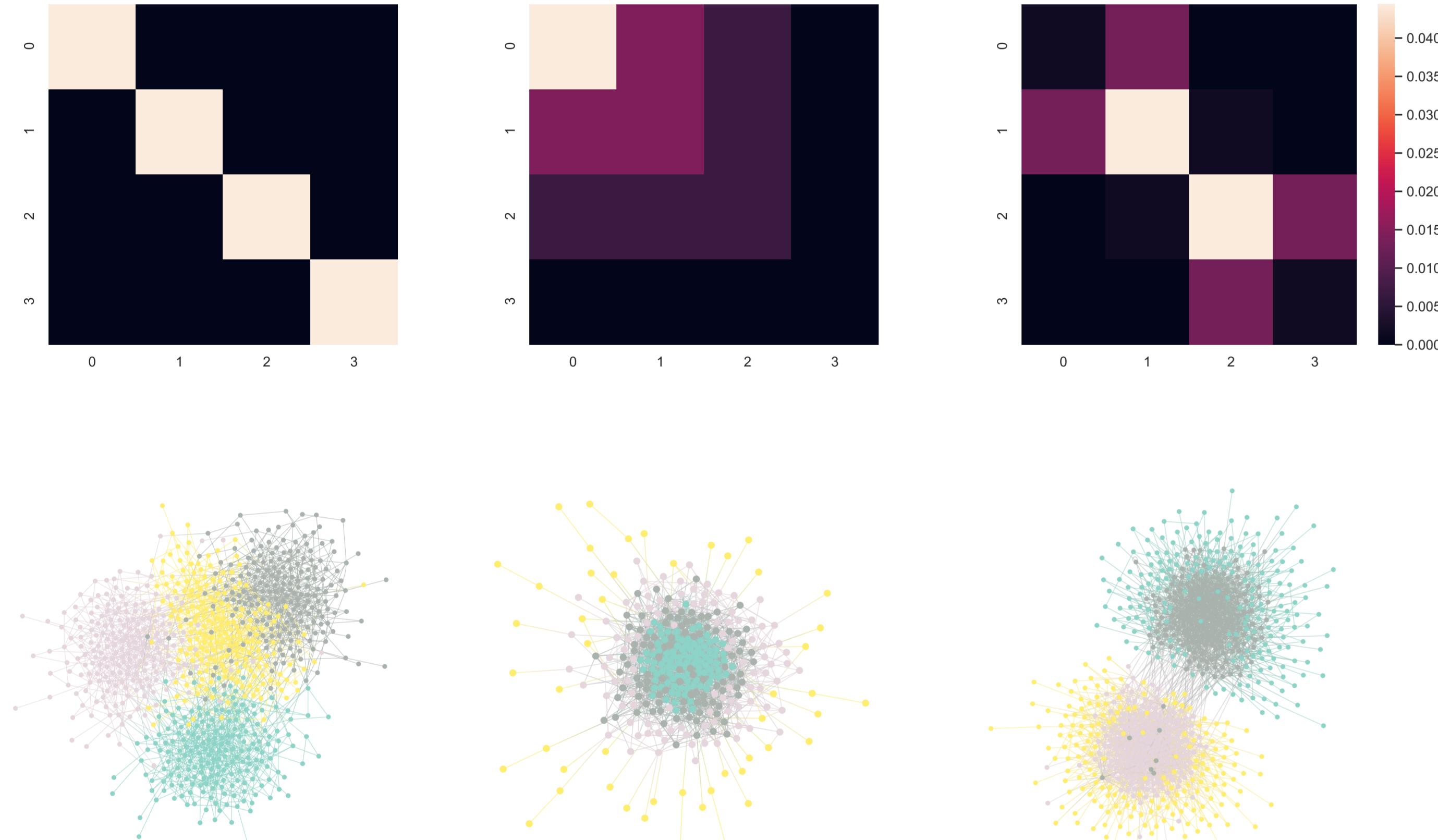


Motivation

- We are interested in finding **assortative** structure in networks
- The general stochastic block models (**SBMs**) can describe general mixing patterns including assortativity as a special case
- However, when assortativity is indeed the dominating pattern, the general model gives more than we need

Our contribution: develop a nonparametric Bayesian approach based on a constrained variant of SBM to detect assortative structure



Top panel: connection matrix indicating the probability of placing edges between different groups with assortative (left) core-periphery (middle) and a mixture of the former two structures (right). Bottom panel: networks generated from SBMs with community structure.

Bayesian inference for community detection

- For an observed network with adjacency matrix A , we sample or maximise from the posterior distribution of vertices partition \mathbf{b}
- The Bayes' rule

$$P(\mathbf{b}|\mathbf{A}) = \frac{P(\mathbf{A}|\mathbf{b})P(\mathbf{b})}{P(\mathbf{A})}$$

- The marginal likelihood of our model, the planted partition model (**PPM**), reads as

$$P(\mathbf{A}|\mathbf{b}) = \frac{e_{in}!e_{out}!}{\binom{B}{2}^{e_{in}} \binom{B}{2}^{e_{out}} (E+1)^{1-\delta_{B,1}}} \times \prod_r \frac{(n_r-1)!}{(e_r+n_r-1)!} \times \frac{\prod_i k_i}{\prod_{i < j} A_{ij}! \prod_i A_{ii}!!}$$

- With any appropriate choice of the prior $P(\mathbf{b})$, we can approximate the posterior distribution $P(\mathbf{b}|\mathbf{A})$ via sampling with Markov Chain Monte Carlo (MCMC)
- For model selection, we compute the description length of the data

$$\Sigma = -\ln P(\mathbf{A}|\mathbf{b}) - \ln P(\mathbf{b})$$

Modularity optimisation and maximum likelihood are not equivalent

- As shown in the literature, there is a connection between the log-likelihood function of PPM and the modularity function

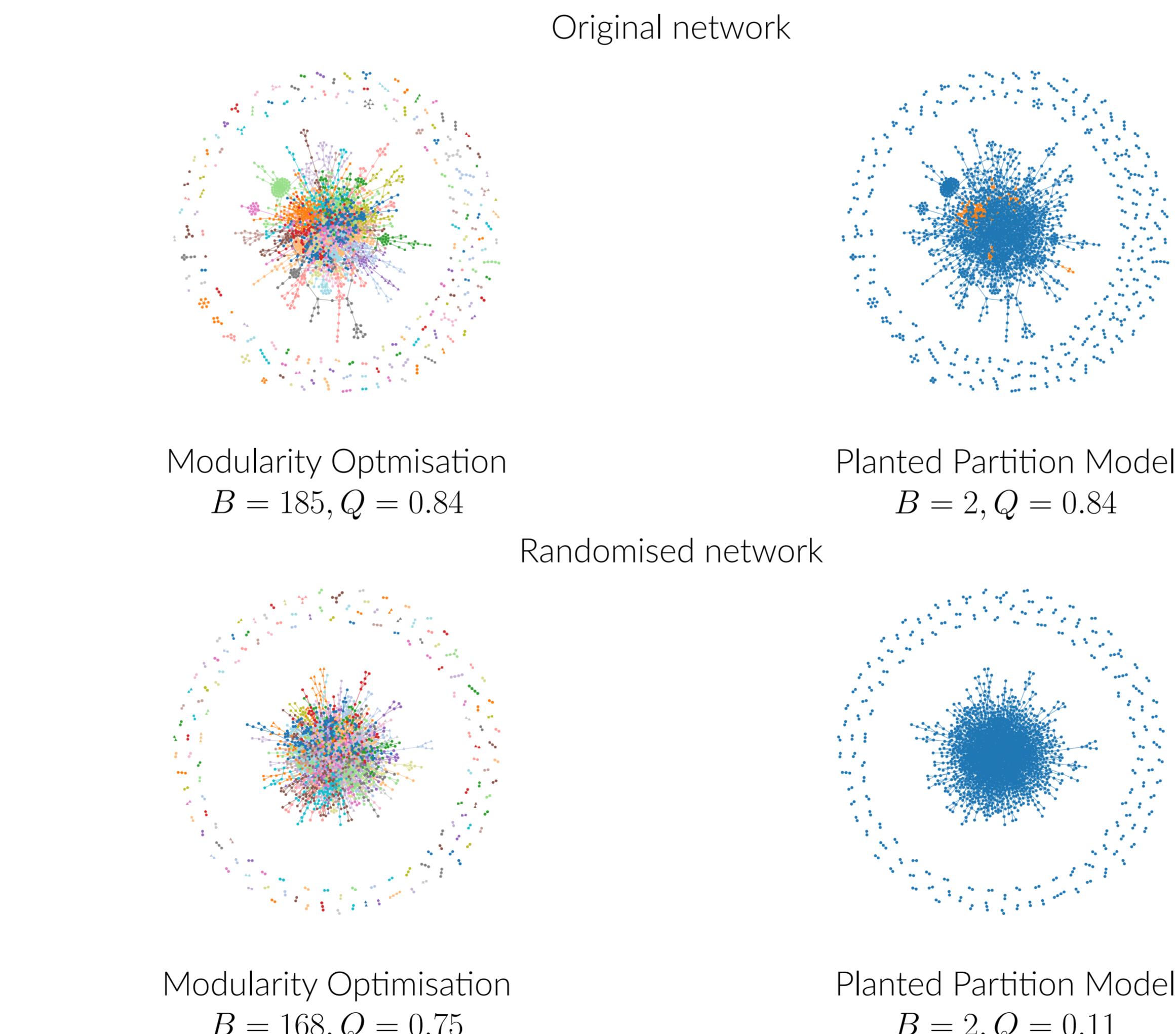
$$\text{Log-likelihood: } \ln \mathcal{L} = \frac{\mu}{2}(A_{ij} - \gamma\theta_i\theta_j)\delta_{b_ib_j} + E \log \lambda_{out} - \frac{\lambda_{out}}{2} \left(\sum_i \theta_i \right)^2 + \sum_i k_i \ln \theta_i$$

$$\text{Modularity: } Q = \frac{1}{2E} \sum_{ij} \left(A_{ij} - \frac{k_i k_j}{2E} \right) \delta_{b_ib_j}$$

- Maximising modularity is equivalent to maximising the log-likelihood of PPM when the model parameters are set to constant (i.e. $\mu, \gamma, \lambda_{out}$, and $\{\theta_i\}$)

- **However**, such equivalence is tenuous since model parameters should be estimated via the maximum likelihood principle
- Even when it holds, modularity optimisation is prone to overfitting just as the maximum likelihood approach does

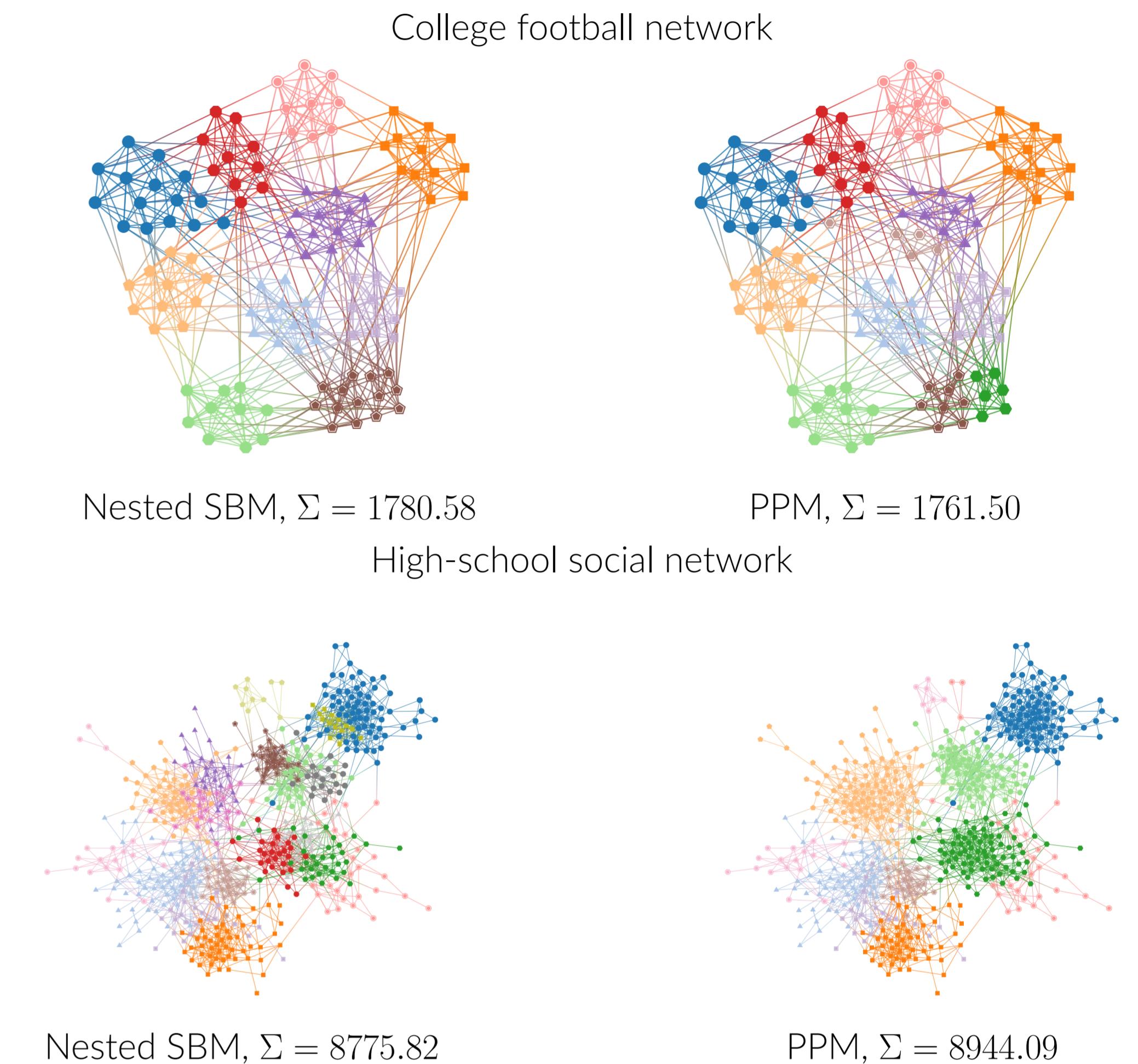
Robust against overfitting



- We applied modularity optimisation and our Bayesian approach with PPM to a network of protein-protein interactions

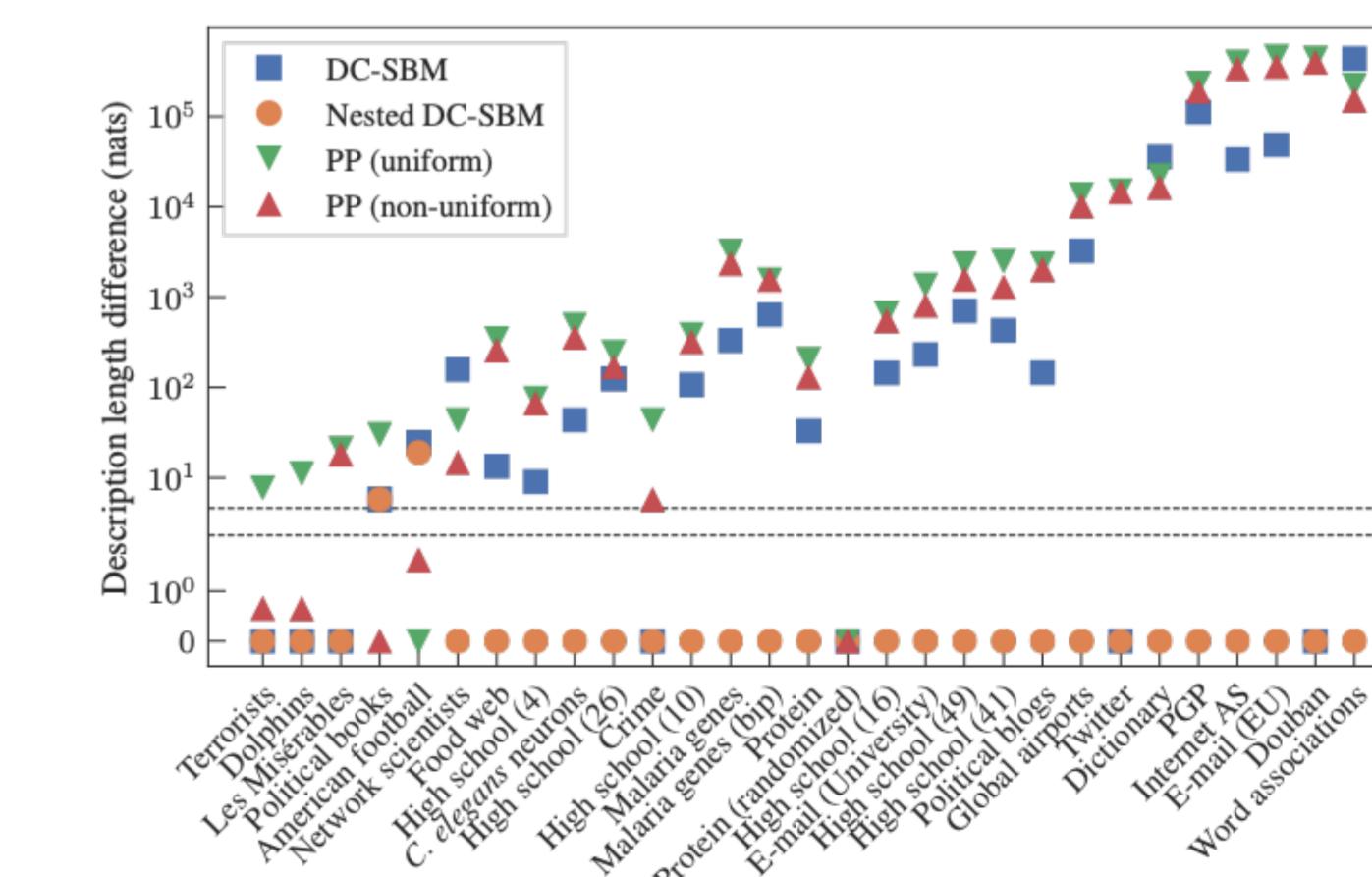
- Results obtained in the original network (top panel) and a randomised version of the network (bottom panel) are shown above
 - Modularity optimisation finds over a hundred of communities in the original and the randomised network, **with high value of modularity in both cases**
 - In comparison, the Bayesian approach **does not** return spurious communities in the random case

Model selection



Rather taking for granted, we can check the assumption of assortativity by model selection. The best model is the one has the **minimum description length Σ**

- If assortativity is indeed the dominating pattern, partitions given by PPM should ascribe the smallest Σ compared to other model variants (e.g. college football network)
- When more general pattern is the dominating pattern, other model variants allowing a general mixing pattern should outperform PPM (e.g. high-school social network)



In our study of a selection of empirical networks,

- Only a few networks with assortativity being the dominating pattern
- Most of the time (especially in large networks) more general mixing pattern are preferred, raising a **caveat** on the practice of exclusively searching for assortative structure

Further materials

paper: available on arXiv <https://arxiv.org/abs/2006.14493>

code: available in the *graph-tool* library <https://graph-tool.skewed.de/>

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