Network Inference Part 2

Tiago P. Peixoto

 $University \ of \ Bath$

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NETWORK MEASUREMENTS ARE NOISY



(A social network)

- ▶ As with any empirical measurement, network data are unreliable.
- ▶ However, very few datasets contain any kind of error estimate!
- ▶ We know there must be errors, but we do not know how many, or where they are located.

NETWORK RECONSTRUCTION TASK



So that \hat{A} is as close as possible to A^* .

Caveats:

- With a single copy of A.
- ▶ Without knowing how strong the noise is (i.e. the number of missing or spurious edges).

HOW IS RECONSTRUCTION POSSIBLE?



(a)

(b)

HOW IS RECONSTRUCTION POSSIBLE?



We need:

- ► A model for structure.
- ▶ A model for noise.

HOW IS RECONSTRUCTION POSSIBLE?



We need:

- ► A model for structure.
- ▶ A model for noise.

(but for networks)

NONPARAMETRIC BAYESIAN INFERENCE

- \blacktriangleright A model for structure, $P({\pmb A}|\theta)$
- ▶ A model for noise, $P(\mathcal{D}|\mathbf{A}, \phi)$

 $A \rightarrow$ Network, $\mathcal{D} \rightarrow$ Measured data, $(\theta, \phi) \rightarrow$ Parameters



Marginal probabilities:

$$P(\mathbf{\mathcal{D}}|\mathbf{A}) = \int P(\mathbf{\mathcal{D}}|\mathbf{A}, \phi) P(\phi) d\phi$$
$$P(\mathbf{A}) = \int P(\mathbf{A}|\theta) P(\theta) d\theta$$

STRUCTURE: THE STOCHASTIC BLOCK MODEL (SBM)

Planted partition: N nodes divided into B groups.



Degree-corrected: Arbitrary degree sequence: $\{\kappa_i\}$

- ▶ Not restricted to assortative structures ("communities").
- ► Easily generalizable (edge direction, overlapping groups, etc.)

BAYESIAN SBM

$$P(\boldsymbol{A}|\boldsymbol{\lambda},\boldsymbol{\kappa},\boldsymbol{b}) = \prod_{i < j} \frac{(\kappa_i \kappa_j \lambda_{b_i b_j})^{A_{ij}} e^{-\kappa_i \kappa_j \lambda_{b_i b_j}}}{A_{ij}!} \times \prod_i \frac{(\kappa_i^2 \lambda_{b_i b_i}/2)^{A_{ii}/2} e^{-\kappa_i^2 \lambda_{b_i b_i}/2}}{(A_{ii}/2)!}$$

Noninformative priors:
$$P(\boldsymbol{\lambda}|\boldsymbol{b}) = \prod_{r \leq s} e^{-\lambda_{rs}/(1+\delta_{rs})\bar{\lambda}}/(1+\delta_{rs})\bar{\lambda}$$

$$P(\boldsymbol{\kappa}|\boldsymbol{b}) = \prod_{r} (n_r - 1)! \delta(\sum_{i} \kappa_i \delta_{b_i, r} - 1)$$

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Marginal likelihood:

$$P(\boldsymbol{A}|\boldsymbol{b}) = \int P(\boldsymbol{A}|\boldsymbol{\lambda}, \boldsymbol{\kappa}, \boldsymbol{b}) P(\boldsymbol{\lambda}|\boldsymbol{b}) P(\boldsymbol{\kappa}|\boldsymbol{b}) \, \mathrm{d}\boldsymbol{\lambda} \mathrm{d}\boldsymbol{\kappa}$$

$$= \frac{\bar{\lambda}^E}{(\bar{\lambda}+1)^{E+B(B+1)/2}} \times \frac{\prod_{r < s} e_{rs}! \prod_r e_{rr}!!}{\prod_{i < j} A_{ij}! \prod_i A_{ii}!!} \times \prod_r \frac{(n_r - 1)!}{(e_r + n_r - 1)!} \times \prod_i k_i!$$

$$= P(\boldsymbol{A}|\boldsymbol{k}, \boldsymbol{e}, \boldsymbol{b}) P(\boldsymbol{k}|\boldsymbol{e}, \boldsymbol{b}) P(\boldsymbol{e})$$

BAYESIAN SBM

$$P(\boldsymbol{A}|\boldsymbol{\lambda},\boldsymbol{\kappa},\boldsymbol{b}) = \prod_{i < j} \frac{(\kappa_i \kappa_j \lambda_{b_i b_j})^{A_{ij}} e^{-\kappa_i \kappa_j \lambda_{b_i b_j}}}{A_{ij}!} \times \prod_i \frac{(\kappa_i^2 \lambda_{b_i b_i}/2)^{A_{ii}/2} e^{-\kappa_i^2 \lambda_{b_i b_i}/2}}{(A_{ii}/2)!}$$

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Marginal likelihood:

Edge counts e.

Degrees, k.

NESTED SBM: GROUP HIERARCHIES



Deeper Bayesian hierarchy:

- ▶ Prevents underfitting.
- ▶ Multiple scales of description.



Measurement model

 $\operatorname{Edge-o-meter}$

 $\begin{array}{l} p \rightarrow \text{probability of a missing edge } (1 \rightarrow 0) \\ q \rightarrow \text{probability of a spurious edge } (0 \rightarrow 1) \end{array}$



 $n_{ij} \rightarrow$ number of measurements of pair (i, j) $x_{ij} \rightarrow$ number of edges recorded

$$P(x_{ij}|n_{ij}, A_{ij}, p, q) = \binom{n_{ij}}{x_{ij}} \left[(1-p)^{x_{ij}} p^{n_{ij} - x_{ij}} \right]^{A_{ij}} \left[q^{x_{ij}} (1-q)^{n_{ij} - x_{ij}} \right]^{1-A_{ij}}$$

$$\begin{split} P(\boldsymbol{x}|\boldsymbol{n},\boldsymbol{A},\boldsymbol{\alpha},\boldsymbol{\beta},\boldsymbol{\mu},\boldsymbol{\nu}) &= \int P(\boldsymbol{x}|\boldsymbol{n},\boldsymbol{A},p,q) P(p|\boldsymbol{\alpha},\boldsymbol{\beta}) P(q|\boldsymbol{\mu},\boldsymbol{\nu}) \, \mathrm{d}p \, \mathrm{d}q \\ P(p|\boldsymbol{\alpha},\boldsymbol{\beta}), P(q|\boldsymbol{\mu},\boldsymbol{\nu}) \to \text{Beta priors} \end{split}$$

The Edge-o-meter



(α, β) = (1, 10) → accurate measurement (low noise)
(α, β) = (50, 100) → high noise, good calibration
(α, β) = (5, 10) → high noise, bad calibration
(α, β) = (1, 1) → <u>noninformative</u> (i.e. uniform distribution)

THE FULL RECONSTRUCTION METHOD

Posterior distribution:

$$P(\boldsymbol{A}, \boldsymbol{b} | \boldsymbol{n}, \boldsymbol{x}, \alpha, \beta, \mu, \nu) = \frac{P(\boldsymbol{x} | \boldsymbol{n}, \boldsymbol{A}, \alpha, \beta, \mu, \nu) P(\boldsymbol{A} | \boldsymbol{b}) P(\boldsymbol{b})}{P(\boldsymbol{x} | \alpha, \beta, \mu, \nu)}$$

We infer both the network \boldsymbol{A} as well as the SBM latent variables \boldsymbol{b} via MCMC:

Move proposals $P(\mathbf{b}'|\mathbf{A}, \mathbf{b})$ and $P(\mathbf{A}'|\mathbf{A}, \mathbf{b})$, accept with probability

$$\min\left(1, \frac{P(\boldsymbol{A}', \boldsymbol{b}' | \boldsymbol{\mathcal{D}}) P(\boldsymbol{A} | \boldsymbol{A}', \boldsymbol{b}') P(\boldsymbol{b} | \boldsymbol{A}', \boldsymbol{b}')}{P(\boldsymbol{A}, \boldsymbol{b} | \boldsymbol{\mathcal{D}}) P(\boldsymbol{A}' | \boldsymbol{A}, \boldsymbol{b}) P(\boldsymbol{b}' | \boldsymbol{A}, \boldsymbol{b})}\right).$$

(Efficient, scales to very large networks.)

HOW DOES IT WORK?



HOW DOES IT WORK?





HOW DOES IT WORK?



EXAMPLE: TERRORIST ASSOCIATIONS



 $$\rm Node\,pair$$ V. Krebs, "Mapping networks of terrorist cells", Connections 24 (3), 43-52

EXAMPLE: ZACHARY'S KARATE CLUB



W. W. Zachary, J. Anthro. Research 33(4), 452-473 (1977)

WAIT! IS THIS JUST EDGE PREDICTION?

It <u>is</u> edge prediction, but it yields a full posterior distribution P(A|n, x) that is **nonparametric**.

We can:

▶ Perform maximum marginal posterior estimation,

$$\hat{A}_{ij} = \begin{cases} 1 & \text{if } \pi_{ij} > 1/2 \\ 0 & \text{if } \pi_{ij} < 1/2, \end{cases}$$

where $\pi_{ij} = \sum_{A} A_{ij} P(A|n, x)$ is the marginal posterior edge probability.

• Estimate network properties $y(\mathbf{A})$ and their error estimates:

$$\hat{y} = \sum_{\boldsymbol{A}} y(\boldsymbol{A}) P(\boldsymbol{A}|\boldsymbol{n}, \boldsymbol{x})$$

$$\sigma_y^2 = \sum_{\boldsymbol{A}} (\hat{y} - y(\boldsymbol{A}))^2 P(\boldsymbol{A}|\boldsymbol{n}, \boldsymbol{x}).$$

RECONSTRUCTION PERFORMANCE

Real network (political blogs) + simulated noise: $p \in [0, 1], \ q = pE/[\binom{N}{2} - E]$



RECONSTRUCTION PERFORMANCE: DEGREES



(p,q) = (0.41, 0.0094)

INFERRING THE NOISE



EMPIRICAL RECONSTRUCTION REDUX

C. elegans neural network



White et al., Phil. Trans. R. Soc. London 314, 1 (1986).

EMPIRICAL RECONSTRUCTION REDUX

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White et al., Phil. Trans. R. Soc. London 314, 1 (1986). π_{ij}

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C. elegans NEURAL NETWORK



C. elegans NEURAL NETWORK



ARXIV.ORG CO-AUTHORSHIP NETWORK



UNCERTAINTY ASSESSMENT OF EMPIRICAL DATA

Dataset Similarity		Nodes	Edges		Degree assortativity		Local clustering		Be	\hat{p}	ĝ
			Direct	Estimated	Direct	Estimated	Direct	Estimated			
karate	0.94(4)	34	78	77(7)	-0.47561	-0.49(5)	0.57064	0.58(5)	2.7(6)	0.06(5)	0.012(10)
terrorists	0.96(2)	62	152	154(8)	-0.08048	-0.096(20)	0.48637	0.50(2)	5.4(5)	0.05(4)	0.003(2)
football	0.857(16)	115	613	500(18)	0.16244	0.18(7)	0.40322	0.68(4)	12.7(3)	0.05(3)	0.0226(19)
netscience	0.9981(17)	379	914	915(3)	-0.08168	-0.0823(18)	0.74123	0.741(3)	29.6(14)	0.004(3)	$3.1(19) \times 10^{-5}$
celegans	0.754(20)	302	2345	3850(150)	-0.16320	-0.165(7)	0.28752	0.374(12)	17.25(19)	0.39(3)	$6(3) \times 10^{-5}$
malaria	0.9981(15)	1103	2965	2973(9)	-0.30013	-0.2997(20)	0	0(0)	30.8(3)	0.004(3)	$4(3) \times 10^{-6}$
power	0.80(7)	4941	6594	9900(1300)	0.00346	0.043(17)	0.08010	0.058(7)	15.6(7)	0.33(10)	$2.5(19) \times 10^{-7}$
polblogs	0.965(5)	1222	16714	17860(190)	-0.22133	-0.2226(16)	0.32025	0.343(5)	16.6(3)	0.066(10)	$4.4(17) \times 10^{-5}$
dlbp	0.64(1)	12590	49744	106 000(2000)	-0.04572	-0.0559(19)	0.11718	0.164(7)	86.4(20)	0.529(11)	$9(5) \times 10^{-9}$
openflights	0.9916(9)	3286	39.430	40100(70)	-0.00531	-0.0071(11)	0.49647	0.507(2)	117.1(5)	0.0167(18)	$1.0(3) \times 10^{-7}$
reactome	0.999977(10)	6327	146160	146164(3)	0.24487	0.24487(4)	0.58838	0.5887(3)	318.7(10)	$4.1(18) \times 10^{-5}$	$1.3(8) \times 10^{-7}$
cond-mat	0.999986(13)	40421	175693	175 695(4)	0.18633	0.18633(2)	0.63616	0.63615(3)	1014(6)	$3(2) \times 10^{-5}$	$3(2) \times 10^{-9}$
Enron	0.99986(5)	36692	183831	183 885(18)	-0.11076	-0.11075(2)	0.49698	0.49692(8)	188.9(11)	0.00028(10)	$2.9(19) \times 10^{-9}$
linux	0.9973(3)	30837	213424	214 600(120)	-0.17468	-0.17467(7)	0.12849	0.1322(10)	351.2(7)	0.0055(5)	$1.7(10) \times 10^{-9}$
brightkite	0.9985(3)	58228	214078	214740(80)	0.01082	0.01100(11)	0.17233	0.17234(10)	151(3)	0.0029(5)	$1.7(12) \times 10^{-8}$
pgp	0.99799(9)	39 796	301498	301 660(60)	0.00076	0.00049(8)	0.461 09	0.4617(2)	929(2)	0.00227(16)	$3.35(18) \times 10^{-7}$
caida	0.99967(13)	53387	496731	497 070(130)	-0.18697	-0.186959(17)	0.68097	0.68126(14)	218.0(16)	0.0007(3)	$1.0(8) \times 10^{-9}$
web-Stanford	0.9999987(8)	281903	2312497	2312494(4)	-0.11244	-0.1124447(2)	0.59763	0.597634(3)	4168(2)	$1.0(2) \times 10^{-6}$	$7(5) \times 10^{-11}$
flickr	0.999976(13)	105938	2316948	2 316 830(60)	0.24685	0.246 823(16)	0.08913	0.089138(7)	617(2)	$6(3) \times 10^{-7}$	$2.0(11) \times 10^{-8}$

NOISE AND DETECTABILITY OF COMMUNITIES

Planted partition model:

$$\omega_{rs} = \omega_{\rm in} \delta_{rs} + \omega_{\rm out} (1 - \delta_{rs})$$

Single observation, n = 1, effectively:

$$\omega_{rs}' = (1 - p - q)\omega_{rs} + q$$



 $N|\omega_{\rm in} - \omega_{\rm out}| < B\sqrt{\langle k \rangle}, \qquad N|\omega_{\rm in} - \omega_{\rm out}| < \frac{B\sqrt{(1-p-q)\langle k \rangle + qN}}{(1-p-q)}.$

Multiple measurements and heterogeneous errors

Observational error does not need to be uniform for every pair (i, j). Non-uniform model, w/ pair-specific error rates: p_{ij} and q_{ij}

$$P(x_{ij}|n_{ij}, A_{ij}, p_{ij}, q_{ij}) = \binom{n_{ij}}{x_{ij}} \left[(1 - p_{ij})^{x_{ij}} p_{ij}^{n_{ij} - x_{ij}} \right]^{A_{ij}} \left[q_{ij}^{x_{ij}} (1 - q_{ij})^{n_{ij} - x_{ij}} \right]^{1 - A_{ij}}$$

Marginal probability,

$$\begin{split} P(x_{ij}|n_{ij},A_{ij},\alpha,\beta,\mu,\nu) \\ &= \int P(x_{ij}|n_{ij},A_{ij},p_{ij},q_{ij})P(p_{ij}|\alpha,\beta)P(q_{ij}|\mu,\nu) \, \mathrm{d}p_{ij}\mathrm{d}q_{ij} \\ &= \binom{n_{ij}}{x_{ij}} \left[\frac{\mathcal{B}(n_{ij}-x_{ij}+\alpha,x_{ij}+\beta)}{\mathcal{B}(\alpha,\beta)} \right]^{A_{ij}} \times \\ & \qquad \left[\frac{\mathcal{B}(x_{ij}+\mu,n_{ij}-x_{ij}+\nu)}{\mathcal{B}(\mu,\nu)} \right]^{1-A_{ij}}. \end{split}$$

HUMAN CONNECTOME

418 INDIVIDUALS



HUMAN CONNECTOME 418 INDIVIDUALS

Uniform errors





Nonuniform errors

 π_{ij}



 $Q_{ij} \in [0,1] \rightarrow$ experimentally determined uncertainties

$$P_Q(\mathbf{A}|\mathbf{Q}) = \prod_{i < j} Q_{ij}^{A_{ij}} (1 - Q_{ij})^{1 - A_{ij}}$$

Example:

STRING Protein-Protein interaction network database, Szklarczyk et al, Nucleic Acids Research 45, D362–D368 (2017).

Errors are estimated via a combination of: (i) direct experiments, (ii) database curation, (iii) publication text-mining, (iv) co-expression data, (v) genome proximity, (vi) ortholog fusion, (vii) phylogenetic co-ocurrence.

The distribution $P_Q(\boldsymbol{A}|\boldsymbol{Q})$ implies the following noisy measurement process,

$$P(\boldsymbol{Q}|\boldsymbol{A}) = \frac{P_Q(\boldsymbol{A}|\boldsymbol{Q})P_Q(\boldsymbol{Q})}{P_Q(\boldsymbol{A})},$$

with prior

$$P_Q(\boldsymbol{Q}) = \prod_{i < j} P(Q_{ij}),$$

and normalization constant

$$P_Q(\boldsymbol{A}) = \int P_Q(\boldsymbol{A}|\boldsymbol{Q}) P_Q(\boldsymbol{Q}) \, \mathrm{d}\boldsymbol{Q} = \prod_{i < j} \bar{Q}^{A_{ij}} (1 - \bar{Q})^{1 - A_{ij}},$$

with $\bar{Q} = \int_0^1 Q P(Q) dQ$. Combining these together we have

$$P(\boldsymbol{Q}|\boldsymbol{A}) = P_Q(\boldsymbol{Q}) \prod_{i < j} \left(\frac{Q_{ij}}{\bar{Q}}\right)^{A_{ij}} \left(\frac{1 - Q_{ij}}{1 - \bar{Q}}\right)^{1 - A_{ij}}$$

$$P(\boldsymbol{A}|\boldsymbol{Q}) = \frac{P(\boldsymbol{Q}|\boldsymbol{A})P(\boldsymbol{A})}{P(\boldsymbol{Q})}, \qquad \bar{Q} = \frac{\sum_{i < j} Q_{ij}}{\binom{N}{2}}.$$

$$P(\boldsymbol{A}|\boldsymbol{Q}) = \frac{P(\boldsymbol{Q}|\boldsymbol{A})P(\boldsymbol{A})}{P(\boldsymbol{Q})}, \qquad P(\boldsymbol{A}|\boldsymbol{Q}) \neq P_Q(\boldsymbol{A}|\boldsymbol{Q})!$$

We are keeping the same noise generating process, but changing our prior assumption about the data.

E. coli proteins:







For code, see:

https://graph-tool.skewed.de

(See also HOWTO at: https://graph-tool.skewed.de/ static/doc/demos/inference/inference.html)