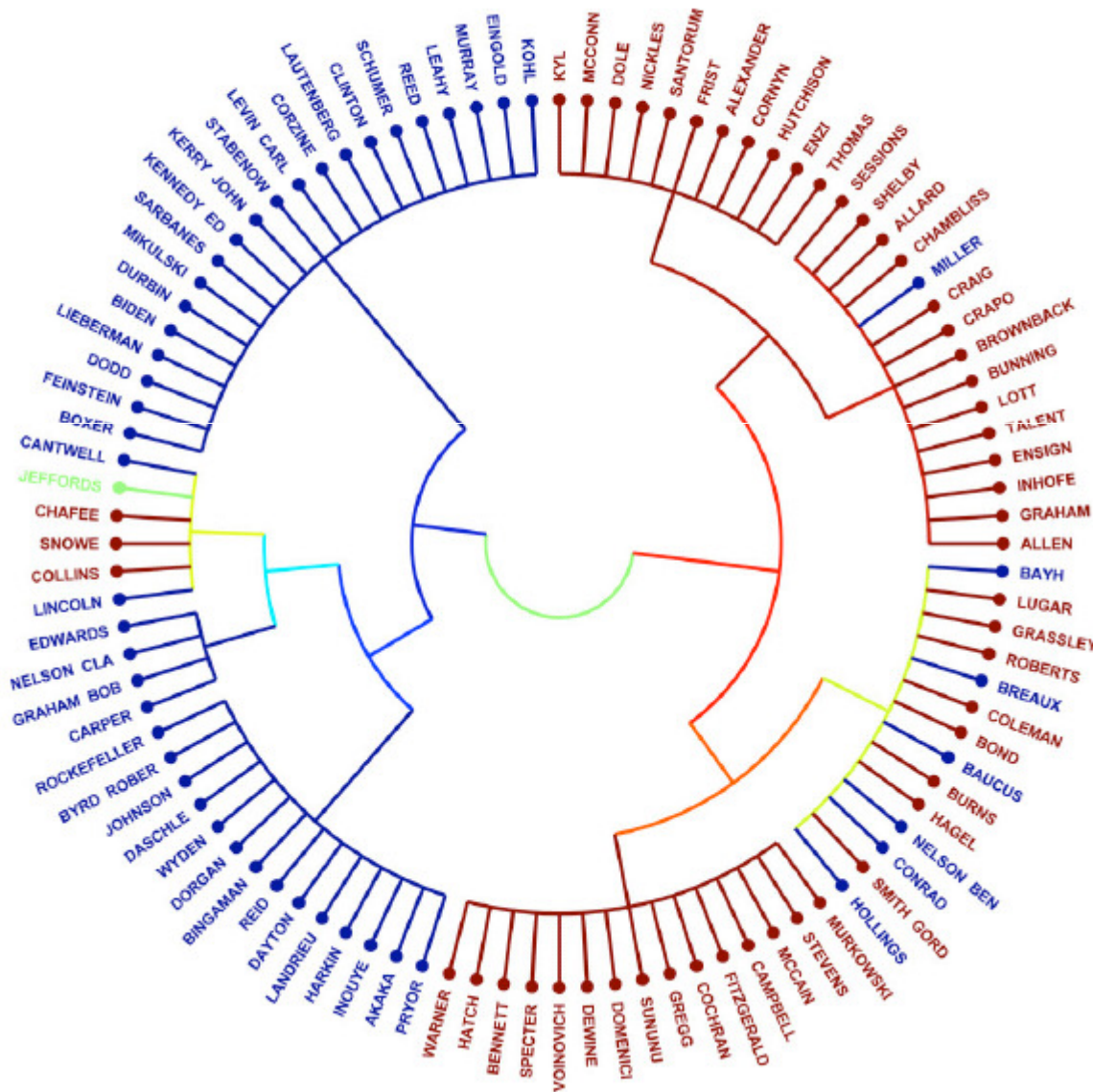
# Congressional Committees

(MAP, PJM, Newman, Warmbrand & Friend 2005, 2006 & 2007)



# Congressional Cosponsorship

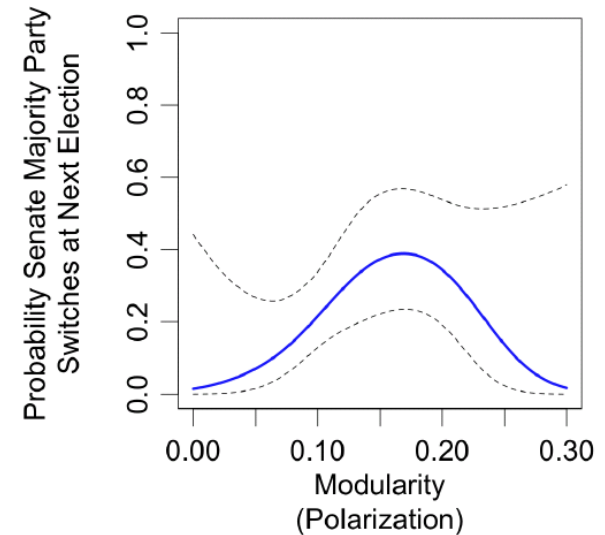
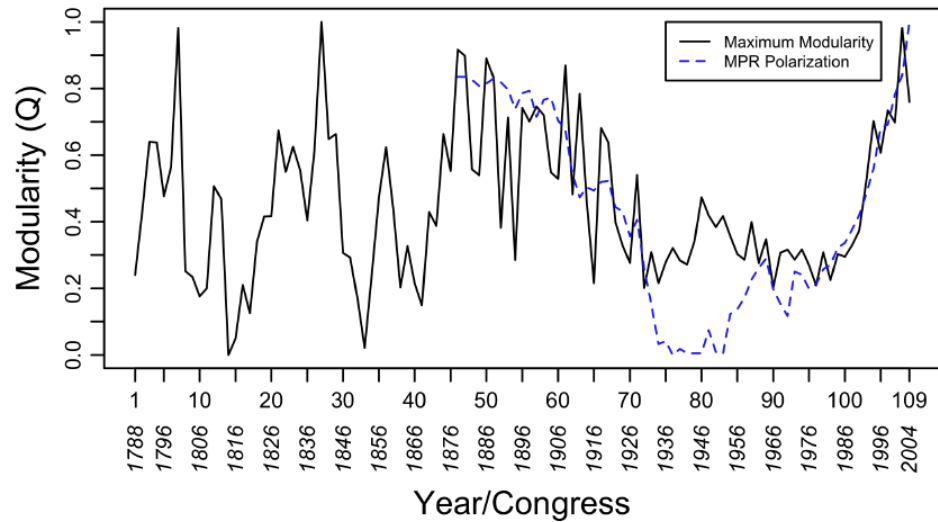
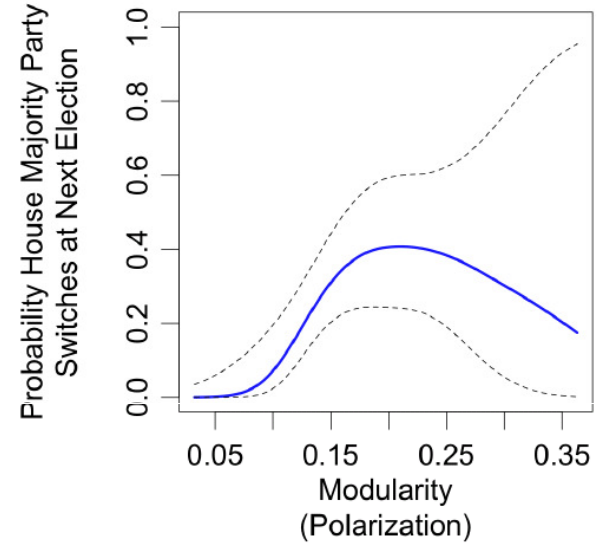
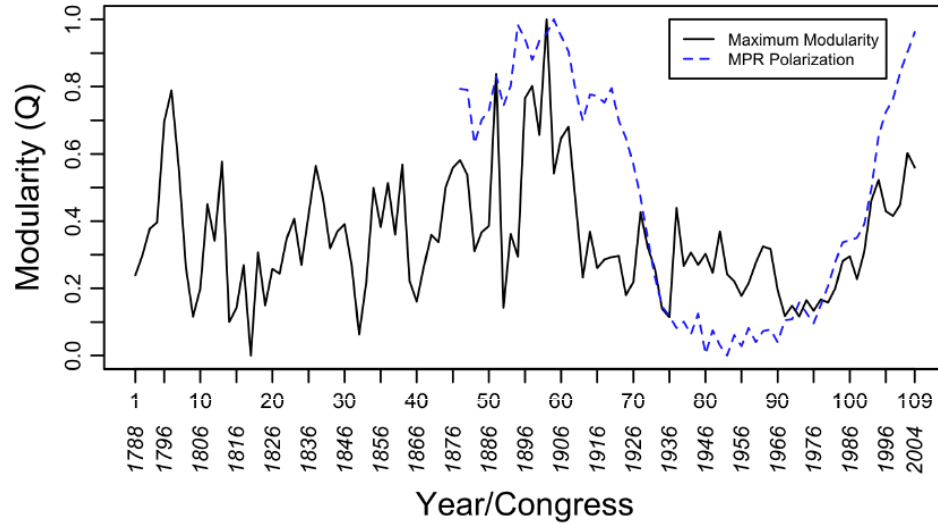
(Zhang, Friend, Traud, MAP, Fowler & PJM 2008)





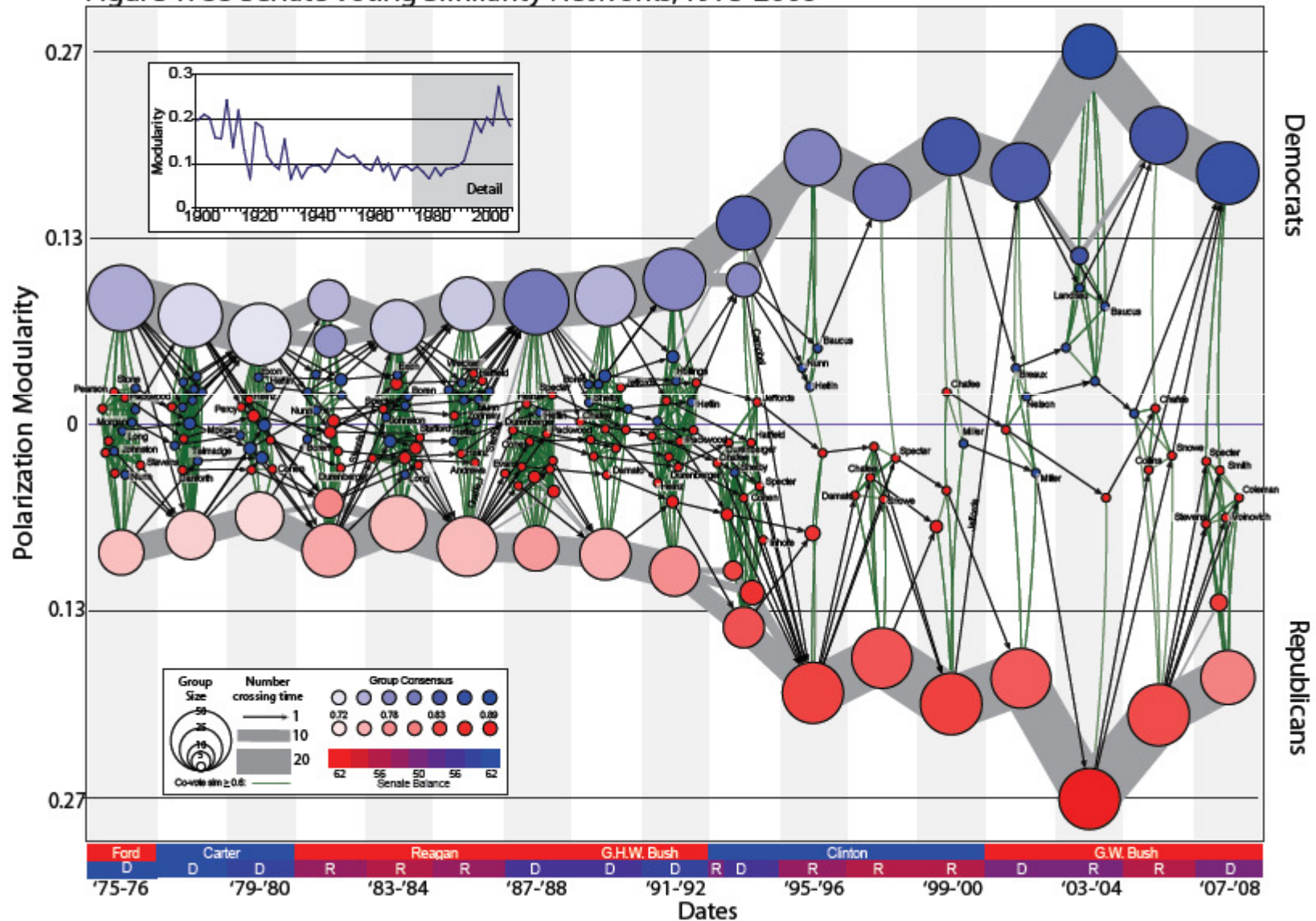
# Congressional Roll Call

(Waugh, Pei, Fowler, PJM & MAP [arXiv])



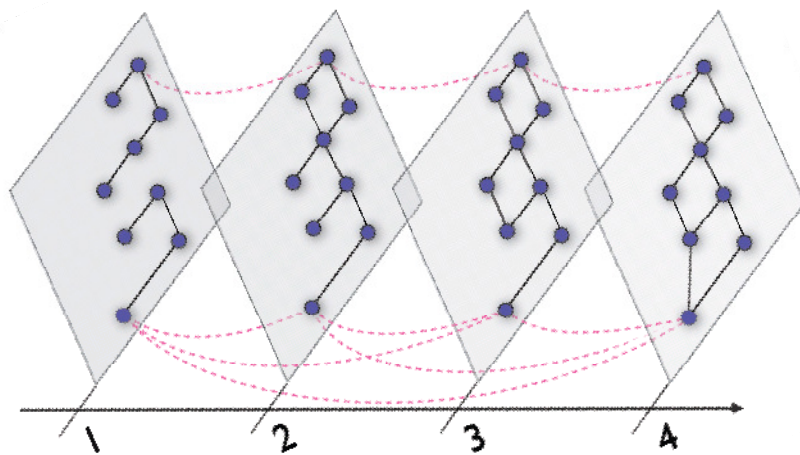
# Congressional Roll Call (Moody & Mucha)

Figure 1. US Senate Voting Similarity Networks, 1975-2008



## 2. Multislice Networks

- All of the examples above are on static networks, with a single kind of tie, partitioned at a single spatial resolution
- Real-world networks: dynamic, multiplex, and with communities at multiple scales!
- Easy Part: Glue together common individuals
- **Hard Part: Include identity arcs in null model**



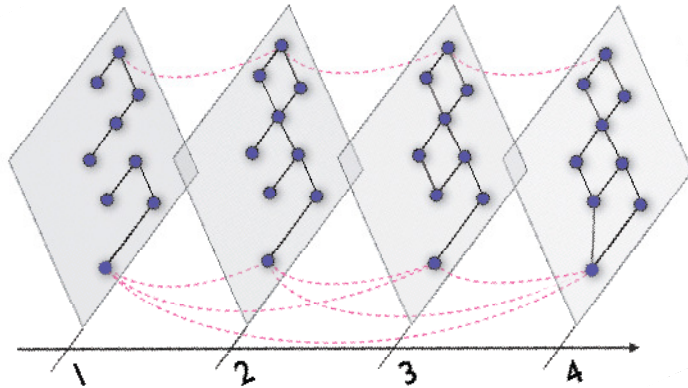
$$\begin{pmatrix} A^{(1)} & I & 0 & 0 \\ I & A^{(2)} & I & 0 \\ 0 & I & A^{(3)} & I \\ 0 & 0 & I & A^{(4)} \end{pmatrix} \text{Ordered}$$

$$\begin{pmatrix} A^{(1)} & I & I & I \\ I & A^{(2)} & I & I \\ I & I & A^{(3)} & I \\ I & I & I & A^{(4)} \end{pmatrix} \text{Categorical}$$

# What is the appropriate null model?

$$Q = \frac{1}{2W} \sum_{i,j} B_{ij} \delta(C_i, C_j), \quad B_{ij} = A_{ij} - P_{ij}$$

- Each slice is a network (static, single type) with a specified spatial resolution of interest
- Cross-slice ties are structurally defined, so they are always there “at random” and therefore do not contribute to modularity?!?



$$\begin{pmatrix} A^{(1)} & I & 0 & 0 \\ I & A^{(2)} & I & 0 \\ 0 & I & A^{(3)} & I \\ 0 & 0 & I & A^{(4)} \end{pmatrix}$$

# A Way Out: Laplacian Dynamics

- Lambiotte, Delvenne & Barahona [arXiv:0812.1770] showed a way to **derive** modularity from normalized Laplacian dynamics, defining partition quality in terms of stability (autocovariance in Markov process)

$$\dot{p}_i = \sum_j \frac{A_{ij}}{k_j} p_j - p_i, \quad p_i^* = k_i/2m.$$

$$R_{\text{NL}}(t) = \sum_C \sum_{i,j \in C} \left[ (e^{t(B-I)})_{ij} \frac{k_j}{2m} - \frac{k_i}{2m} \frac{k_j}{2m} \right]. \quad B_{ij} = A_{ij}/k_j$$

Expansion of matrix exponential to first-order in  $t$  recovers Newman-Girvan modularity with resolution  $\gamma = 1/t$ .

***So how do we apply this idea to multislice networks?***

# Multislice Modularity Derivation

- Generalized Lambiotte *et al.* to rederive standard null models for bipartite (Barber), directed (Leicht-Newman), and signed networks (Traag *et al.*).
  - (1) Conditional probabilities based on link type
  - (2) Multiple types of flows (direction/signs)
  - (3) Different time scales along different links

# Multislice Modularity Derivation

- Generalized Lambiotte *et al.* to rederive standard null models for bipartite (Barber), directed (Leicht-Newman), and signed networks (Traag *et al.*).
- Resulting generalization applied to multislice:

$$Q_{\text{multislice}} = \frac{1}{2\mu} \sum_{ijsr} \left\{ \underbrace{\left( A_{ijs} - \gamma_s \frac{k_{is}k_{js}}{2m_s} \right)}_{\text{within slices adjacency data}} \delta_{sr} + \underbrace{\delta_{ij} C_{jsr}}_{\text{cross-slice identity arcs}} \right\} \delta(g_{is}, g_{jr})$$

# Examples

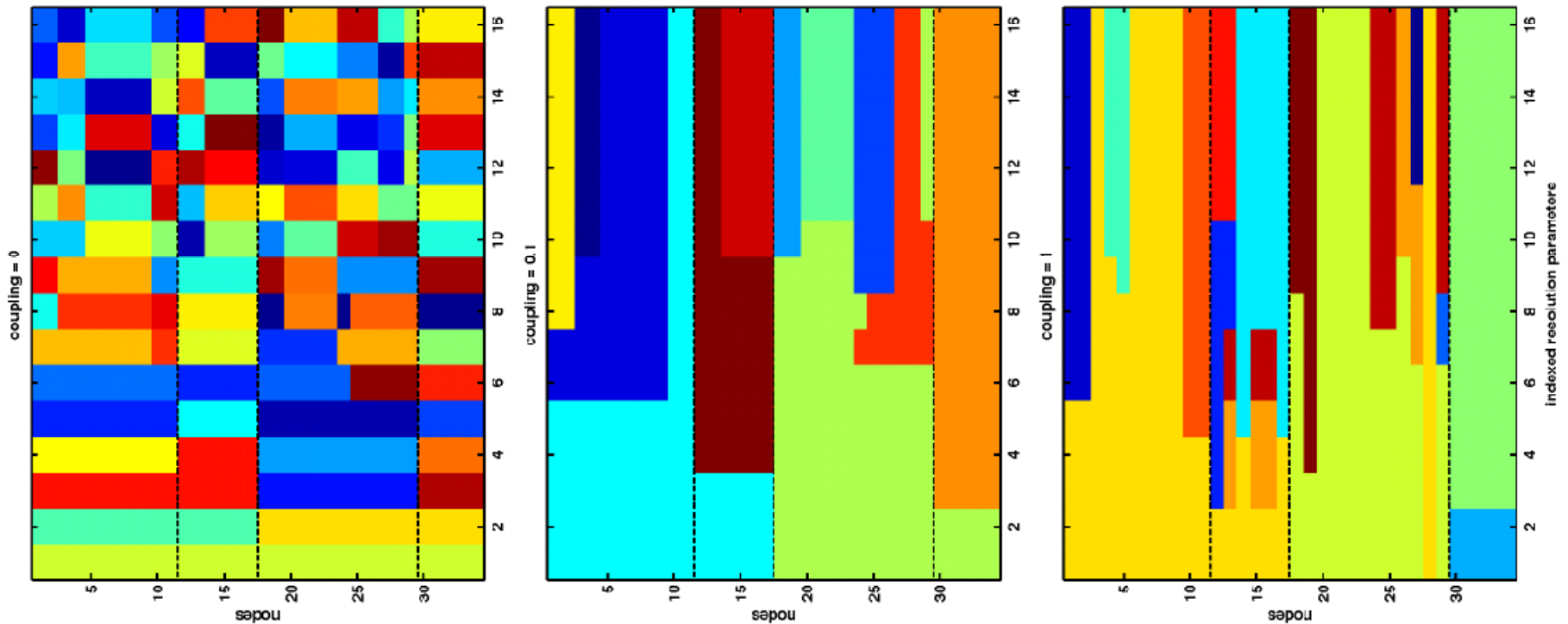
- Return of the Zachary Karate Club
- Tastes, Ties & Time
- Historical Congressional Roll Call

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# Zachary Karate Club

## 16 resolution slices by 34 nodes



*Note presence of obviously non-optimal assignments  
(value to making multislice-specific algorithms)*

# Tastes, Ties & Time

- Lewis *et al.* 2008
- First wave of private northeastern school
- Facebook friends
- Picture friends
- Roommates
- Housing Groups

$\omega$	#Communities	#Communities per Individual			
		1	2	3	4
0	1036	0	0	0	1640
0.1	122	230	664	611	135
0.2	66	326	805	415	94
0.3	49	430	792	354	64
0.4	36	522	770	302	46
0.5	31	645	695	276	24
1	16	1640	0	0	0

# Roll Call Networks

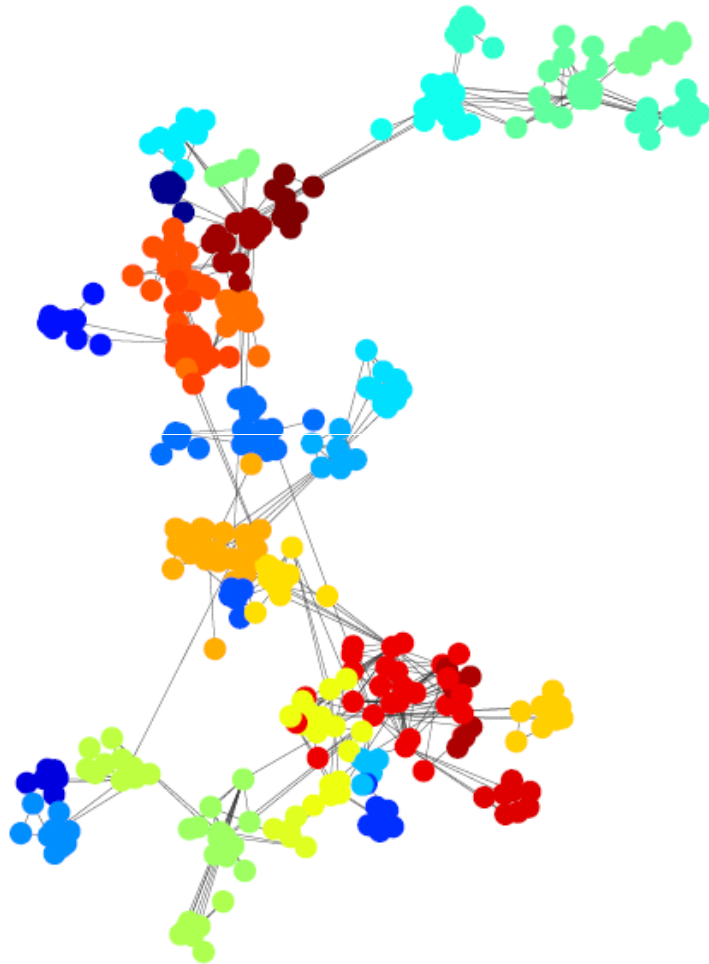
into an  $n \times n$  *adjacency matrix*  $A$ , with elements  $A_{ij} \in [0, 1]$  representing the extent of voting agreement between legislators  $i$  and  $j$ , with elements defined here by

$$A_{ij} = \frac{1}{b_{ij}} \sum_k \alpha_{ijk}, \quad (1)$$

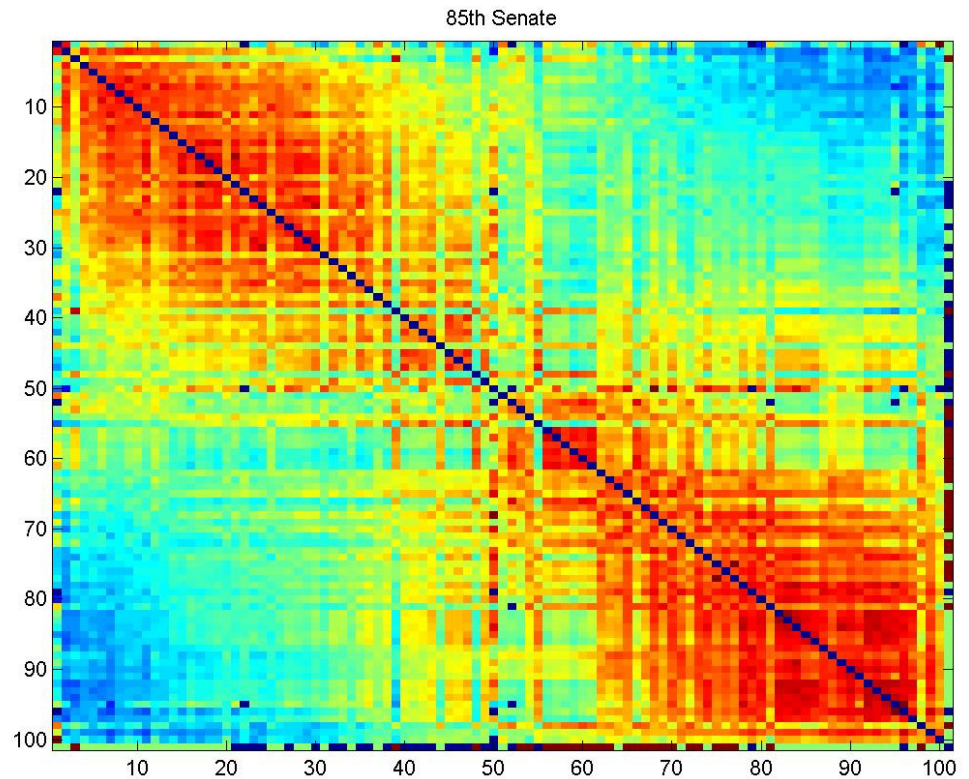
where  $\alpha_{ijk}$  equals 1 if legislators  $i$  and  $j$  voted the same on bill  $k$  and 0 otherwise and  $b_{ij}$  is the total number of bills on which both legislators voted. The matrix  $A$  encodes a network of weighted affiliations between legislators, with weights determined by the similarity of their roll-call records

- Modularity as a measure of polarization
- Modularity as a predictor of majority turnover (the “partial polarization hypothesis”)

# Roll call as a network?

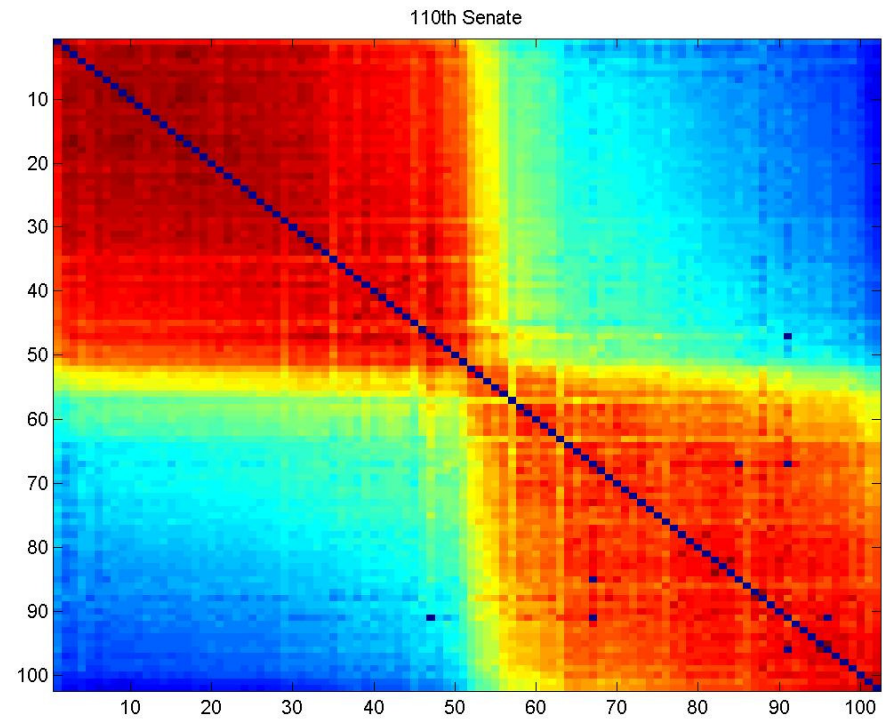
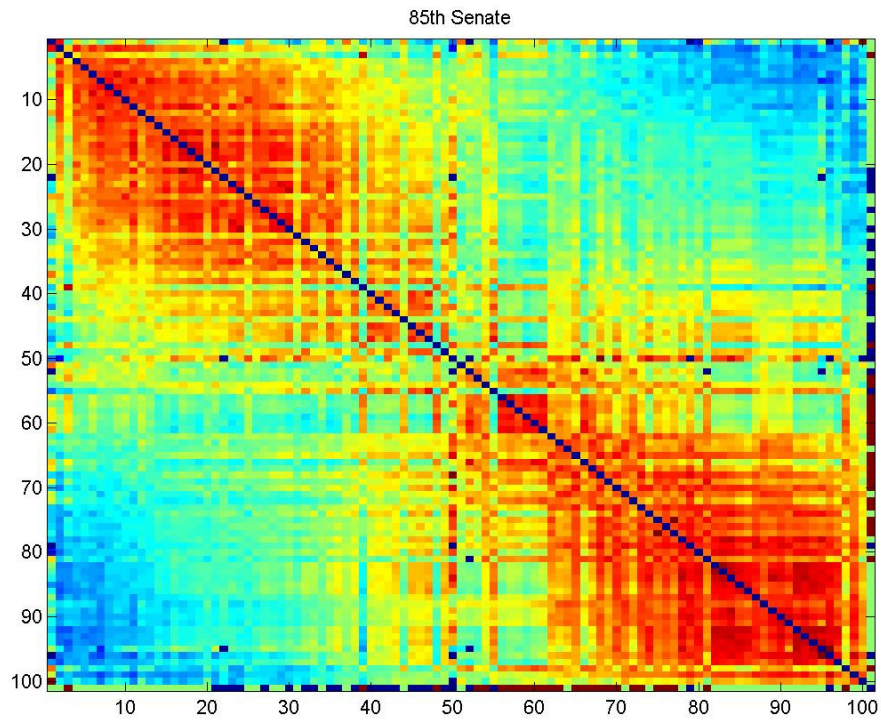


Scientific Coauthorship

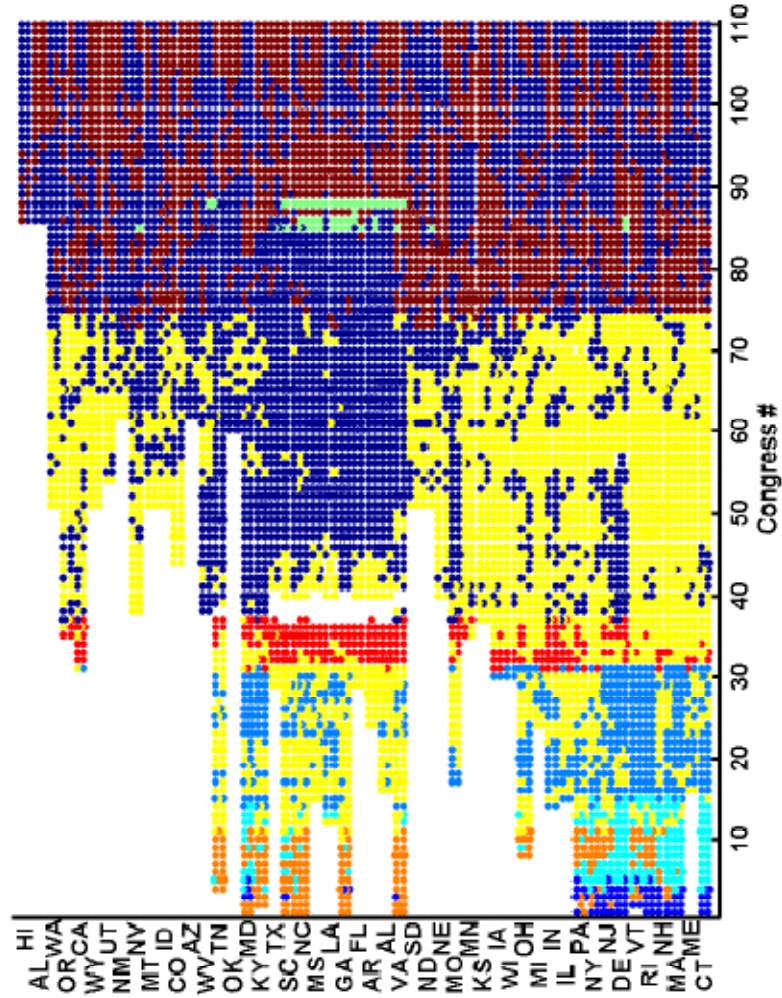
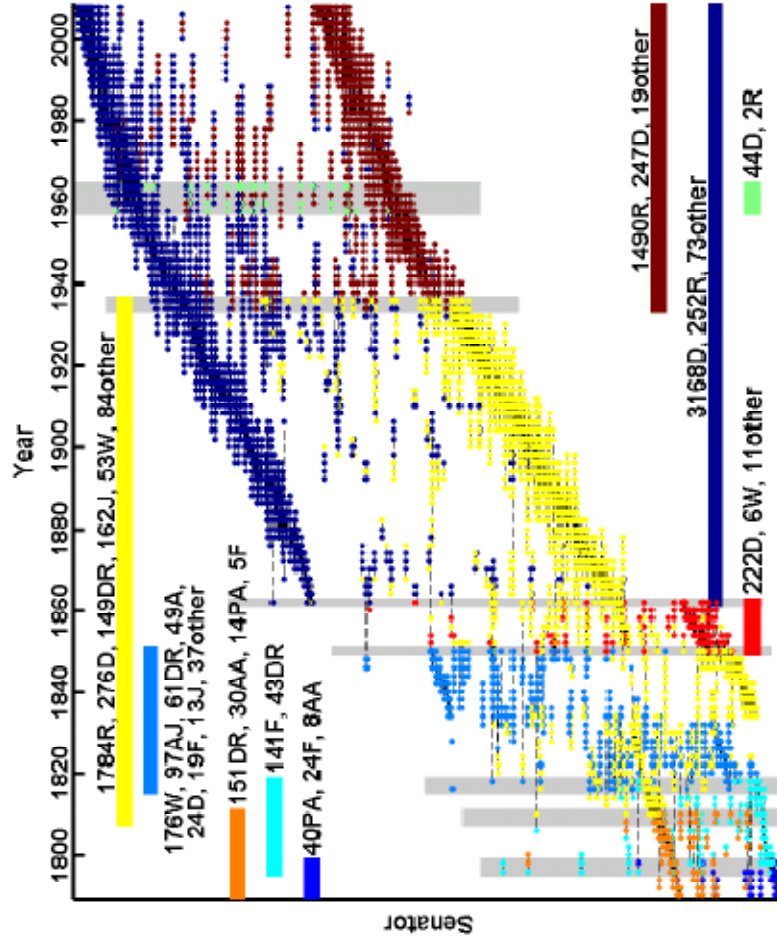


v. Roll Call Similarities

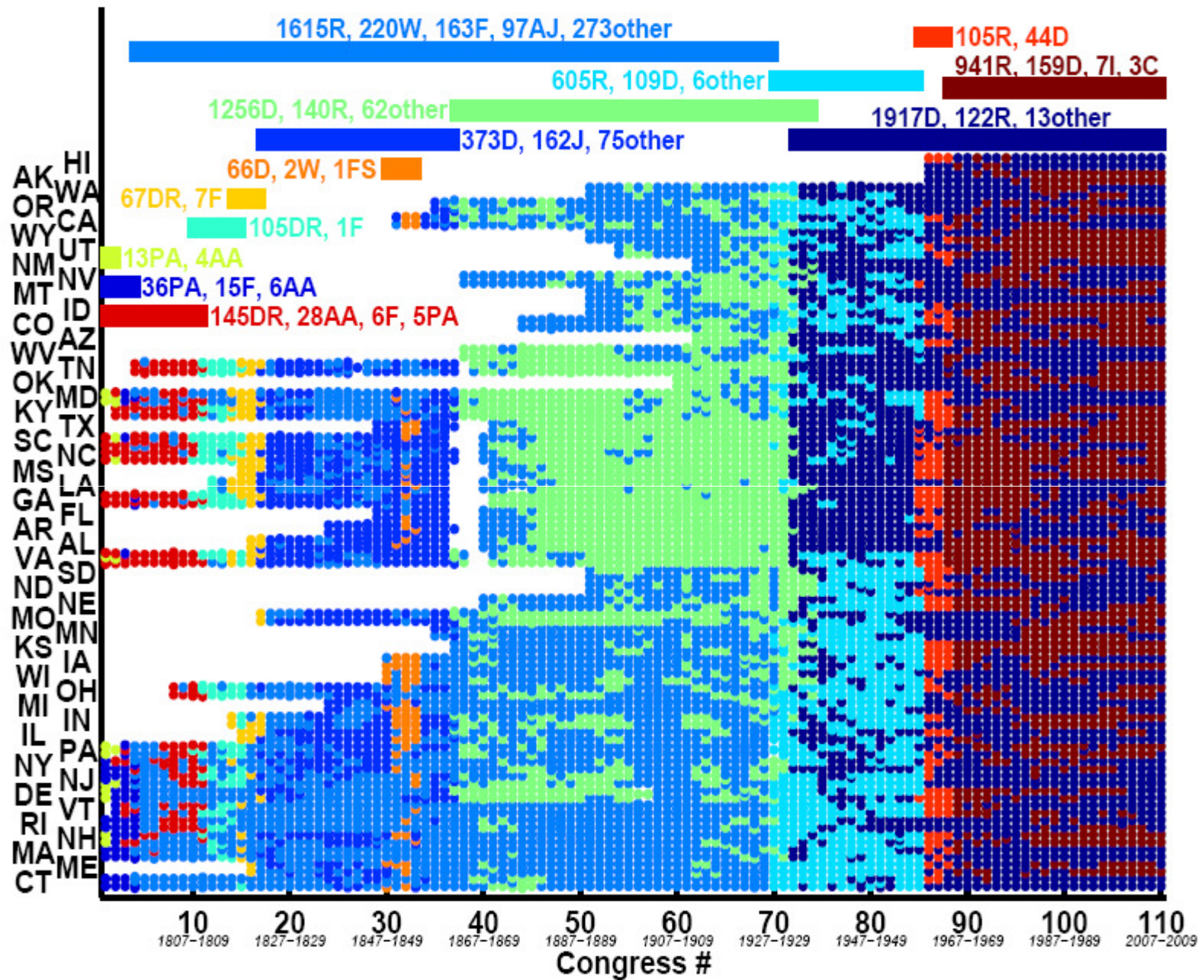
# Polarization in Roll Call Networks



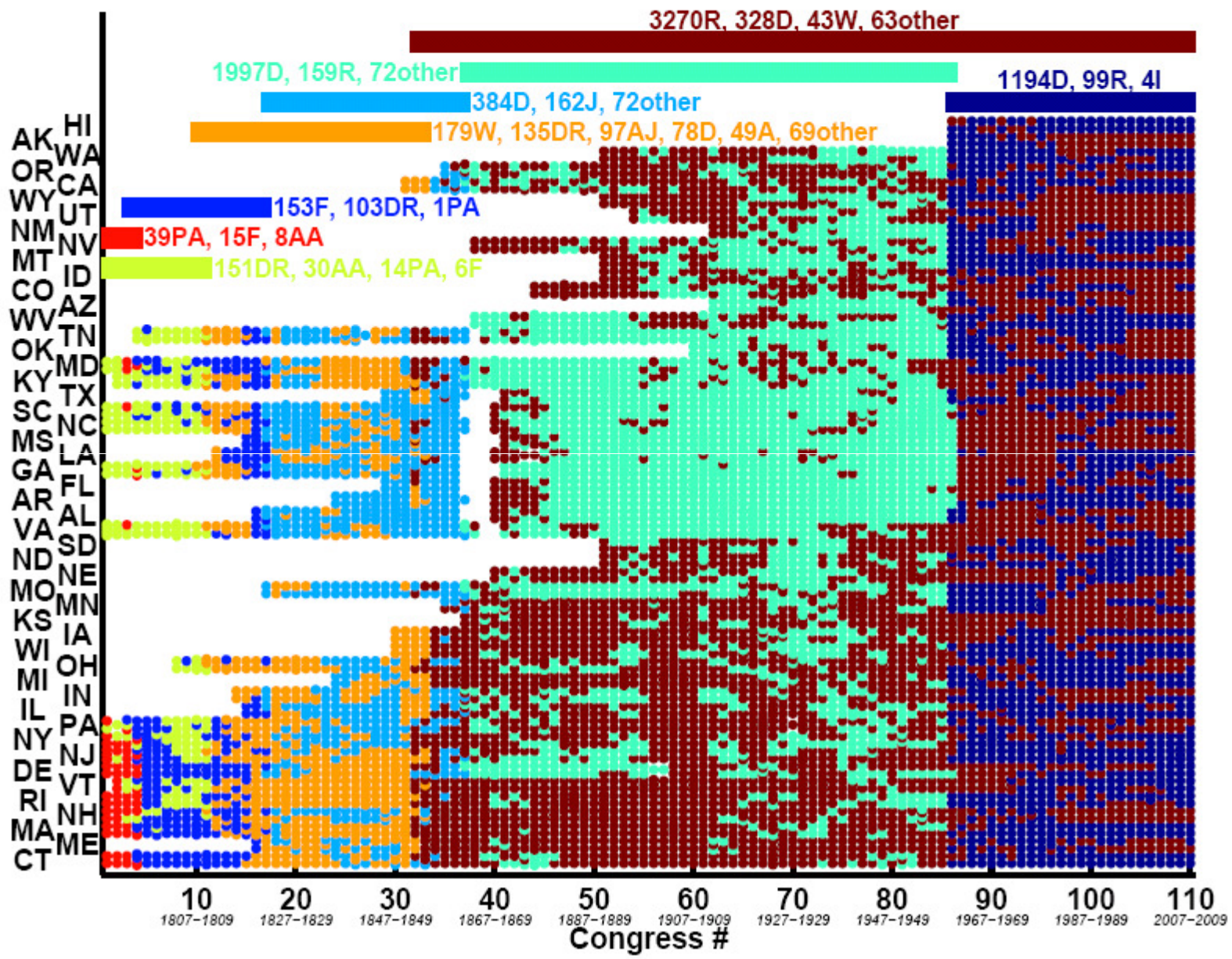
# 110 Senates (two-year Congresses)



Coupling = 0.2: 13 communities

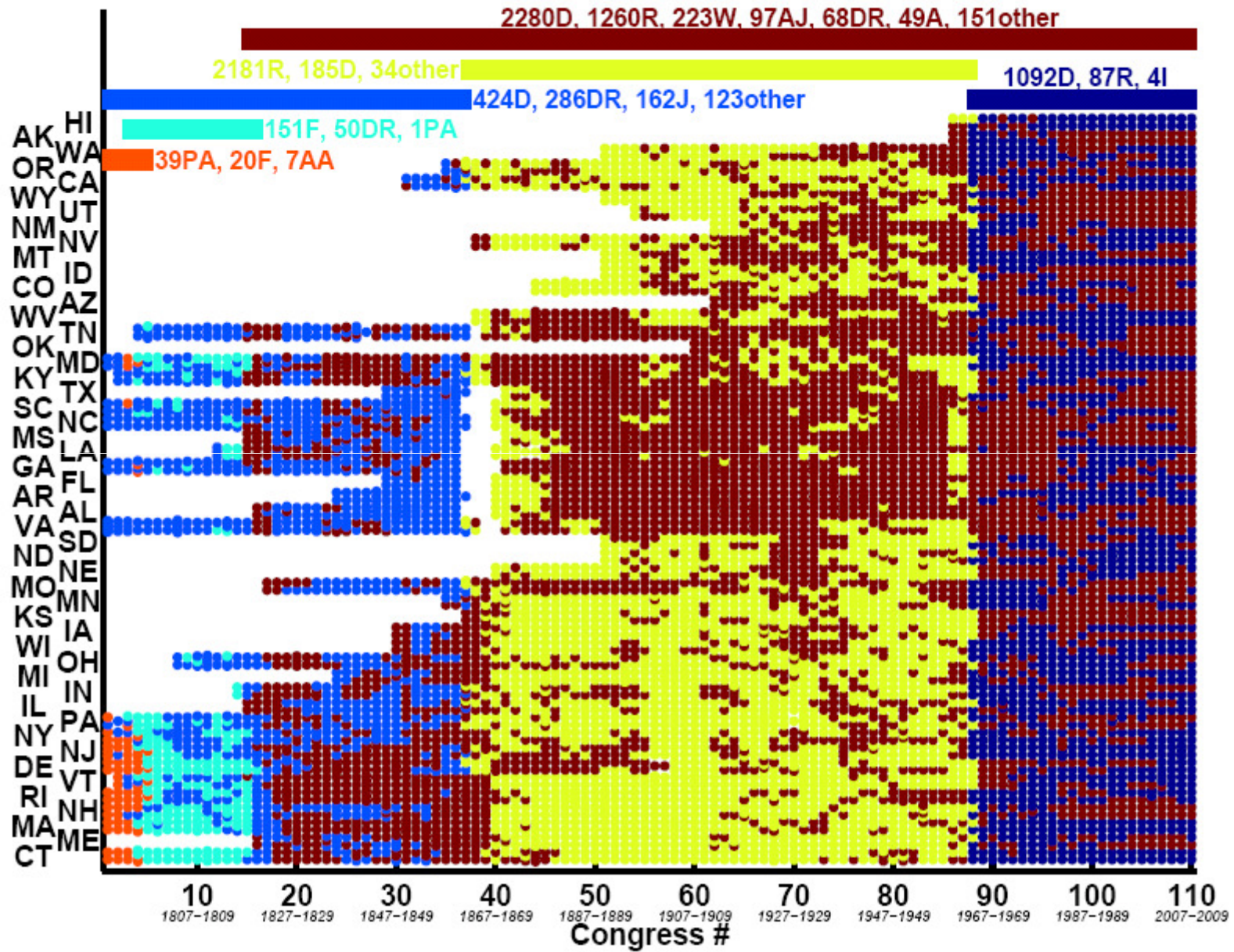


Coupling = 0.5: 8 communities

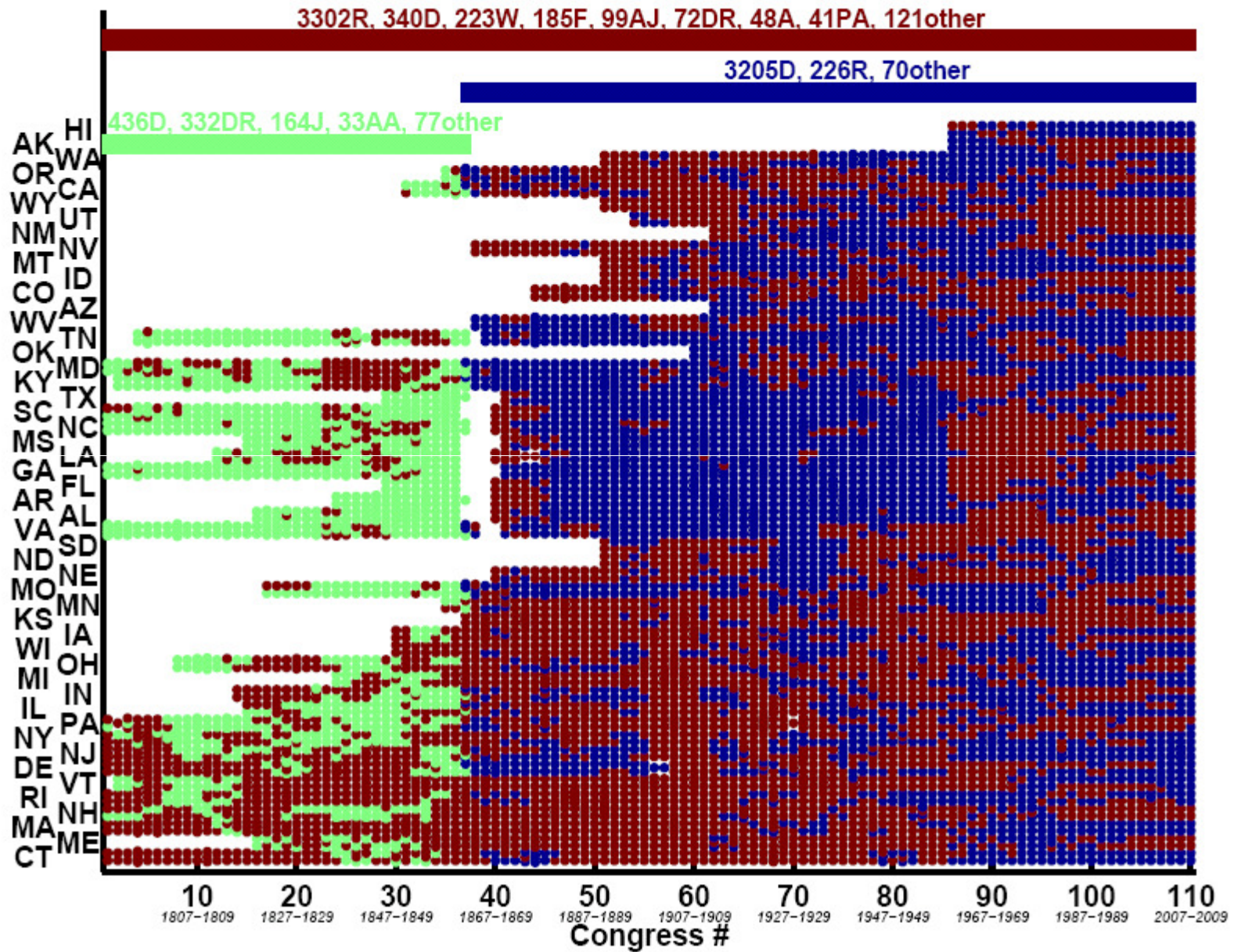




### Coupling = 0.8: 6 communities



Coupling = 4: 3 communities



# Generalized Dynamics

- a) Calculate stability (to first-order-in-t) corresponding to independent probability of observing nodes  $i$  and  $j$ , *conditional on the type of connection necessary to move  $j \rightarrow i$ .*
- b) Generalize dynamics to include motion along different types of edges.
- c) Different spreading weights on different types (in stability definition, cf. in dynamics)

## a) Bipartite Networks

- Recover Barber null model with resolution:

$$\sum_{ij} [(\delta_{ij} + tL_{ij}) p_j^* - \rho_{i|j} p_j^*] \delta(c_i, c_j).$$

$$L_{ij} = A_{ij}/k_j - \delta_{ij} \quad p_j^* = k_j/(2m)$$

→  $\rho_{i|j} = b_{ij} k_i / m,$

$$\gamma = 1/t \quad Q_{\text{bipartite}} = \frac{1}{2m} \sum_{ij} \left[ A_{ij} - \gamma b_{ij} \frac{k_i k_j}{m} \right] \delta(c_i, c_j),$$

## b) Directed Networks

- Recover Leicht-Newman null model w/resolution:

$$\sum_{ij} [(\delta_{ij} + tL_{ij}) p_j^* - \rho_{i|j} p_j^*] \delta(c_i, c_j).$$

$$\dot{p}_i = \sum_j L_{ij} p_j = \sum_j \frac{1}{k_j} (A_{ij} + A_{ji}) p_j - p_i.$$

$$p_j^* = k_j / (2m) \quad k_j = k_j^{\text{in}} + k_j^{\text{out}}.$$

$$\rho_{i|j} p_j^* = \left( \frac{k_i^{\text{in}} k_j^{\text{out}}}{m k_j} + \frac{k_i^{\text{out}} k_j^{\text{in}}}{m k_j} \right) \frac{k_j}{2m} = \frac{k_i^{\text{in}} k_j^{\text{out}} + k_i^{\text{out}} k_j^{\text{in}}}{2m^2},$$

$$\gamma = 1/t$$

$$Q_{\text{directed}} = \frac{1}{m} \sum_{ij} \left[ A_{ij} - \gamma \frac{k_i^{\text{in}} k_j^{\text{out}}}{m} \right] \delta(c_i, c_j),$$

## c) Signed Networks


- Recover null model of Traag *et al.* & Gomez *et al.*:

$$\sum_{ij} [(\delta_{ij} + tL_{ij}) p_j^* - \rho_{i|j} p_j^*] \delta(c_i, c_j).$$

$$L_{ij} = (A_{ij}^+ + A_{ij}^-) / k_j - \delta_{ij} \text{ (with } k_j = k_j^+ + k_j^- \text{)}$$

$$\rho_{i|j} p_j^* = \left( \frac{k_i^+ k_j^+}{2m^+ k_j} - \frac{k_i^- k_j^-}{2m^- k_j} \right) \frac{k_j}{2m} = \frac{1}{2m} \left( \frac{k_i^+ k_j^+}{2m^+} - \frac{k_i^- k_j^-}{2m^-} \right)$$

$$\gamma = 1/t$$

$$Q_{\text{signed}} = \frac{1}{2m} \sum_{ij} \left[ A_{ij}^+ - A_{ij}^- - \left( \gamma^+ \frac{k_i^+ k_j^+}{2m^+} - \gamma^- \frac{k_i^- k_j^-}{2m^-} \right) \right] \delta(c_i, c_j)$$


# Multislice Networks

(note extra indices explicitly denoting slices here)

$$k_{js} = \sum_i A_{ijs}, c_{js} = \sum_r C_{jstr}, \kappa_{js} = k_{js} + c_{js}.$$

$$\dot{p}_{is} = \sum_{jr} (A_{ijs} \delta_{sr} + \delta_{ij} C_{jstr}) p_{jr} / \kappa_{jr} - p_{is}$$

$$\sum_{ij} [(\delta_{ij} + tL_{ij}) p_j^* - \rho_{i|j} p_j^*] \delta(c_i, c_j).$$

$$p_{jr}^* = \kappa_{jr} / (2\mu), \text{ where } 2\mu = \sum_{jr} \kappa_{jr}.$$

$$\rho_{is|jr} p_{jr}^* = \left[ \frac{k_{is}}{2m_s} \frac{k_{jr}}{\kappa_{jr}} \delta_{sr} + \frac{C_{jstr}}{c_{jr}} \frac{c_{jr}}{\kappa_{jr}} \delta_{ij} \right] \frac{\kappa_{jr}}{2\mu}$$

$$\gamma = 1/t$$

$$Q_{\text{multislice}} = \frac{1}{2\mu} \sum_{ijsr} \left\{ \left( A_{ijs} - \gamma_s \frac{k_{is} k_{js}}{2m_s} \right) \delta_{sr} + \delta_{ij} C_{jstr} \right\} \delta(g_{is}, g_{jr})$$

# Summary

- *Community structure provides a powerful tool to simplify the description of a network*
- “Multislice” framework extends modularity to more complicated (and more interesting!) situations of **dynamic** data, **multiplexed** ties, and communities across **multiple scales**
- **Applications:** fMRI (Bassett et al.), international relations (w/Cranmer), finance (w/Blocher)
- **Issues** to address: Many local optima (see, e.g., Good, de Montjoye & Clauset) means we need a good statistical mechanics of partitions