

What is the core distribution of a graph telling us?

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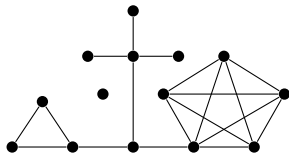


Setting: statistical models for random graphs

How to capture node importance?

In some applications, it matters not just to **how many** other nodes a particular node in the network is connected, but also to **which** other nodes it is connected.

→ Is degree-centric analysis suitable? ←



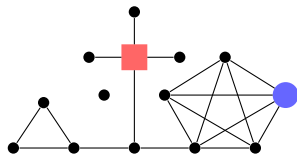
- Examples: information dispersal, the spread of disease or viruses, or robustness to node failure...
- Social network setting: record 'node celebrity status'.

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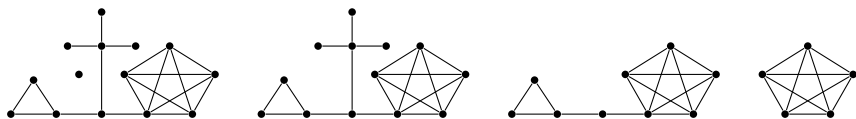
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Classifying vertices: coreness (a.k.a. shell index)

[Seidman83]: A k -core decomposition of a graph captures precisely this:



Any vertex may live in **many cores**, but only **one shell**.

Vast literature on:

- Fast computation of shell indices;
- Interesting applications and heuristic studies.

Not surfaced in stats literature so far:

- A rigorous statistical model for networks relying on core structure.

→ Core structure is summarized by **shell distribution**. ←

The shell distribution model.

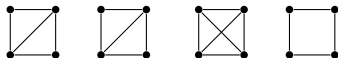
- $G = g$: a random instance of a graph on n nodes
- $n_i(g)$: number of vertices in shell i ; p_i : the “shell parameter”

$$P(G = g; p) = \varphi(p) \prod_{i=0}^{n-1} p_i^{n_i(g)}$$

Exponential family form

$$P(G = g; p) = \exp\left\{\sum_{i=0}^{n-2} n_i(g)\theta_i - \psi(\theta)\right\}.$$

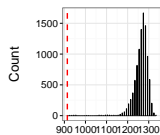
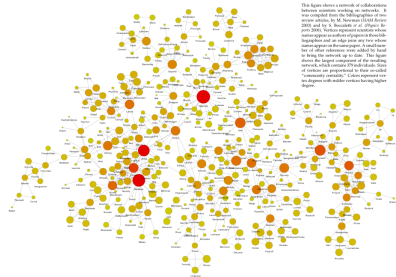
- Shell $\not\leftrightarrow$ degree distribution:
- Erdős-Rényi not a formal submodel
- Log-linear structure only on ‘atomic level’.



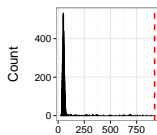
Sampling from the model - Authorship dataset

The largest connected component of the network science co-authorship network (379 nodes)

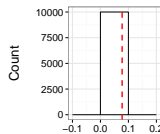
Collaboration Between Network Scientists



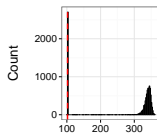
Edges



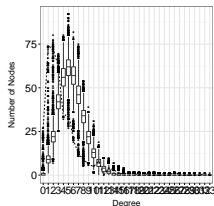
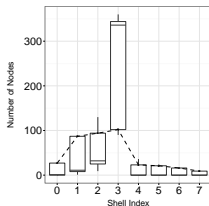
Triangles



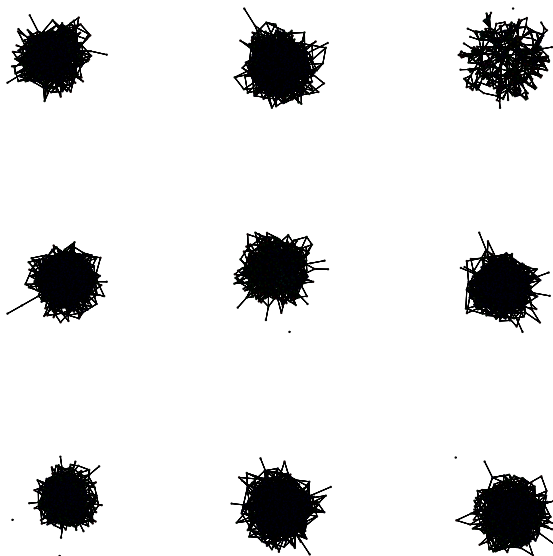
Centrality



Largest Core Size



Typical graphs from the model - Authorship dataset

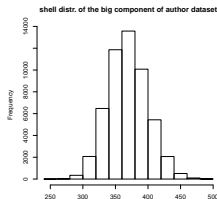


... what to
do with
this??

Exploring structure of graphs within a fiber

- The author network component core distribution can be realized with graphs that have from about 250 to 500 triangles.
- Simulations: examples from $n = 18$ to $n = 57$ nodes, algorithm never visited the same graph twice, min and max number of triangles differ by a factor of 2 or 3.

A typical histogram of number of triangles:



So what do we have?

- Model that provides necessary formalism for using k -cores in statistical considerations
- Algorithm for constructing all graphs with given shell structure
- MCMC algorithm for simulating from the model

3 problems

(... or: the usual ERGM suspects)

- Model fitting questions lead to three important subproblems;
- * Solving these is crucial for MLE estimates and goodness of fit tests *
- 1) Existence of MLE - captured by the **model polytope**:

Theorem

The polytope of all shell distribution vectors is a dilate of a simplex.

All **realizable** lattice points lie on the **boundary** of this polytope.

The MLE **never** exists for a sample of size 1.

- 2) Sampling from the fibers (via the Metropolis algorithm):

Algorithm

Randomly construct a graph with a given shell distribution.

Constructs **all** graphs with positive probability.

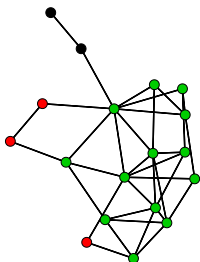
Experiments: fast graph discovery.

3 problems (continued)

(... or: the usual ERGM suspects)

3) Sampling from the model: direct sampling intractable

- Sampson data set: 18 monks in a New England Monastery: $n_S(g) = (0, 2, 3, 15, 0, 0, \dots)$
- MCMC scheme: “tie-no-tie” proposal [Caimo et al] - good mixing
- Probability of accepting: $\pi = \min\left(1, \prod_i p_i^{n_i(g') - n_i(g)}\right)$.

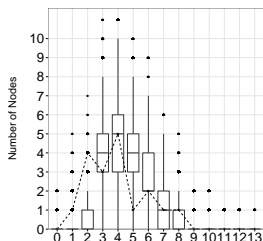
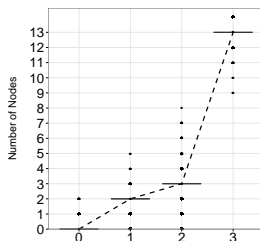
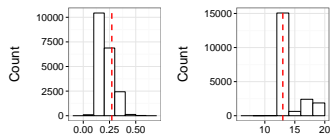
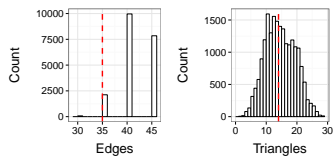
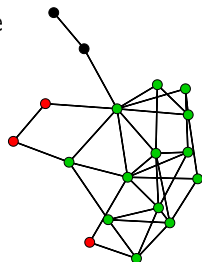


3 problems (continued)

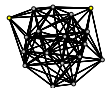
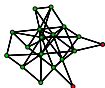
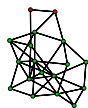
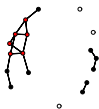
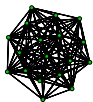
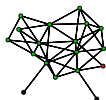
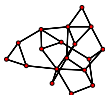
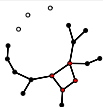
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Model degeneracy! - example



Extending the model family

Introduce a parameter for the degeneracy of a graph:

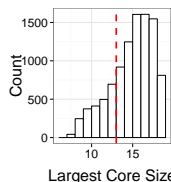
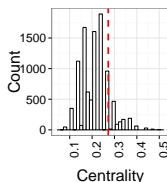
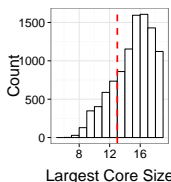
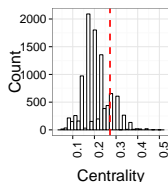
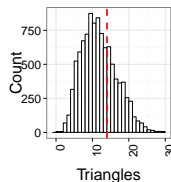
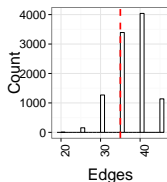
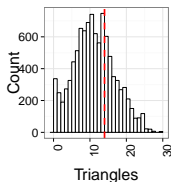
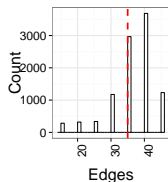
$$P(G = g; p, m) = \varphi(p) \prod_{i=0}^{n-1} p_i^{n_i(g)}, \text{ if } g \in \mathcal{G}_{n,m} := \{G : dgen(G) \leq m\}.$$

It means that all graphs under this model will have degeneracy at least m .

- Treat m as a parameter (that needs to be estimated)
 - analogous to choosing the number of components in a mixture model vs. assuming that it is known.
- We treat m as fixed - select the observed value of m .
- Estimation - open; but at least the new model is not degenerate.

Simulations - Sampson network

Two submodels: support graphs with degeneracy ≤ 3 , or $= 3$ (observed).



- Note heavier tails in one model
- Parameter used = good estimate of MLE (moment equations)
(expected shell distrib. under the MLE very close to observed)

Simulations - Sampson network - typical graphs

