Hierarchical Block Models

Lecture 7, Fall 2014
CSCI 5352, Network Analysis and Models

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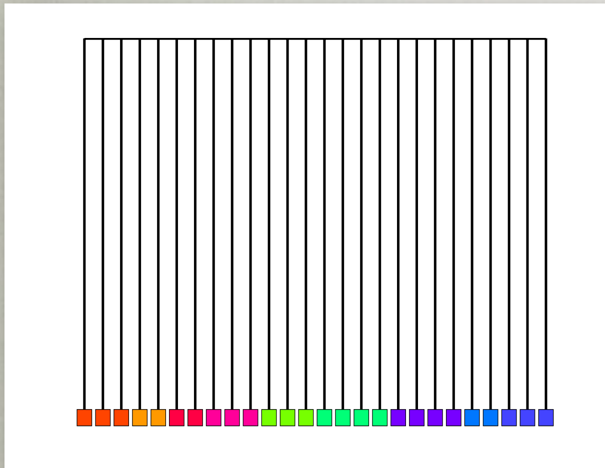
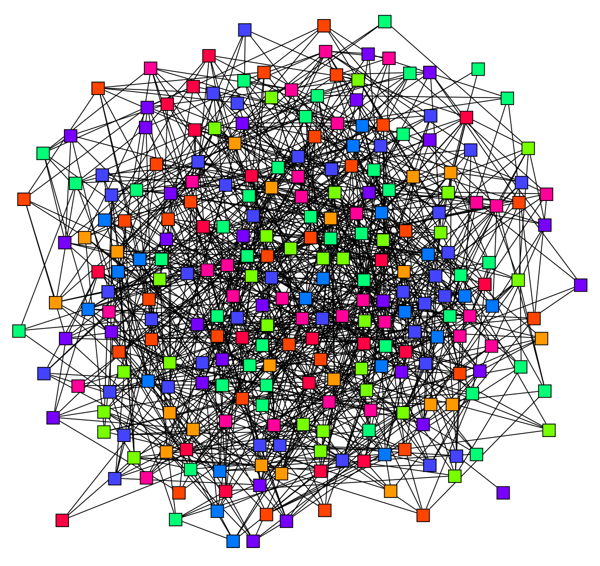
University of Colorado, Boulder

Advanced Generative Models

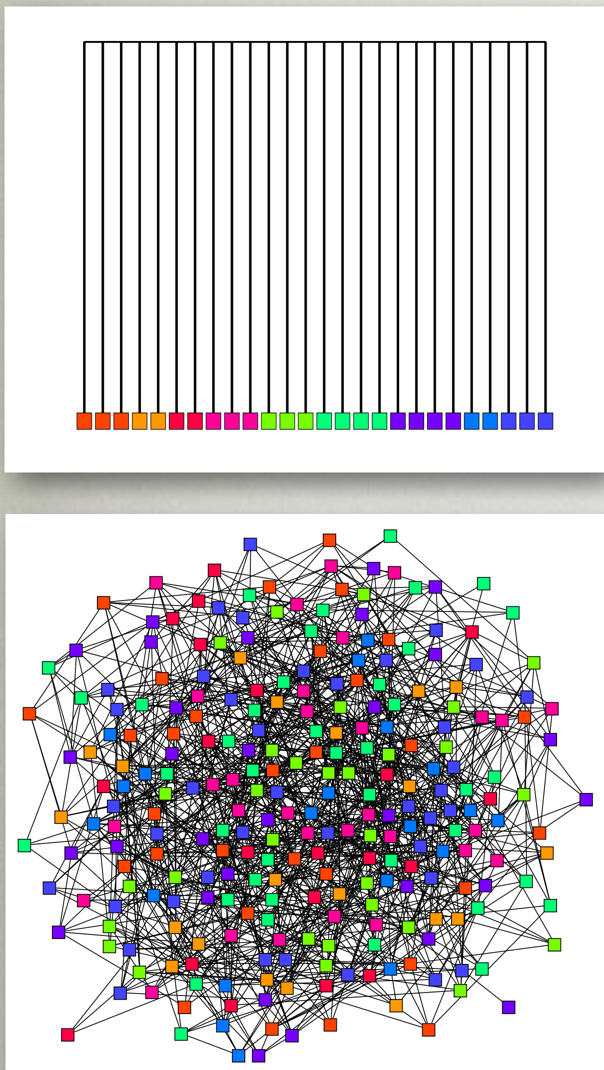
1. hierarchical random graph model example
2. examples of tasks generative models can do
3. application to some real-world data sets

no structure

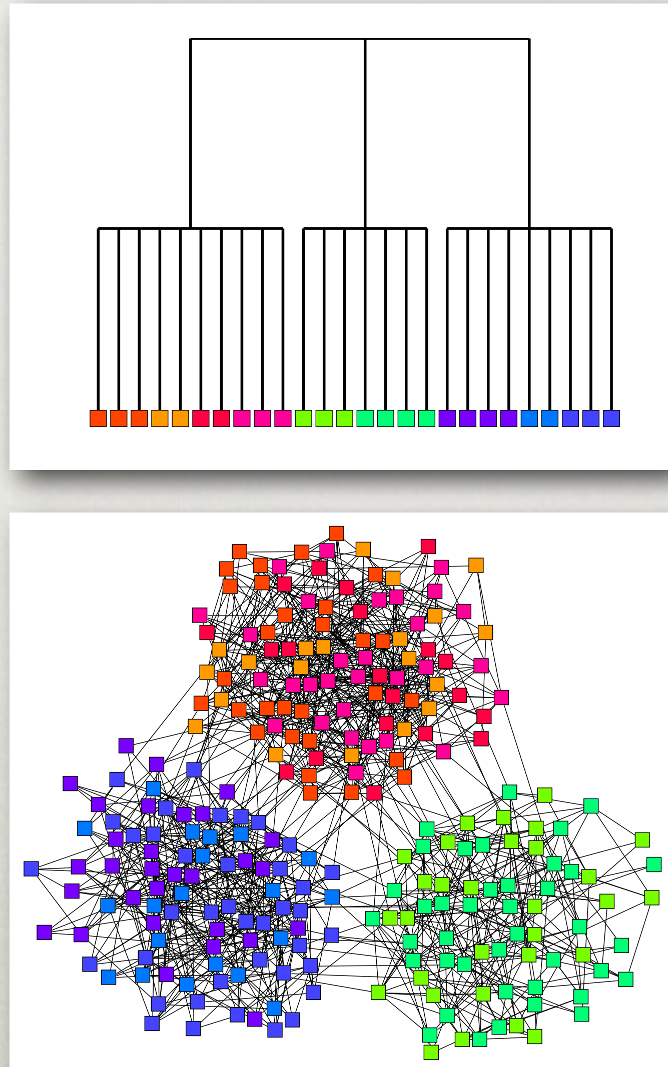




no structure

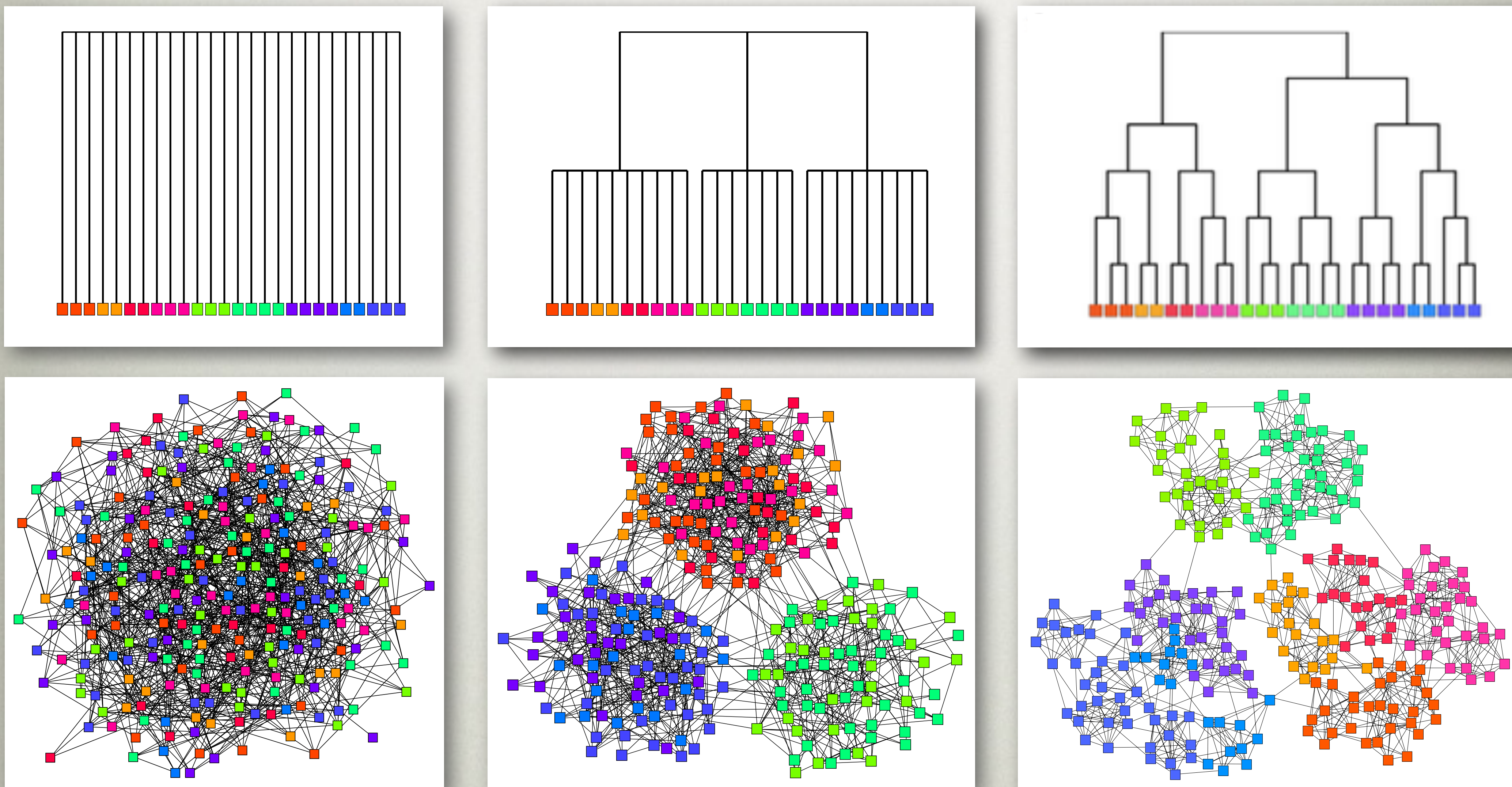


block structure



one scale

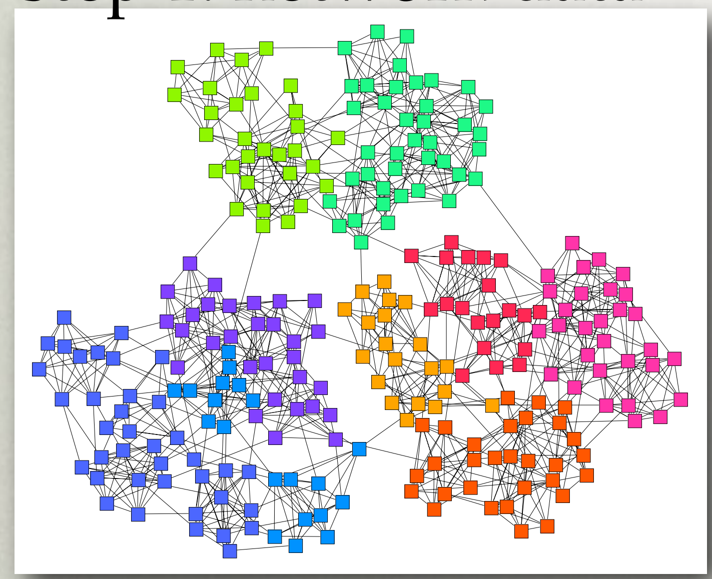
no structure **block structure** **hierarchical structure**



one scale **multi-scale**

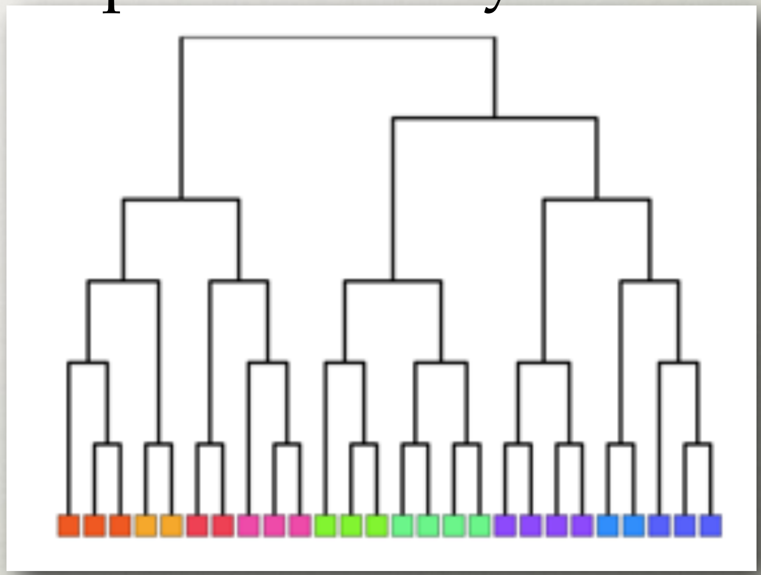
how can we extract a network's hierarchy?

step 1: network data



?

step 3: hierarchy



GENERATIVE MODELS

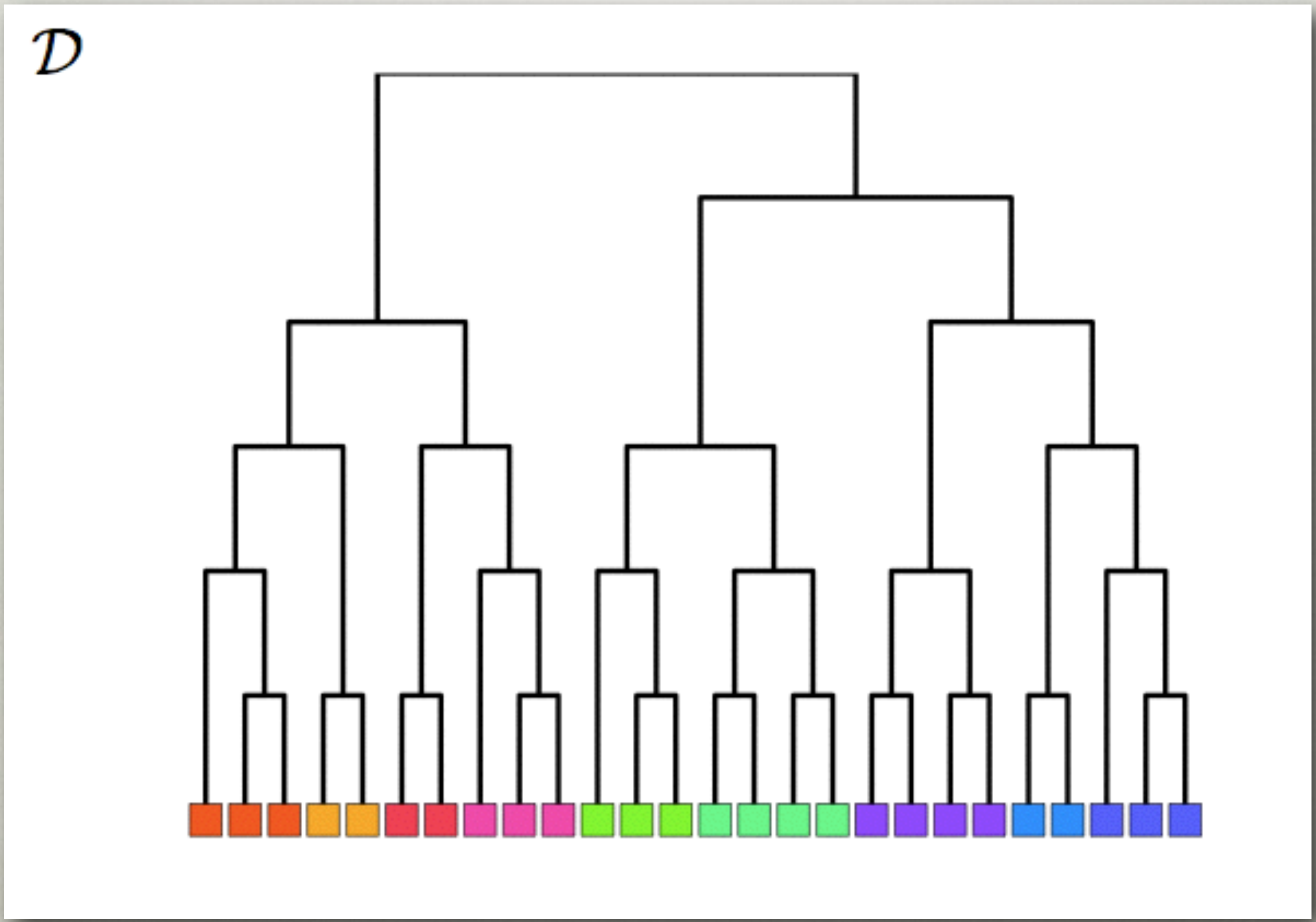
1. write down hierarchical stochastic block model

2. estimate / learn model from data

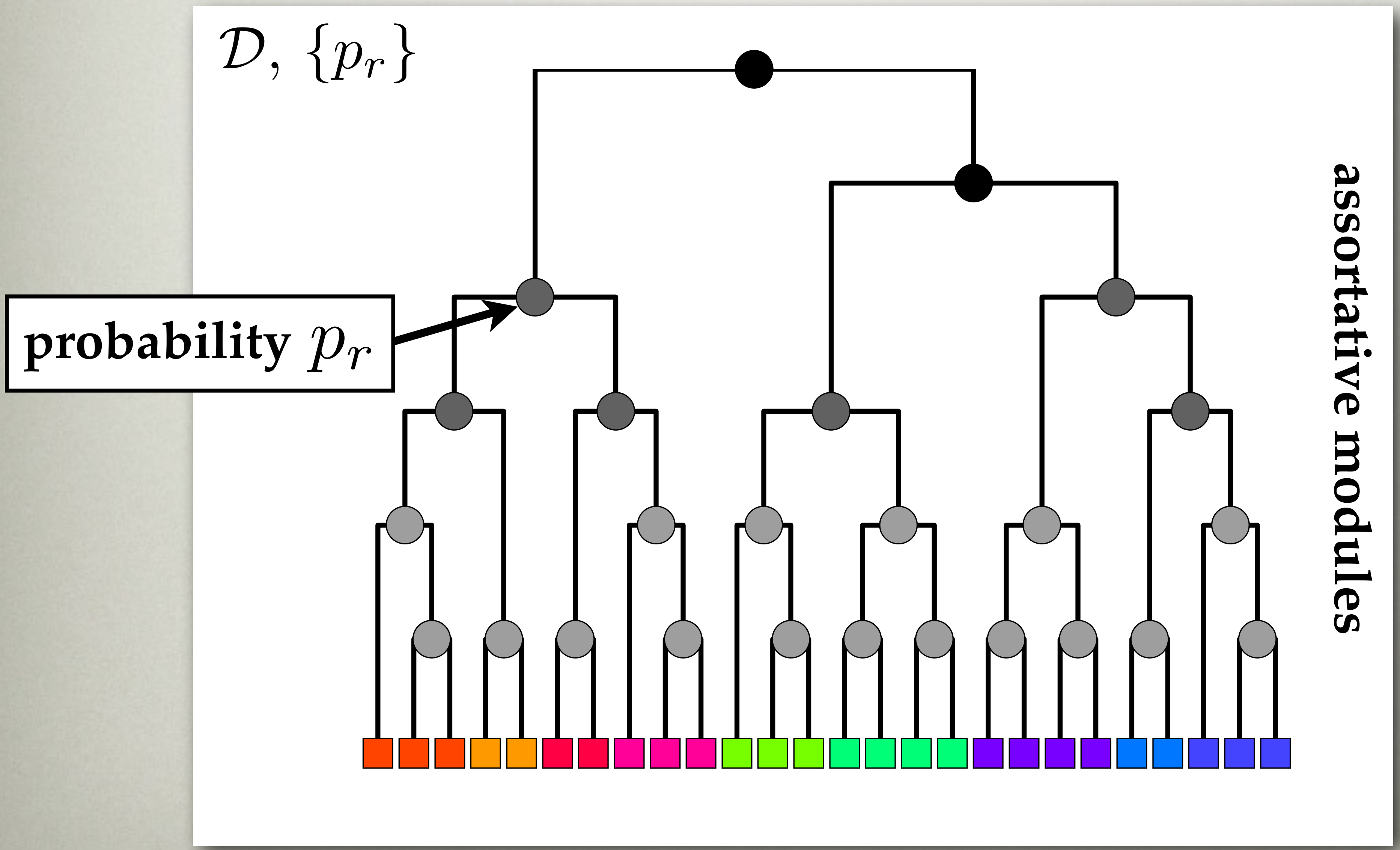
3. evaluate model goodness-of-fit

4. evaluate model predictions

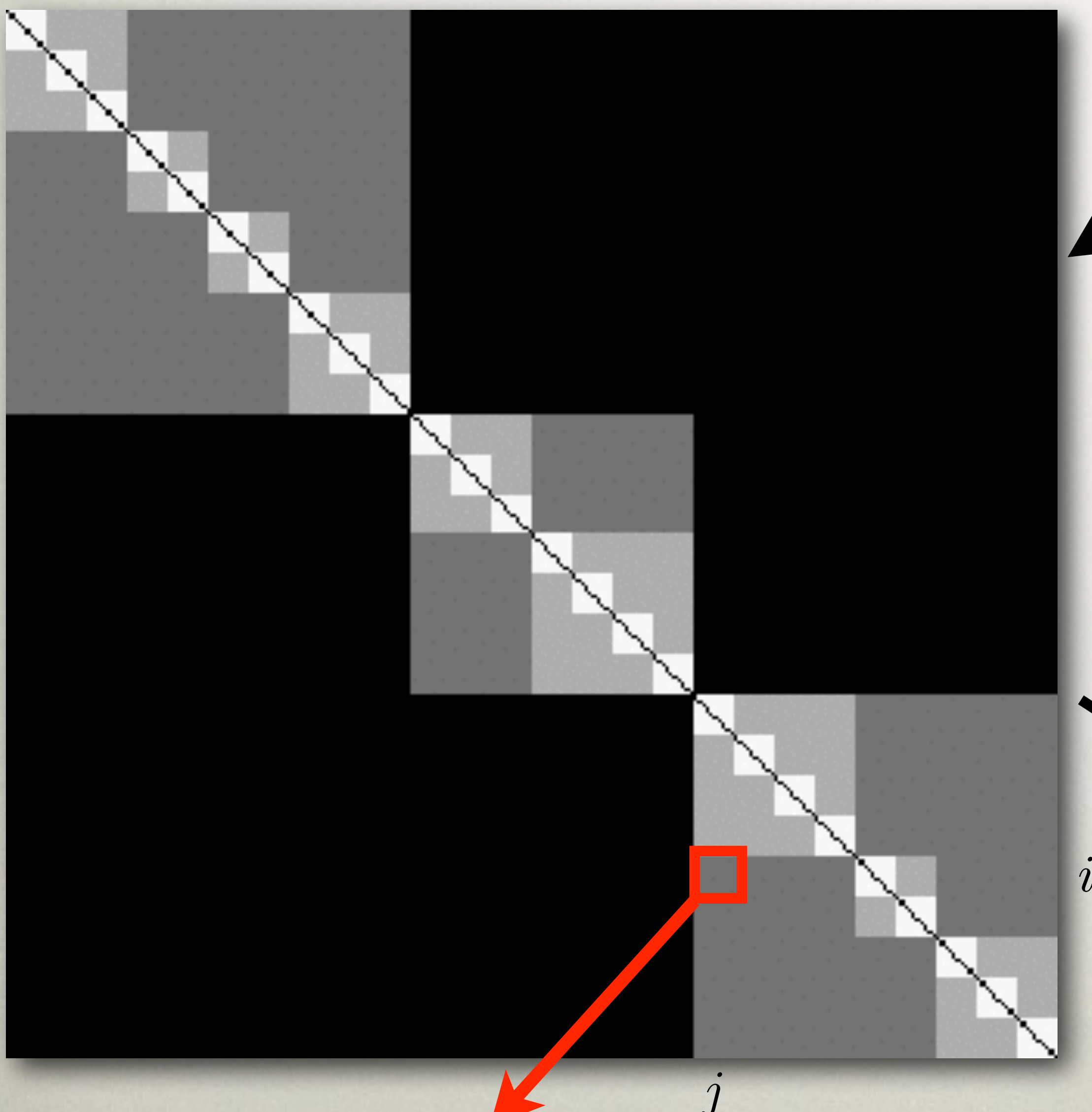
A Model of Hierarchy



A Model of Hierarchy

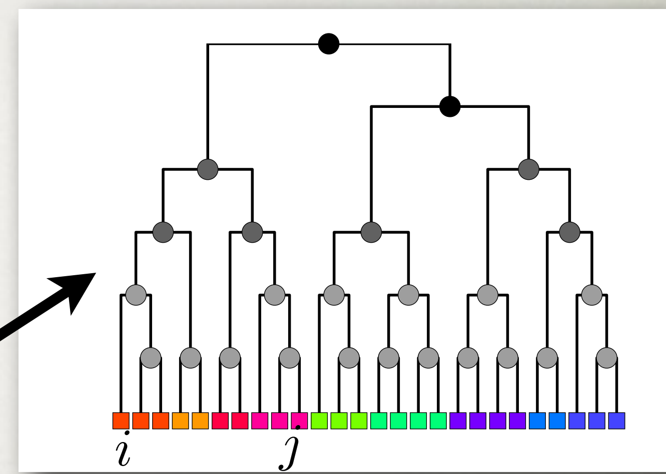


“inhomogeneous” random graph

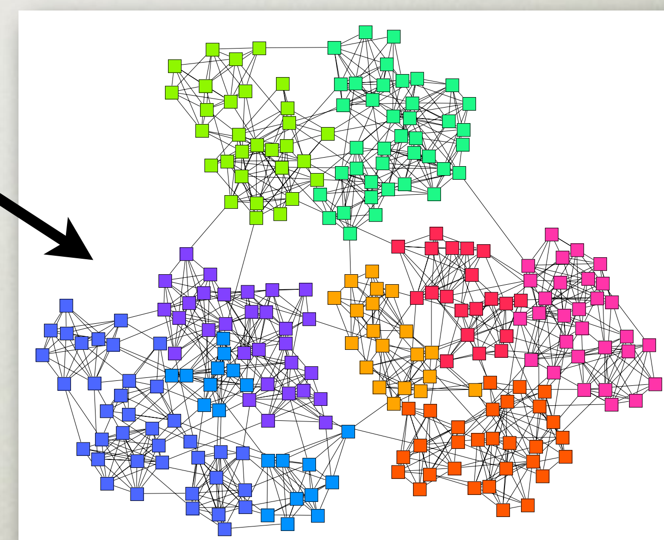


$$\Pr(i, j \text{ connected}) = p_r$$
$$= p_{(\text{lowest common ancestor of } i,j)}$$

model



instance



Hierarchical Random Graph

advantages

- explicit hierarchical structure
- flexible (2n parameters)
- captures structure at all scales
- captures mixtures of assortativity, disassortativity
- like SBM, decomposes adjacencies into "bundles" (each a random bipartite graph)
- learnable directly from data
- nice interpretable structure

disadvantages

- flexible (2n parameters)
- computationally slow
- can overfit to degree structure (like SBM)

Fitting the model

- **likelihood function** $\mathcal{L} = \Pr(\text{ data } | \text{ model })$

  ($\mathcal{L}$ scores **quality** of model)

- **sample all good models**

  via Markov chain Monte Carlo*
  over all dendrograms

- **technical details in**

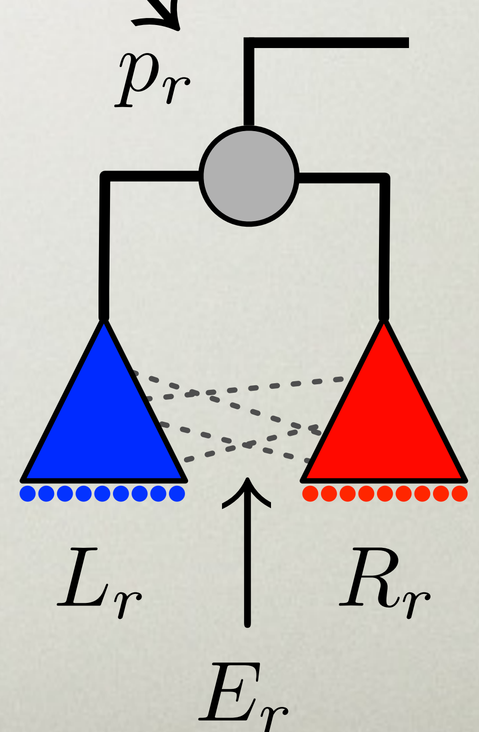
  Clauset, Moore and Newman, *Nature* **453**, 98-101 (2008) and

  Clauset, Moore and Newman, *ICML* (2006)

* other sampling or optimization methods possible

Likelihood Function

$$\mathcal{L}(\mathcal{D}, \{p_r\}) = \prod_r p_r^{E_r} (1 - p_r)^{L_r R_r - E_r}$$

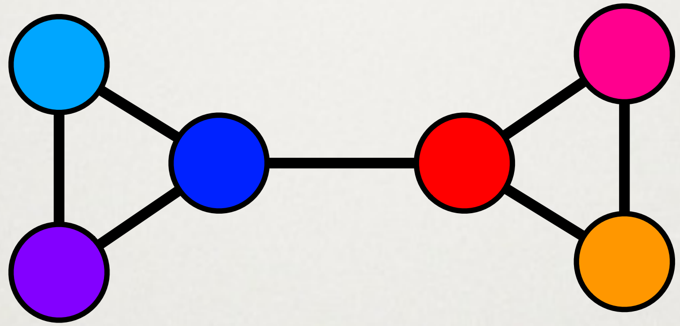


L_r = number nodes in left subtree

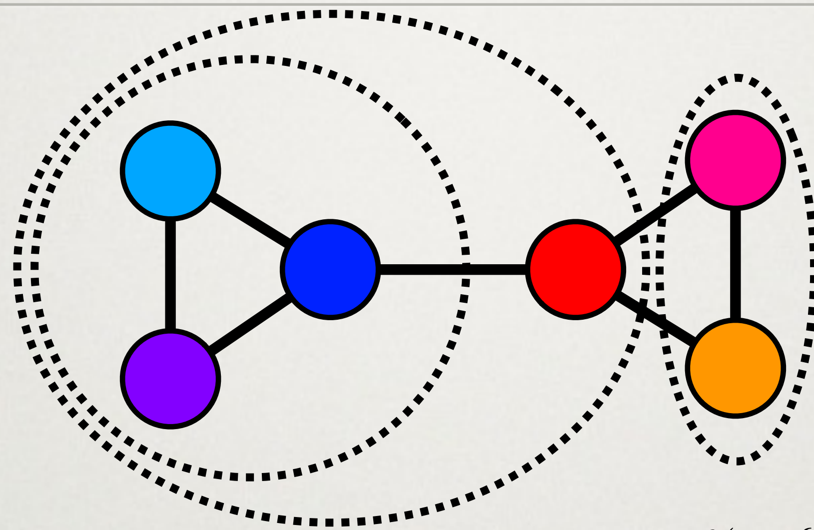
R_r = number nodes in right subtree

E_r = number edges with r as lowest common ancestor

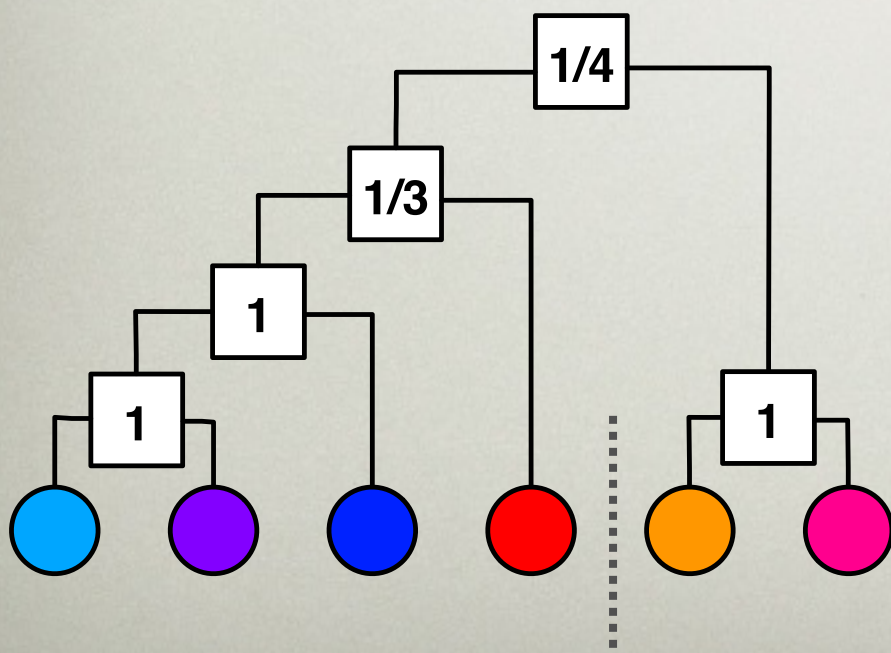
Example



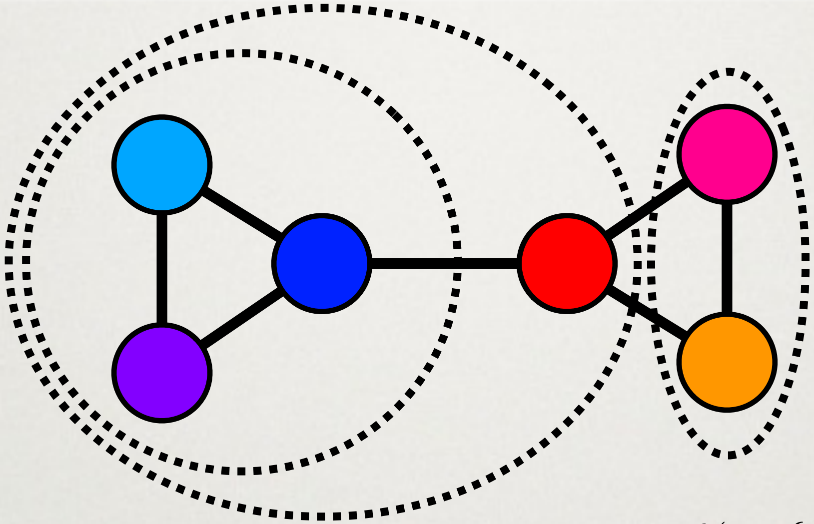
Bad Dendrogram



$$\mathcal{L}(\mathcal{D},\, \{p_r\}) = \prod_r p_r^{E_r}\, (1-p_r)^{L_r R_r - E_r}$$



Bad Dendrogram



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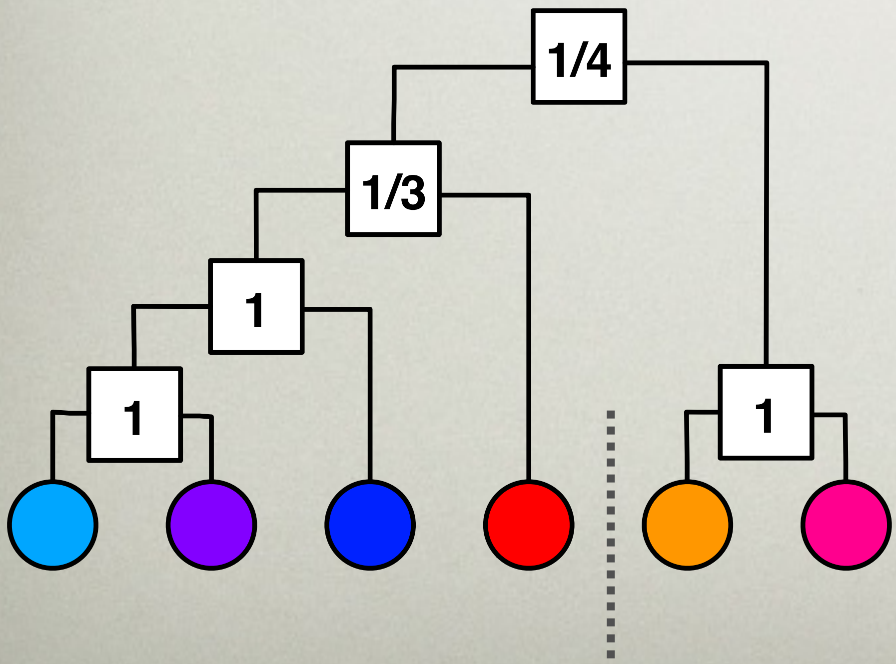
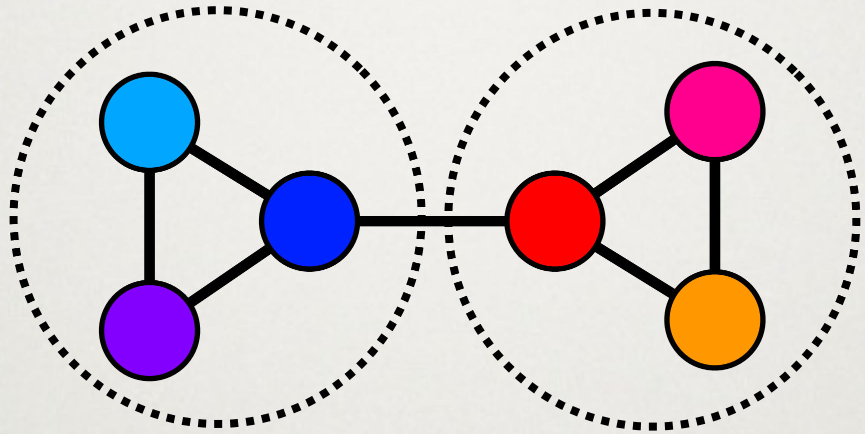


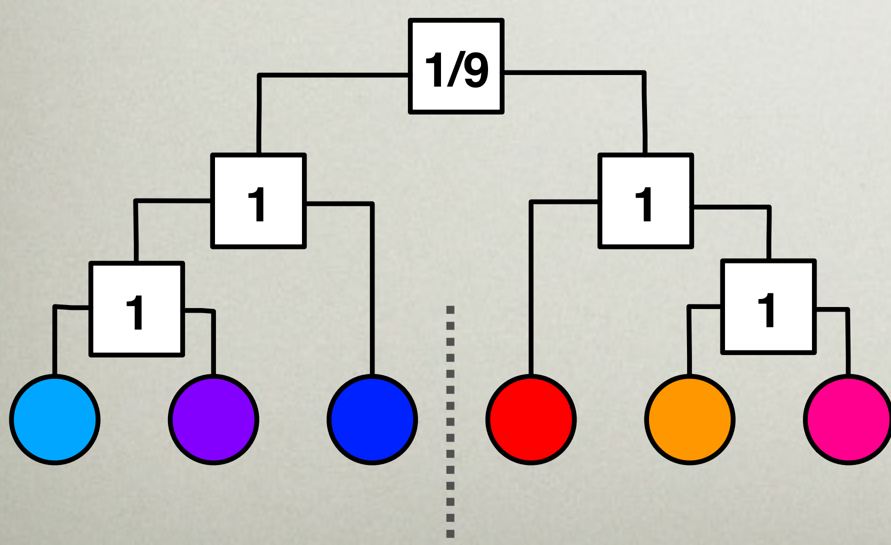
$$\mathcal{L} = \left[\left(\frac{1}{3}\right)^1\left(\frac{2}{3}\right)^2\right]\cdot\left[\left(\frac{1}{4}\right)^2\left(\frac{3}{4}\right)^6\right]$$

$$\mathcal{L} = 0.0016$$

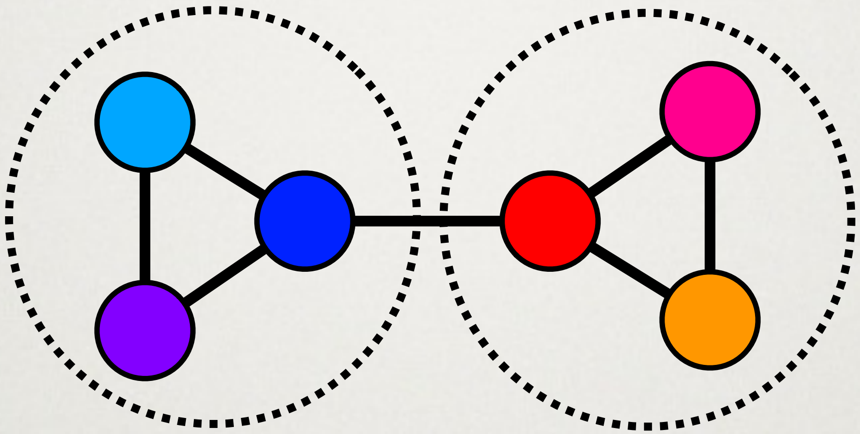
Good Dendrogram



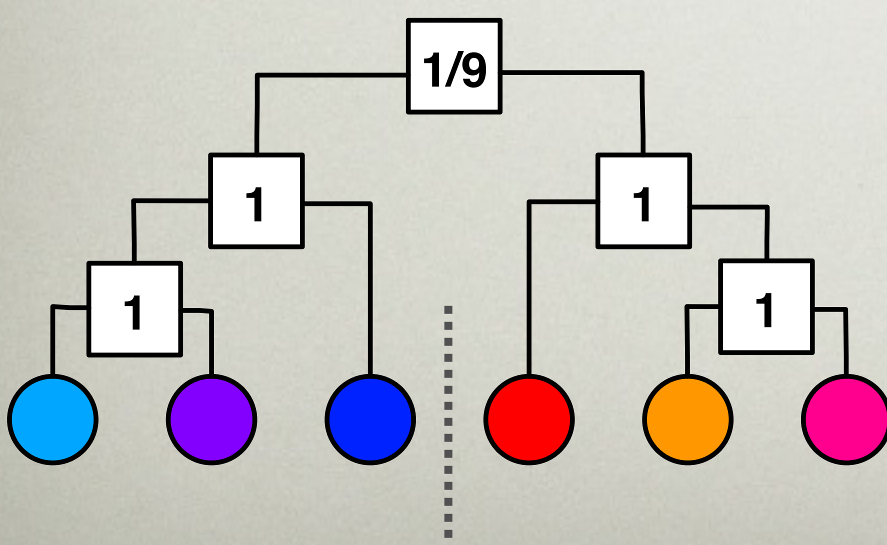
$$\mathcal{L}(\mathcal{D},\, \{p_r\}) = \prod_r p_r^{E_r}\, (1 - p_r)^{L_r R_r - E_r}$$



Good Dendrogram



$$\mathcal{L}(\mathcal{D}, \{p_r\}) = \prod_r p_r^{E_r} (1 - p_r)^{L_r R_r - E_r}$$



$$\mathcal{L} = \left[\left(\frac{1}{9}\right)^1 \left(\frac{8}{9}\right)^8 \right]$$

$$\mathcal{L} = 0.0433$$

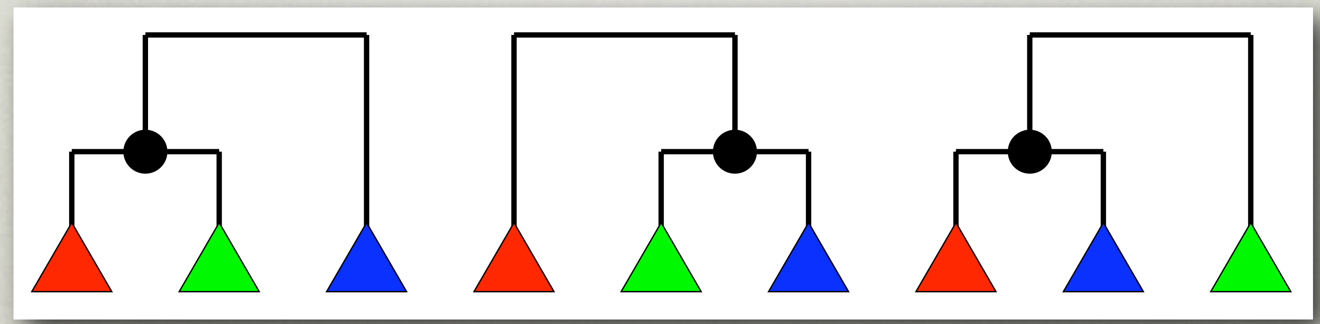
Markov chain Monte Carlo (MCMC)

Given $\mathcal{D}$, choose random internal node

Choose random reconfiguration of subtrees [ergodicity]

Recompute probabilities $\{p_r\}$ and likelihood $\mathcal{L}$

Sampling states according to their likelihood [detailed balance]



three subtree configurations

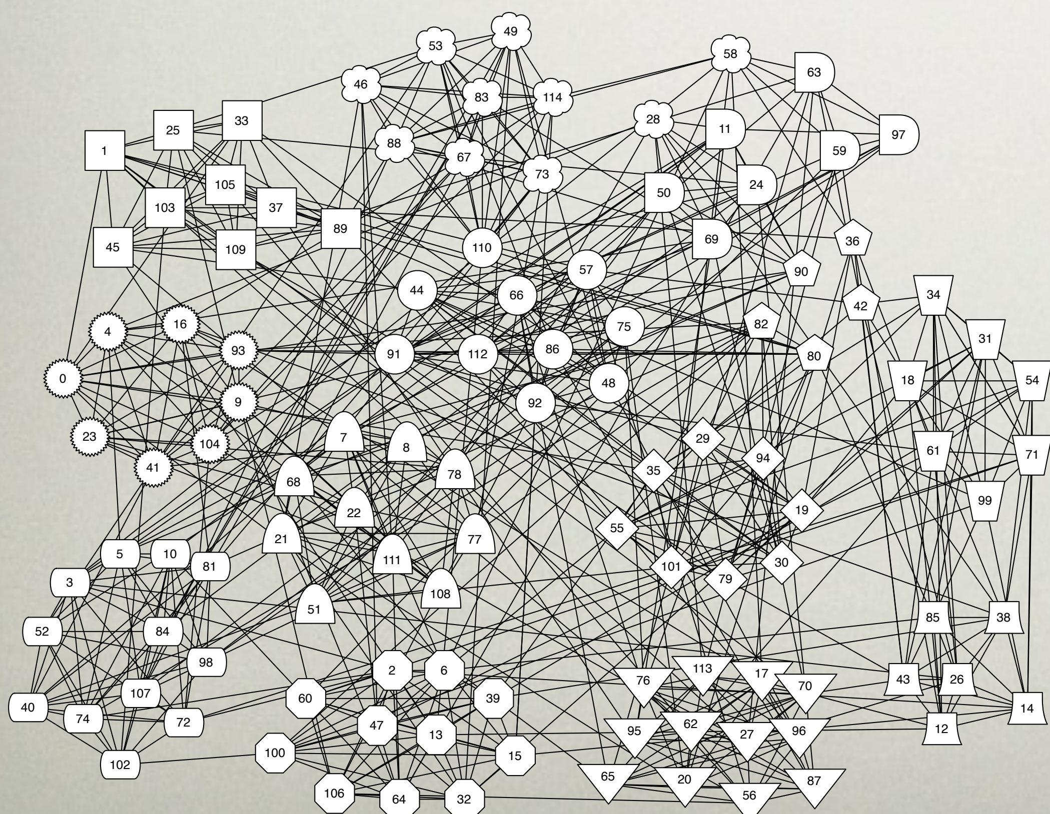
(up to relabeling)

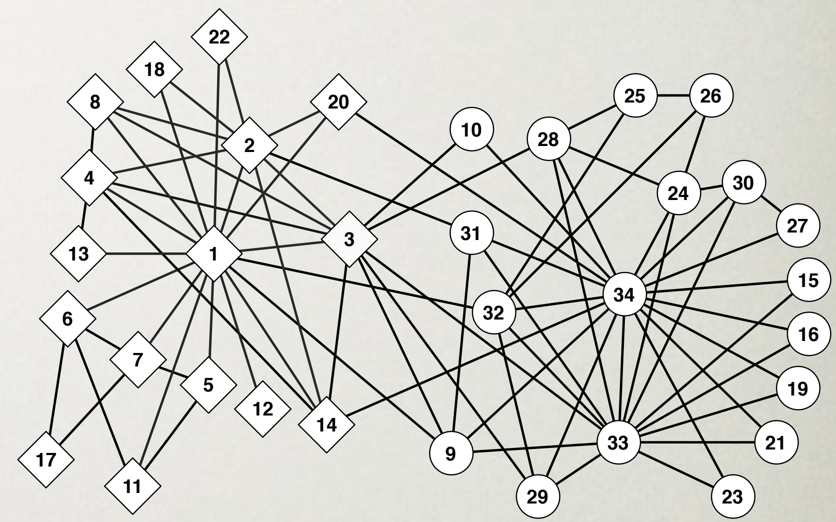
Some applications

Two Case Studies

NCAA Schedule 2000

$n = 115 \quad m = 613$





Zachary's Karate Club

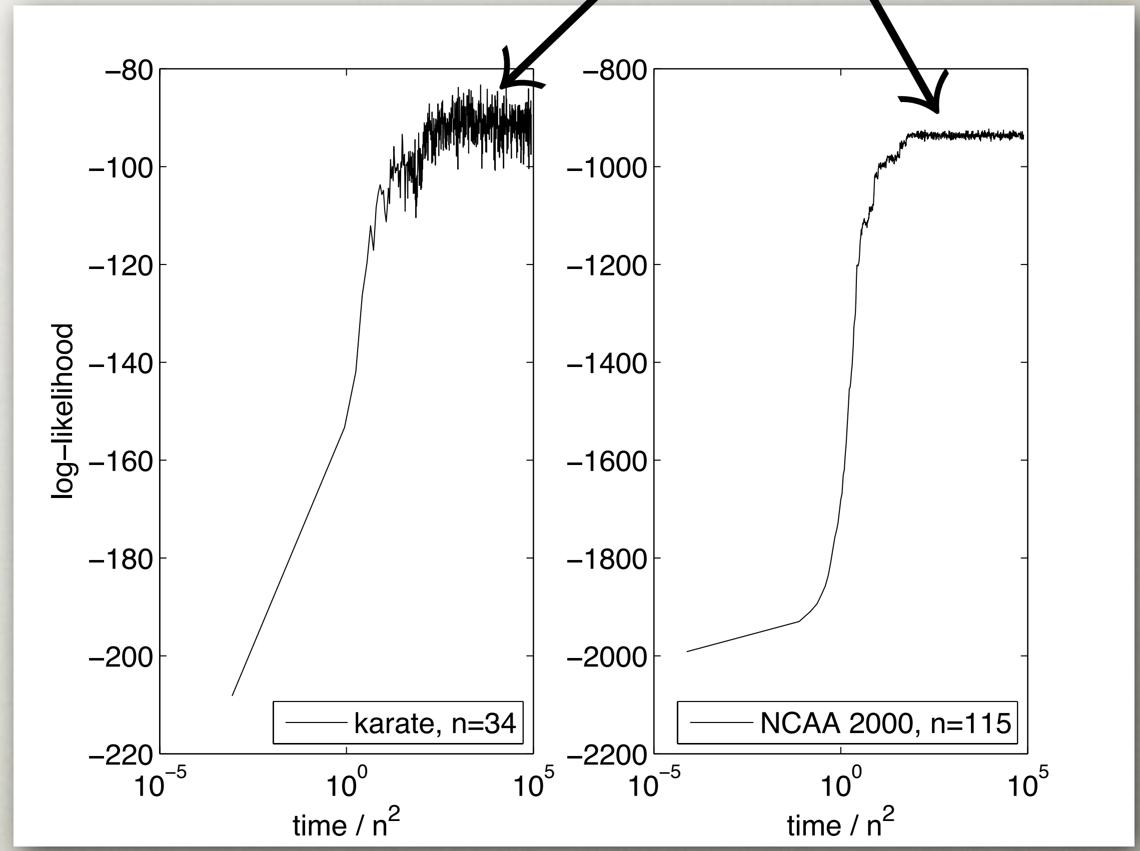
$n = 34 \quad m = 78$

Mixing Times

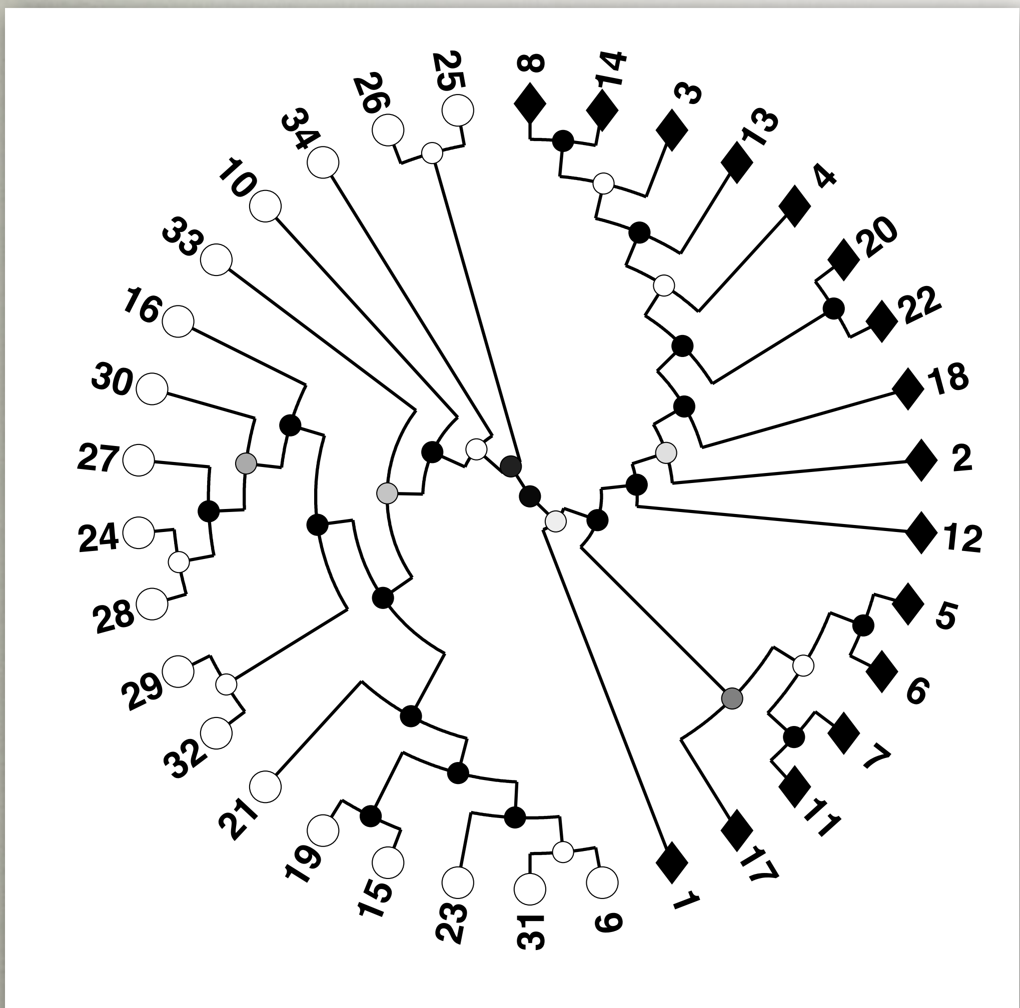
MCMC mixes relatively quickly

Equilibrium in $\sim O(n^2)$ steps

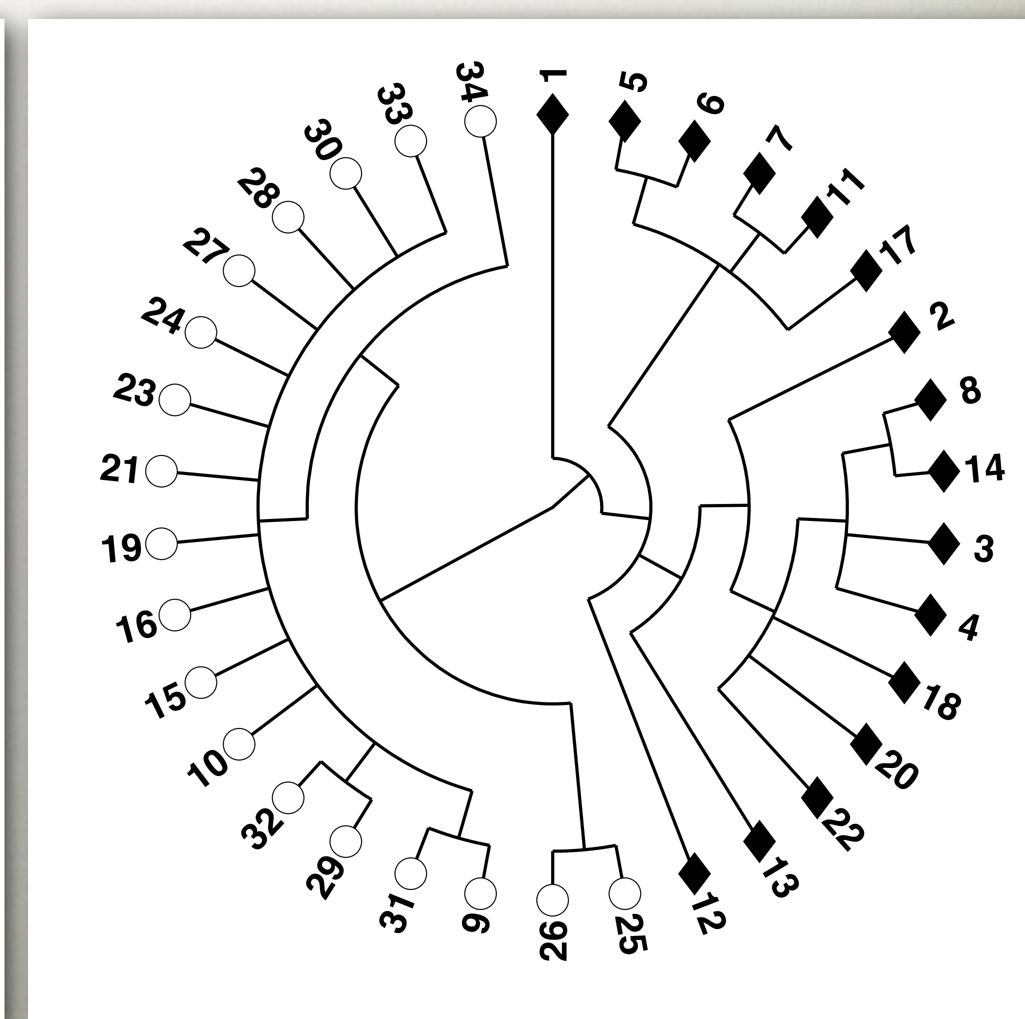
equilibrium



Hierarchies

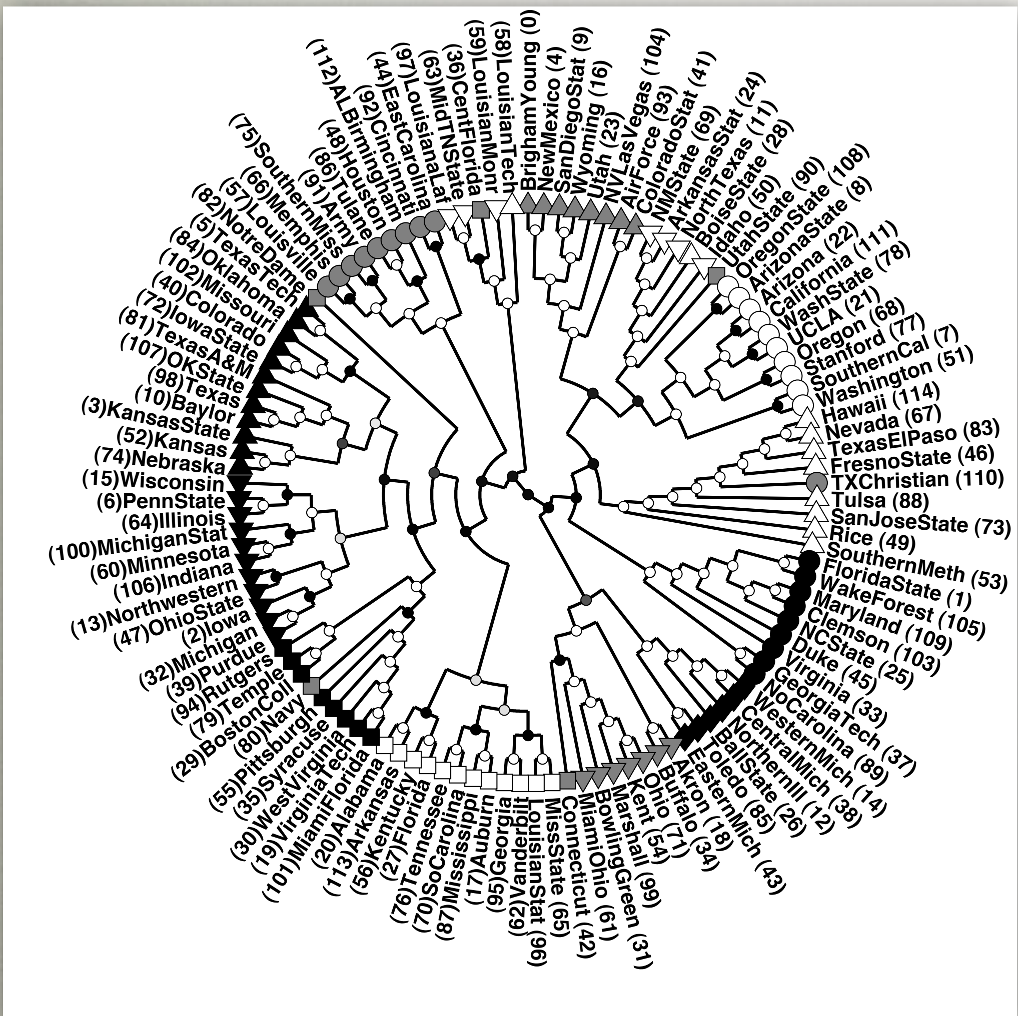


point estimate

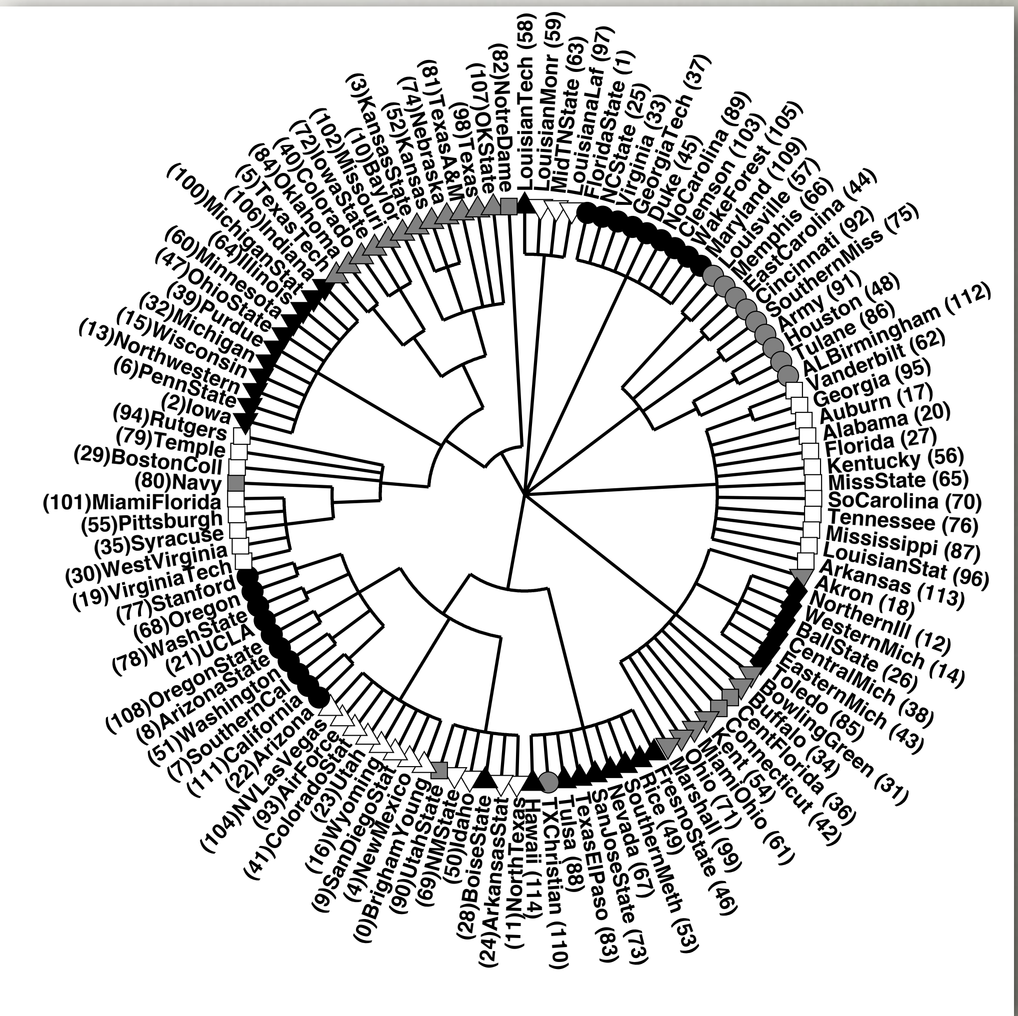


consensus hierarchy

Hierarchies



point estimate



consensus hierarchy

Edge Annotations

Average likelihood of edge existing

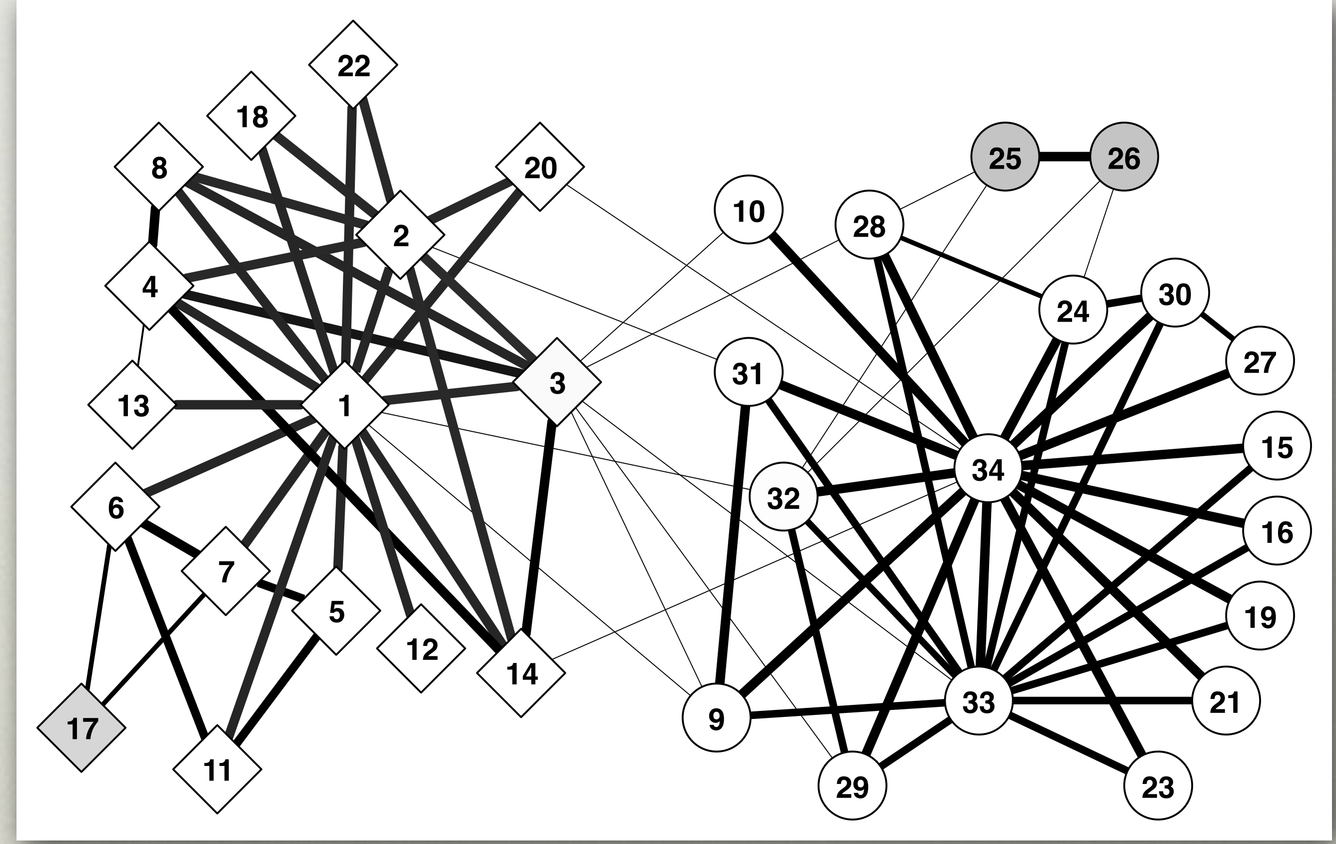
- For each edge (i, j) in *G*, compute average associated parameter $\langle \theta_r \rangle_{(i,j)}$ over sampled models
- $\langle \theta_r \rangle_{(i,j)}$ is edge annotation (weight)

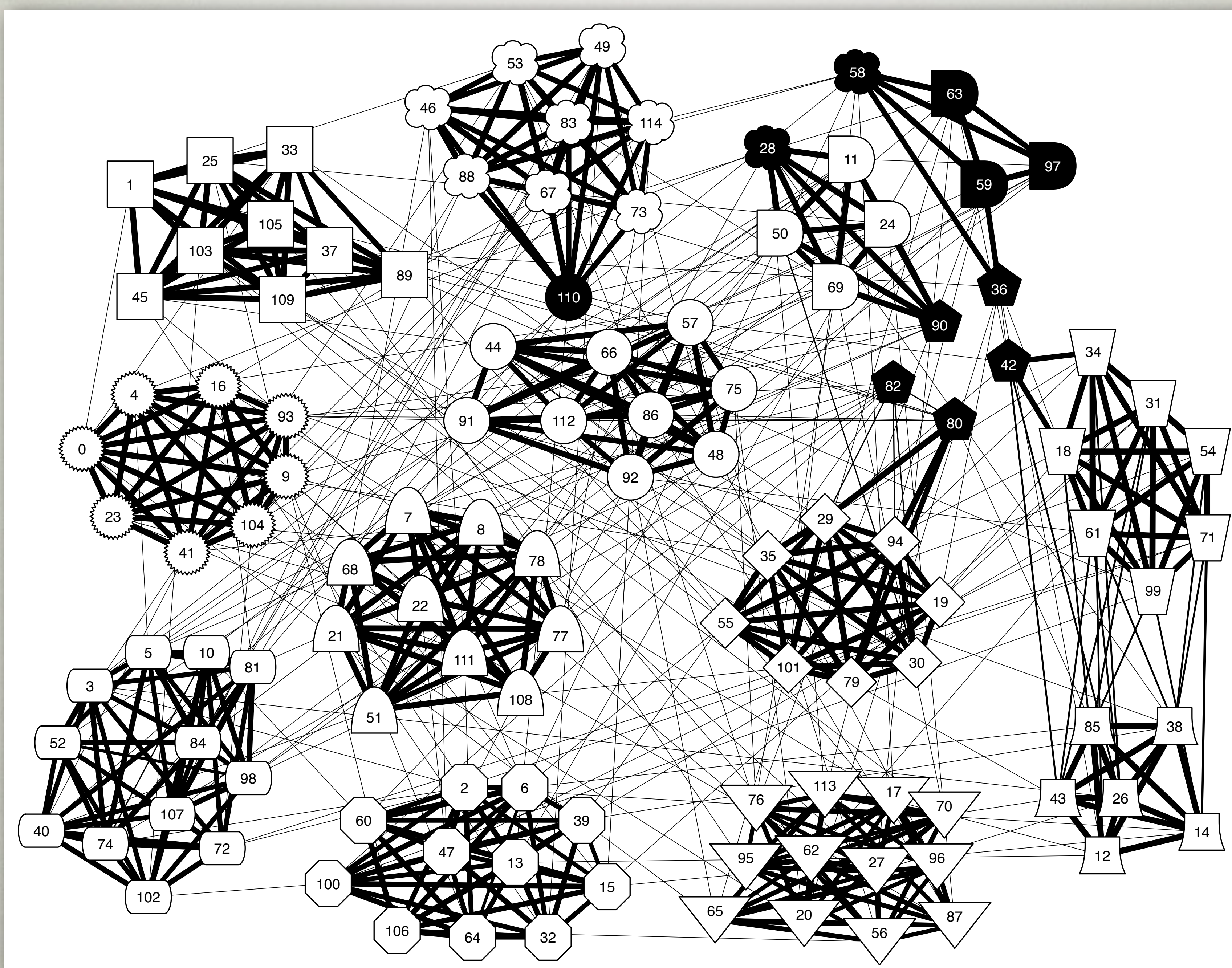
Vertex Annotations

Group-affiliation strengths

- If each vertex has known group label
- Ask, how often does vertex i appear in a subtree with majority of its fellows?
- Frequency is vertex annotation (strength)

Edge, Note Annotations




49
53
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63
46
83
114
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1
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89
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110
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91
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80
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72
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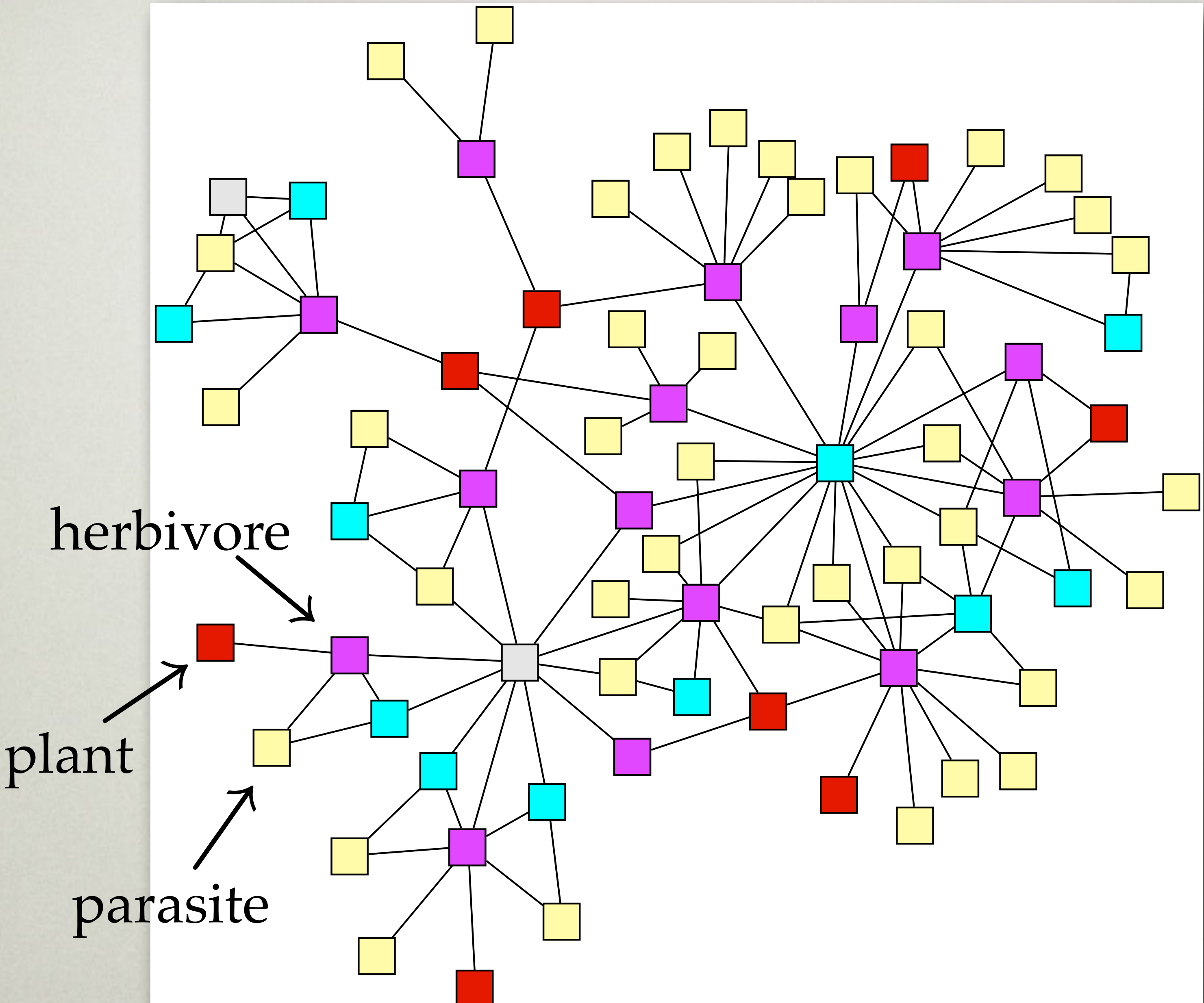
62
27
96
14
12
100
15
102
65
20
87
56
106
64
32

Model Checking

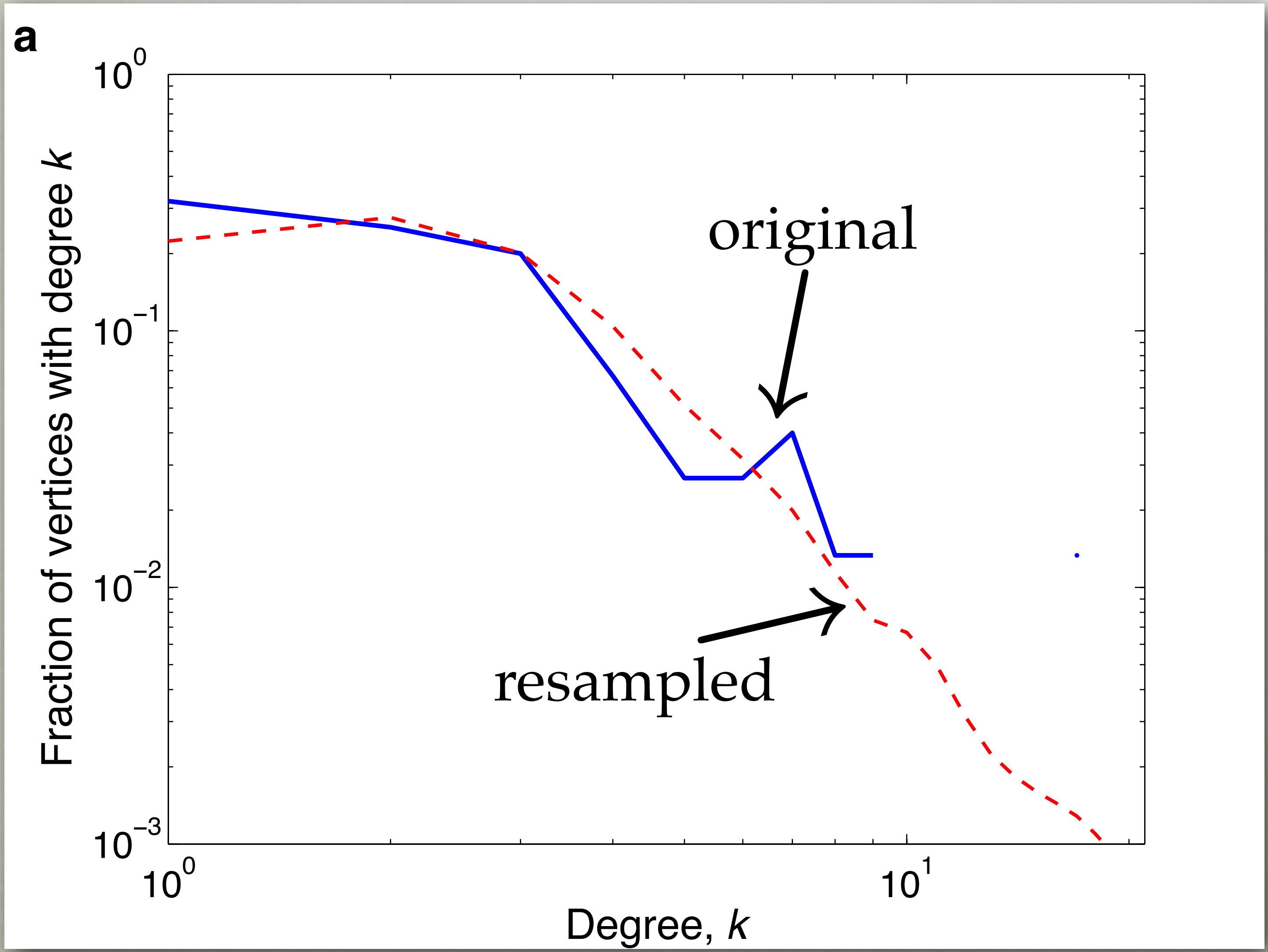
Model Checking

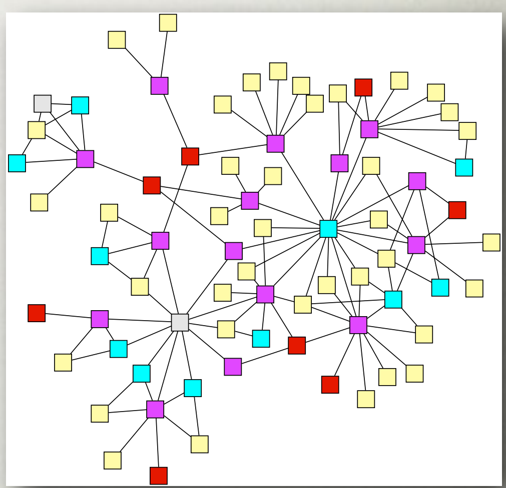
- Given graph G
- run MCMC to equilibrium
- then, for each sampled $\mathcal{D}$, draw a **resampled** graph G' from ensemble

Checking the model (goodness-of-fit):
do resampled graphs look like original?

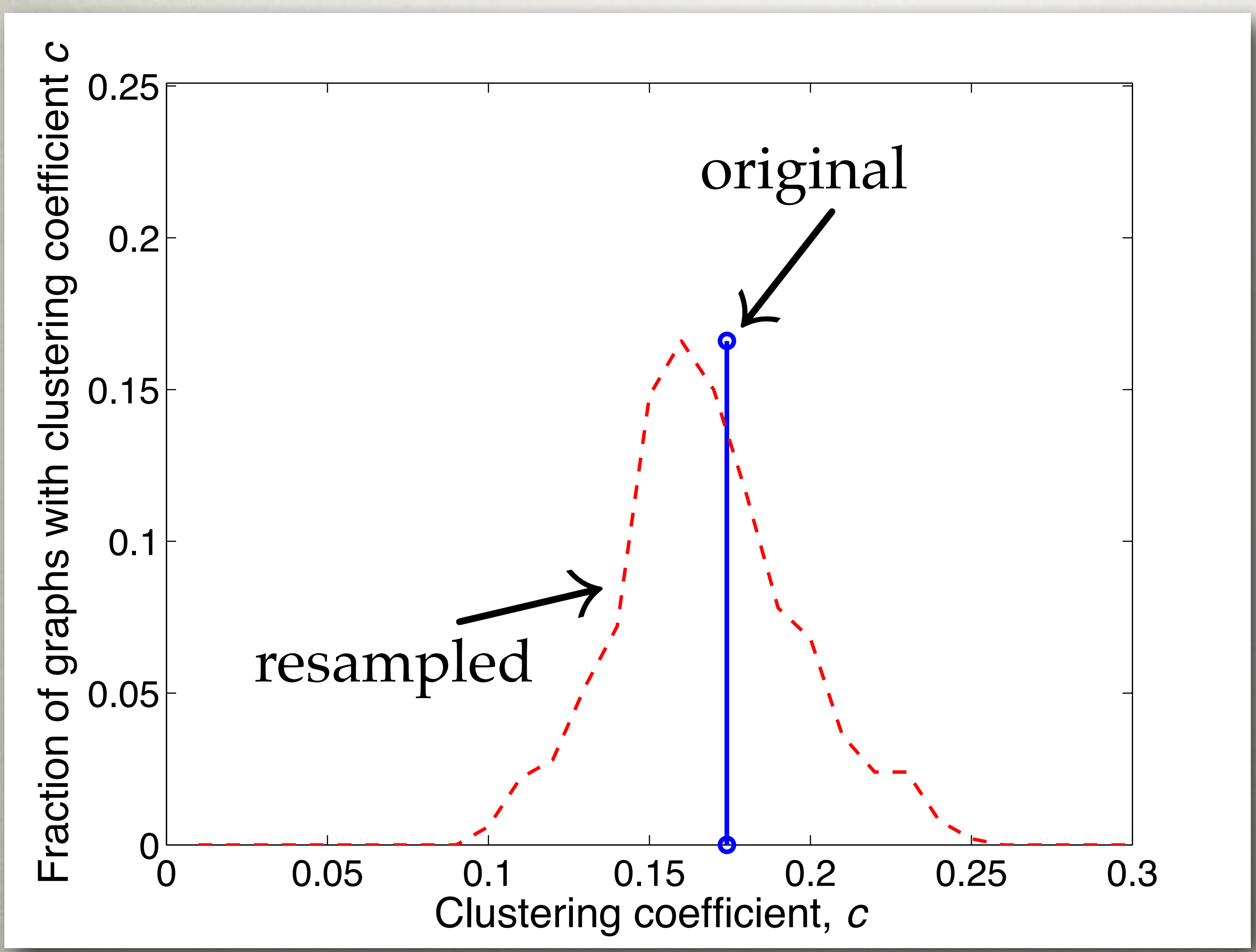

herbivore
plant
parasite

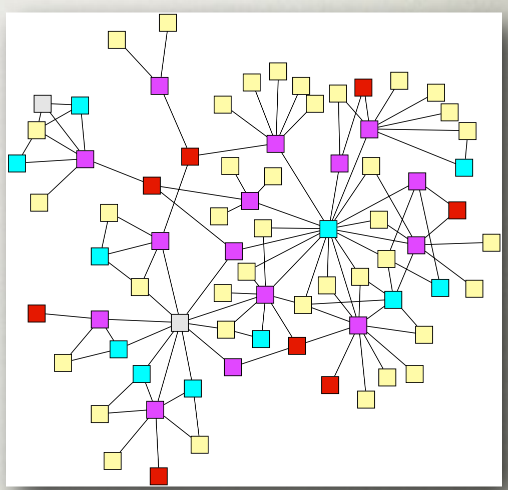
Degree Distribution



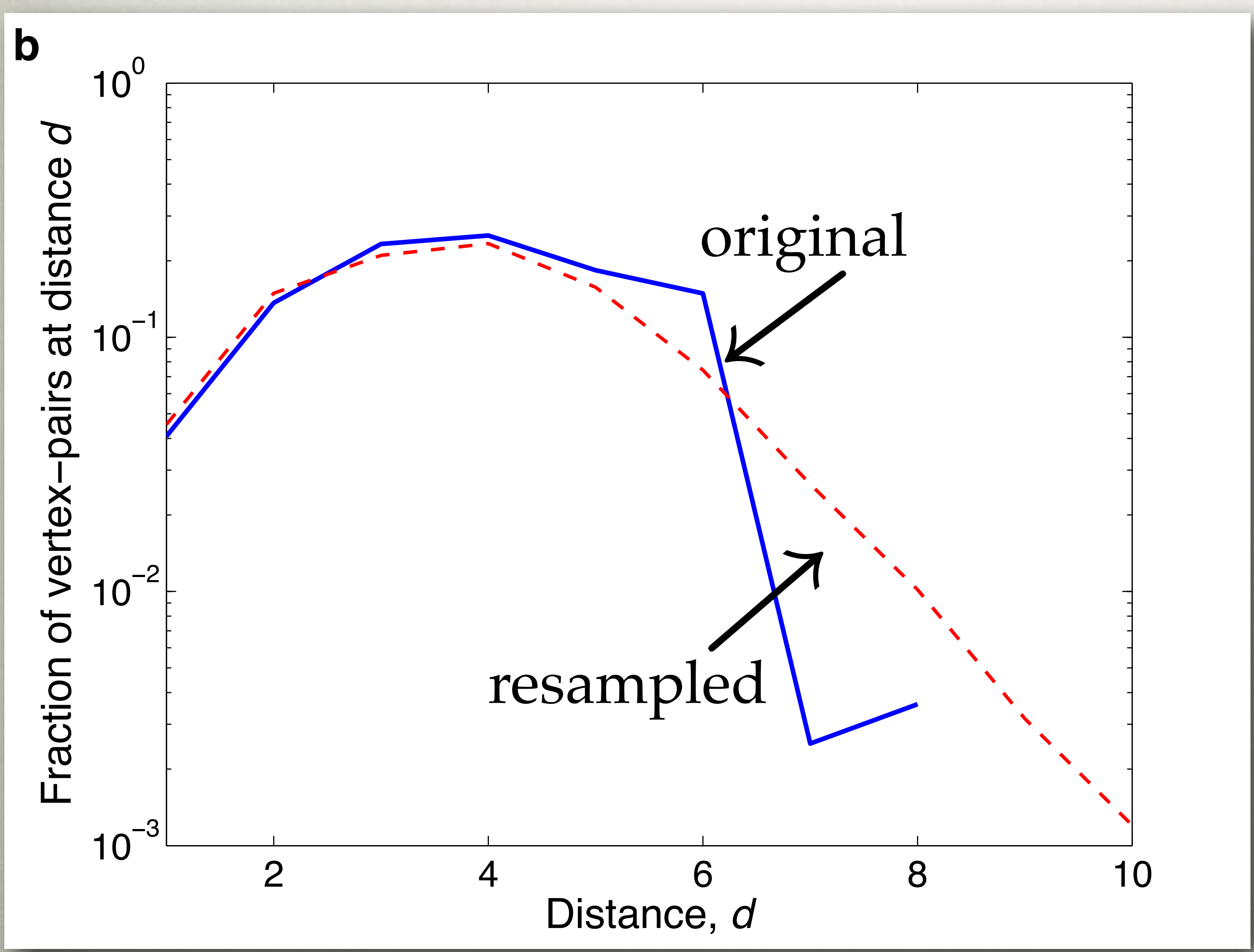


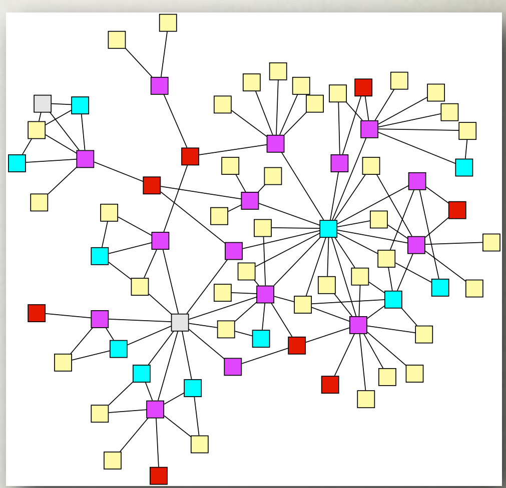
Clustering Coefficient





Distance Distribution





Predicting Missing Links

many networks partially known, noisy

- social nets, food webs, protein interactions, etc.

can hierarchies predict their **missing links**?

previous approaches

- Liben-Nowell & Kleinberg (2003)
- Goldberg & Roth (2003)
- Szilágyi et al. (2005)
- many more now

Accuracy is Hard

- remove k edges from G
- how easy to guess a missing link?

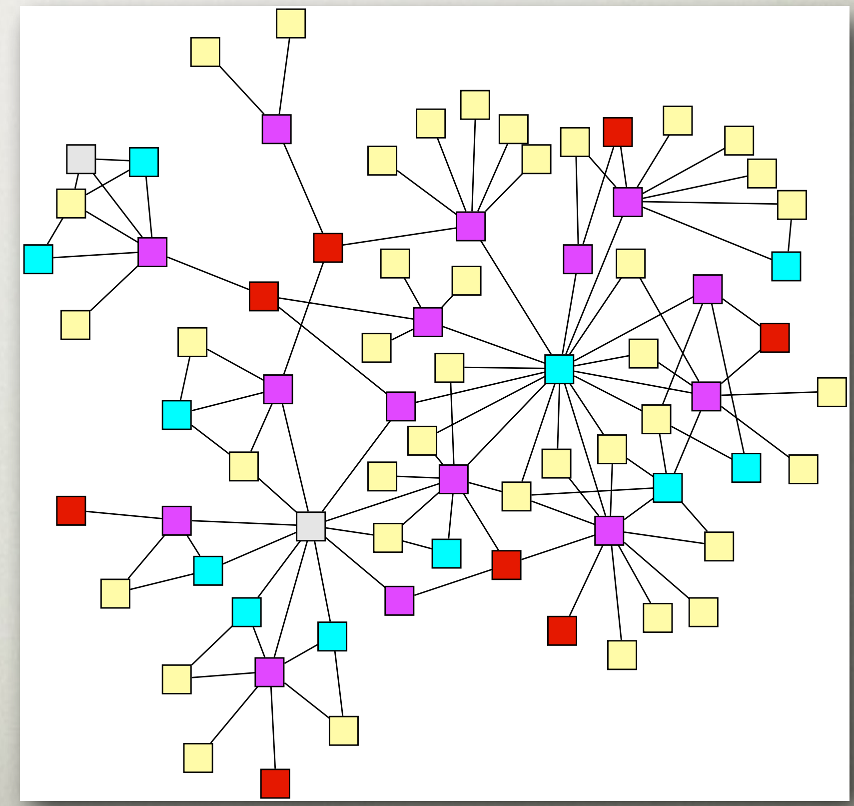
$$p_{\text{guess}} \approx \frac{k}{n^2 - m + k}$$

$$= O(n^{-2})$$

$$n = 75$$

$$m = 113$$

$$p_{\text{guess}} = k/(2662 + k)$$



Generative Model Aproach

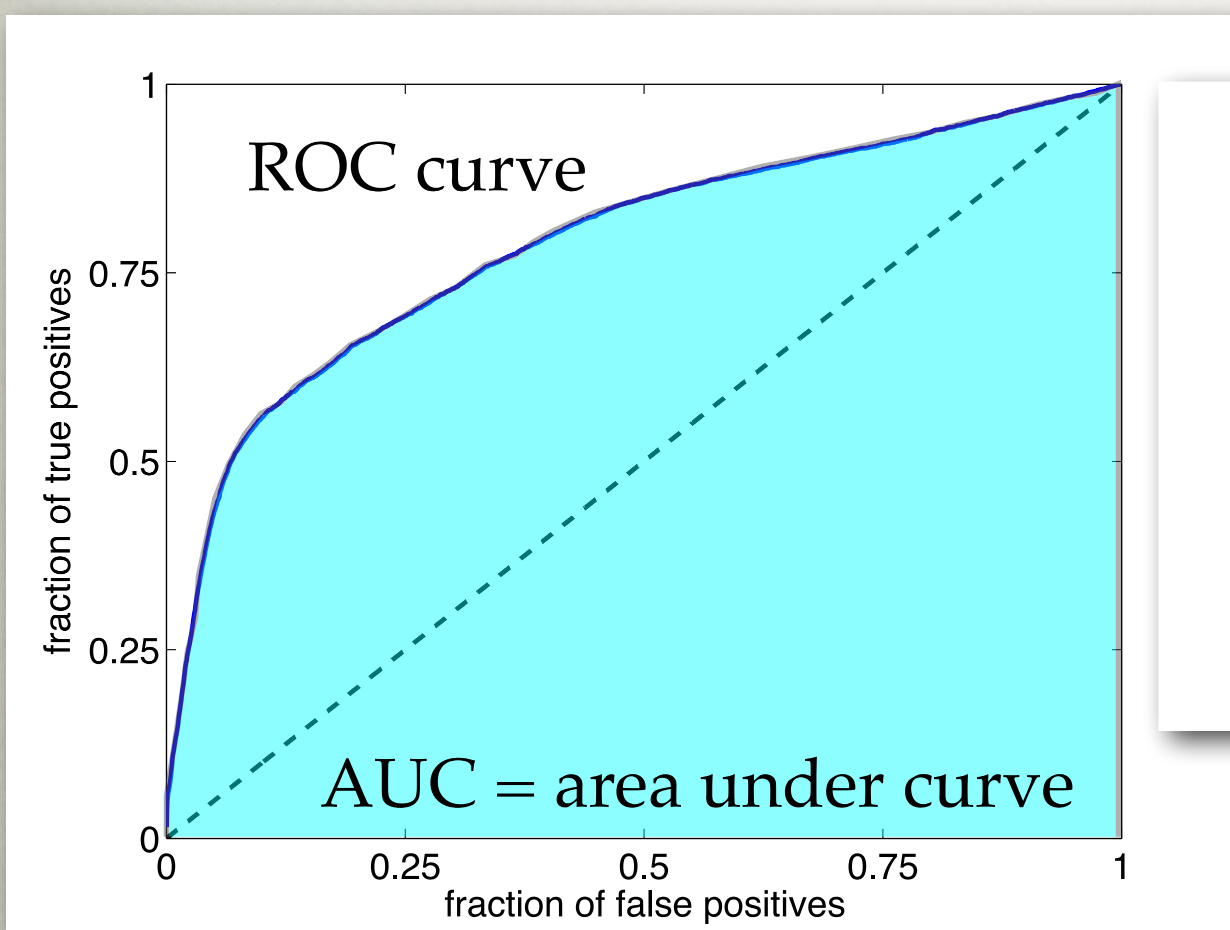
- Given incomplete graph G
- run MCMC to equilibrium
- then, over sampled $\mathcal{D}$, compute average $\langle p_r \rangle$ for links $(i, j) \notin G$
- predict links with high $\langle p_r \rangle$ values are missing

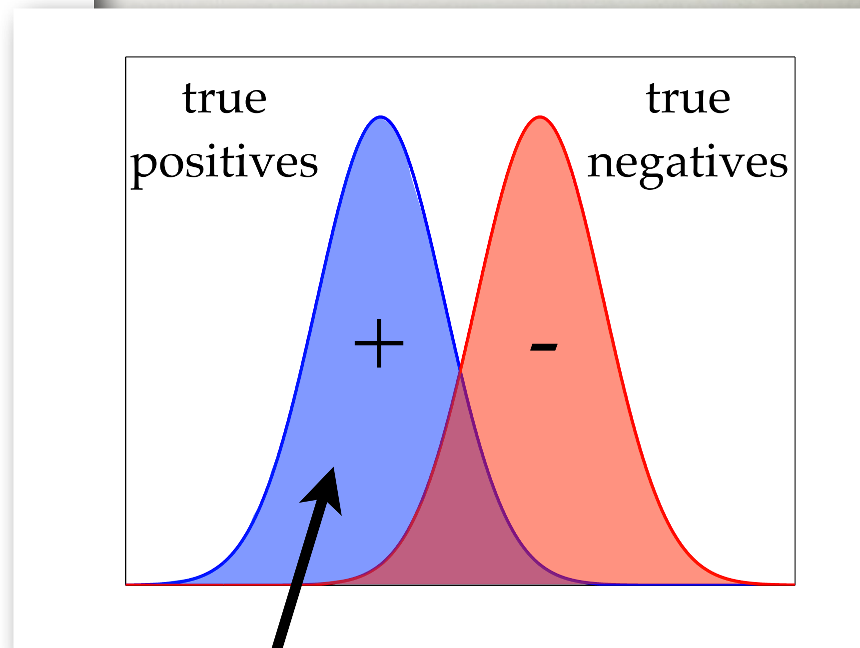
Test via leave-*k*-out cross-validation

perfect accuracy: AUC = 1

no better than chance: AUC = 1/2

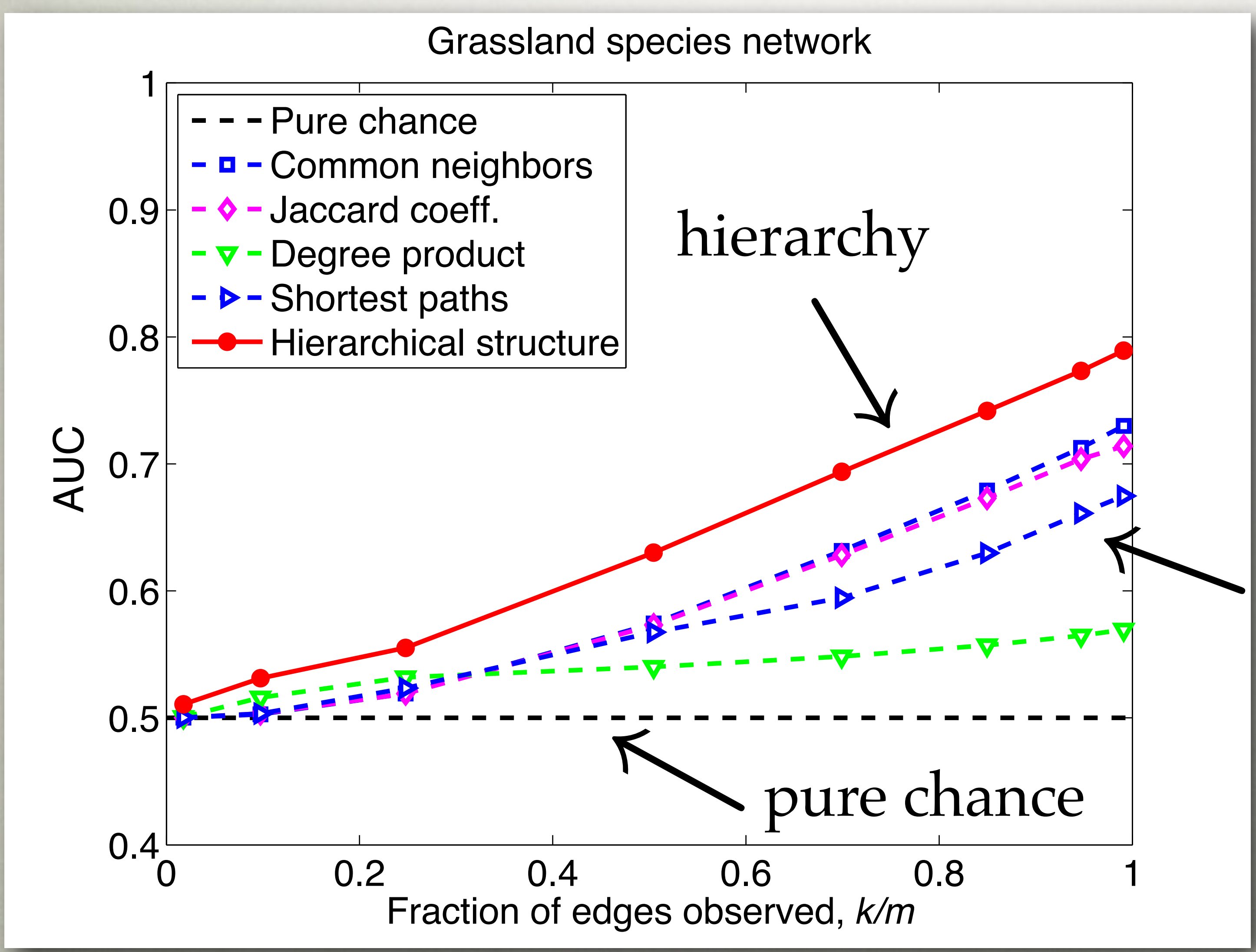
Scoring the Predictions

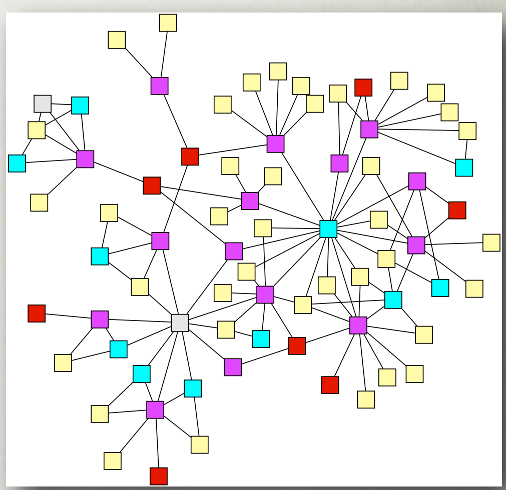




AUC =
Pr(distinguish
+ from -)

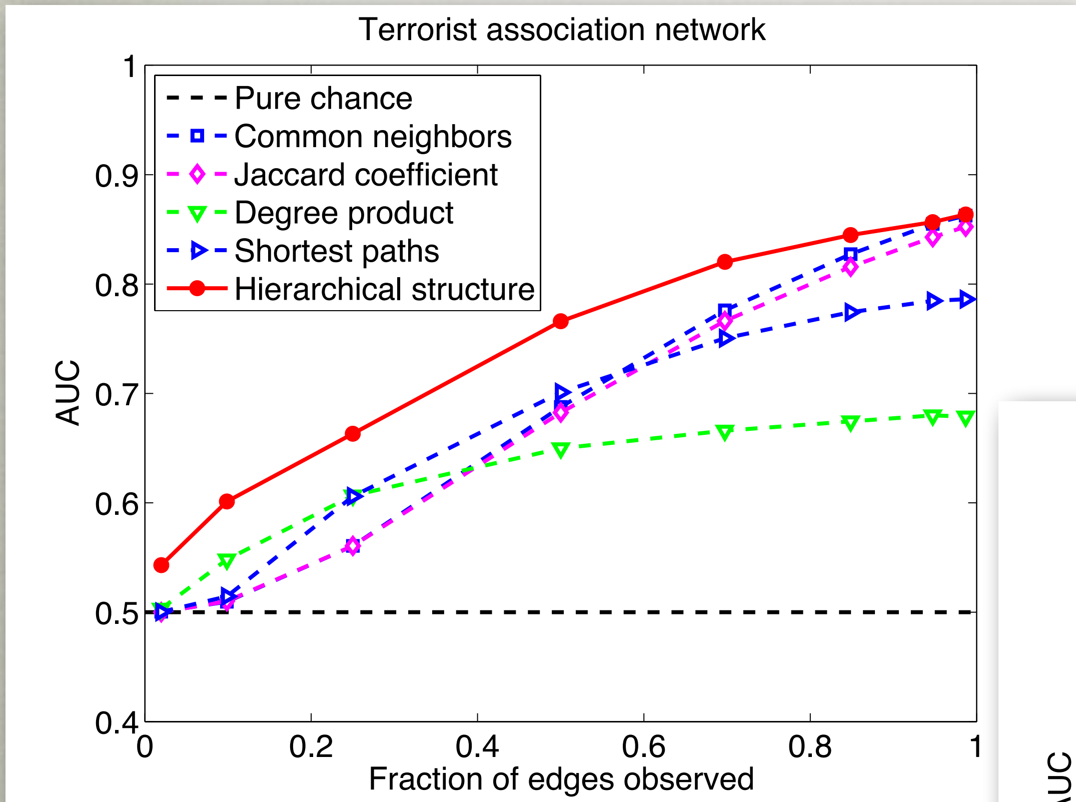
Performance 1

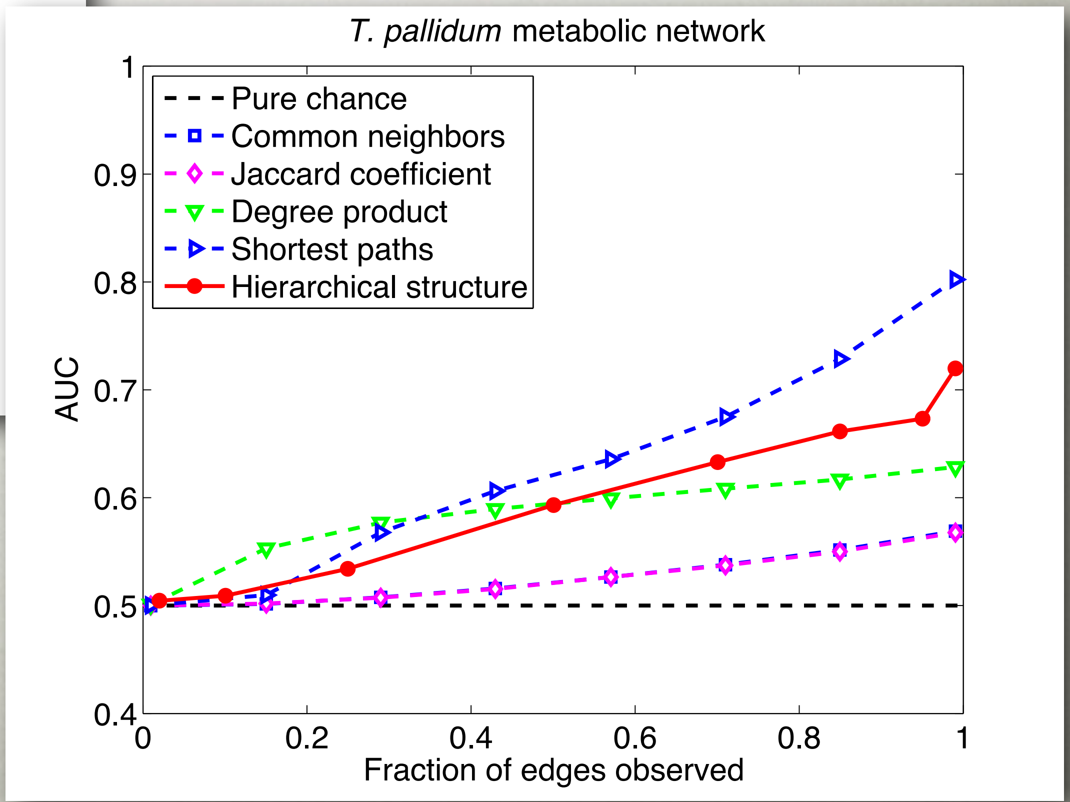




simple predictors

Performance 2





Some Final Thoughts

- what processes create these hierarchical structures?
- scaling up the running time from $O(n^2)$?
- active learning
- generalization to weighted, directed edges
- generalization to non-Poisson distributions