Networks & Hierarchies

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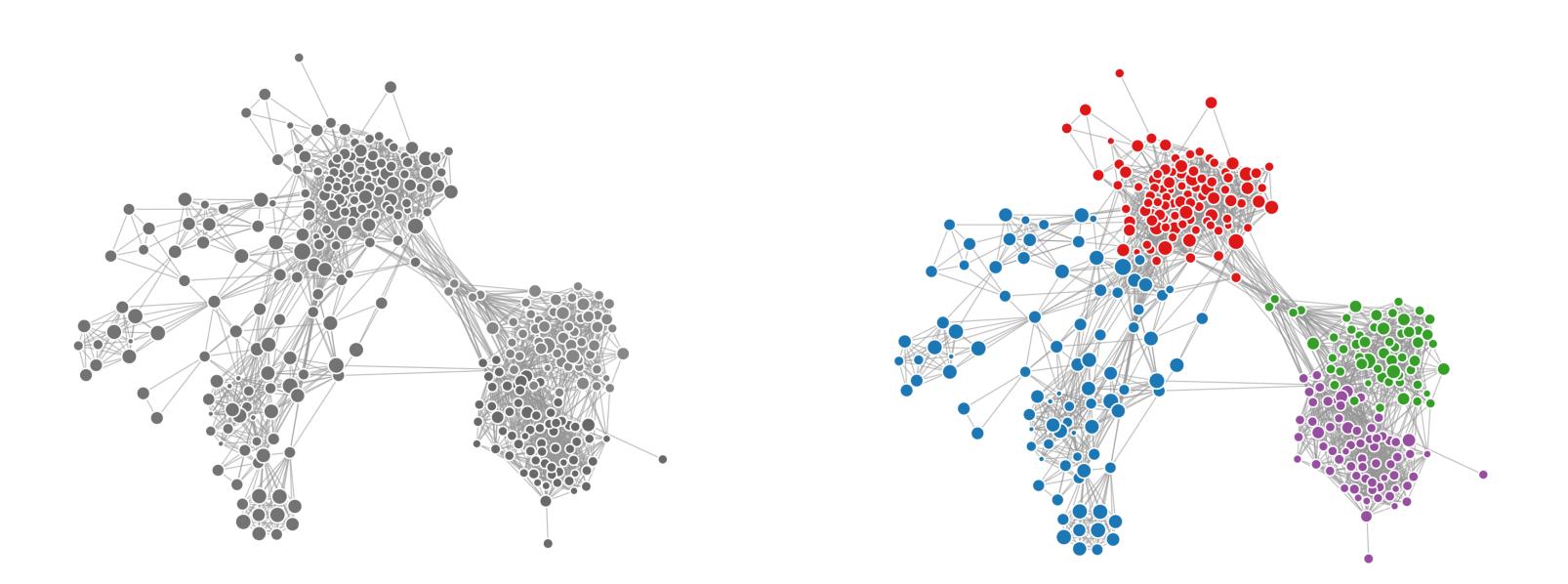
daniel.larremore@colorado.edu @danlarremore

Goals for these two lectures:

- 1. Why do we look for large-scale structure? 🤥
- 2. **How** do we find linear hierarchies? (2)
- 3. Where can we read more details?

Simplicity is a great virtue but it requires hard work to achieve it and education to appreciate it. And to make matters worse: complexity sells better.

E. W. Dijkstra



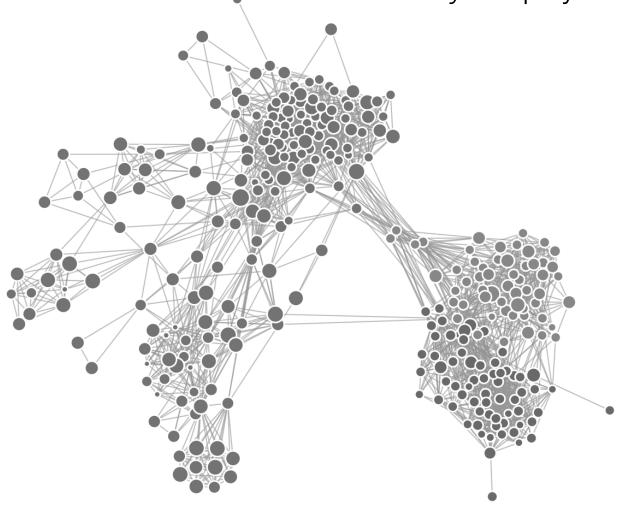
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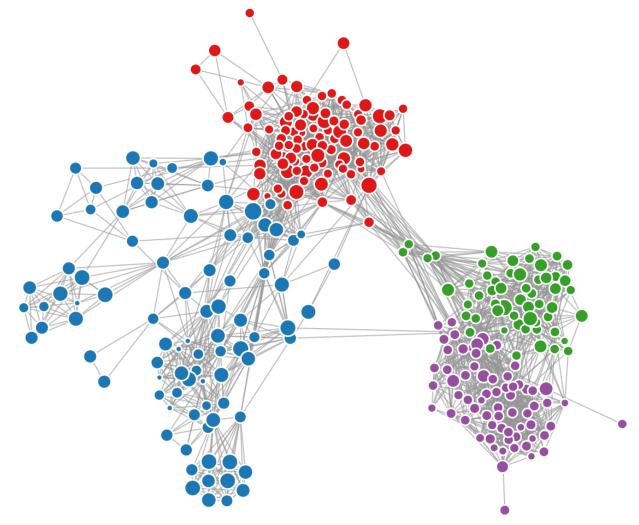
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We can interpret this in two ways:

The Cynic: Pictures of networks can be *really cool* but our goal is to do good science, not make pretty pictures.

The Scientist: The most beautiful science is when we correctly simplify a complex system.





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We define these large-scale structures—models, really—to compress complex networks.

Goal: understanding, not a list of parts and dimensions



Finding large-scale structures is the same as anything else:

We want a simplified model of something very complicated.

We want to know what the important pieces are, and how they fit together.

Many uses for models of large-scale structure

Treat the network like a system:

Extrapolation. Make predictions for as-yet unseen nodes (in "space" or time). **Interpolation**. Identify missing links.

Generalization. Nodes of this type are like others of the same type.

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Treat the network like a means to an end; an intermediate data structure:

Useful division. Need groups so that we can assign treatments in an A/B test. **Simplification**. Downstream regression model needs ranks or groups.

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The idea of rankings—pervasive!

Assumptions:

- 1. Competitors have some intrinsic quality (or vector of qualities).
- 2. Interactions can (stochastically) reveal differences in qualities.
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Systems of dominance

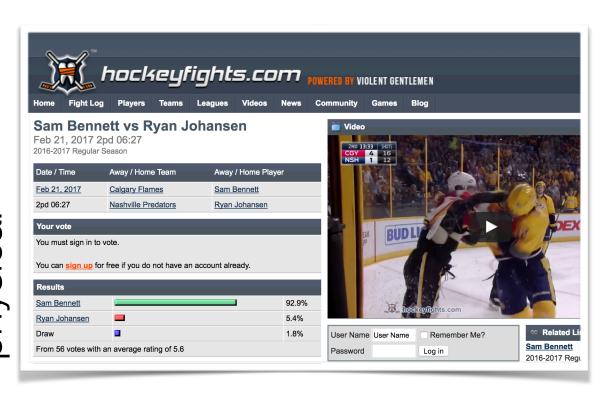


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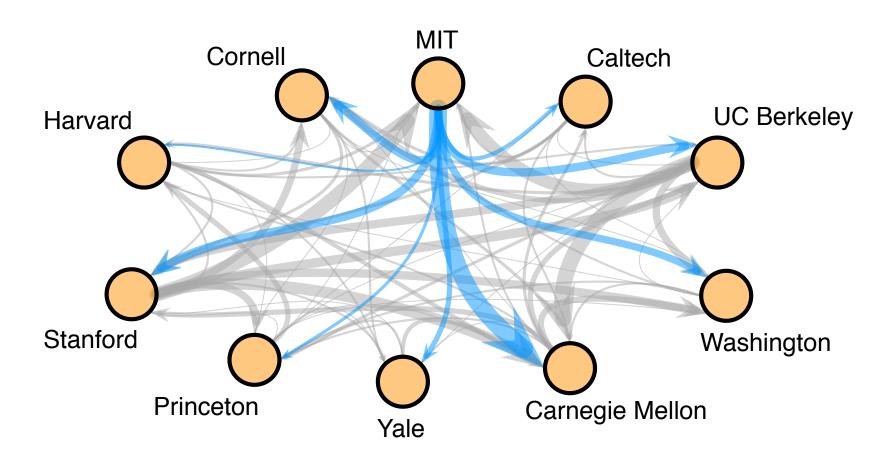
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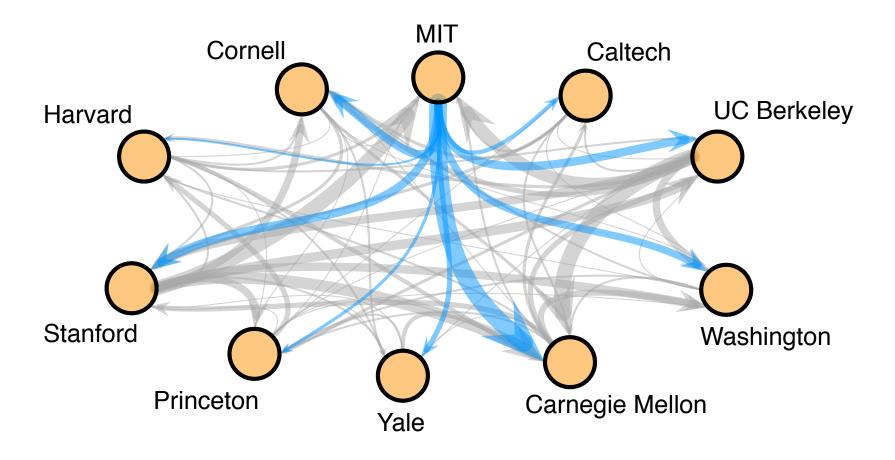


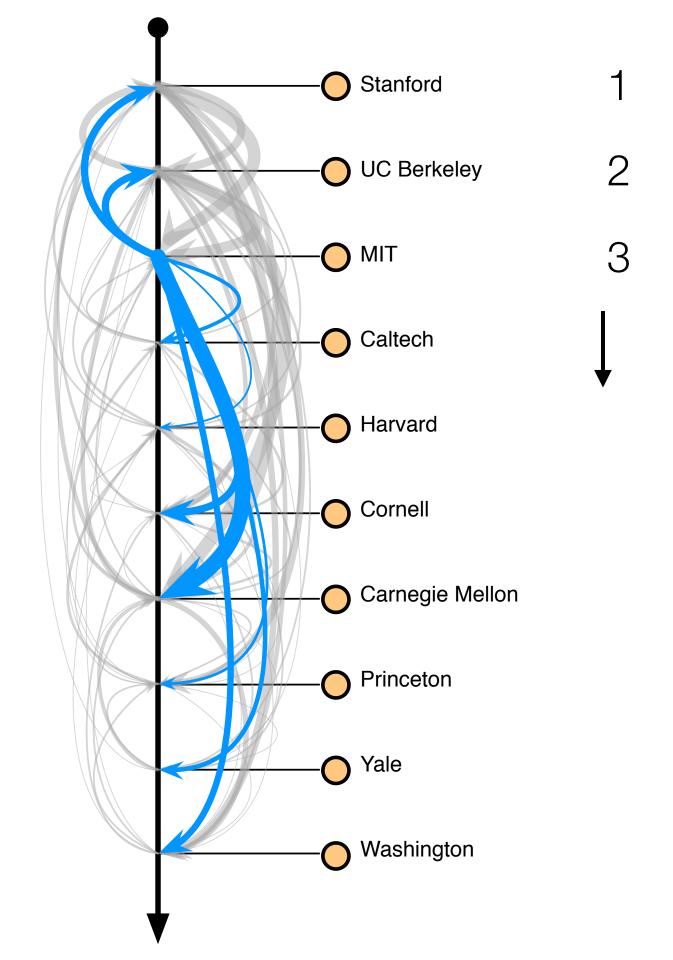
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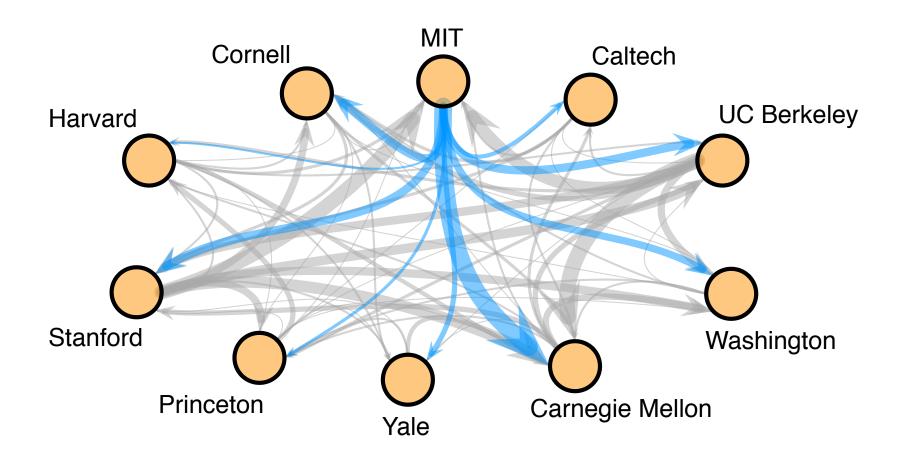


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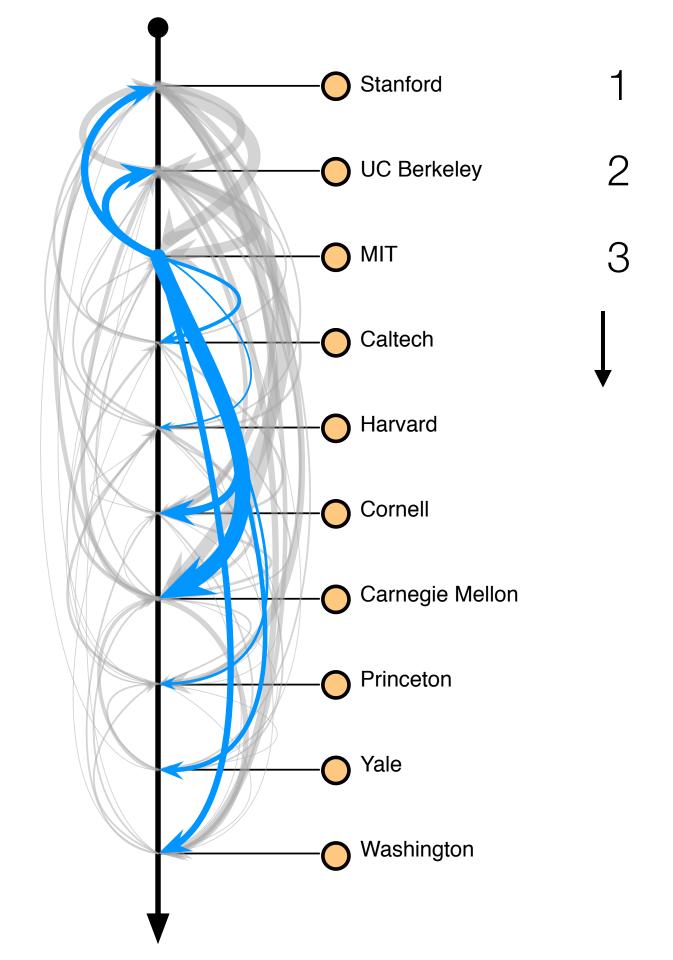


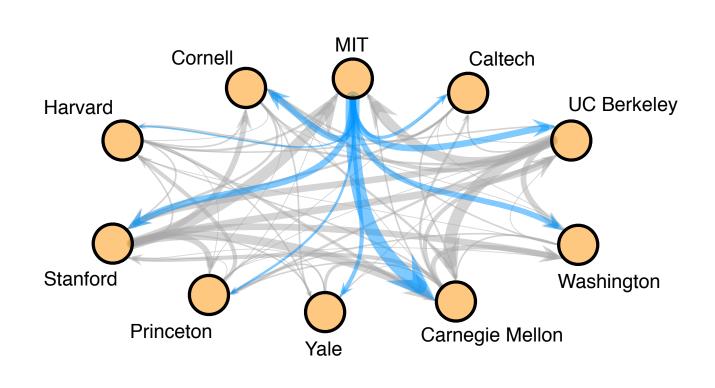




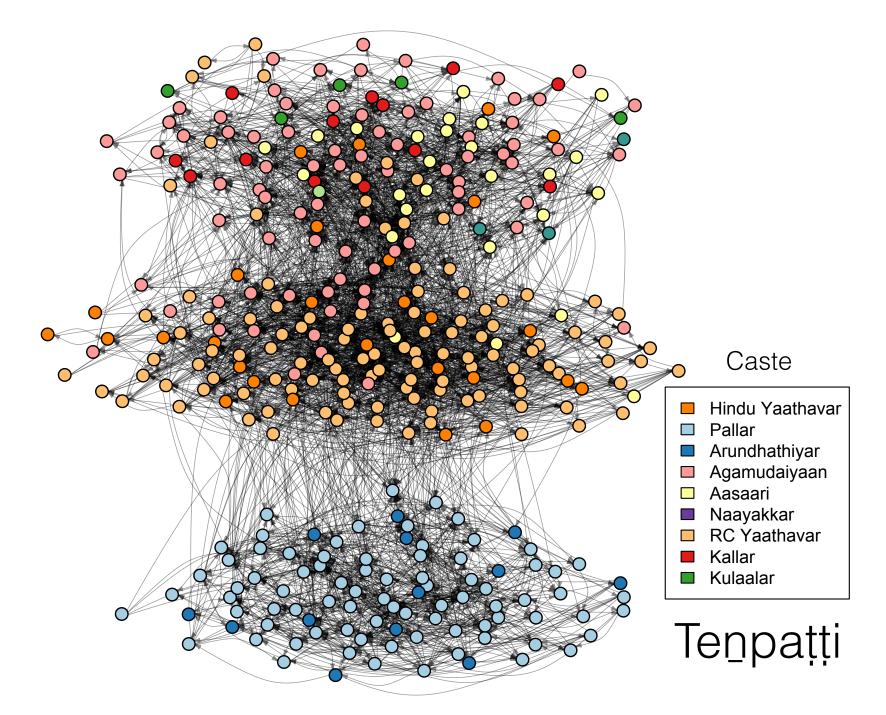
Assumptions:

- 1. Endorsers have some intrinsic quality.
- 2. Interactions can reveal differences in qualities.
- 3. Endorsements are pair-wise.





Latent position can be revealed by dominance or endorsement interactions.



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Its adjacency matrix is A.

 $A_{ij} = A_{i \rightarrow j}$ means i beat j or i was endorsed by j

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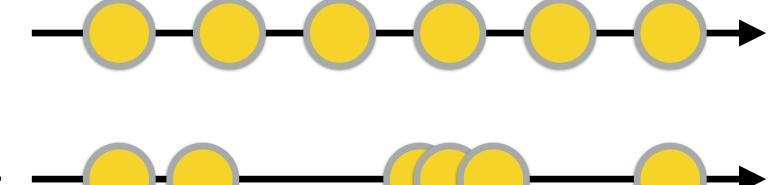
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Alternative problem: Which items should be compared next in order to most/best resolve our estimate of the ranks? (sequential tournament design)

Embeddings vs Orderings

Ordering place the nodes in order:



Embedding assigns a position to each node:



Which one should I use?

- > Depends on the use case.
 - > Is it possible for two nodes to occupy the same rank or position? If so, an embedding is more appropriate. Also better when meaning of 1-rank Δ varies.
 - > Consider that you can always go from an embedding to an ordering, if you have a rule for breaking ties.

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Therefore if we have a whole list of outcomes, we can try to find a total ordering that breaks as few of these implications as possible.

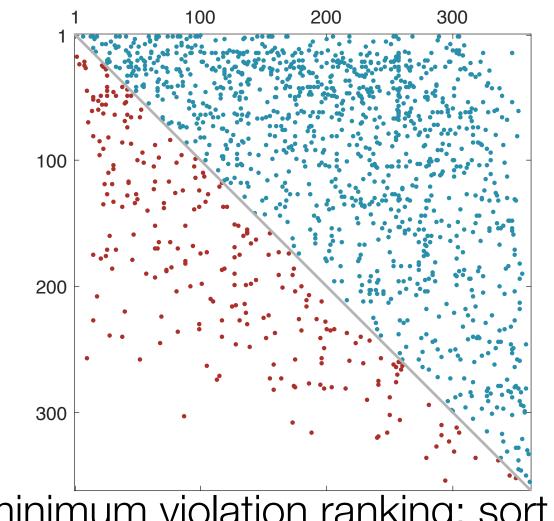
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 A_{ij} = number of times that *i* beat *j*.



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- 6. Repeat until....?

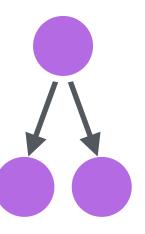
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Notes:

- * The number of violations is non-increasing over time.
- * There may be no unique minimum. Consider this scenario:



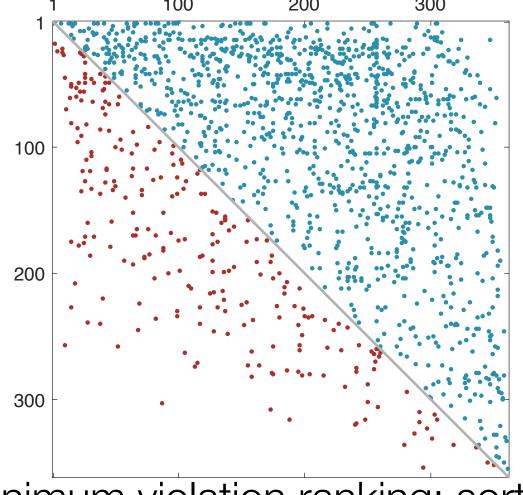
MVR: non-unique & rough optimization landscape

There is no guarantee of a unique minimizing ranking s.

Space of ordinal rankings has n! elements—usually use MCMC to search.

Slow.

Ordinal. No ties. No interpretability of rank differences.



minimum violation ranking: sort A.

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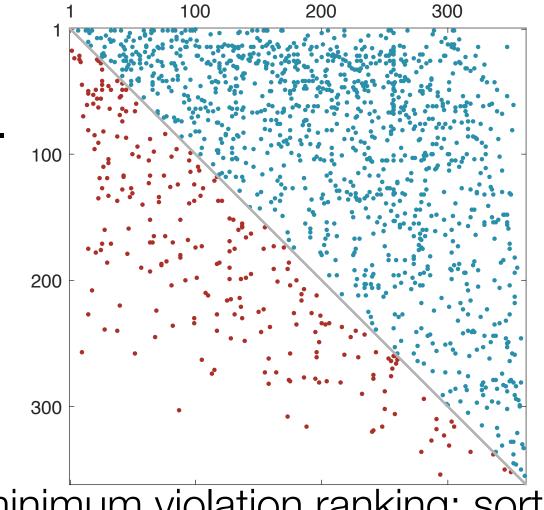
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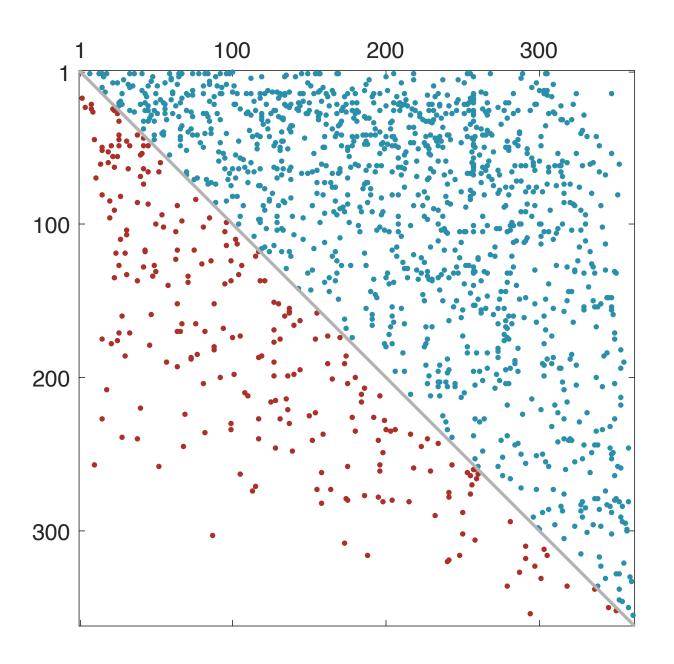
What are other premises on which we can base a ranking model?



minimum violation ranking: sort A.

Embeddings and Orderings 1: MVR & Agony

What if you allowed for **ties** and then ran Minimum Violation Ranking (MVR)? What would happen?

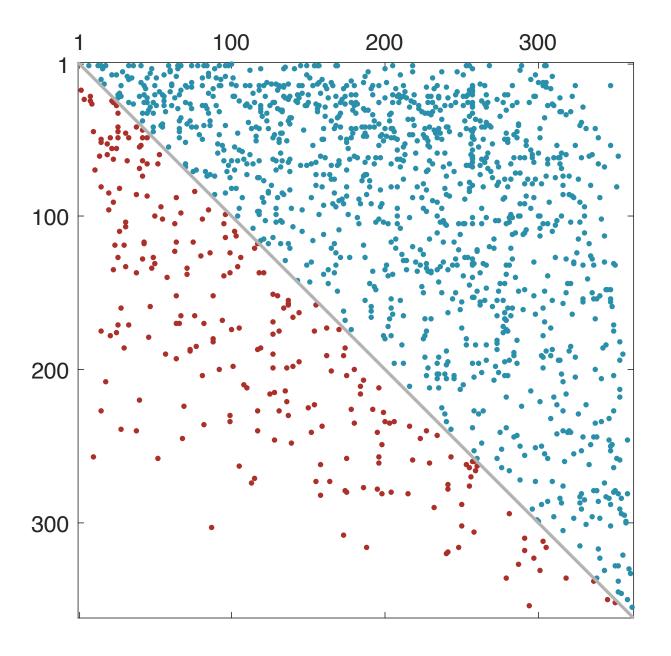


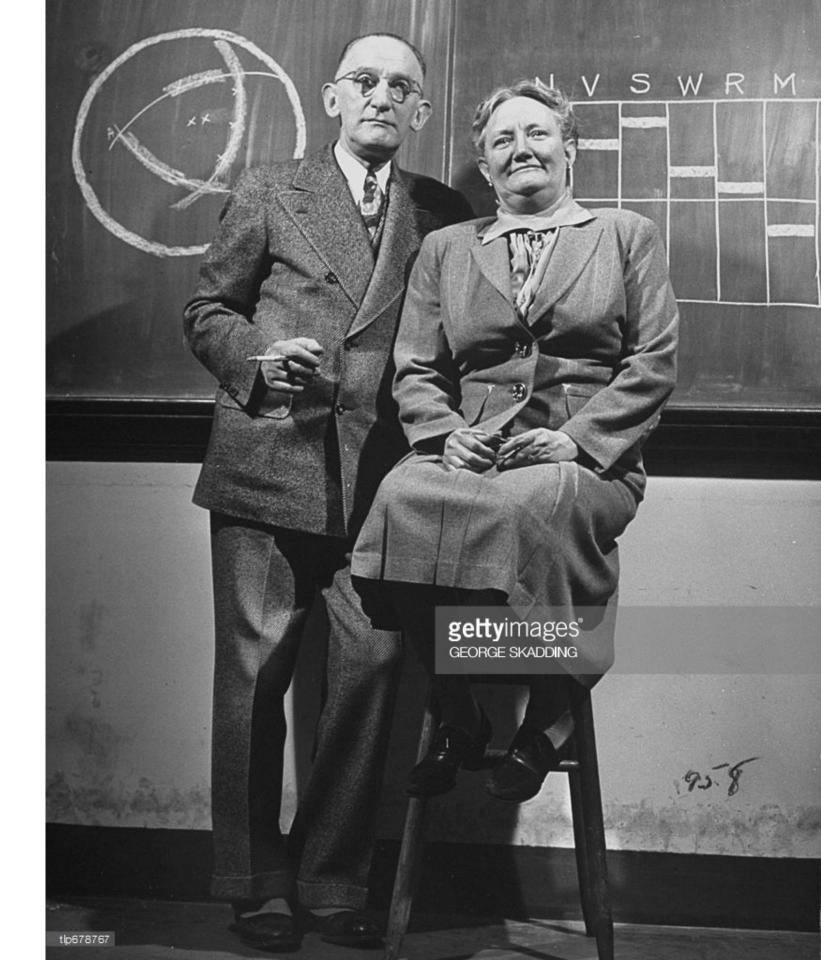
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MVR: uniform cost (1 per edge).

Agony: generic cost function.
for example, difference in ranks.

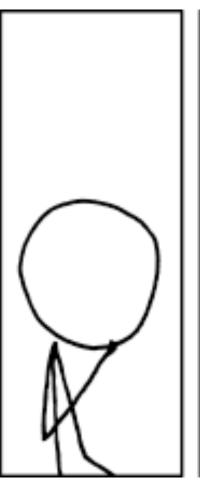


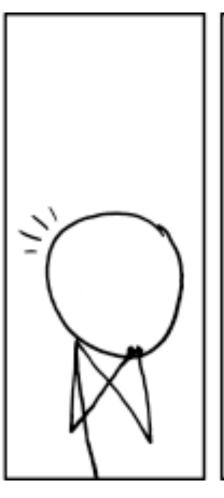






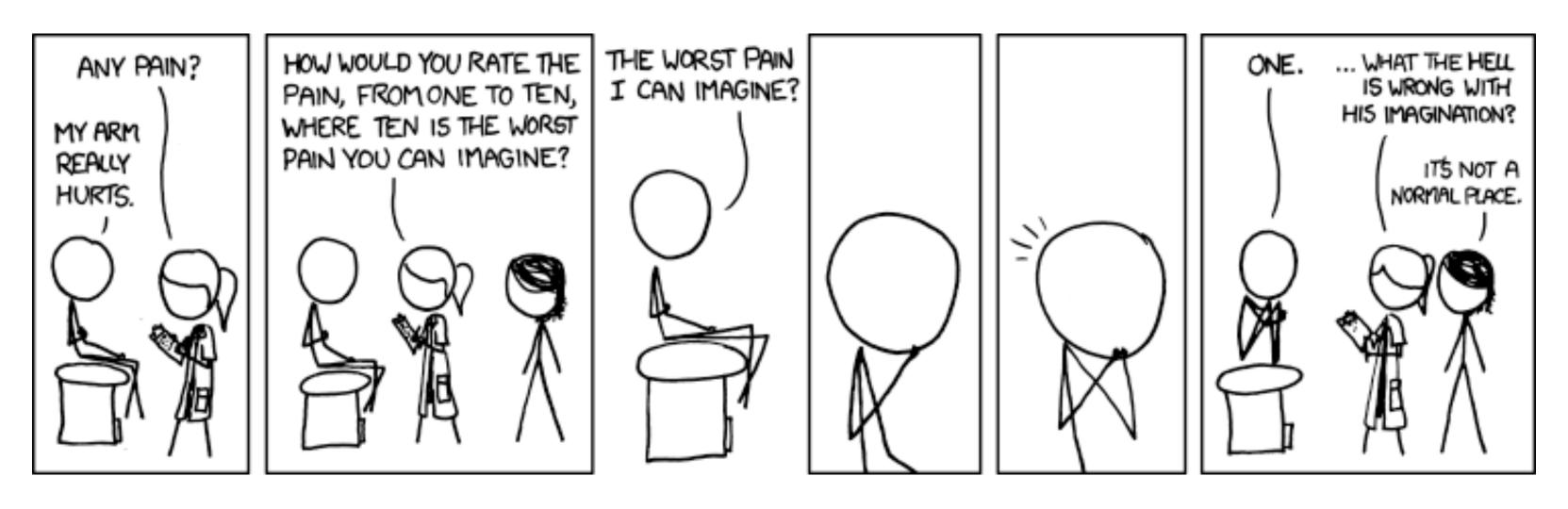








https://xkcd.com/883/



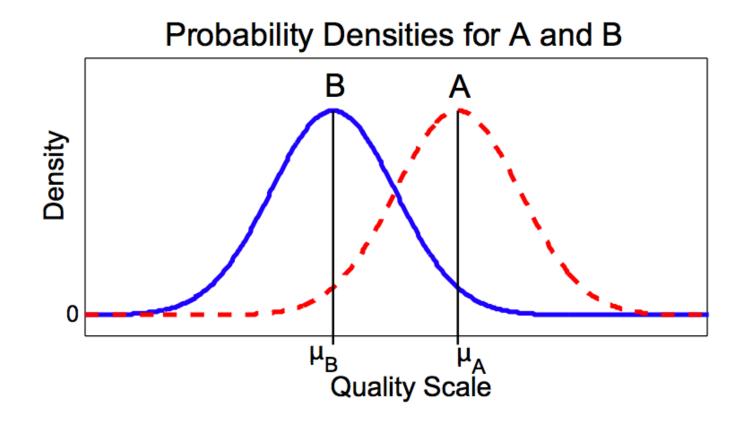
Instead of rating everything from 1 to 10, try paired comparisons.

Do you prefer i or j?

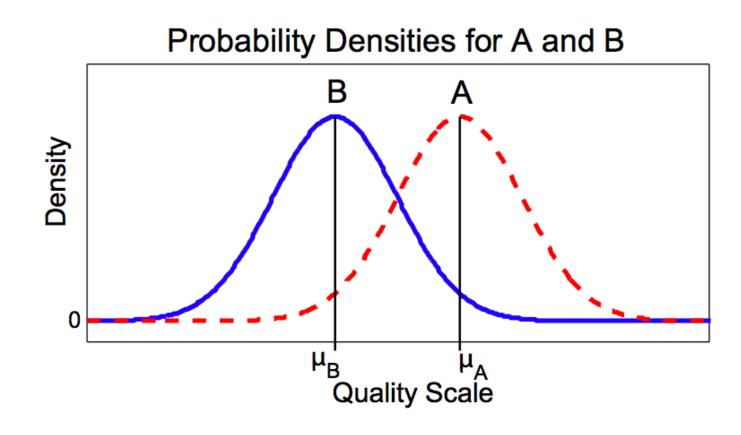
Why? Consider: My 3 is not your 3. What is 1 and what is 10?

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Thurstone: items have quality distributions. When a person judges whether A is better than B they draw from A's distribution and from B's distribution and see which is higher.



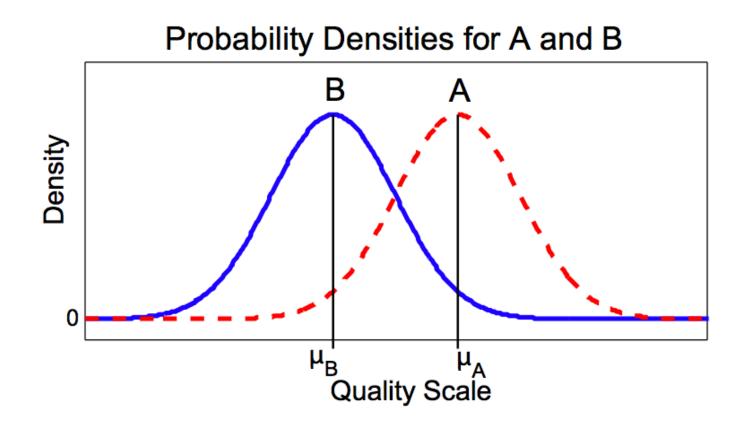
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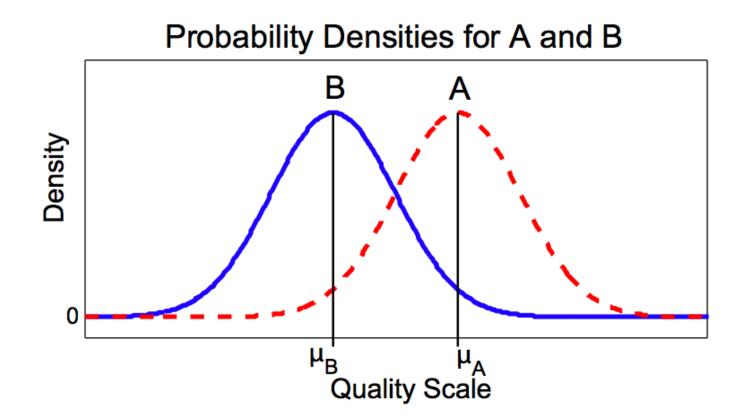


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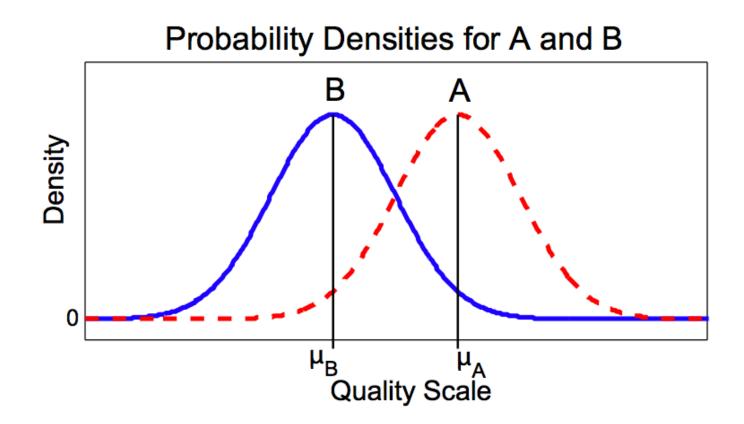
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Where $\Phi^{-1}(x)$ is the inverse CDF of standard normal, a.k.a. the *probit*.

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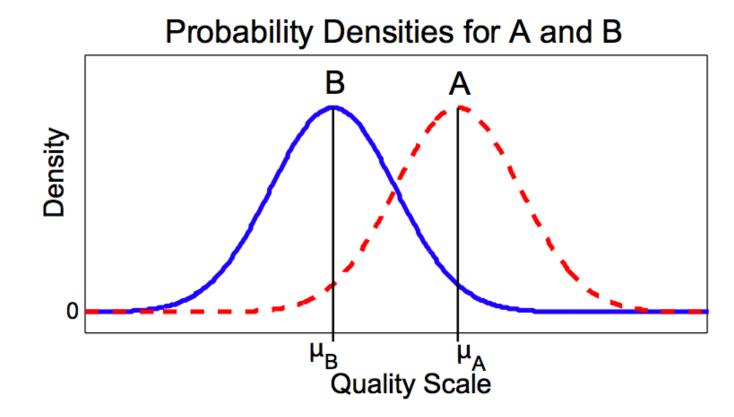
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Powerful idea: lots of pairwise comparisons = estimates of all the qualities! An embedding!

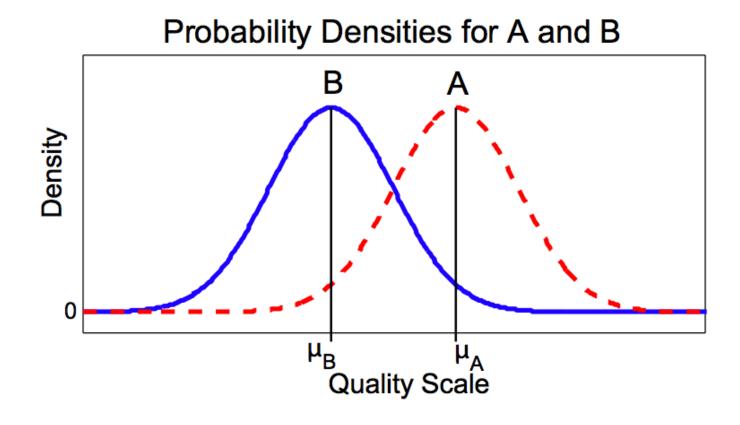
Key: pairwise comparisons = directed network. i preferred to $j = i \rightarrow j$

Finding the qualities of items from pairwise comparisons = Finding embedding of nodes.

Bradley-Terry & Luce: items have quality distributions. When a person judges whether A is better than B they draw from A's and from B's distribution and see which is higher.

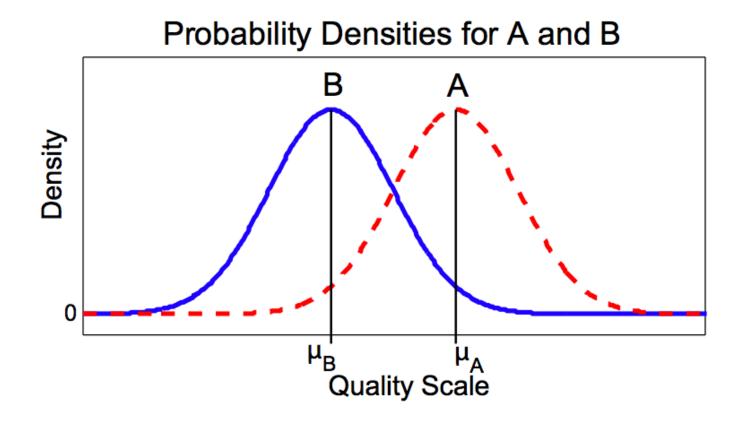


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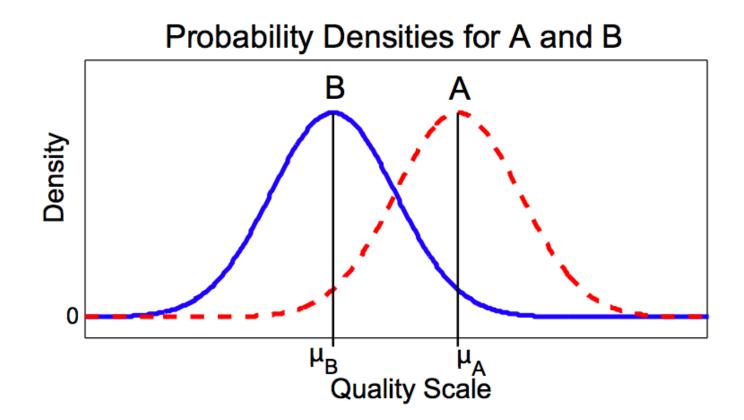
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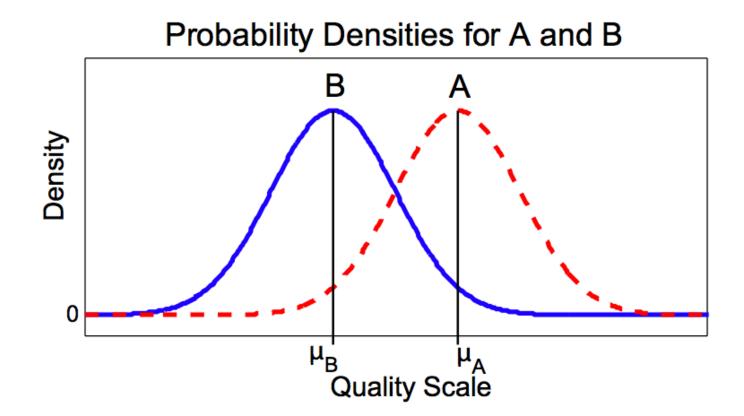
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Introducing: non-transitive dice!

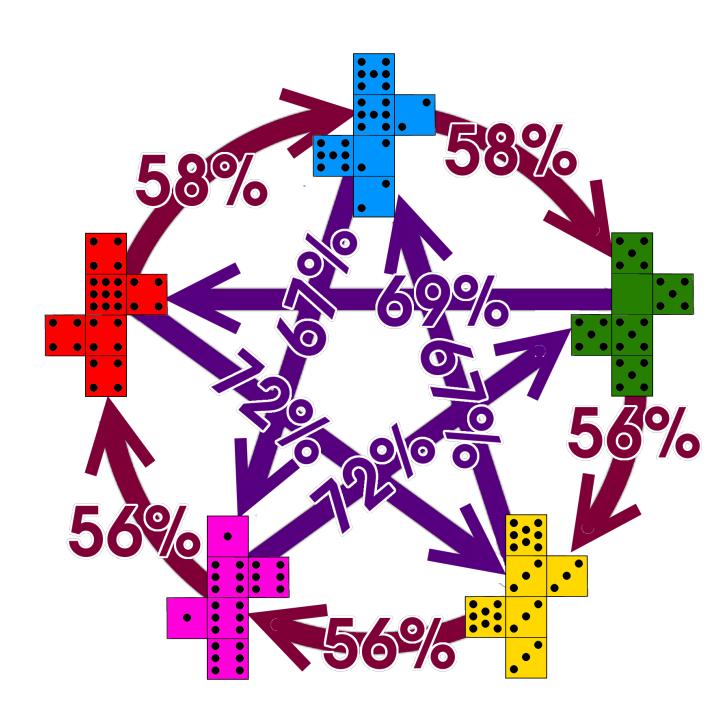
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- 3 (or more) dice {A,B,C}
- faces chosen so that they have the property:
 - A>B more than half the time.
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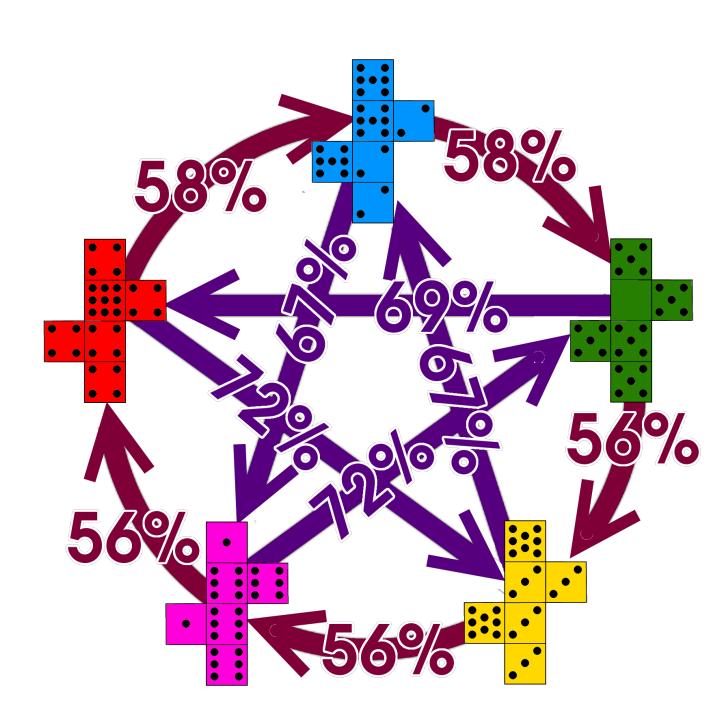


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A great gift for your favorite nerd's desk! Go to the makerspace and laserbeam your own!



Bradley-Terry-Luce

These methods embed items or players in a 1D space.

- Provably avoids non-transitive properties
- Great when lots of data per interaction.

Pairwise ranking is really nice for ordering large sets of preferences too, and this model specifically models the probability that the preference will be for *i* over *j*.

Iterative algorithms exist. Needs a little regularization so the winningest winners don't fly off to infinity.

$$P(i \to j) = \frac{\gamma_i}{\gamma_i + \gamma_j}$$

Introductory tutorial:

http://mayagupta.org/publications/PairedComparisonTutorialTsukidaGupta.pdf

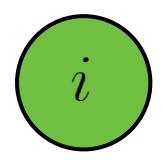
Discrete choice today:

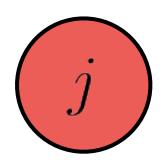
https://web.stanford.edu/~jugander/papers/nips16-pcmc-slides.pdf



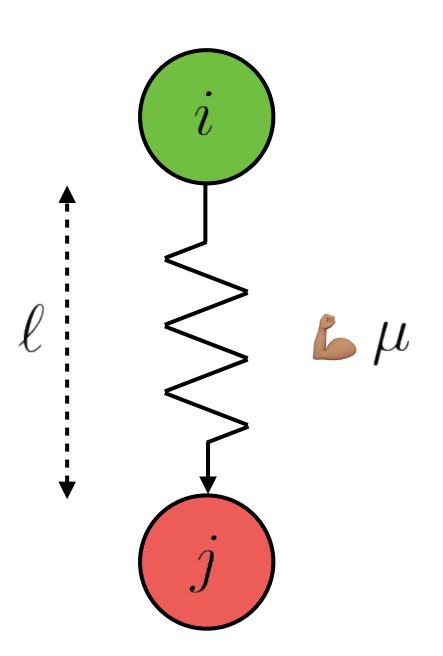
Embeddings & Orderings 2: SpringRank

Each directed edge = directed spring

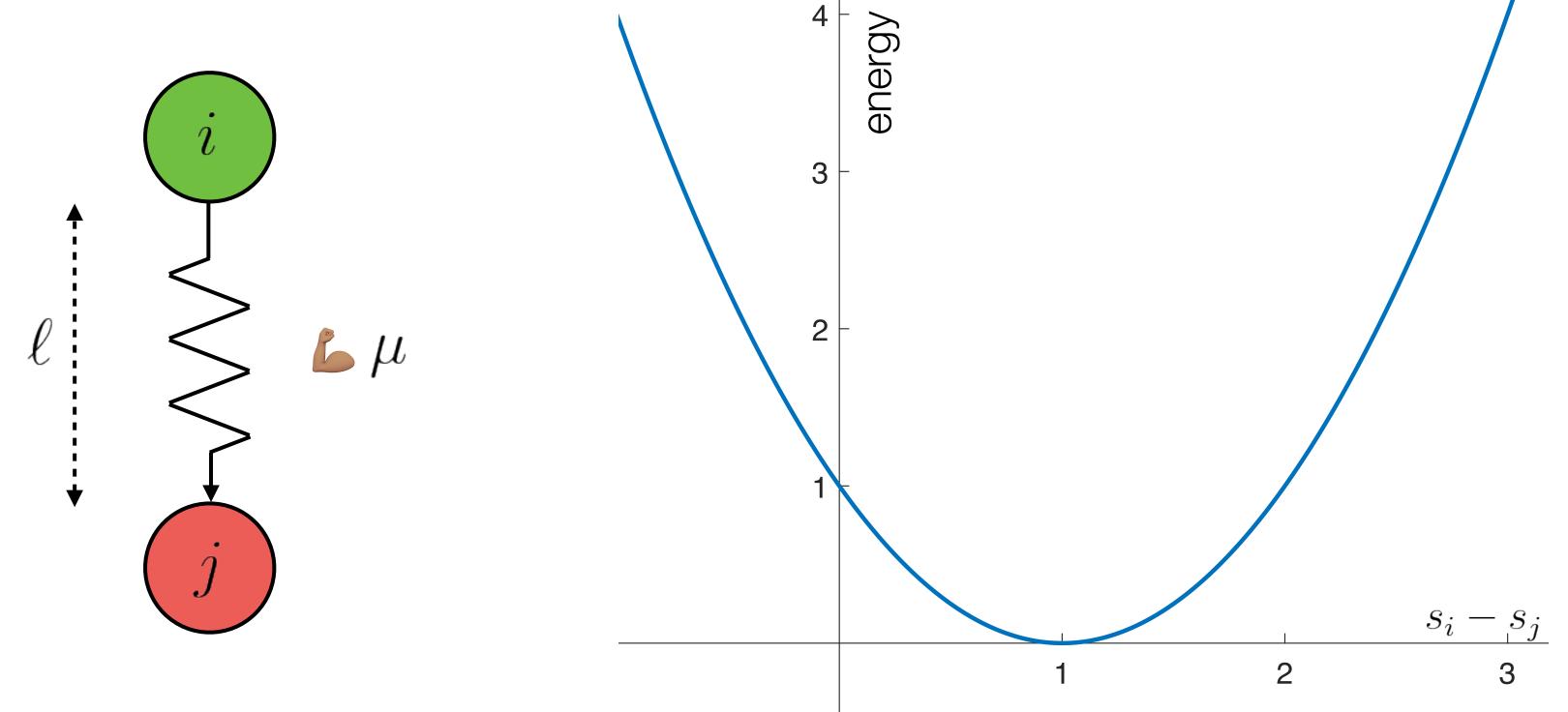


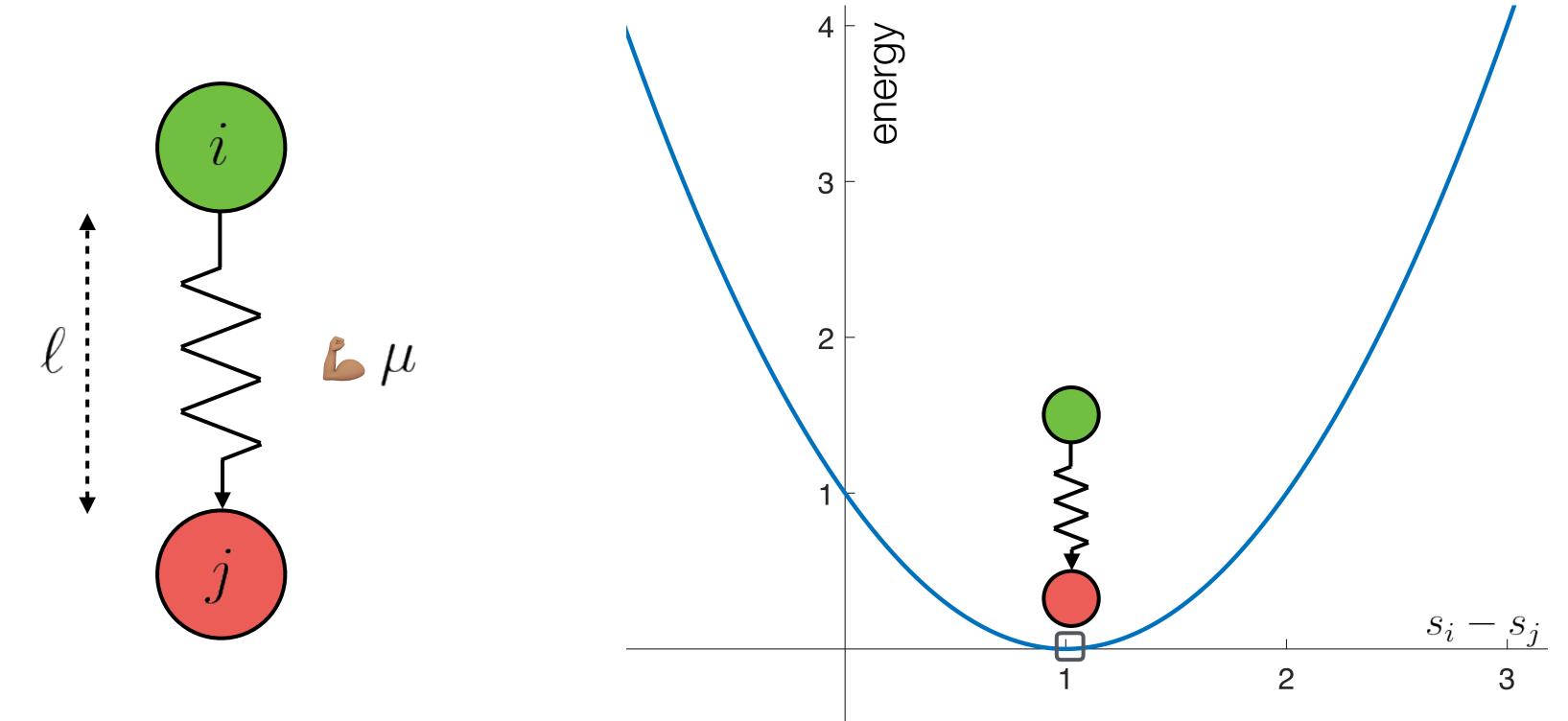


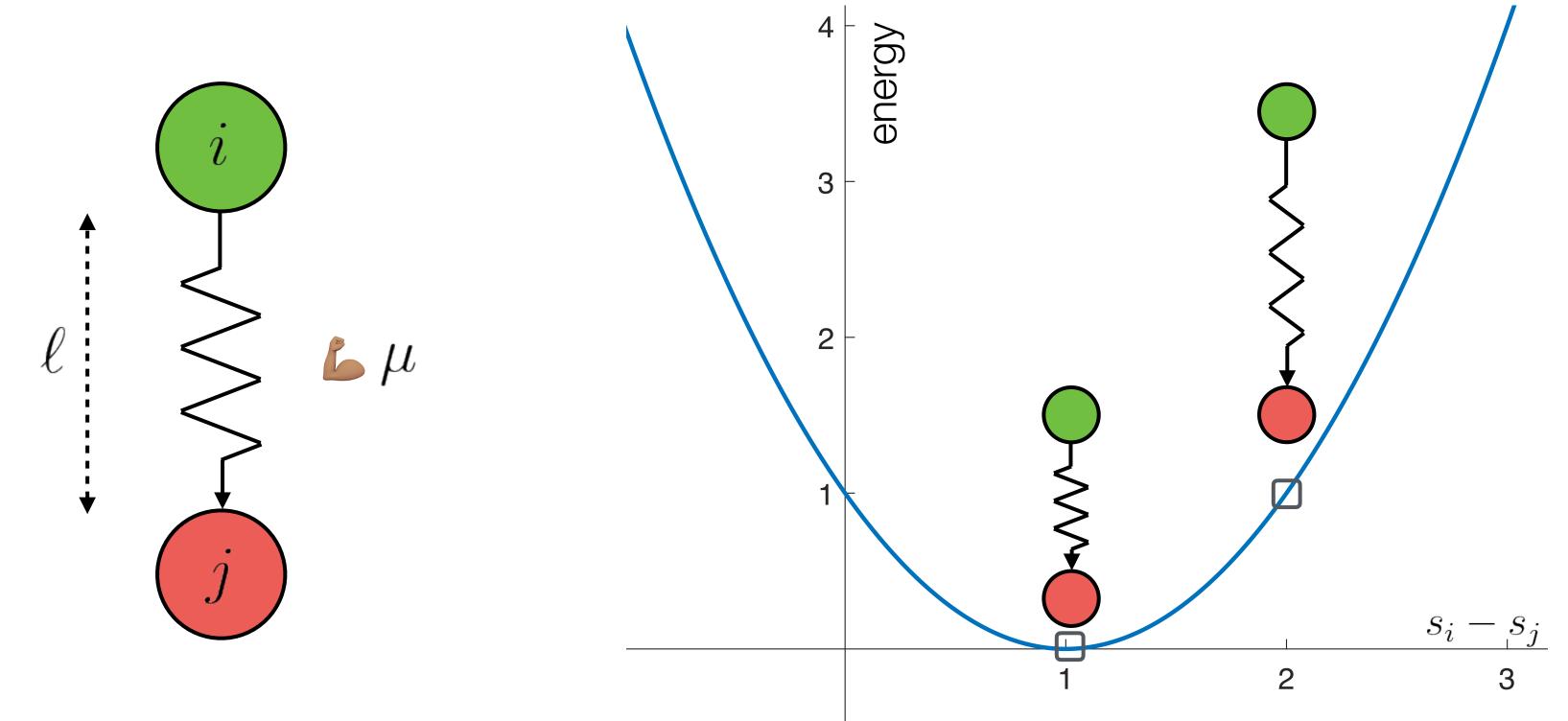
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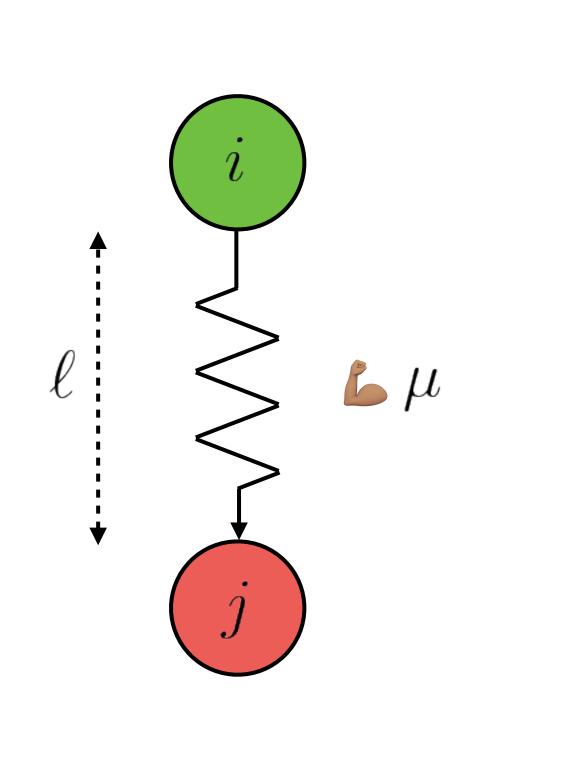


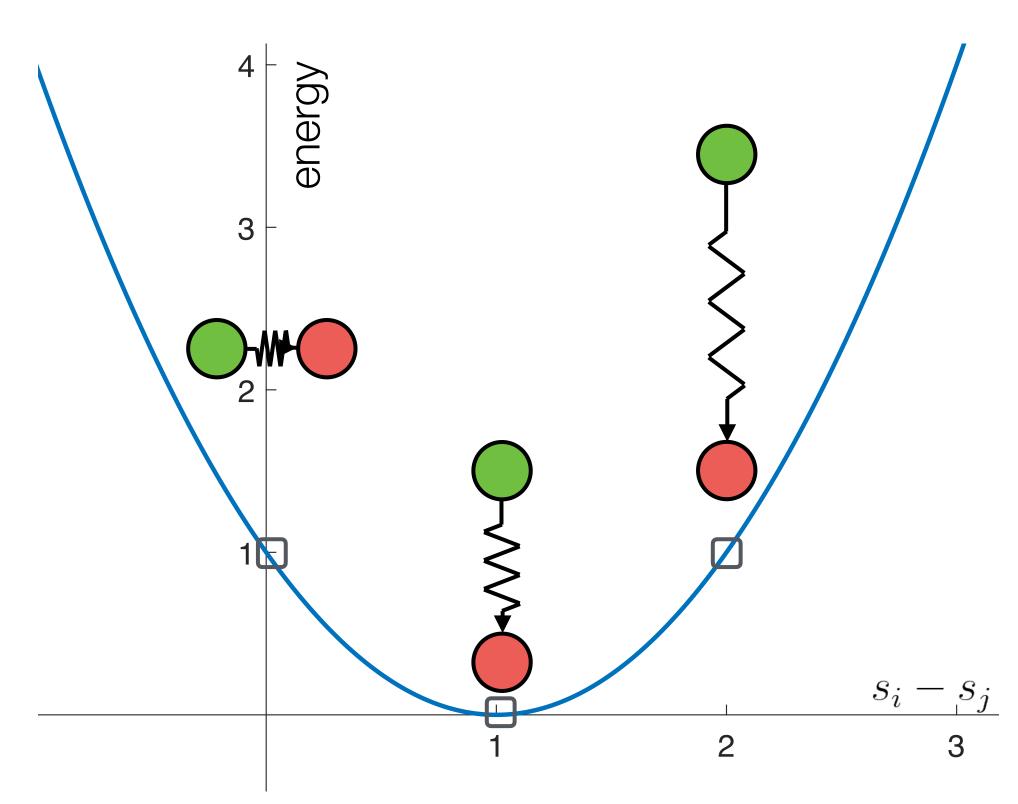
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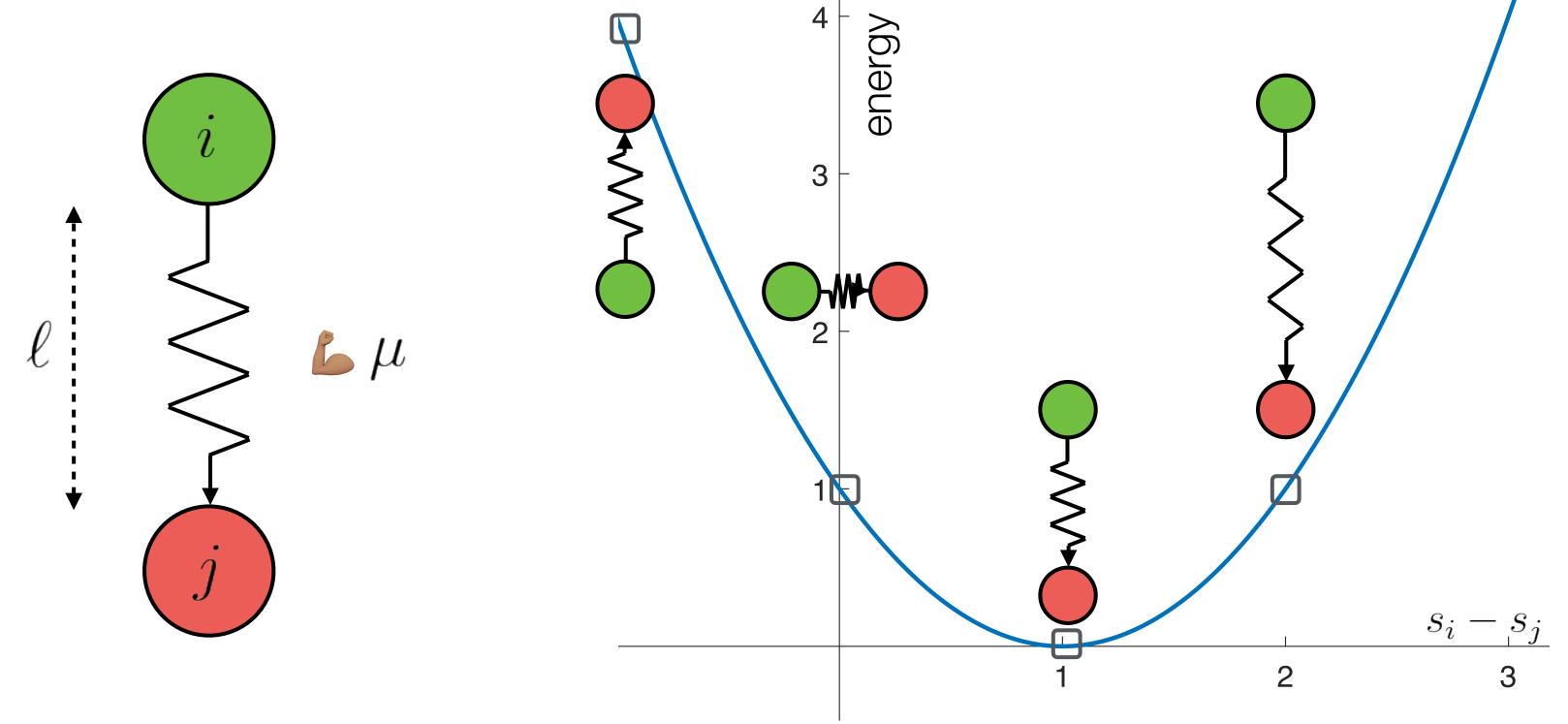












$$(s_i - s_j - 1)^2$$

$$A_{ij}(s_i - s_j - 1)^2$$

$$\sum_{i,j=1}^{N} A_{ij} (s_i - s_j - 1)^2$$

$$H(s) = \frac{1}{2} \sum_{i,j=1}^{N} A_{ij} (s_i - s_j - 1)^2$$

Relax and let the springs decide the ranks

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Because the springs are linear, the potential is quadratic.

The SR Hamiltonian is *convex* in s.

$$\nabla H(s) = 0$$

The solution is unique...up to an additive constant. (Why?)

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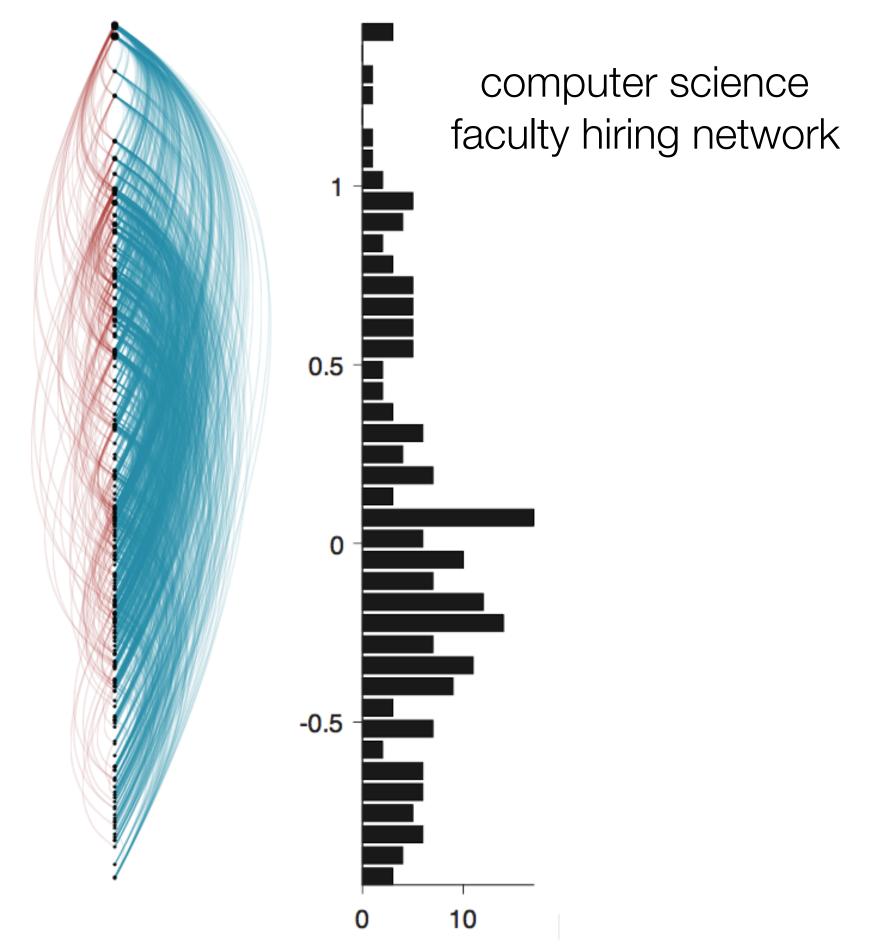
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Notice: the matrix on the left is the *graph Laplacian* of the *undirected* network.

Uniqueness: Set $s_1=0$, min(s)=0, or mean(s)=0. Or use a pseudoinverse. Or regularize.

It works!

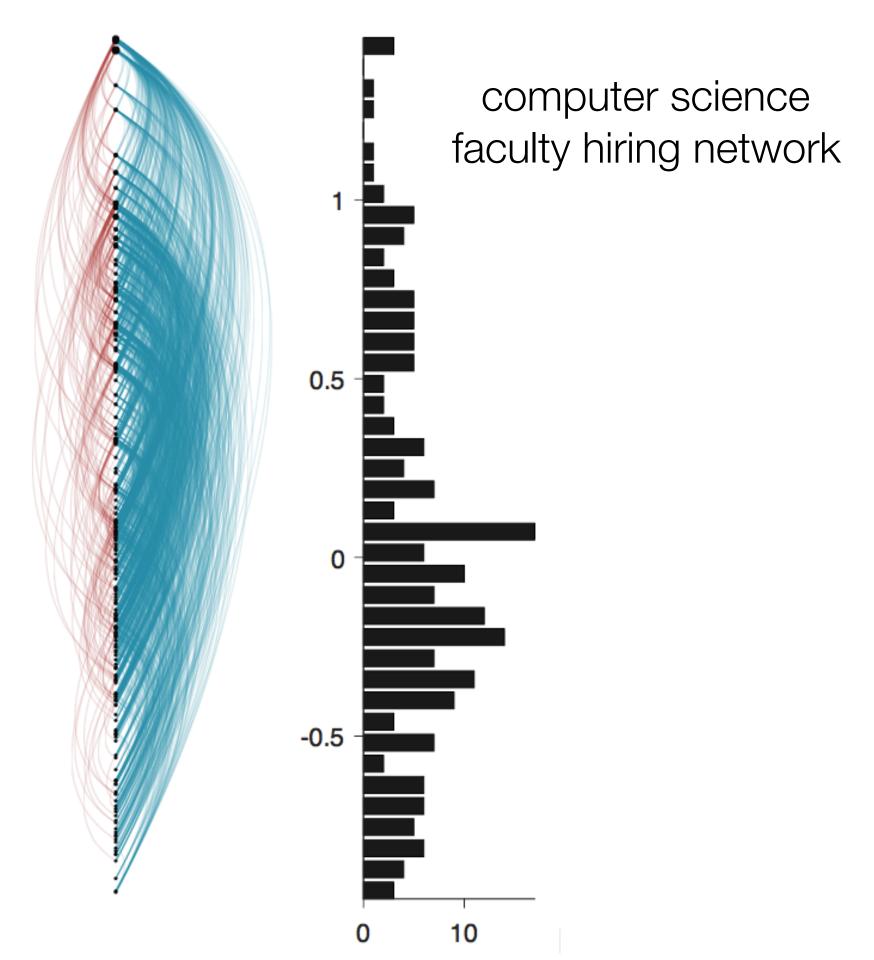


It works!

Real networks tend to be sparse...
our linear algebra problem is sparse...
we can use sparse iterative solvers...
millions of edges in seconds.

Even better: it's a linear-Laplacian system.

Near-linear-time (in |edges|) solutions.



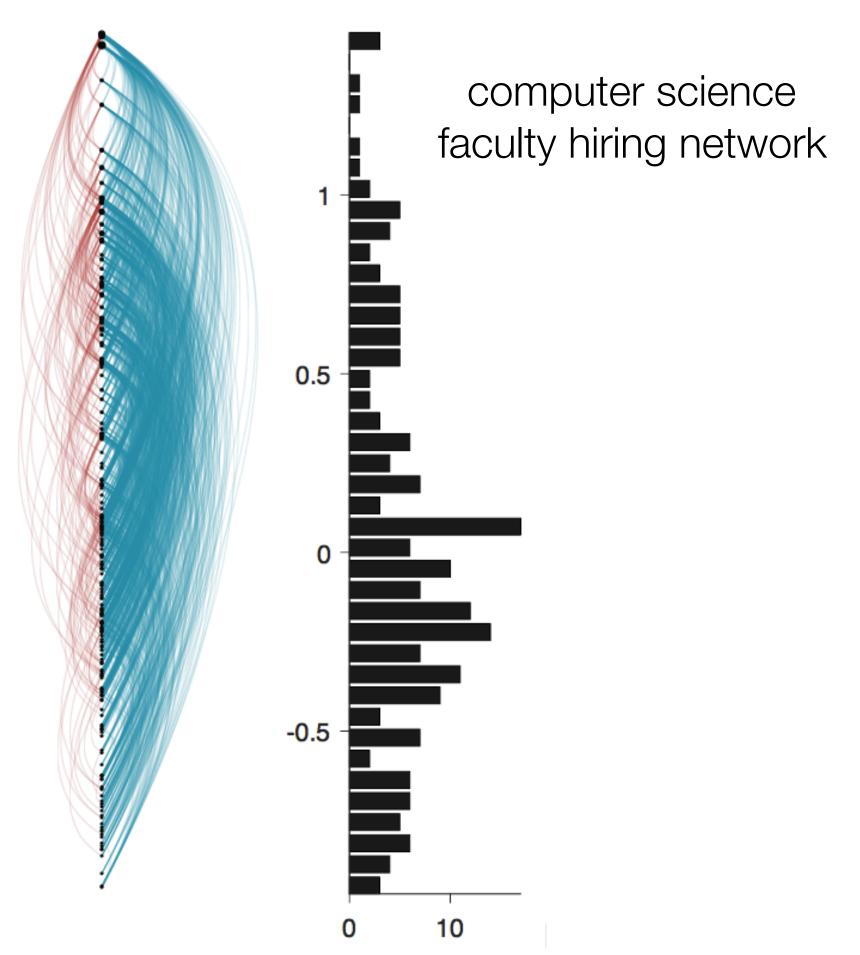
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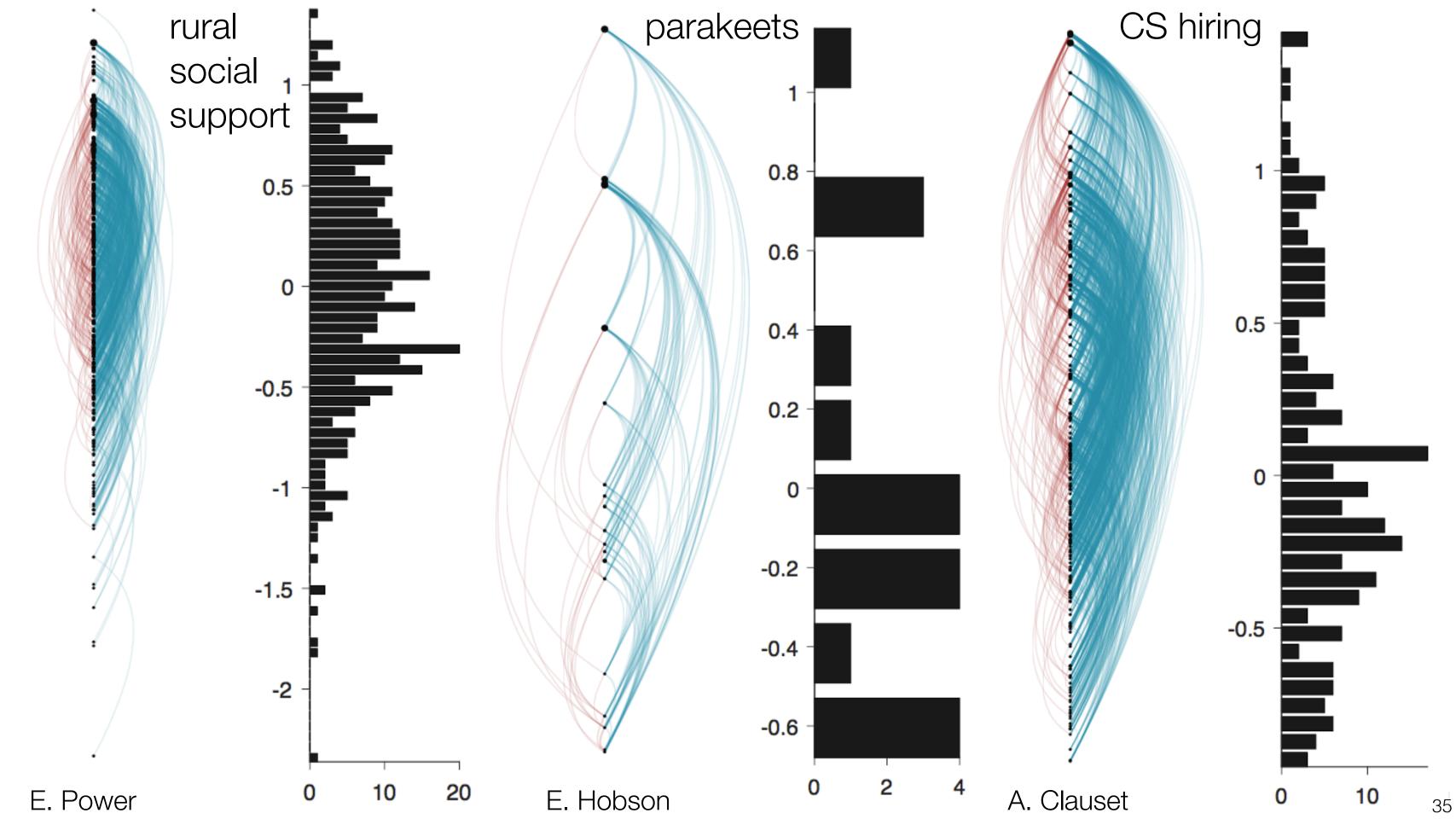
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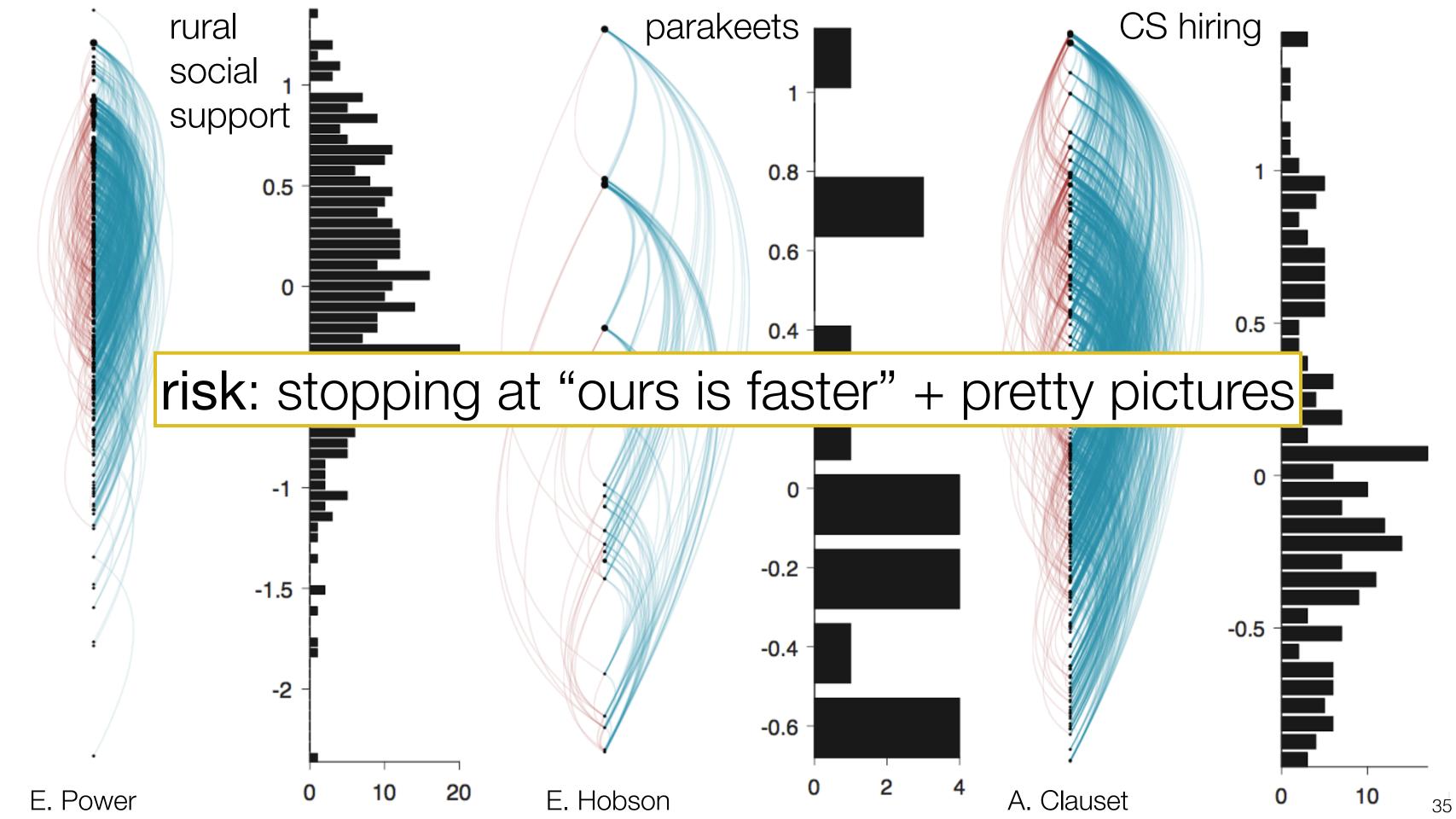
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Note that node positions can be clumpy, since this is an *embedding*.







In a linear hierarchy the key quantity to predict is edge direction, given edge existence.

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SpringRank predicts edge direction based on the relative direction probabilities:

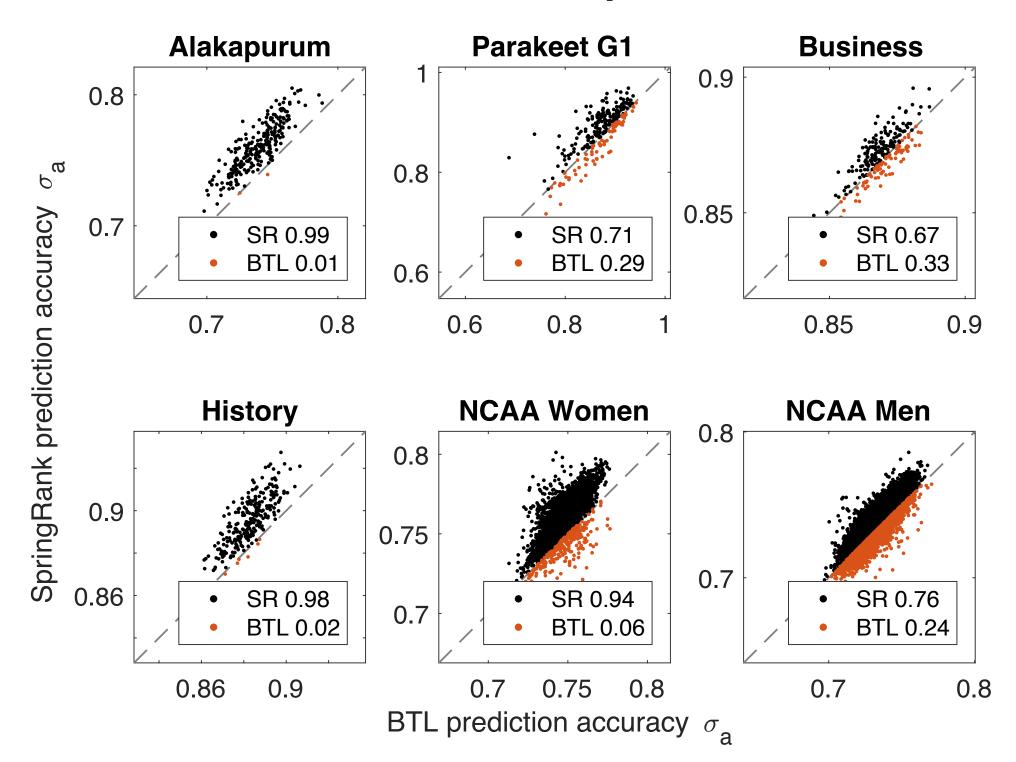
$$P_{ij}(\beta) = \frac{e^{-\beta H_{ij}}}{e^{-\beta H_{ij}} + e^{-\beta H_{ji}}} = \frac{1}{1 + e^{-2\beta(s_i - s_j)}}$$

Cross validation vs BTL: SR makes better predictions

Accuracy:

$$\sigma_a = 1 - \frac{1}{2M} \sum_{i,j} |A_{ij} - (A_{ij} + A_{ji}) P_{ij}|$$

Goal: maximize the number of correctly predicted edge directions.



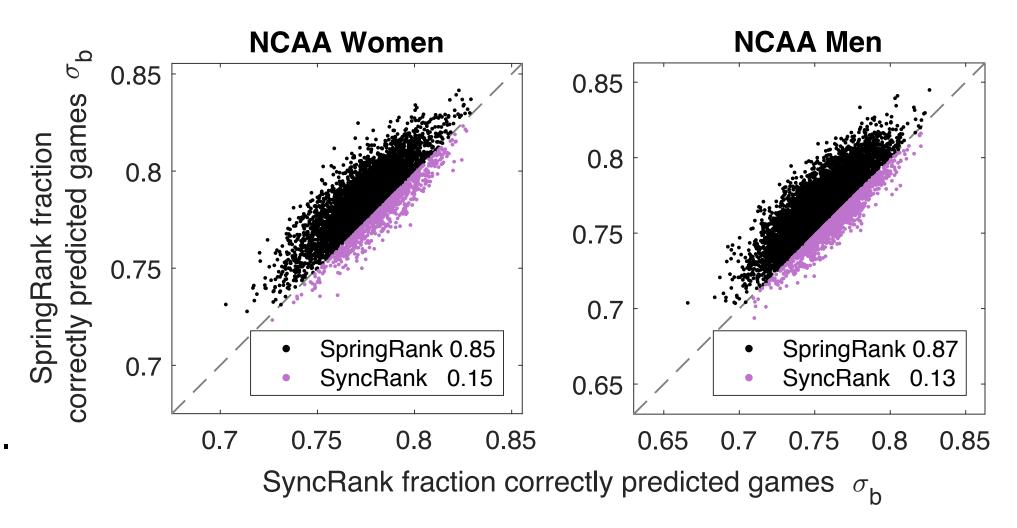
Cross validation vs SyncRank: SR makes better predictions

"One-bit" Accuracy:

Higher ranked player always wins.

- No probabilistic prediction.
- Bad for gambling.

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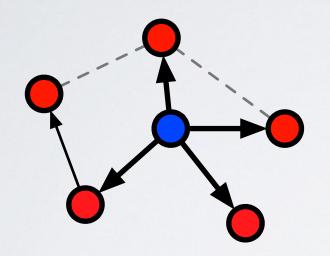


Why/when would a model of springs make better predictions than a model of the choices themselves?

describing networks position = centrality: structural vs. dynamical importance harmonic centrality closeness centrality betweenness centrality degree centrality connectivity eigenvector centrality PageRank Katz centrality many many more... structural importance = cheap estimate of dynamical importance (aka "influence") Boldi & Vigna, arxiv: 1308.2140 (2013) Borgatti, Social Networks 27, 55-71 (2005)

11

describing networks



position = centrality:

harmonic, closeness centrality

importance = being in "center" of the network

harmonic
$$c_i = \frac{1}{n-1} \sum_{j \neq i} \frac{1}{d_{ij}}$$

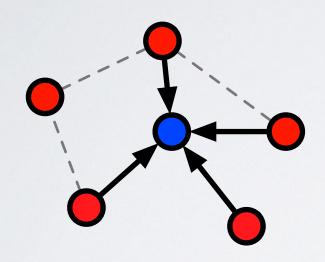
length of shortest path

distance: $d_{ij} = \begin{cases} \ell_{ij} & ext{if } j ext{ reachable from } \\ & ext{otherwise} \end{cases}$

Boldi & Vigna, arxiv:1308.2140 (2013) Borgatti, Social Networks **27**, 55–71 (2005)

network position: harmonic Medici 9.5 Guadagni 7.92 Str Albizzi 7.83 Gu Strozzi 7.67 Ridolfi 7.25 Bischeri 7.2 Tornabuoni 7.17 Alb Barbadori 7.08 Medici Peruzzi 6.87 Gi Castellani 6.87 Sal Salviati 6.58 Acciaiuoli 5.92 Ginori 5.33 Lamberteschi 5.28 Pazzi 4.77

describing networks



position = centrality:

PageRank, Katz, eigenvector centrality

importance = sum of importances* of nodes that point at you

$$I_i = \sum_{j \to i} \frac{I_j}{k_j}$$

or, the left eigenvector of

$$\mathbf{A}\mathbf{x} = \lambda \mathbf{x}$$

Embeddings and Orderings 3: PageRank

PageRank defines scalar rank recursively:

important pages are those that are linked to by important pages.

Great at finding the top 3 but limited predictions available using the PageRank scores.

The PageRank Citation Ranking: Bringing Order to the Web

January 29, 1998

Abstract

The importance of a Web page is an inherently subjective matter, which depends on the readers interests, knowledge and attitudes. But there is still much that can be said objectively about the relative importance of Web pages. This paper describes PageRank, a method for rating Web pages objectively and mechanically, effectively measuring the human interest and attention devoted to them.

We compare PageRank to an idealized random Web surfer. We show how to efficiently compute PageRank for large numbers of pages. And, we show how to apply PageRank to search and to user navigation.

The Anatomy of a Large-Scale Hypertextual Web Search Engine

Sergey Brin and Lawrence Page

Computer Science Department, Stanford University, Stanford, CA 94305, USA sergey@cs.stanford.edu and page@cs.stanford.edu

Abstract

In this paper, we present Google, a prototype of a large-scale search engine which makes heavy use of the structure present in hypertext. Google is designed to crawl and index the Web efficiently and produce much more satisfying search results than existing systems. The prototype with a full

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From that webpage, she looks at the links on the page, and either

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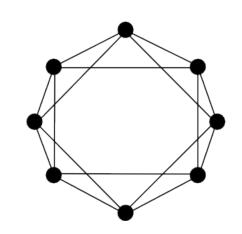
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Jeremy Kun: http://www.infinitelooper.com/?v=K3pT0gTaDec&p=n

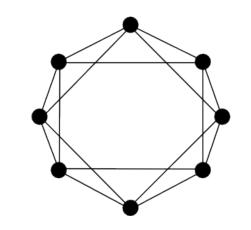




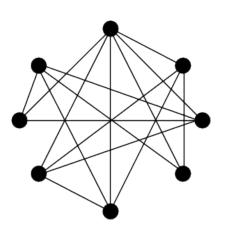
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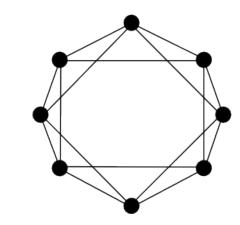
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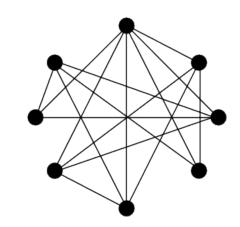
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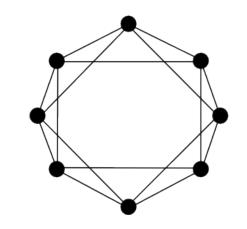


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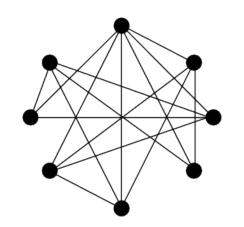


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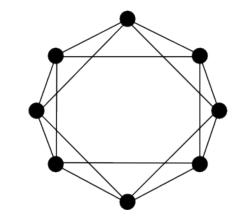


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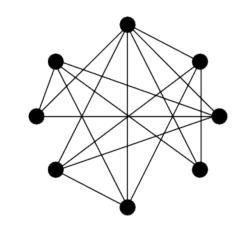


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- and since the generative model itself is some combination or composition of random variables, a **random graph model** is a set of possible networks, each with an associated probability, i.e., a distribution.

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this tangent will introduce the second most popular model for networks: **configuration model(s)**—uniform distributions over networks w/ fixed deg. seq.

Why care about random graphs w/ fixed degree sequence?

Since many networks have broad or peculiar degree sequences, these random graph distributions are commonly used for:

Hypothesis testing:

Can a particular network's properties be explained by the degree sequence alone?

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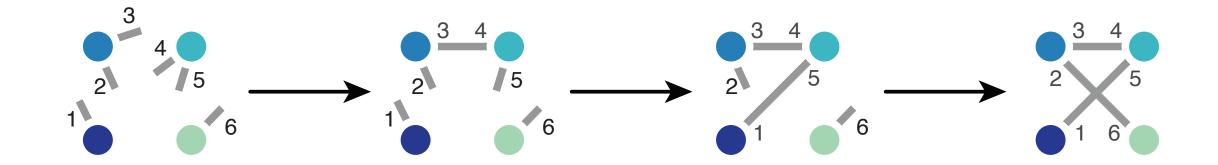
How does the degree distribution affect the epidemic threshold for disease transmission?

Null model for Modularity, Stochastic Block Model:

Compare an empirical graph with (possibly) community structure to the ensemble of random graphs with the same vertex degrees.

Stub Matching to draw from the config. model

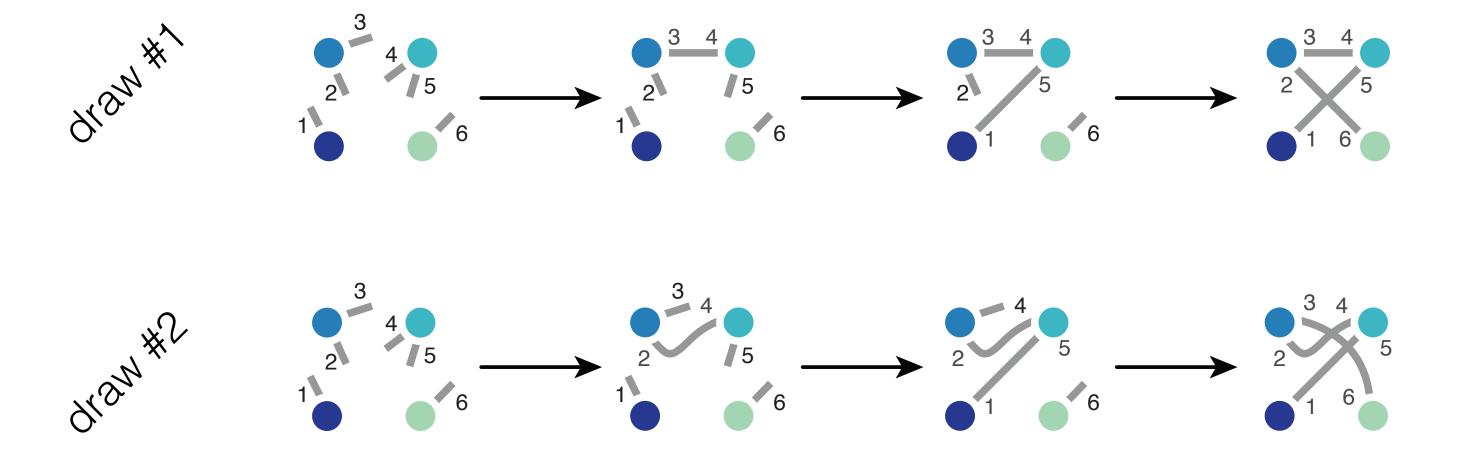
$$\vec{k} = \{1, 2, 2, 1\}$$



the standard algorithm: draw from the distribution by sequential "Stub Matching"

- 1. initialize each node n with k_n half-edges or stubs.
- 2. choose two stubs uniformly at random and join to form an edge.

Stub Matching to draw from the config. model





Are these two different networks? or the same network?





Are these two different networks? or the same network?

Are stubs distinguishable or not?





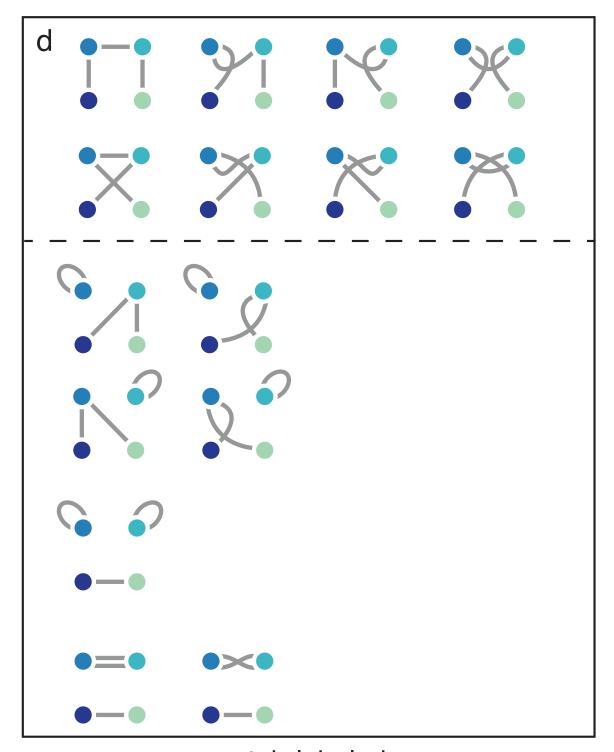
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When it comes to doing science, the answer matters.



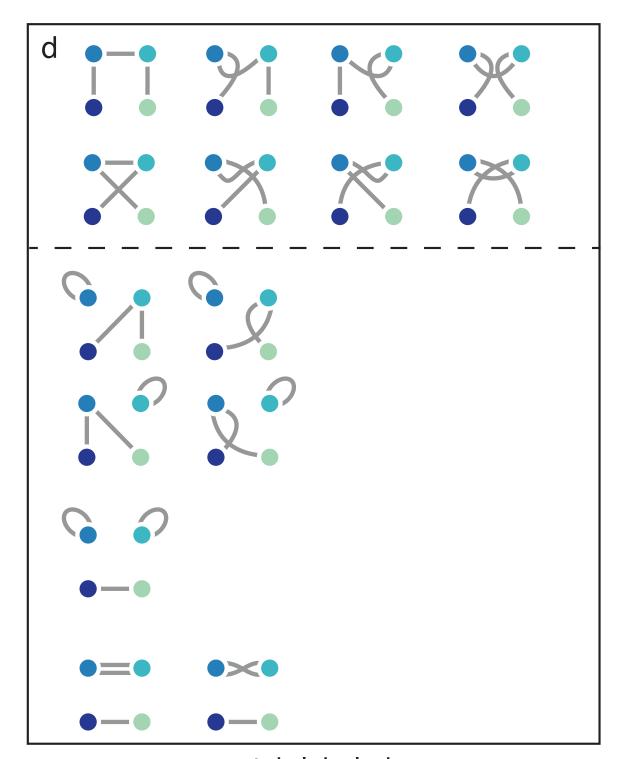
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stub-labeled

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8 of the graphs are simple, while the other 7 have self-loops or multiedges.

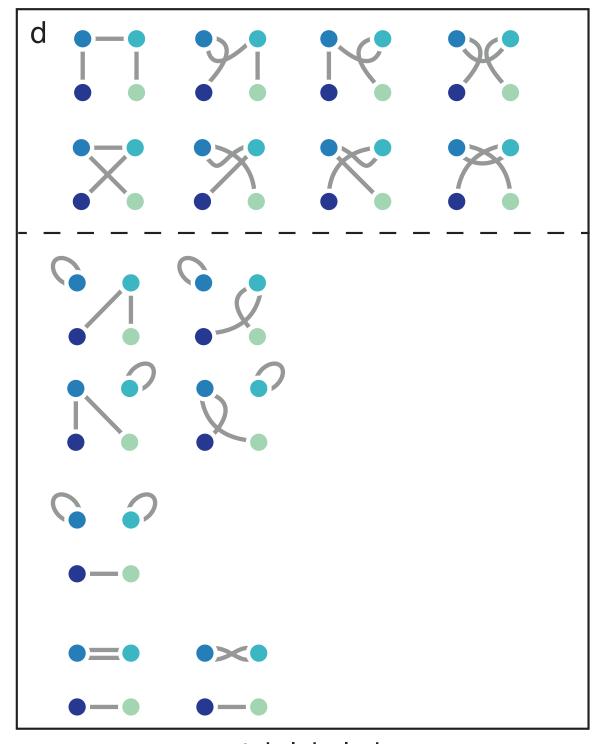


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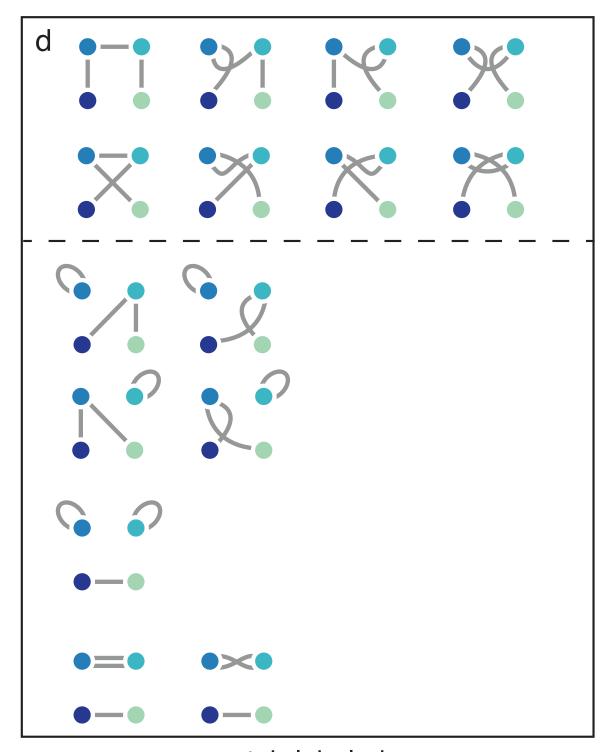
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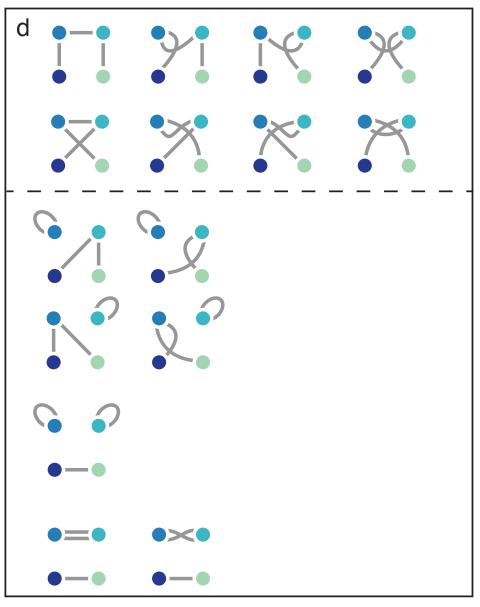
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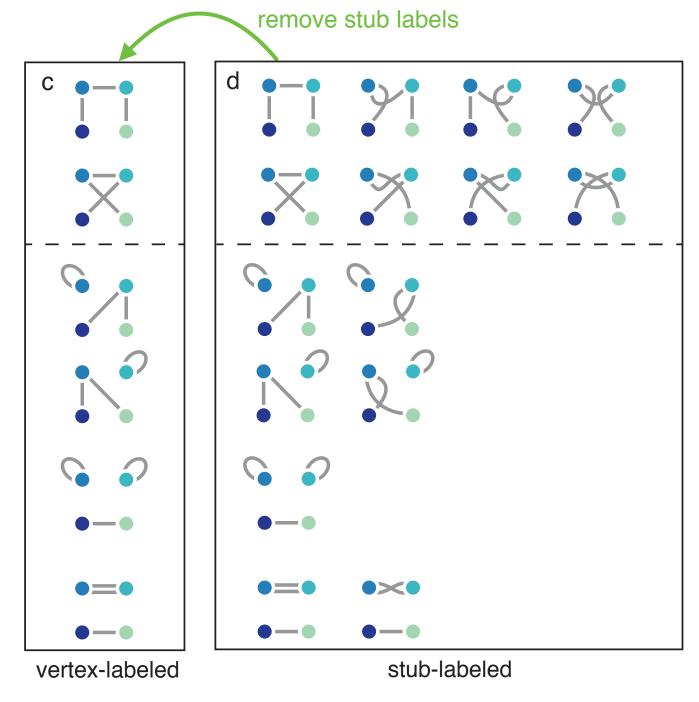
Note, however, that this is not a uniform sample over adjacency matrices (rows).

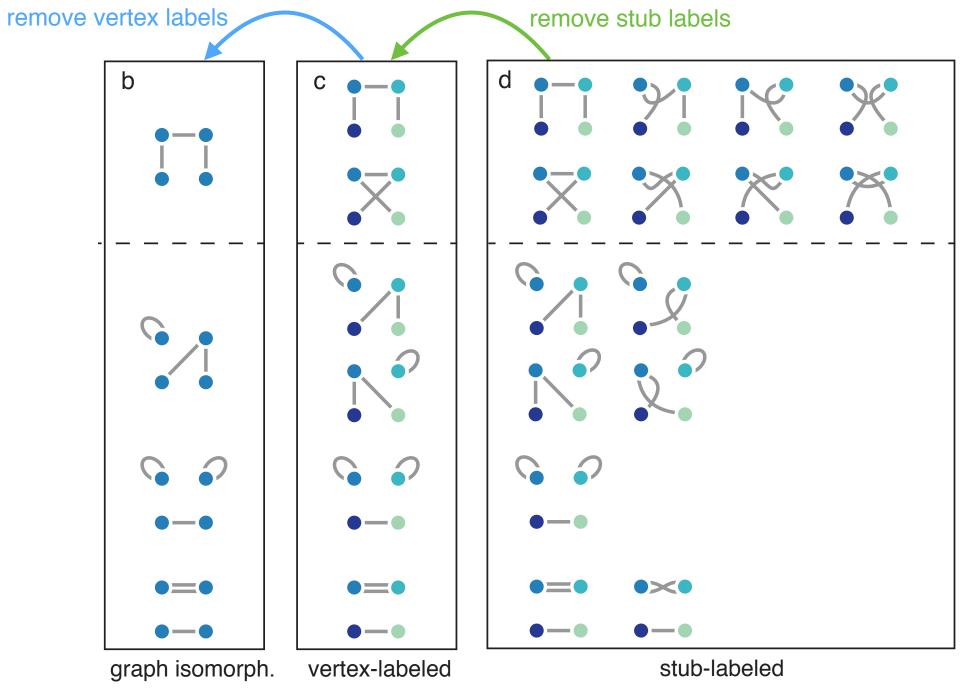


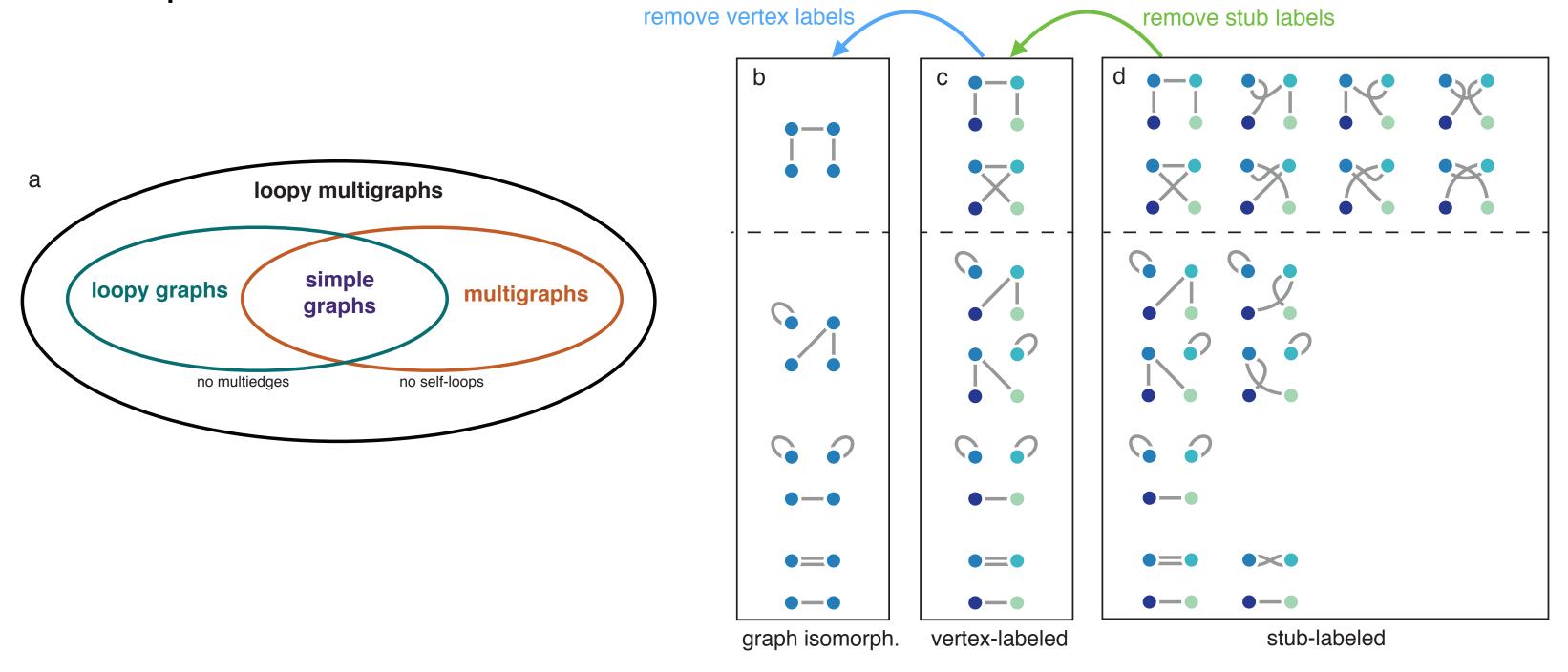
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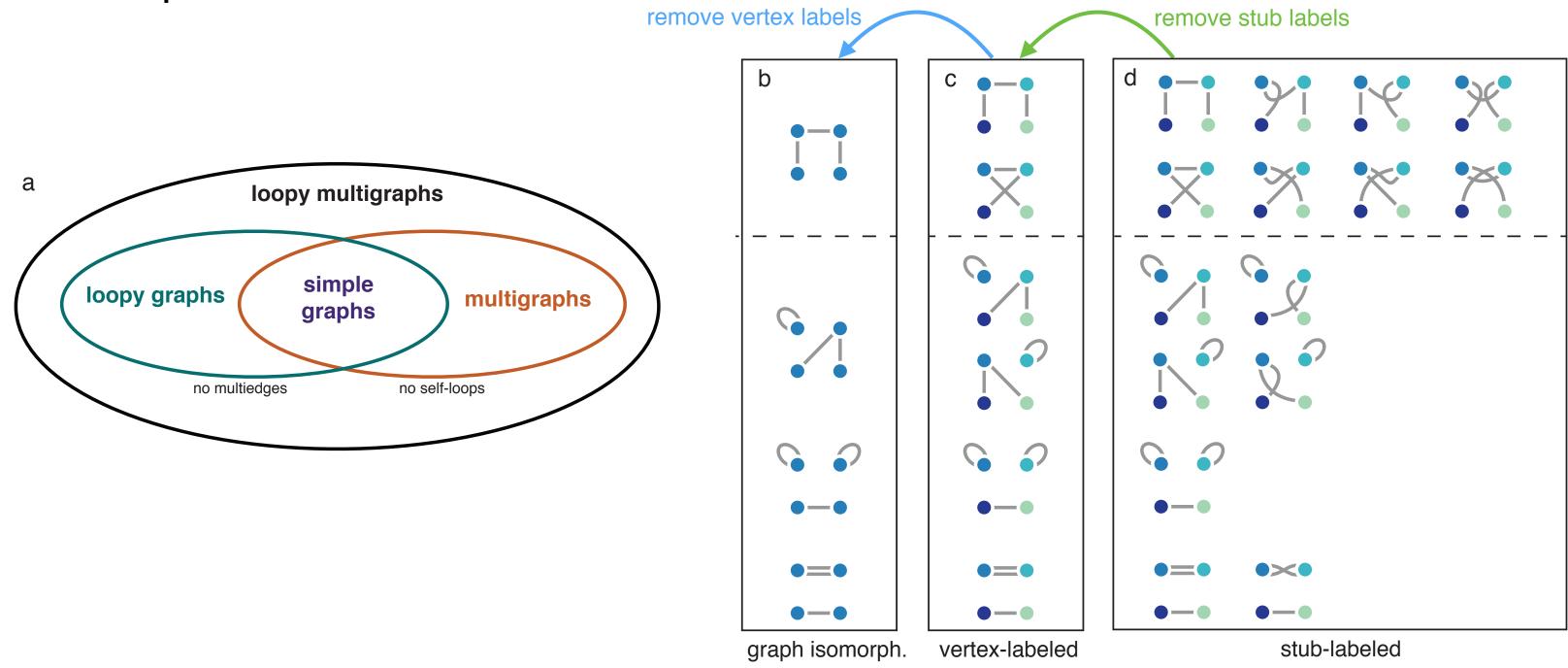


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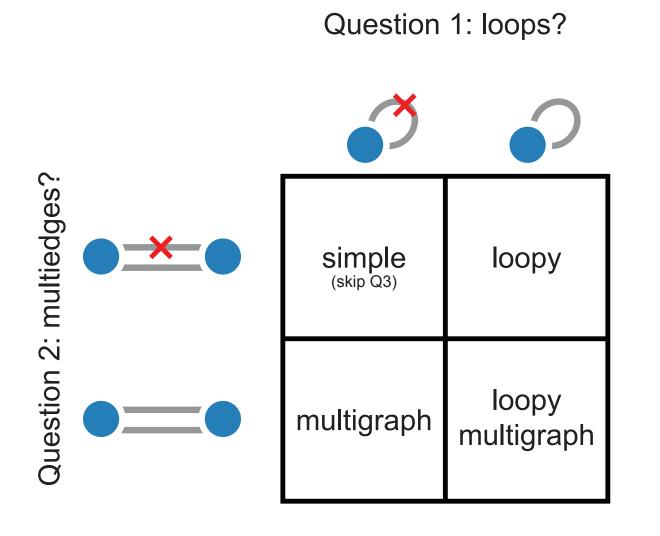


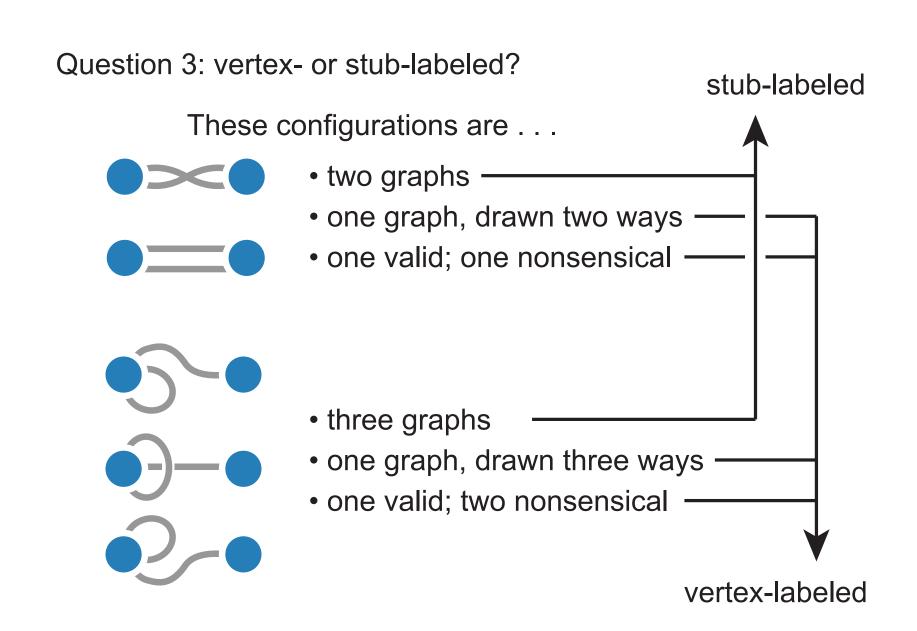


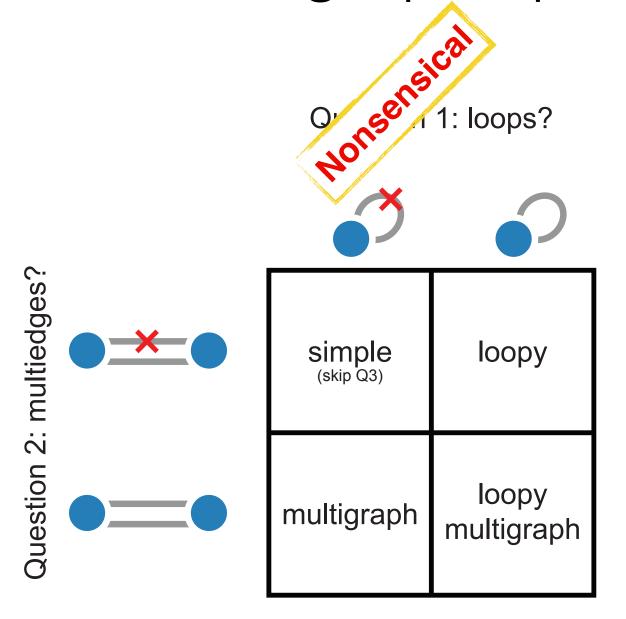
null model hypothesis testing needs uniform sampling for all 8 spaces: loopy{0,1} x multigraph{0,1} x {stub-,vertex-}

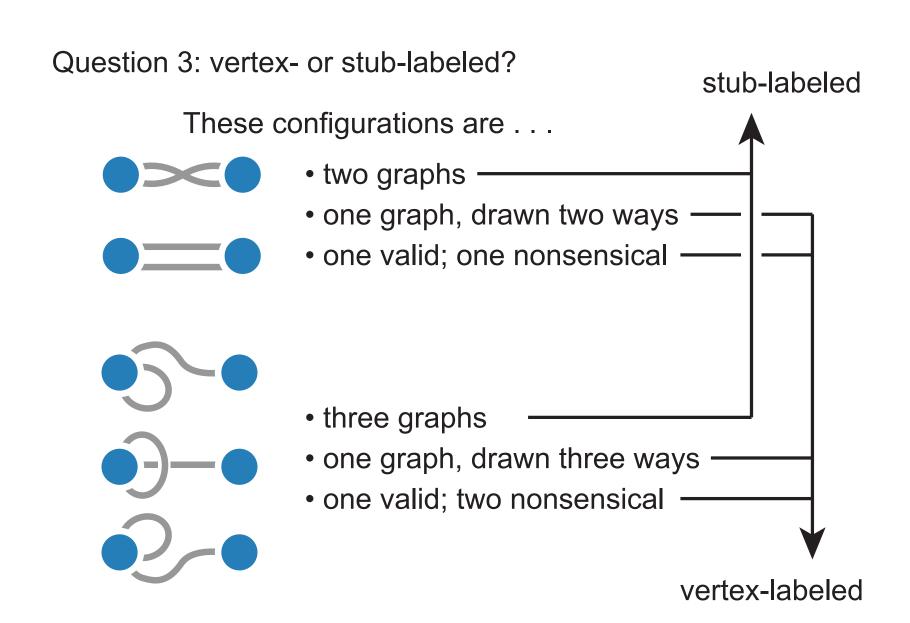
Hypothesis testing

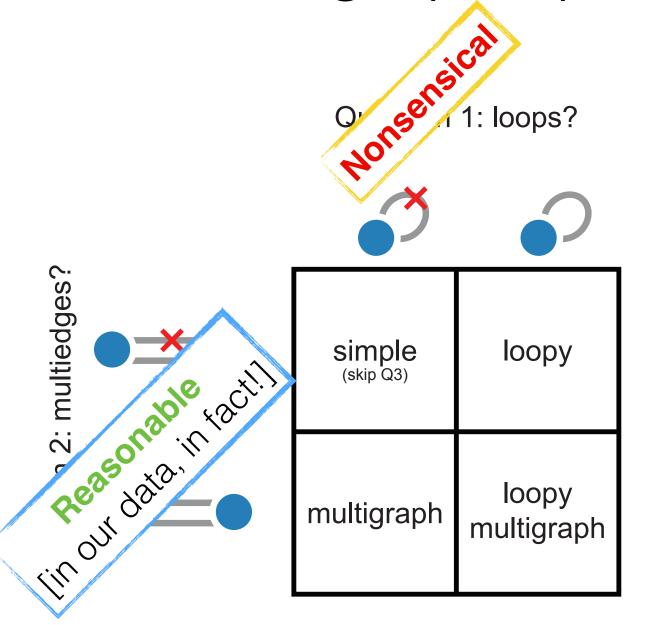


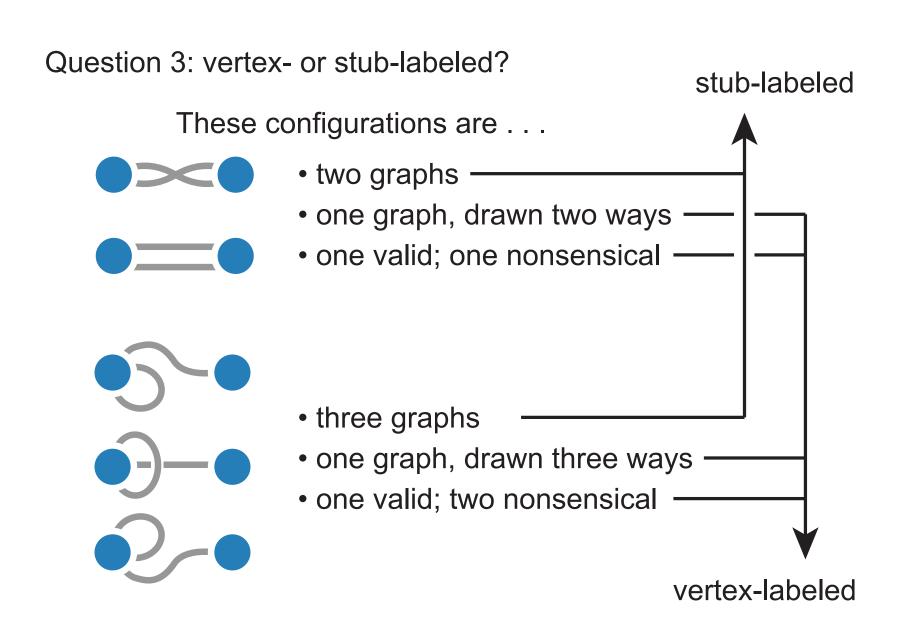


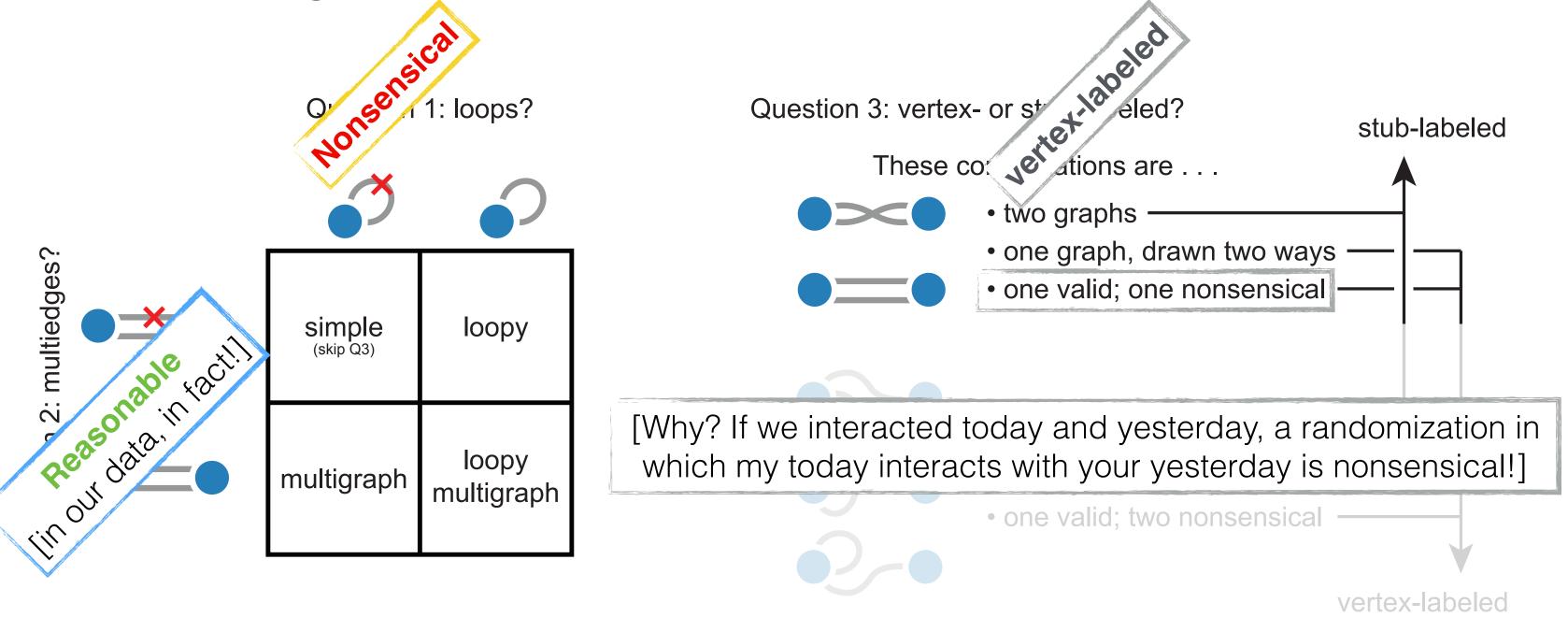




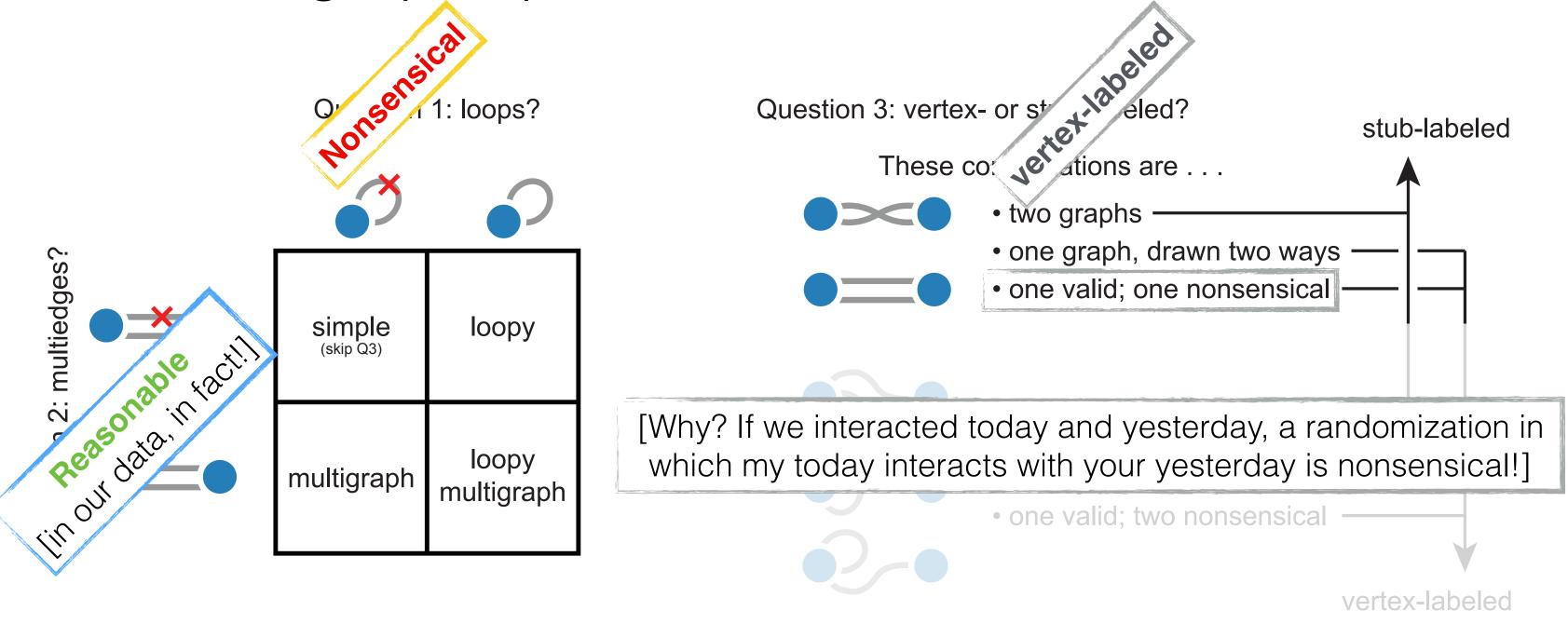




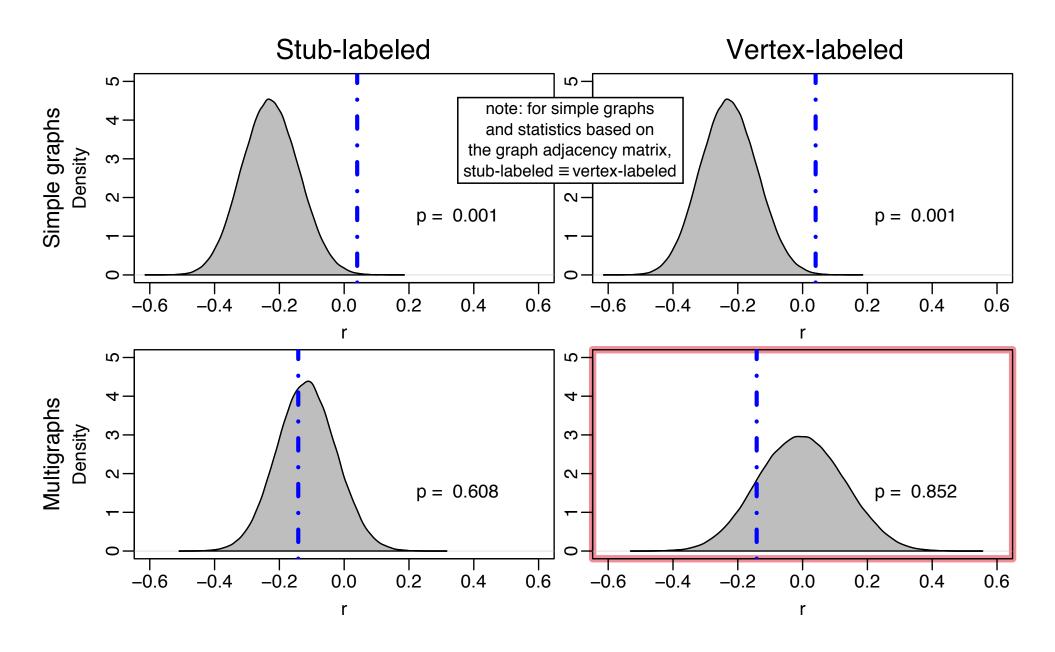




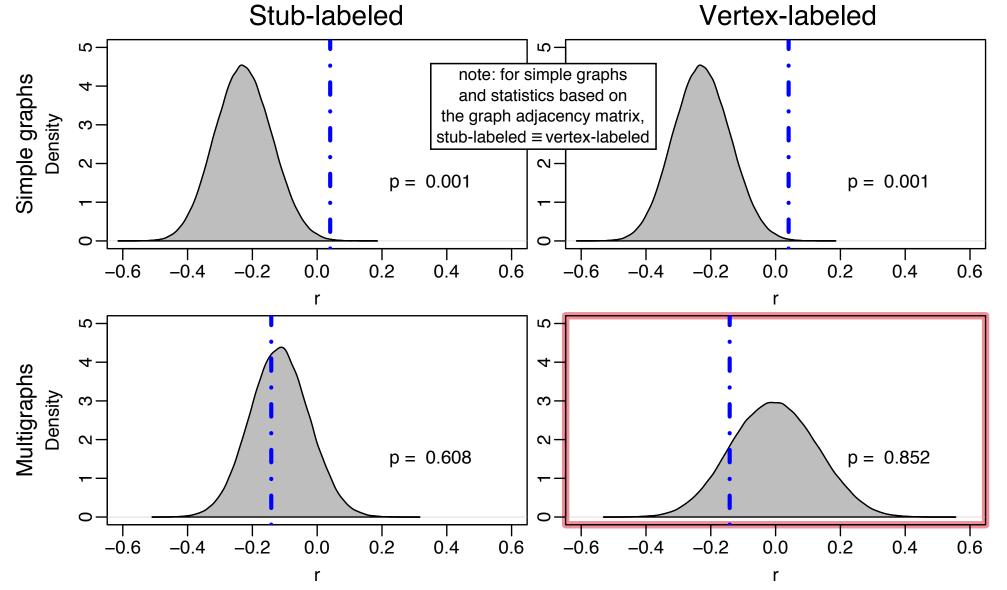
Choose a graph space for barn swallows



This should be modeled as a vertex-labeled multigraph.

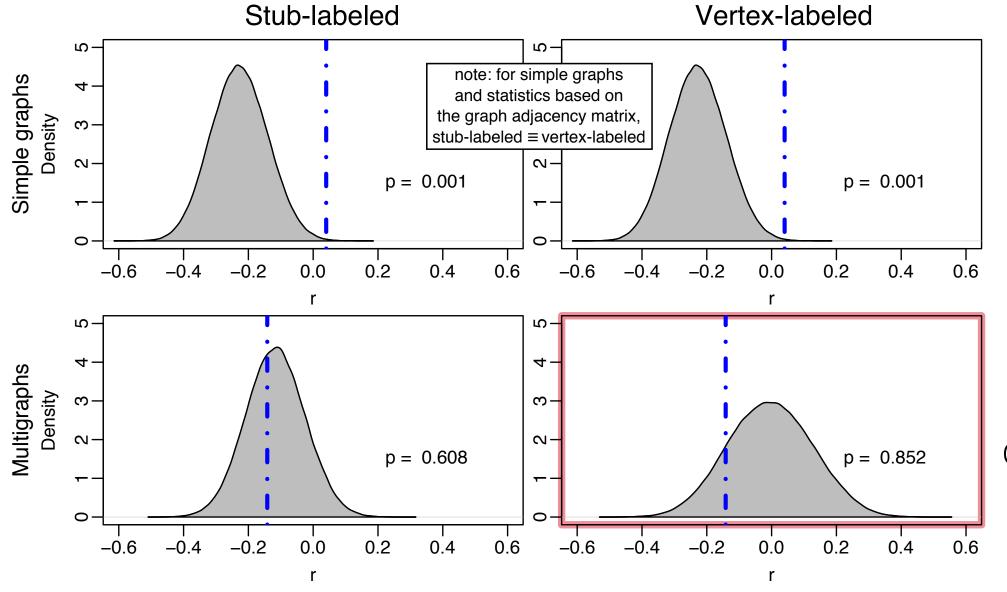


Sanity check: should be = for simple



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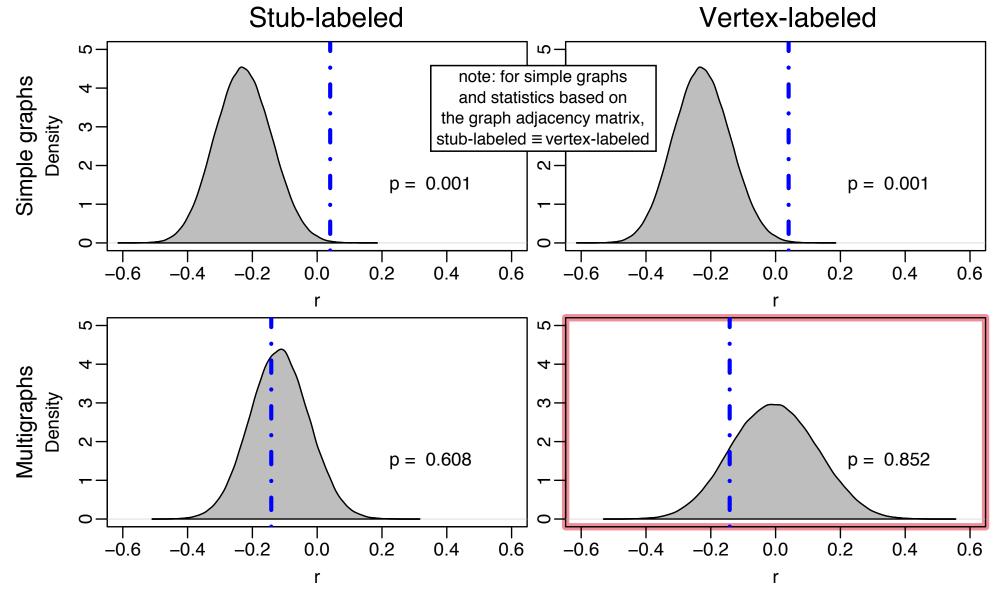
NONE of these is centered at zero. Correct space is *meaningfully* different.



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Uniform sampling means we can compare empirical value to null distribution to draw scientific conclusions.

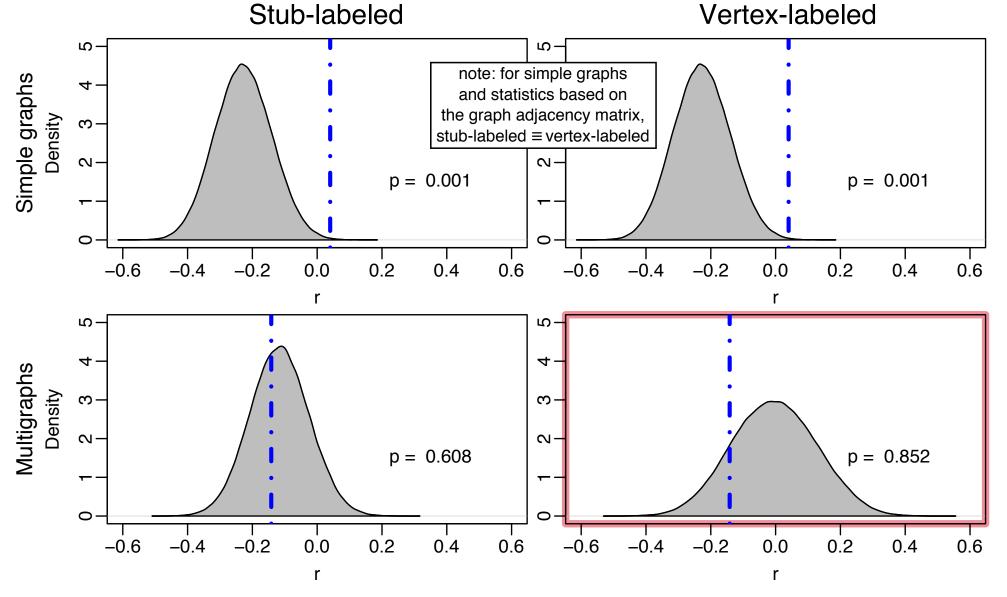


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Another example: Clauset 4:71-75

The choice of graph space matters—careful choice & sampling can flip conclusions!

So, why this tangent?

Random graph models are recipes. You pick the parameters and cook up an ensemble of networks.

How much of [cool property] that we observe is actually just typical of networks from [particular ensemble]?

Null hypothesis: none. Test requires uniform distribution.



olive the dog

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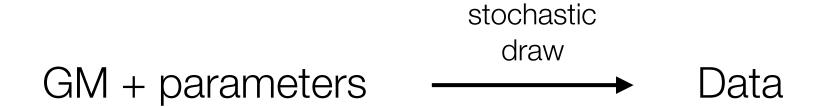
What if we wrote down model whose non-uniformity over its ensemble was a feature?

Generate the structure you wish to infer.

We like generative models because they open the door to inference:

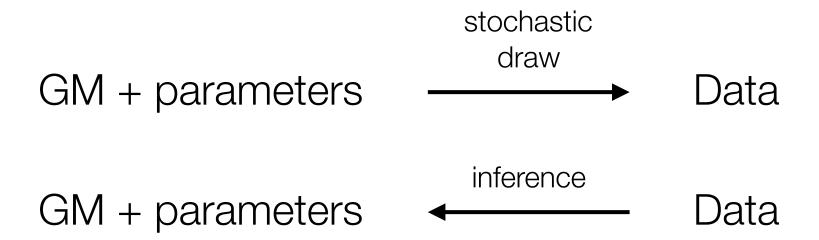
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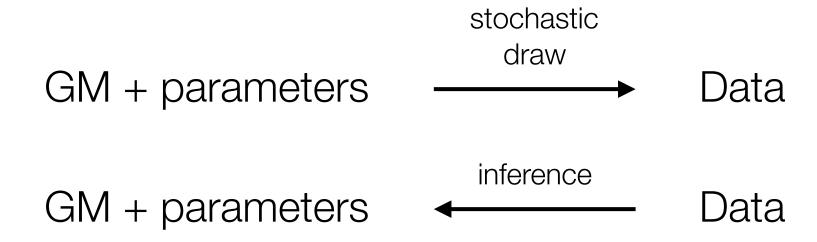
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Generate the structure you wish to infer.

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In other words: let's write down a model whose ensemble's distribution is not uniform but **highly peaked** around networks with structures that we want to see.

The stochastic block model

GM + parameters

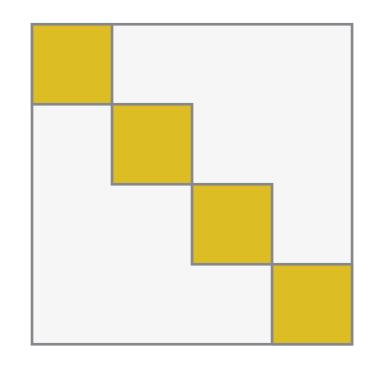


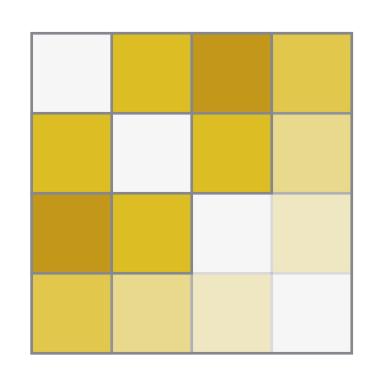
Assign each node to one of B blocks. b_i

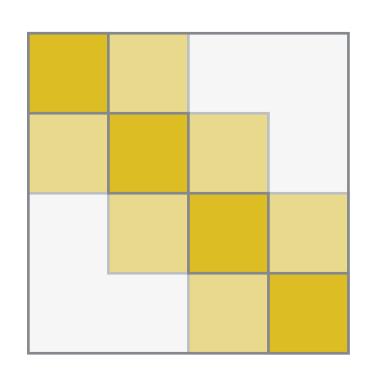
Let the probability that two nodes connect depend only on their blocks:

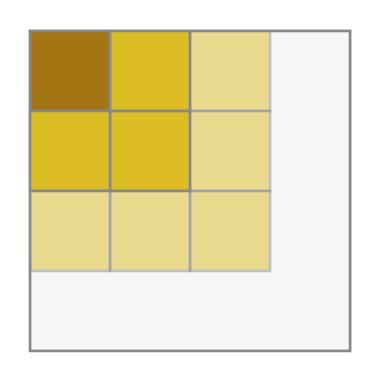
$$Pr(A_{ij}|b_i,b_j) = \omega_{b_i,b_j}$$

Then we can choose the matrix ω to have whatever structure we want!









Assortative

Disassortative

Ordered

Core-periphery

The stochastic block model

GM + parameters

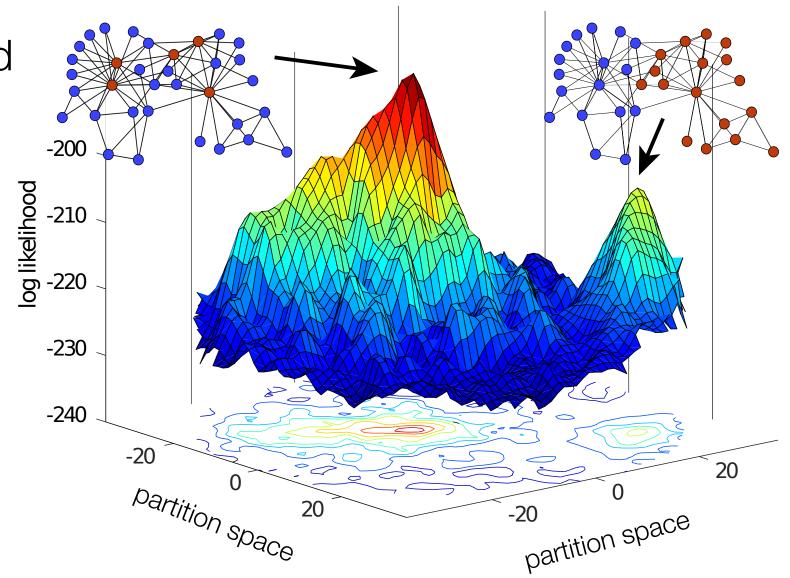


Data

When we run the generative process in reverse (aka inference), we find community structure.

This is nothing more than a statistically principled approach to fitting a model to data.

But instead of fitting a line to a scatter of (x,y) data, we're fitting a model for networks with community structure to data.



Generative model:

Generate the patterns that you want to identify.

Create N nodes.

Assign each node an integer rank r, from 1 to N.

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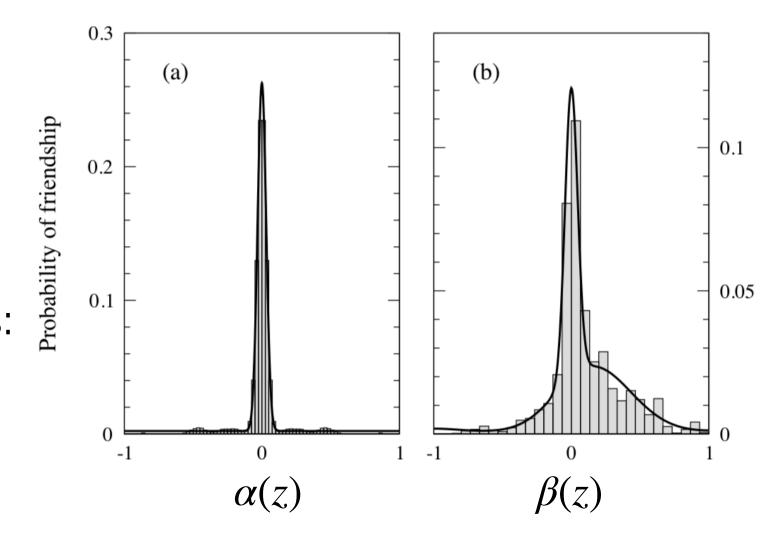
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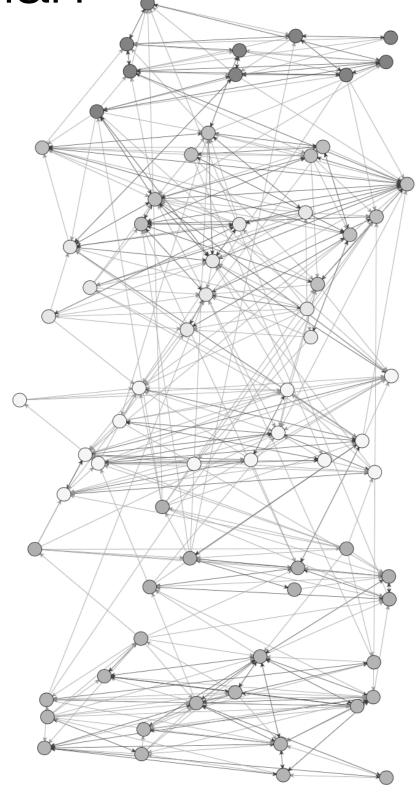


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Inferred parameters of people's attachment preferences & ranks.

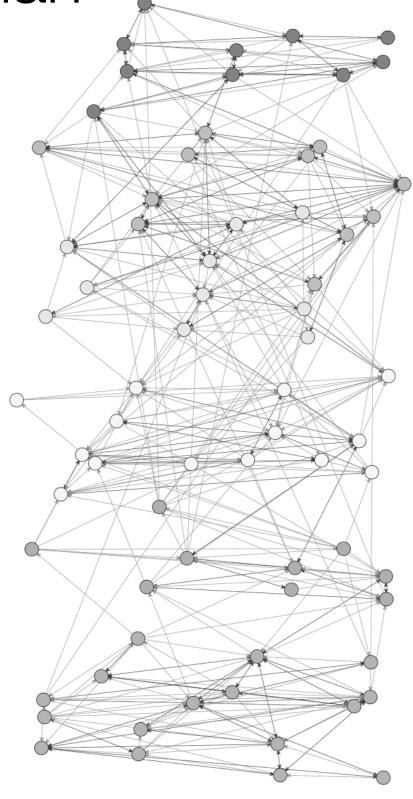
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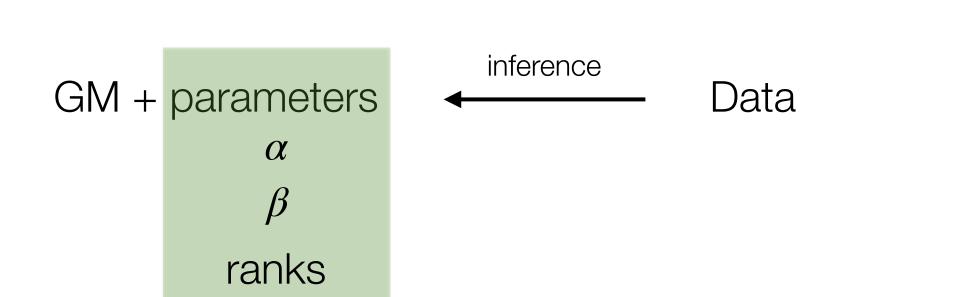


$$\begin{array}{c|c} \mathsf{GM} + \mathsf{parameters} & & & \\ & \alpha & \\ & \beta & \\ & \mathsf{ranks} & & \end{array}$$

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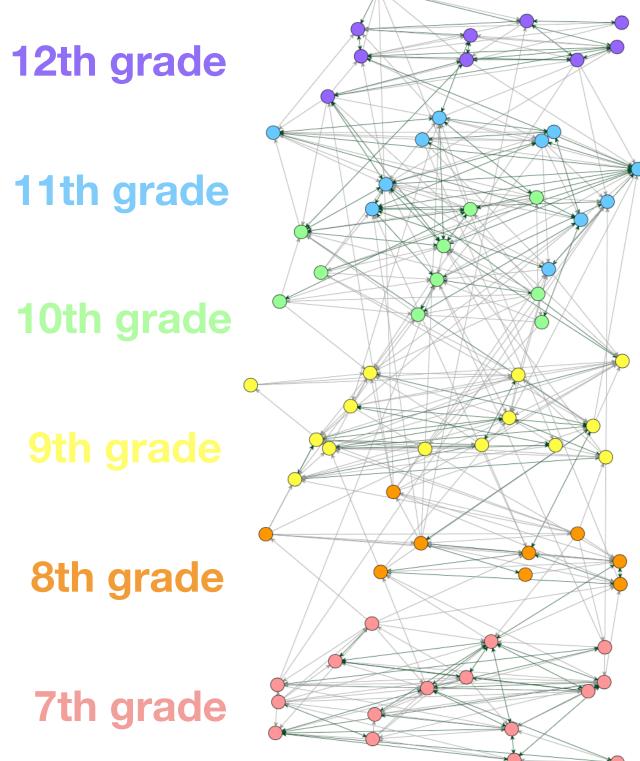
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Embeddings and Orderings 5: Niche Models

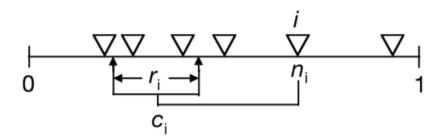


Figure 1 Diagram of the niche model. Each of \boldsymbol{S} species (for example, $\boldsymbol{S} = 6$, each shown as an inverted triangle) is assigned a 'niche value' parameter (n_i) drawn uniformly from the interval [0,1]. Species i consumes all species falling in a range (r_i) that is placed by uniformly drawing the centre of the range (c_i) from $[r/2, n_i]$. This permits looping and cannibalism by allowing up to half of r_i to include values $\ge n_i$. The size of r_i is assigned by using a beta function to randomly draw values from [0,1] whose expected value is 2 c and then multiplying that value by n_i [expected $E(n_i) = 0.5$] to obtain the desired \boldsymbol{c} . A beta distribution with $\alpha = 1$ has the form $f(x|1, \beta) = \beta(1-x)^{\beta-1}$, 0 < x < 1, 0 otherwise, and $E(X) = 1/(1+\beta)$. In this case, $x = 1-(1-y)^{1/\beta}$ is a random variable from the beta distribution if y is a uniform random variable and β is chosen to obtain the desired expected value. We chose this form because of its simplicity and ease of calculation. The fundamental generality of species *i* is measured by r_i . The number of species falling within r_i measures realized generality. Occasionally, model-generated webs contain completely disconnected species or trophically identical species. Such species are eliminated and replaced until the web is free of such species. The species with the smallest n_i has $r_i = 0$ so that every web has at least one basal species.

Embeddings and Orderings 5: Niche Models

Niche Models embed species in a latent space based on feeding preferences:

most species feed from narrow range in a 1-dim. space (~body size).

 Great for food webs. Inference models v slow for all but small networks.

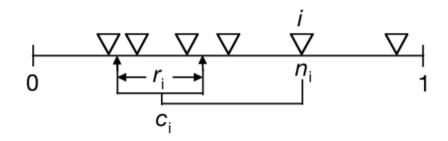


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Want more? Jen Dunne, Cris Moore

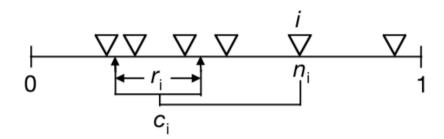


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</methods>

<applications>

Many uses for the same techniques. cf regression

Treat the network like a system:

Extrapolation. Make predictions for as-yet unseen nodes (in "space" or time). **Interpolation**. Identify missing links.

Generalization. Nodes of this type are like others of the same type.

Treat the network like an artifact:

Mechanisms. How did this network arise? What rules governed its assembly? **Explanations**. Coarse-graining or compression.

Treat the network like a means to an end; an intermediate data structure:

Useful division. Need groups so that we can assign treatments in an A/B test. **Simplification**. Downstream regression model needs ranks or groups.





I have a problem with academics using academic data to show something about academics.

9:27 AM - 20 Jun 2018



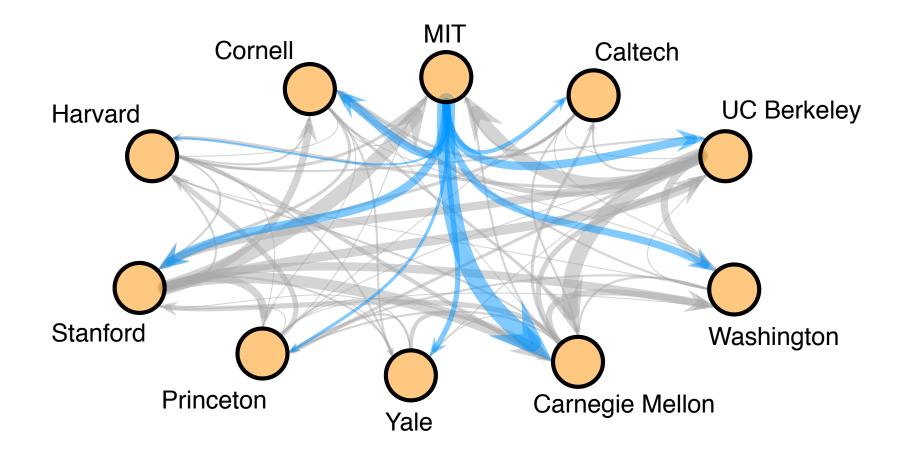


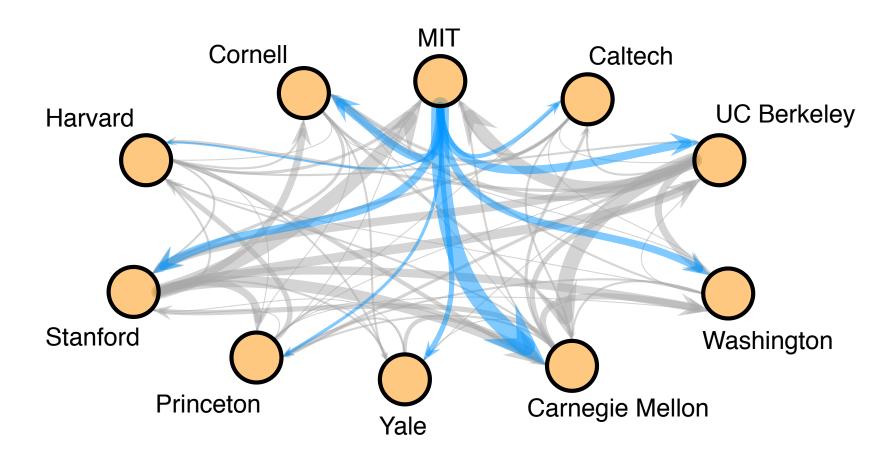
Collect the data (by hand 66)

CVs of all US & Canadian tenure-track faculty in CS, Business, History: 2011-2013.

	Computer Science	Business	History
institutions	205	112	144
tenure-track faculty	5032	9336	4556
mean size	25	83	32
female	15%	22%	36%

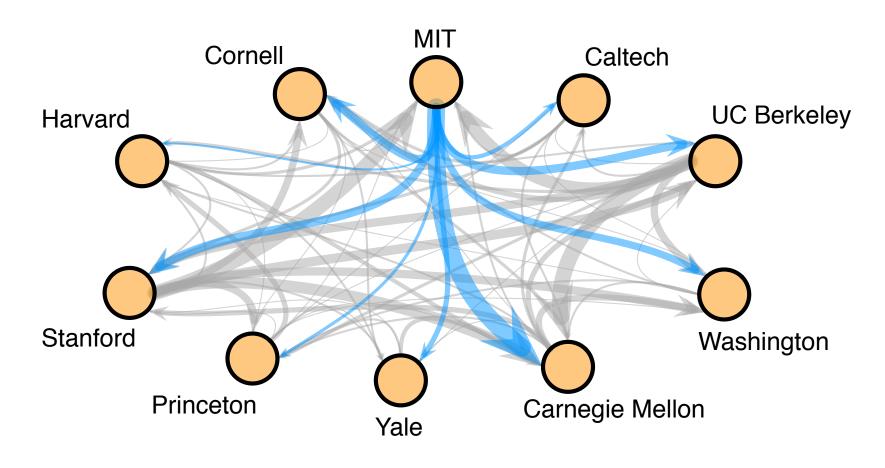
total: **18,924** CVs





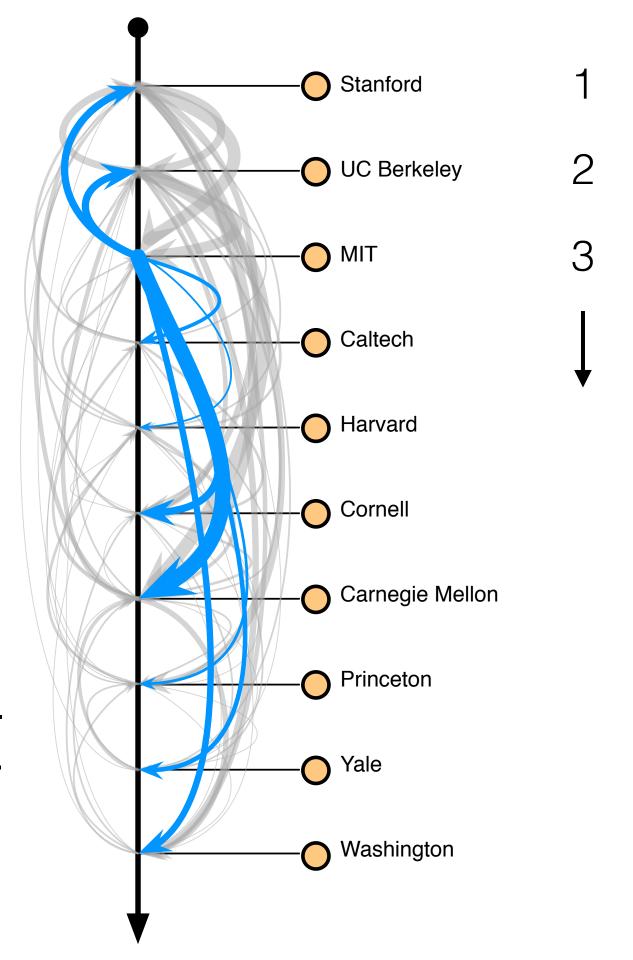
Premises:

- 1. Each hiring committee wants to hire the best.
- 2. Entire network reveals collective preferences.



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systematic

90% of hiring movement is "down" the hierarchy

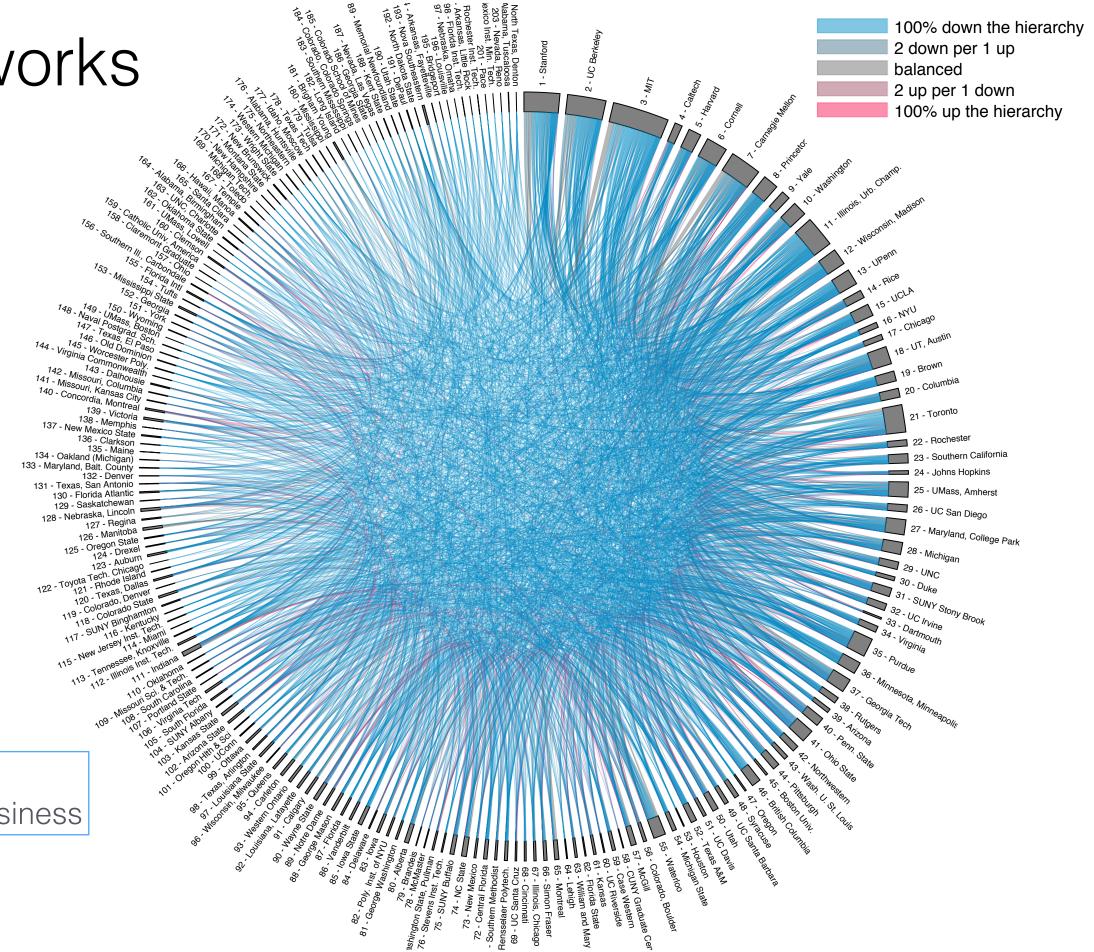
steep

< 7% of faculty have PhD from lower 75% of universities

biased

median change for women ~3 ranks worse than men

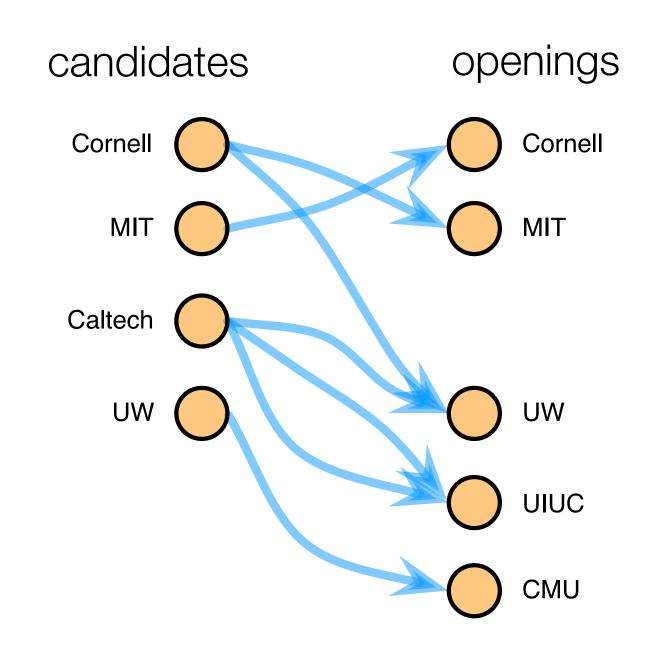
danlarremore.com/faculty/ explore 19,000 hires for History, CS, Business



Generative model:

prestige productivity postdoc experience

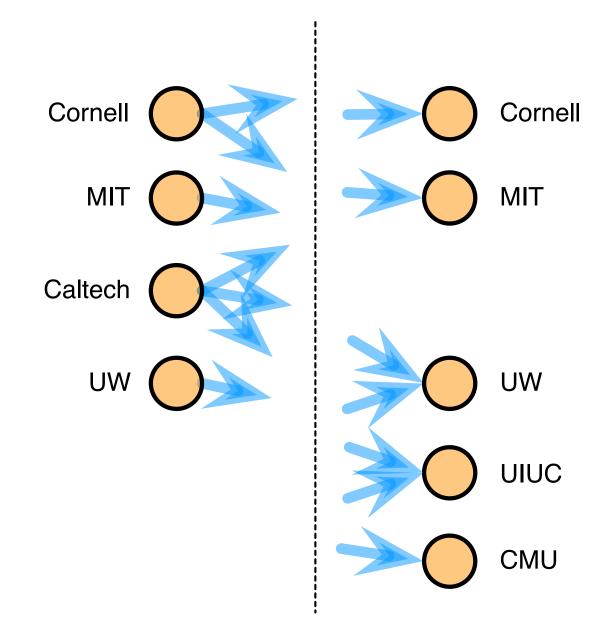
gender geography



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gender geography



accurately generate the links!

1. **Prestige difference**: Faculty Job vs PhD

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 - 2. Productivity

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Gender bias is not uniformly, systematically affecting all hires. But...

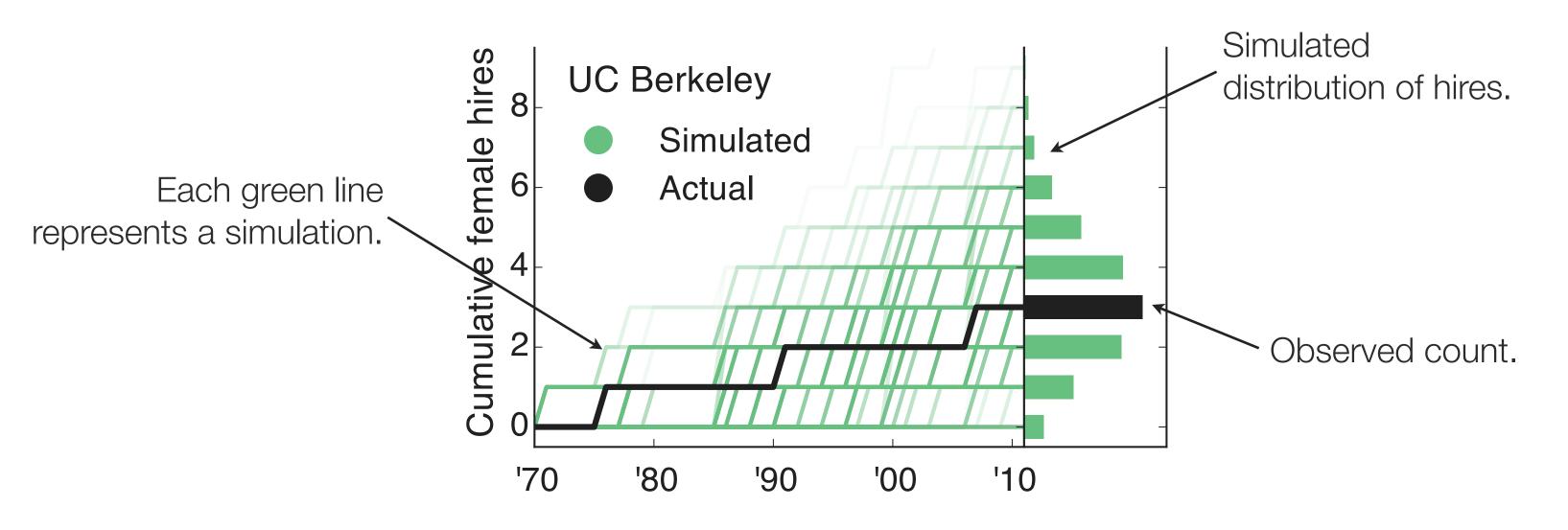
- 1. Prestige difference: Faculty Job vs PhD
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a woman on the job market must have published ~1 additional paper to be placed the same as an equally qualified man.

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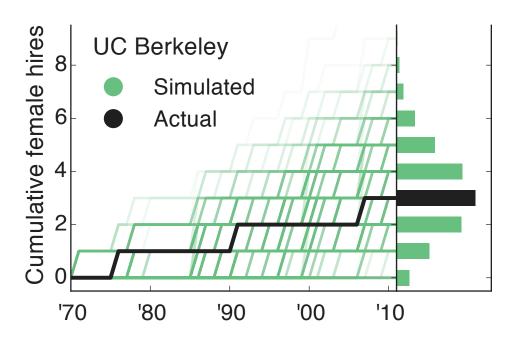
Using 40 years of actual hiring data, simulate hiring patterns for each institution.

Compare actual vs. expected number of female hires.



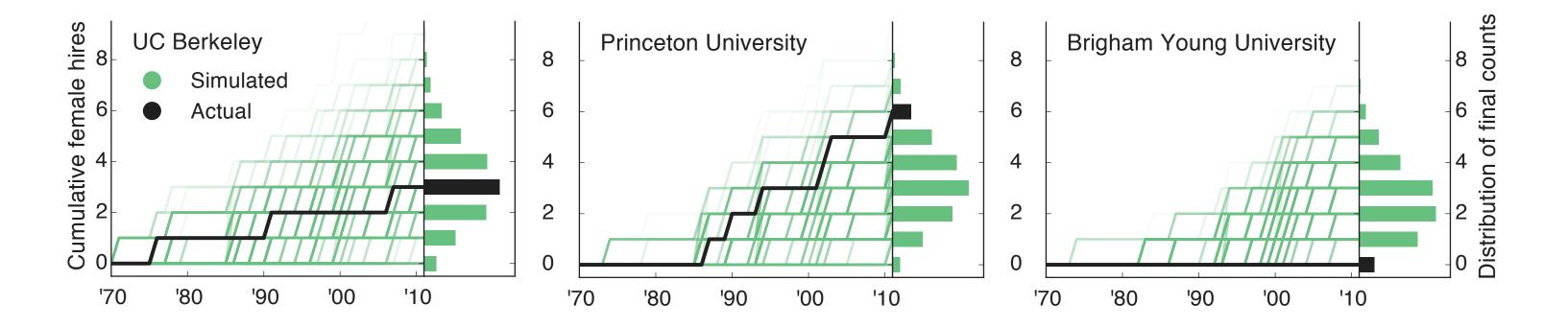
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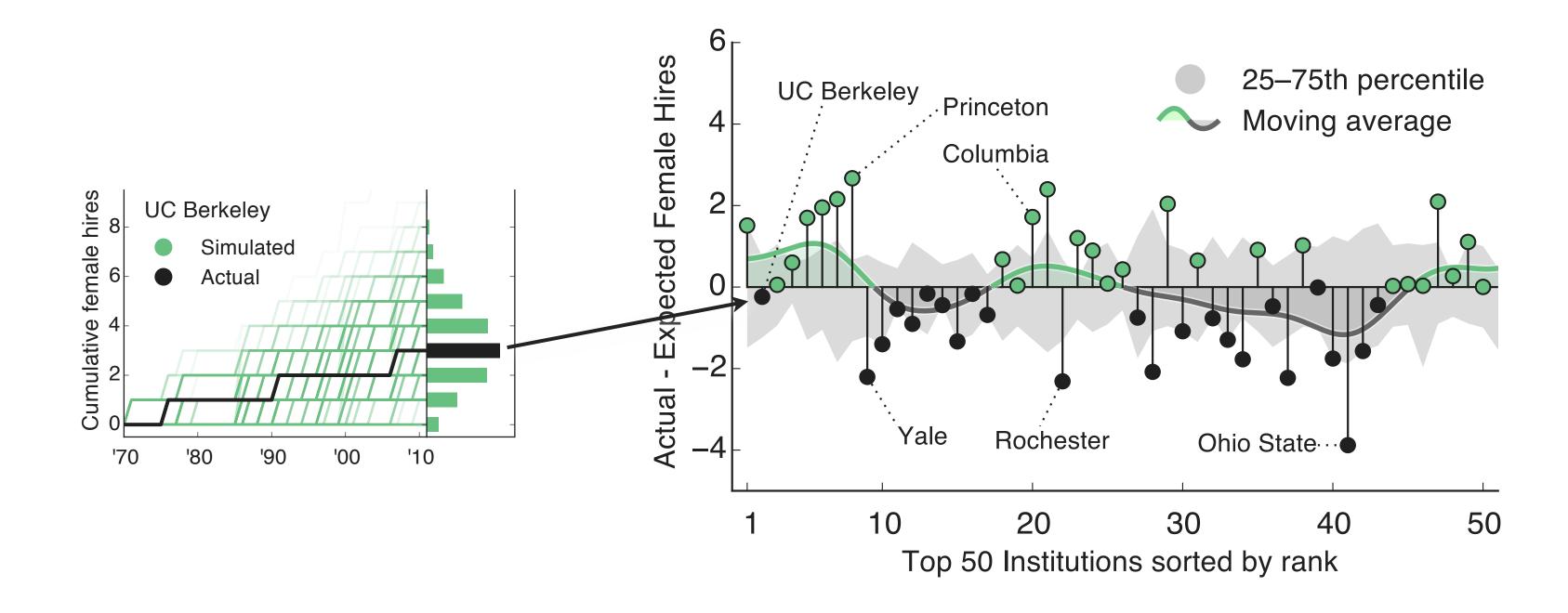
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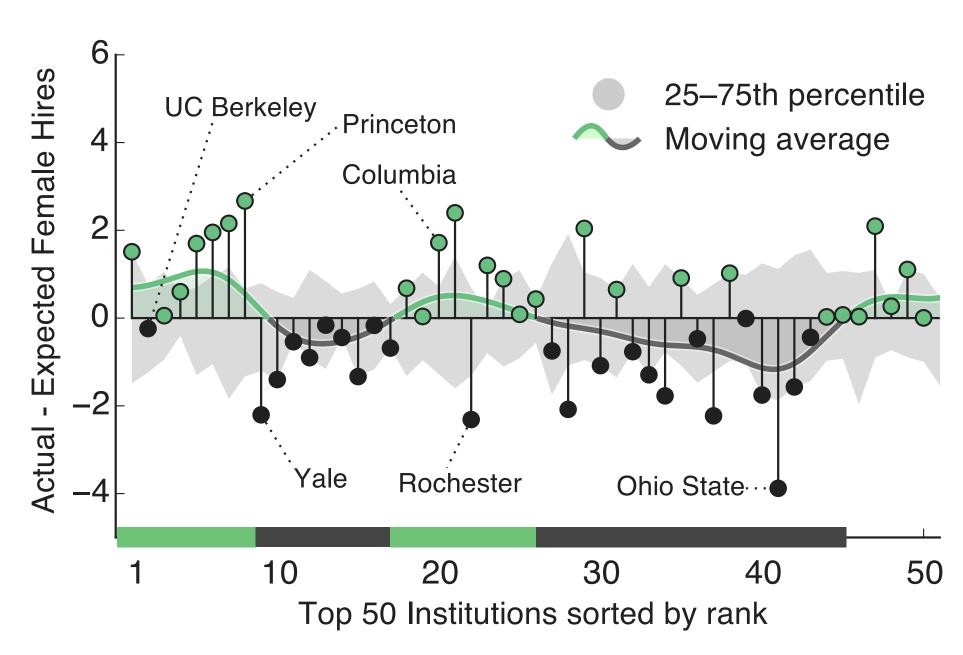


For the top 50 institutions, we see an oscillation.

Why?

An interference effect?
Two distinct candidate pools?

Is it real?

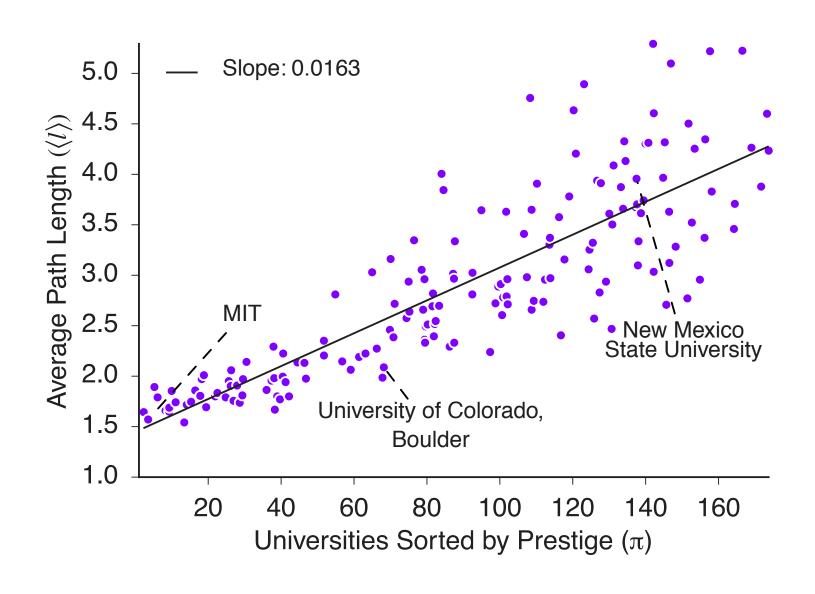


Does the structure of this network affect *ideas?*

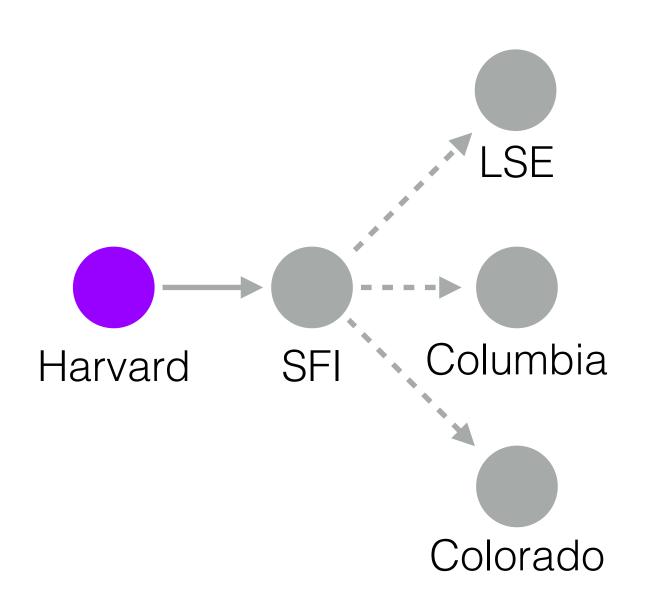
Prestigious institutions are **closer** to all other institutions.

What implications does this have for the **exchange** & **filtration** of ideas?

Does the prestige hierarchy lead to **epistemic inequality**?



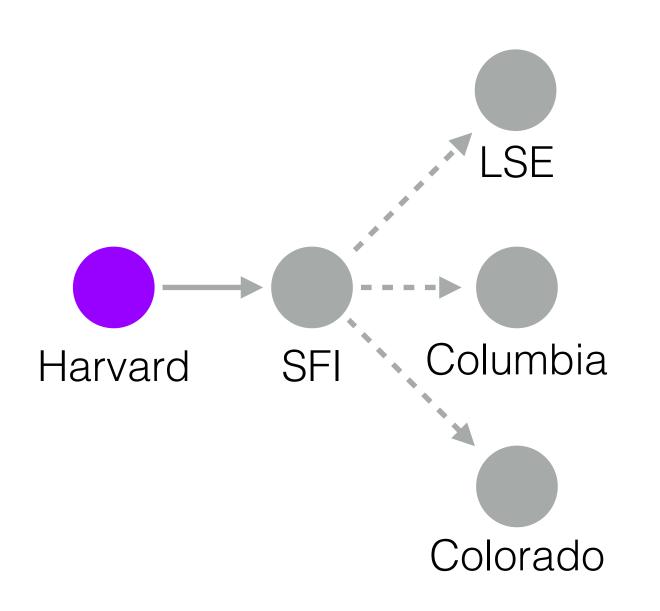
New hires as vectors for infectious ideas?



Do new hires *actually* bring ideas with them? [or would popular topics get there anyway?]

Are some universities better idea exporters?

New hires as vectors for infectious ideas?



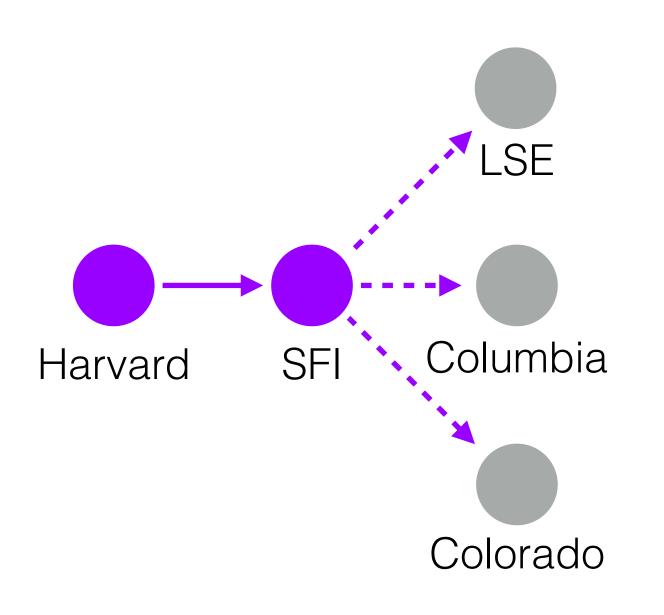
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The probability that a hire transmits the idea to and uninfected university: *p* [idea quality]

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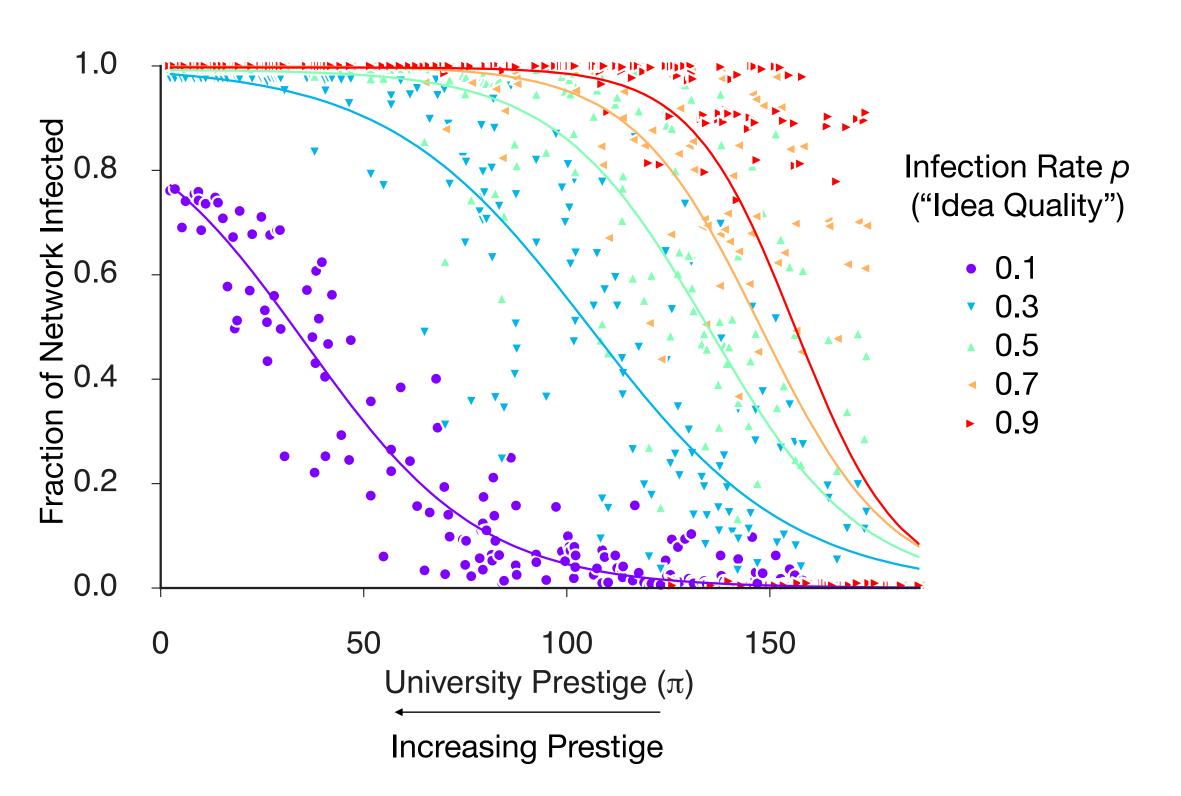
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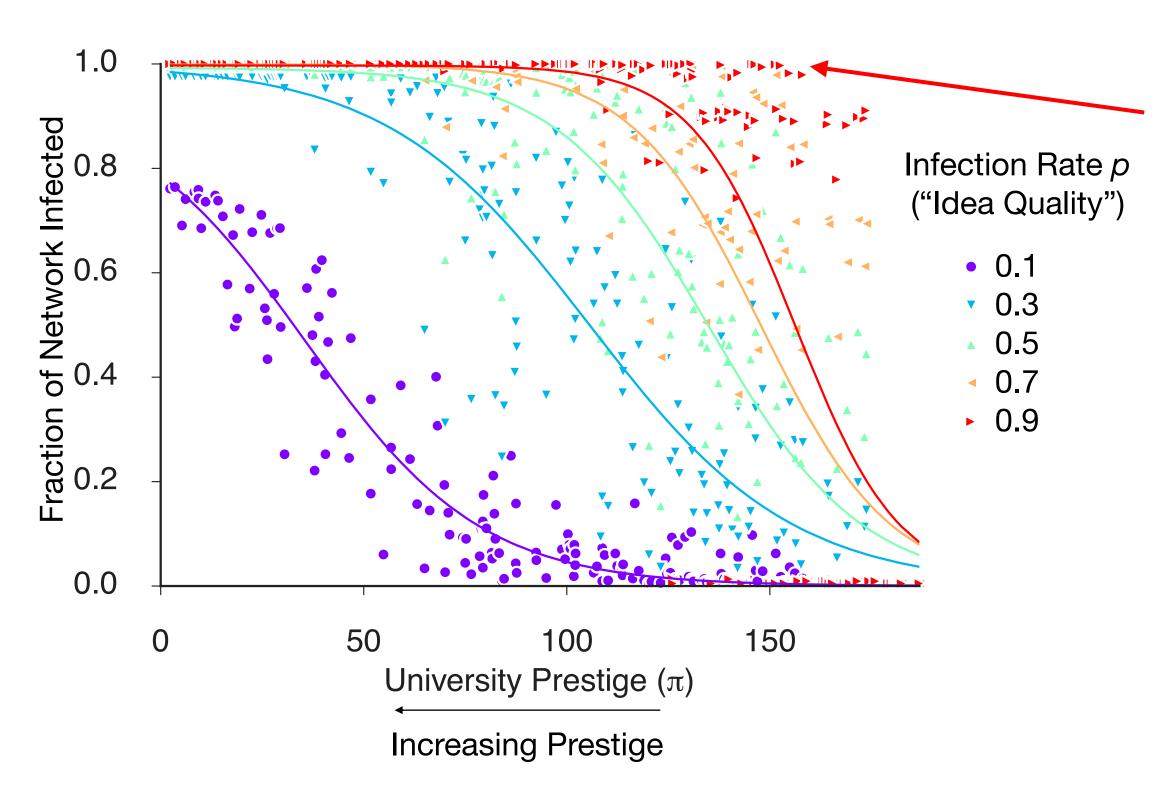
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Network position & the spread of ideas

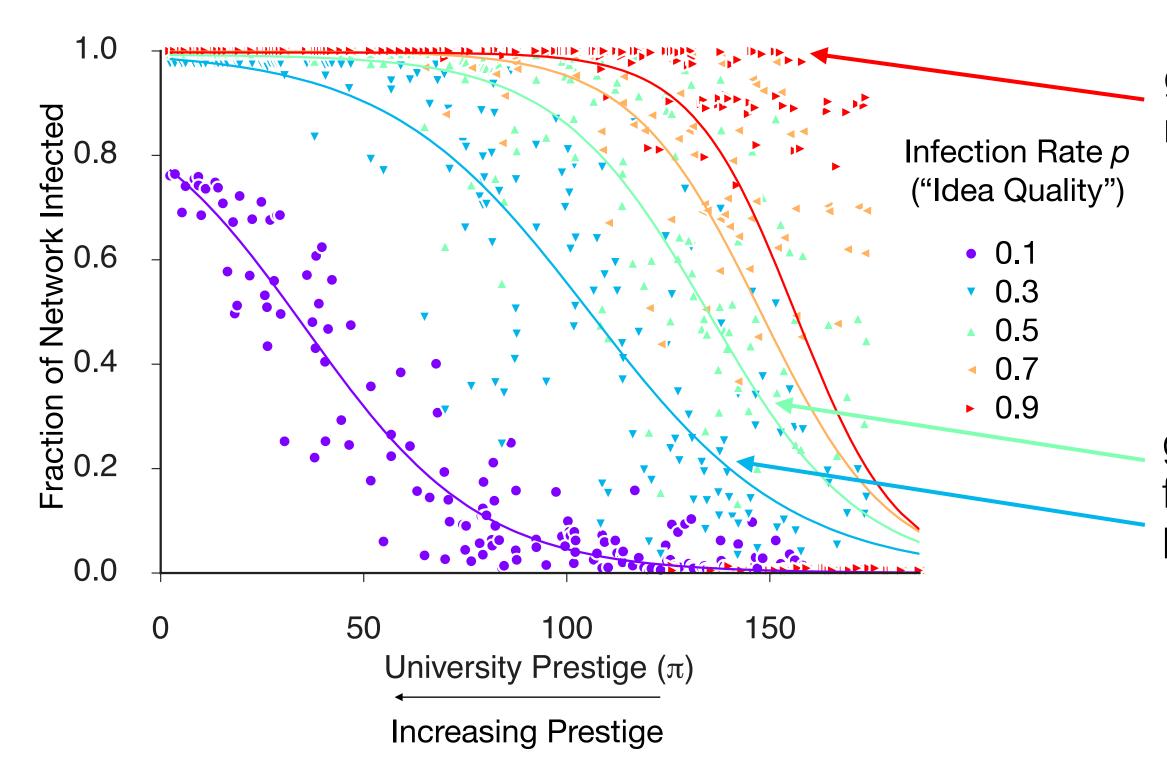


Network position & the spread of ideas



great ideas take root, regardless of starting place

Network position & the spread of ideas



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good ideas spread easily from high-prestige univs, but poorly otherwise.

Analyzed over 200,000 computer science publications and over 2,500 hires. Flagged publications on topic modeling, incremental computing, deep learning.

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Identified faculty who brought [topic] with them when they were hired. Identified faculty who began working on [topic] only 2+ yrs after being hired.

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Compared relative rates of hiring-link spread vs spontaneous spread. (vs random)

Spread of topic modeling (p=0.01) & incremental computing (p=0.01) significantly tied to infection via hiring. Spread of deep learning (p=0.2) not significantly linked to hiring.



Colorado

Sam Way Aaron Clauset Allison Morgan Dimitrios Economou

Kauffman / Lux Sam Arbesman









2018



Allie Morgan



Sam Way



Aaron Clauset

Prestige drives epistemic inequality in the diffusion of scientific ideas Morgan, Economou, Way, Clauset. *Submitted* (2018).

The misleading narrative of the canonical faculty productivity trajectory Way, Morgan, Clauset, Larremore. *PNAS* (2017).

Data-driven predictions in the science of science Clauset, Larremore, Sinatra. *Science* (2017).

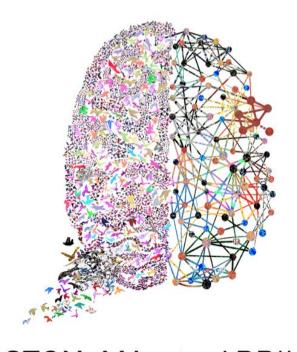
Gender, productivity, and prestige in computer science faculty hiring networks Way, Larremore, Clauset. *Proc. WWW* (2016).

Systematic inequality and hierarchy in faculty hiring networks Clauset, Arbesman, Larremore. *Science Advances*. (2015).

Conference on Complex Networks

COMPLENET '18

Hosted by Northeastern University Network Science Institute



BOSTON, MA APRIL 2018

Xindi Wang





LEARNING TO PLACE OBJECTS: A NETWORK-BASED APPROACH

Xindi Wang

Onur Varol



Tina Eliassi-Rad



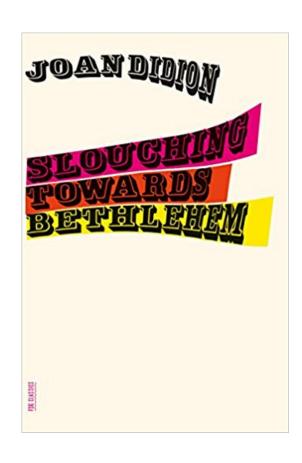
Albert-László Barabási

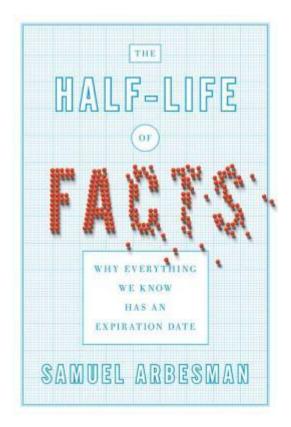


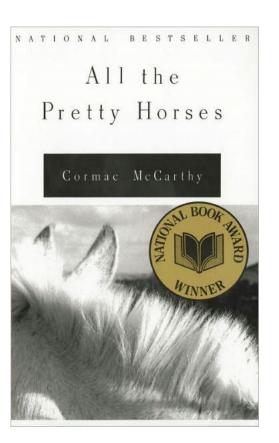
Suppose I give you a book. Predict its sales.

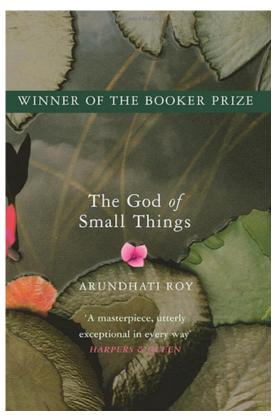
Existing data: books and their sales.

1. turn books into feature vectors.









2. Train a model: $P(\mathsf{book}\,i > \mathsf{book}\,j \mid \overrightarrow{x}_i, \overrightarrow{x}_j, \theta)$

 \overrightarrow{x}_1

 \overrightarrow{x}_2

 \overrightarrow{x}_3

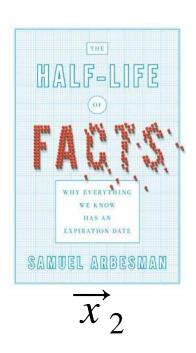
 \overrightarrow{x}_4

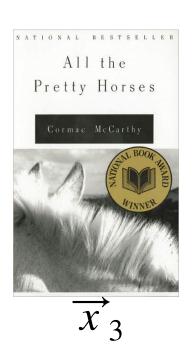
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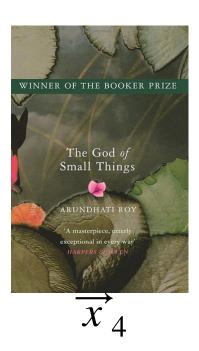
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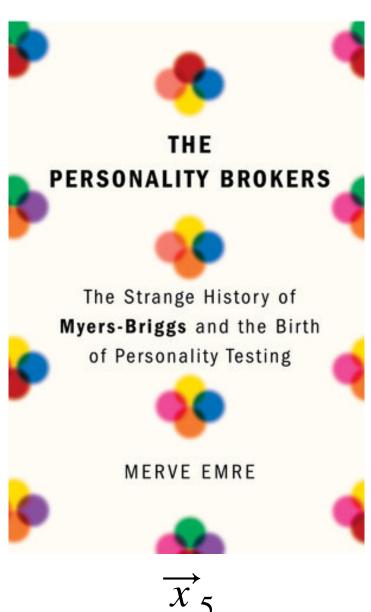








- 2. Train a model.
- 3. Use the model to simulate pairwise competitions. $P(\text{book } i > \text{book } 5 \mid \overrightarrow{x}_i, \overrightarrow{x}_5, \theta)$
- 4. Use [your favo(u)rite algorithm] to infer rank₅ from pairwise comparisons.



Area under the receiver-operator curve (AUC)

Me	ethod	AUC on Fiction	AUC on Biography
	KNN	0.759	0.815
	Cohen et al.	0.892	0.871
	WTG wave	0.910	0.892
Pairwise +	Voting	0.915	0.891
	FAS-PIVOT	0.907	0.892

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Now the question is: why do the top four algorithms perform similarly?

What does that tell us about the structure of the problem and the structure of the space over which we are ranking?

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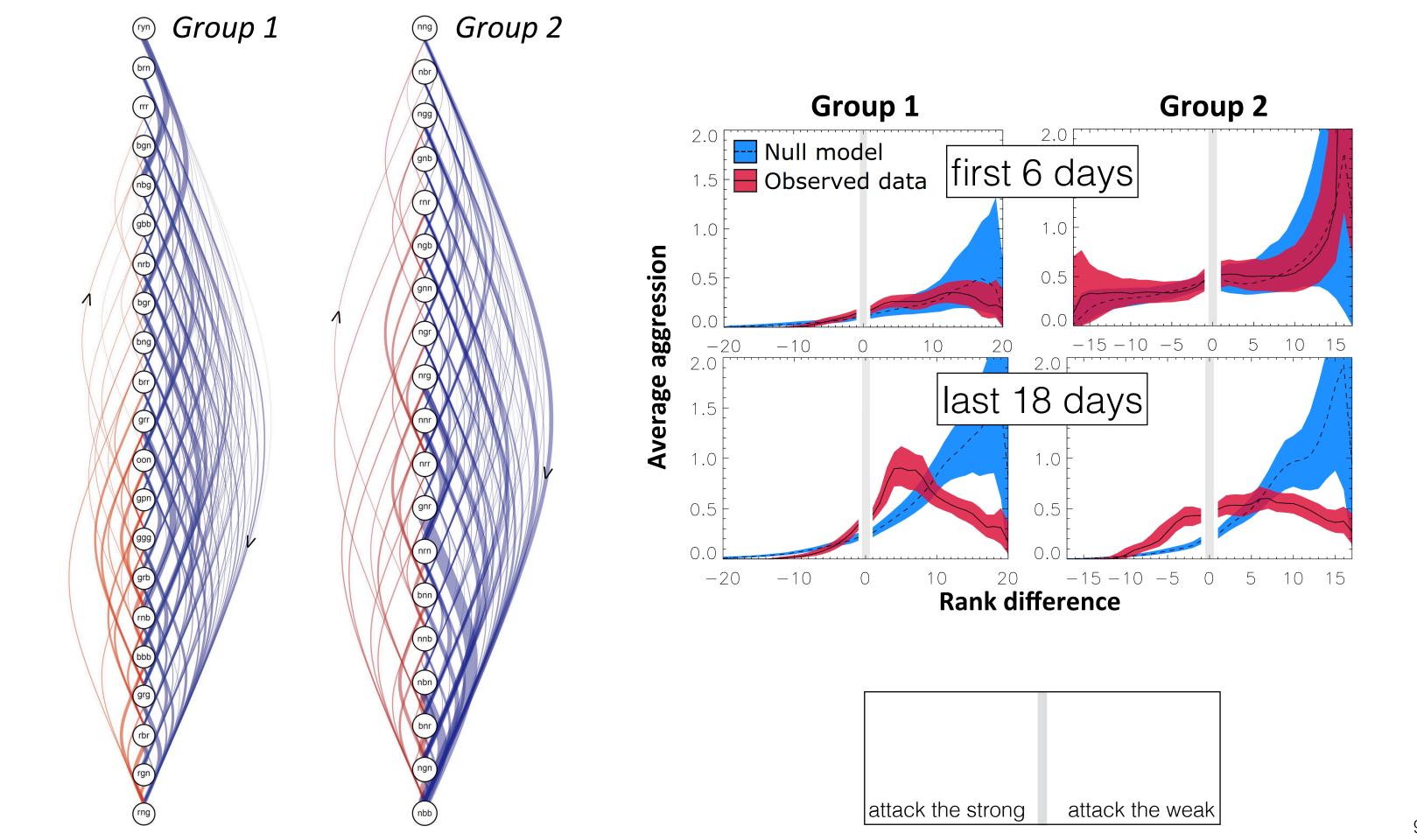
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Want to learn more? xindi.w1993@gmail.com

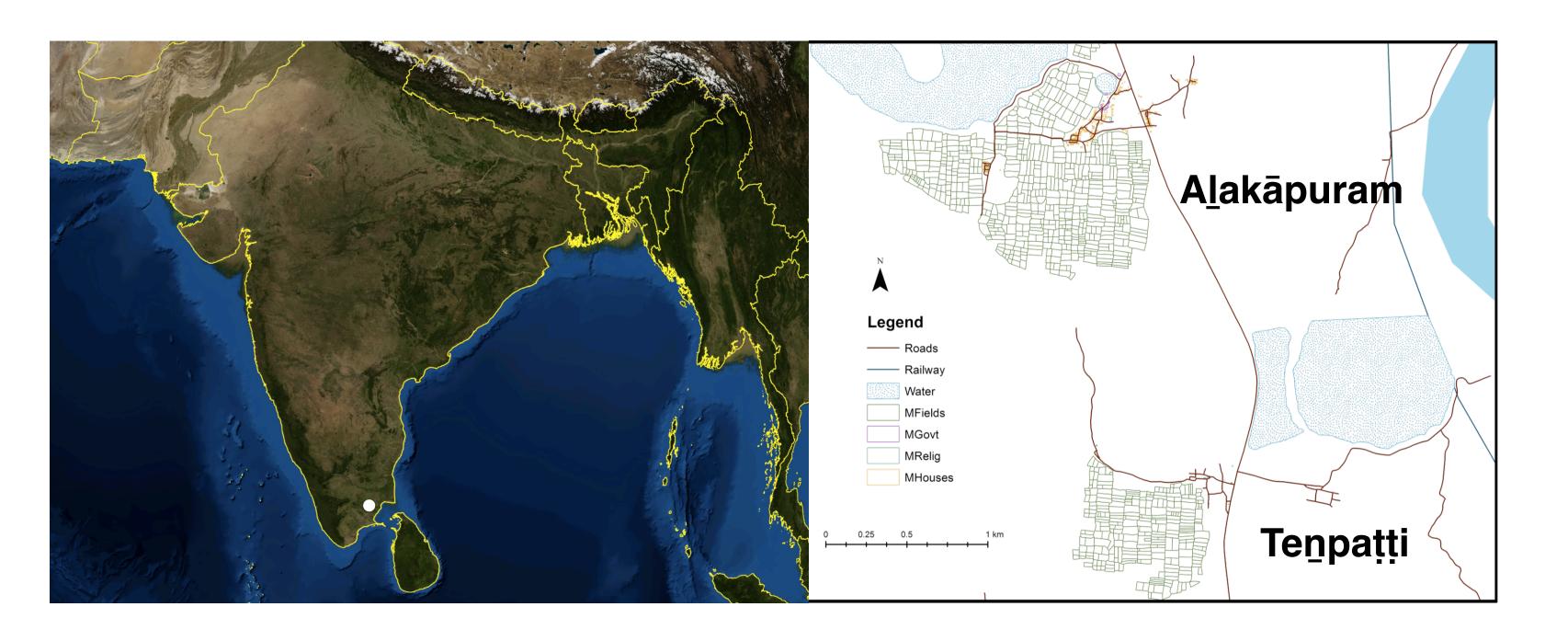








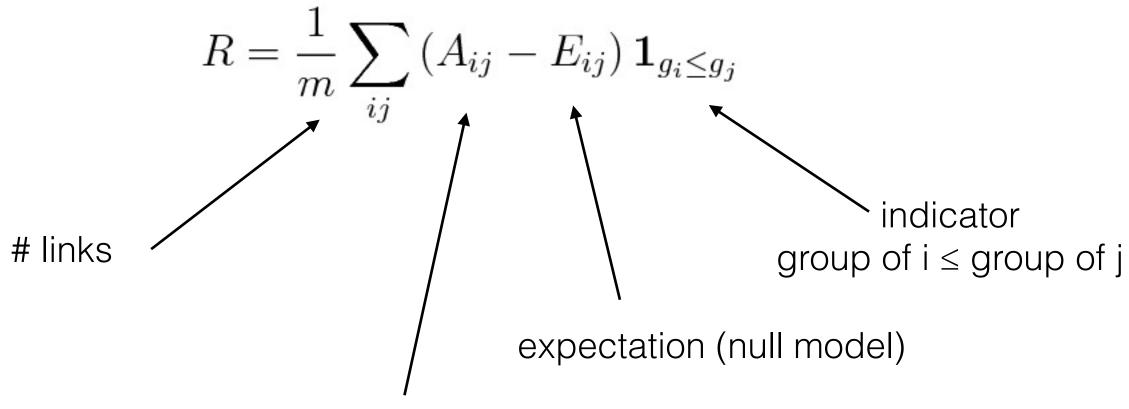
South Indian networks: Tenpaţţi and Alakāpuram



1964 question of Srinavas and Béteille: beyond ethnographic investigations?

Ranked order quality, R

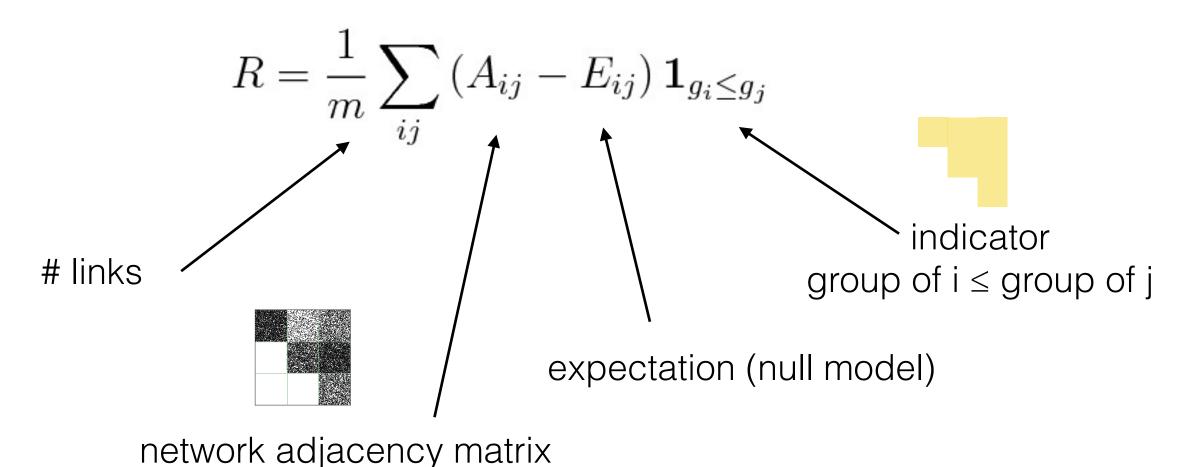
We propose to measure the quality of a ranked ordering by R

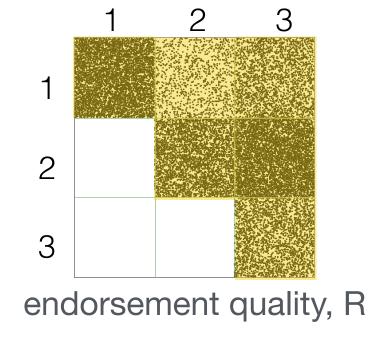


network adjacency matrix

Ranked order quality, R

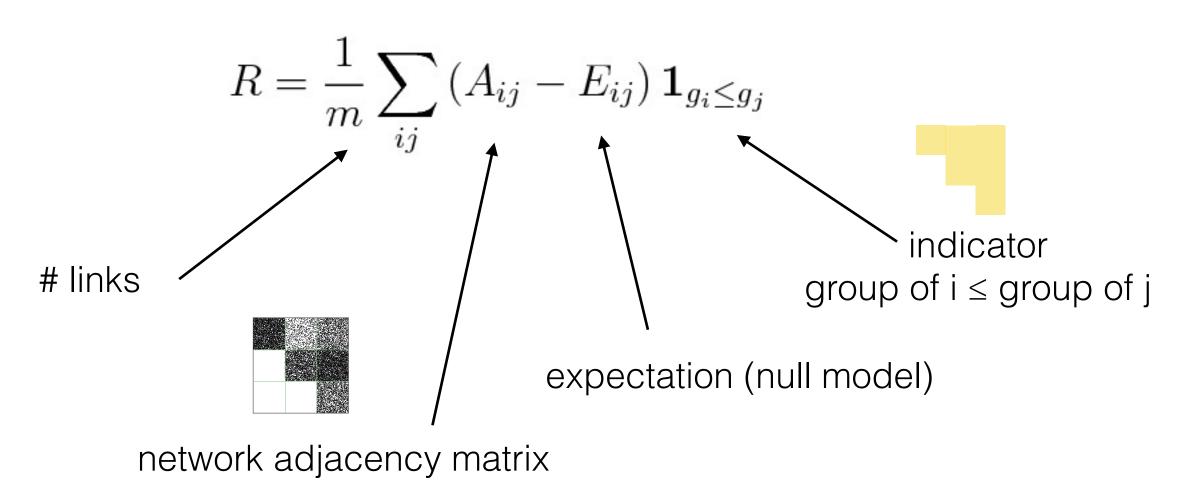
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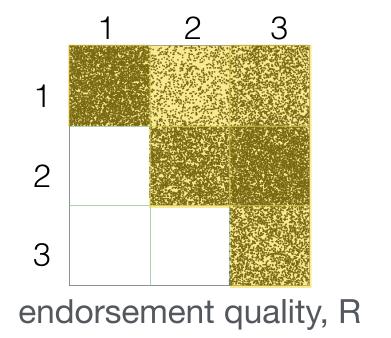


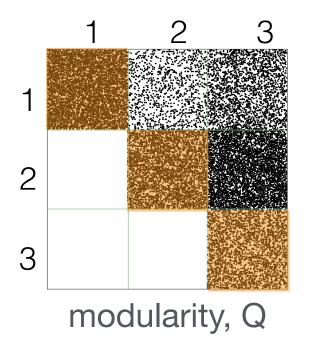


Ranked order quality, R

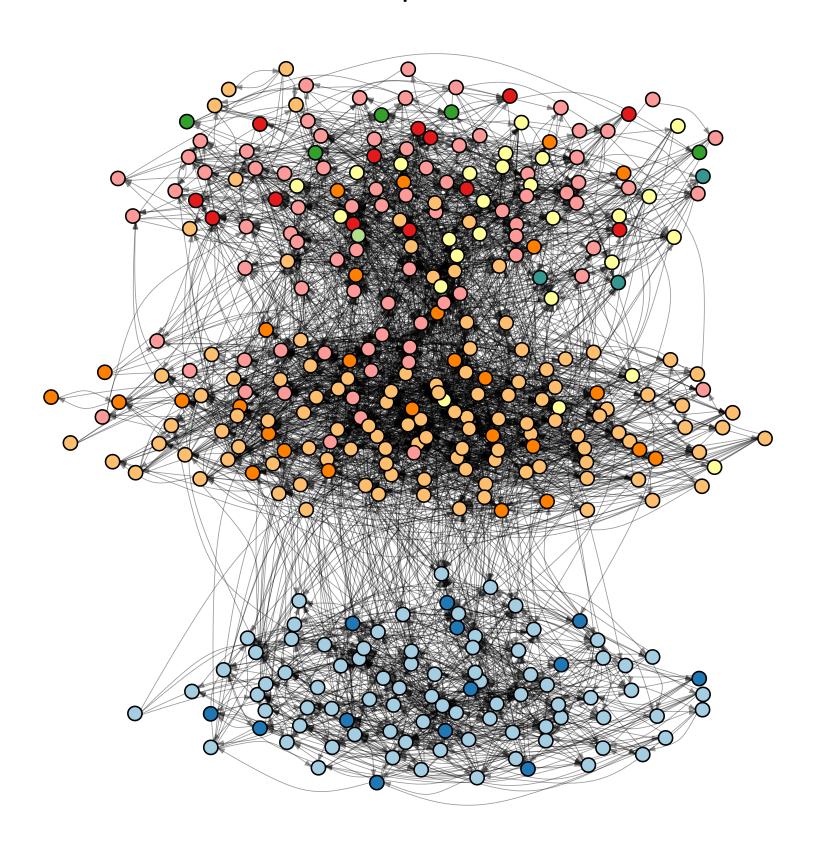
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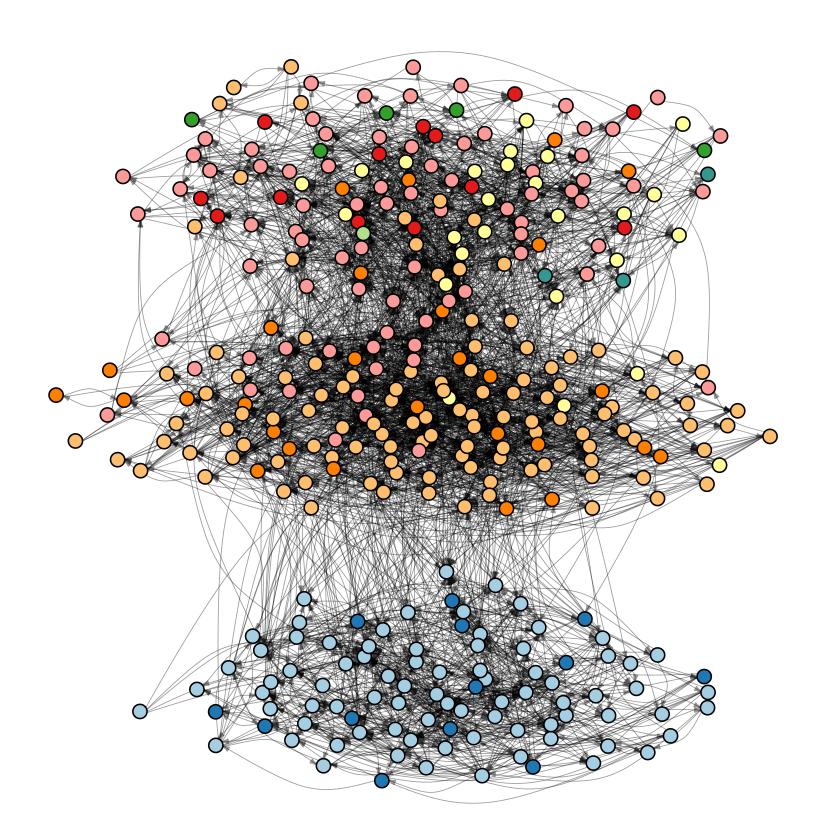




Tenpațți



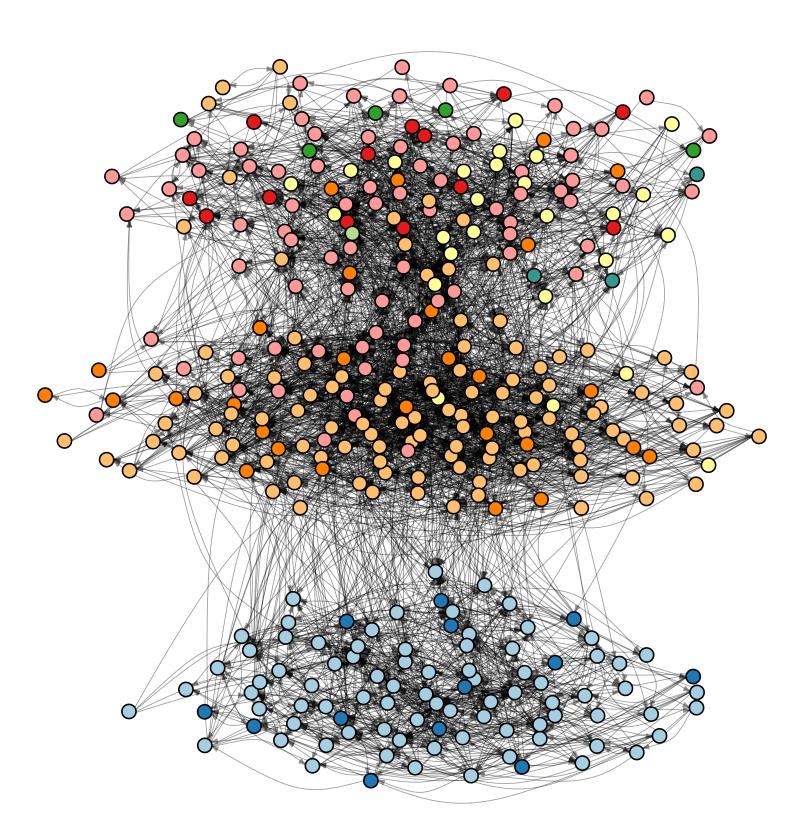
Tenpaţţi



Caste

- Hindu Yaathavar
- Pallar
- Arundhathiyar
- Agamudaiyaan
- Aasaari
- Naayakkar
- RC Yaathavar
- Kallar
- Kulaalar

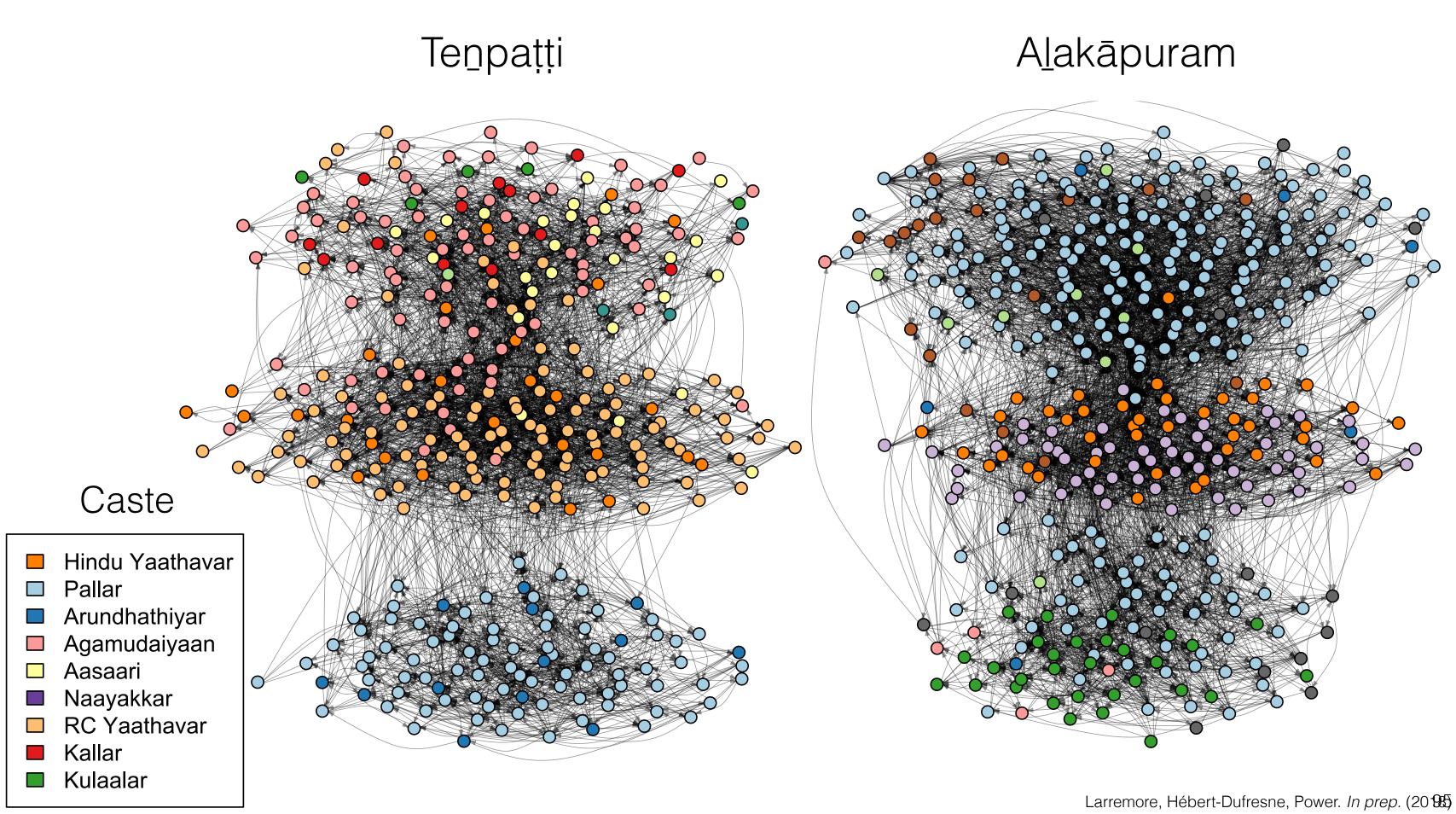
Tenpaţţi



Scheduled castes—*dalit* "untouchable"

Caste

- Hindu Yaathavar
- Pallar
- Arundhathiyar
- Agamudaiyaan
- Aasaari
- Naayakkar
- RC Yaathavar
- Kallar
- Kulaalar



Many uses for models of large-scale structure

Treat the network like a system:

Extrapolation. Make predictions for as-yet unseen nodes (in "space" or time). **Interpolation**. Identify missing links.

Generalization. Nodes of this type are like others of the same type.

Treat the network like an artifact:

Mechanisms. How did this network arise? What rules governed its assembly? **Explanations**. Coarse-graining or compression.

Treat the network like a means to an end; an intermediate data structure:

Useful division. Need groups so that we can assign treatments in an A/B test. **Simplification**. Downstream regression model needs ranks or groups.

intuition: compare this list with the list you would write for regression

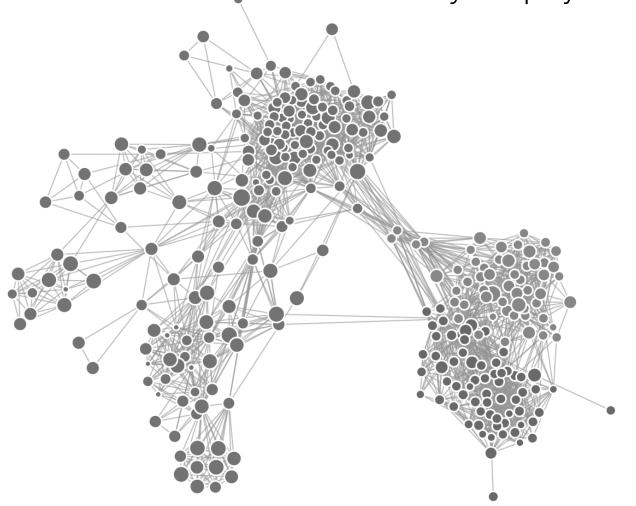
Simplicity is a great virtue but it requires hard work to achieve it and education to appreciate it. And to make matters worse: complexity sells better.

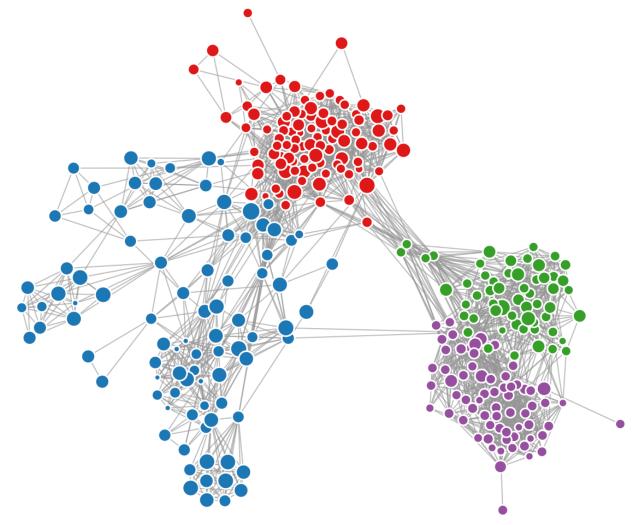
E. W. Dijkstra

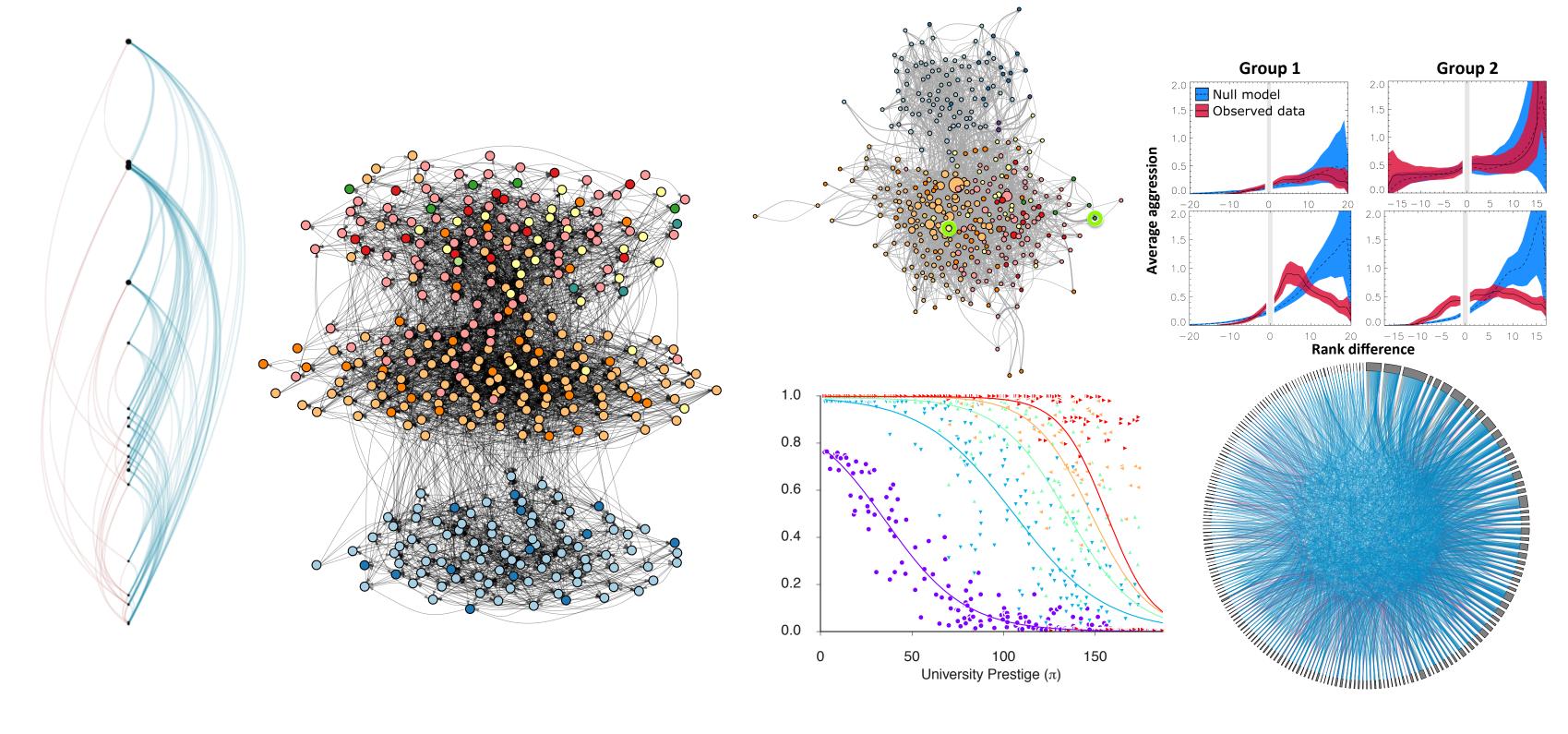
We can interpret this in two ways:

The Cynic: Pictures of networks can be *really cool* but our goal is to do good science, not make pretty pictures.

The Scientist: The most beautiful science is when we correctly simplify a complex system.







Prestige and status structures emerge in networks & we can identify them.

Beyond pictures: these things matter. traps, formation, ideas, & inequalities.

Thank you

@danlarremore daniel.larremore@colorado.edu