Network Inference from Population-Level Observation of Epidemics

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Outline

1 Introduction

- 2 Birth-Death Process Approximation of epidemics on networks
- 3 Network Characterisation
- 4 Bayesian Inference
- 5 Conclusions

Introduction: Network inference

What do we want to infer about Networks?

• Link-based inference: adjacency matrix?

• Topological parameters? (i.e. $\langle k \rangle$)

• Some mesoscopic quantity related to the network structure (comunities, clustering)?

Possibilities

How many ways do we have to infer networks?

The problem				
	1	Correlation (ie. cross-correlation, pearson correlation, and	21	Rate of Information Flow
	2	Correlation + Minimal Spanning Tree	22	Direct directed coherence
	3	Partial correlation	23	Direct directed conerence
	4	Cross-Mutual Information	24	Directed coherence
	5	Free Energy Minimization	25	Directed transfer function
	6	Optimal Causation Entropy	26	Generalized partial directed coherence
	7	Transfer Entropy	27	Partial directed coherence
	8	Static Graphical Lasso	28	Spectral Granger Causality
	9	Convergent Cross-Mapping	29	Cross-distance-correlation
	10	Random	30	Cross-Jaccard-distance
	11	Localization in Covariance Matrices	31	Derivative Variable Correlation
	12	Marchenko-Pastur	32	Higher-Order Network Analysis
	13	Exact mean field approximation	33	Graphical Models
	14	Maximum Likelihood Estimation	34	Mixed-integer Optimisation Approximation
	15	Naive Mean-Field approximation	35	Bayesian GLM for Structure Learning
	16	Thouless-Anderson-Palmer mean field approximation	36	Linear Programming Model
	17	Time Granger Causality	37	Time-Varying Graphical Lasso
	18	Adaptive Granger Causality	38	Integer Programming
	19	Directed Information	39	Partial correlation influence
		Joint Entropy of ISIs	1	

Figure: A lot, apparently [1]! (picture posted on Twitter by S.V. Scarpino, from a talk by B.Klein)

What is new?

Why are we proposing a new approach then?

- Networks of interest: the ones with dynamics on them
- Observing the dynamics can help to infer the network...
- ...But only when detailed (node-level) information is available

Question: what can we infer when little information is available?

The idea behind: observing cascades



Many cascades \rightarrow full inference (Adjacency Matrix) [2].

Remarks

Often full recovery of the graph is not needed

Degree distribution gives a lot of information!

With fewer observations we can infer it, but still too many details (specifically: **continuous** observations)[3]

Can we do `better'?

• Aim: infering at least the **family** a network belongs to...

• ... when only discrete observations of the process are available

• Two ingredients: SIS epidemics and Birth-Death process approximation.

SIS model as a Birth-Death process



Infection with rate τ per S-I link; recovery with rate γ . High dimensionality, many methods try to reduce it [4] Focus on the number of infected nodes:

Space state $S = \{0, ..., N\}$ and events are ± 1 jumps.

Birth-Death process? what rates?

Simple case: Complete network



• a_k is known and not random \Rightarrow exact master equation

• What is a_k in the general case?

Maximum Likelihood Estimation

We are going to learn the rates. Assumptions:

- 1 Infection and recovery are independent Poisson processes of rates a_k and c_k respectively
- 2 We have a sufficient statistics available (i.e. continuous observations)

Maximising the Likelihood [5] leads to:

$$\max_{a_k,d_k} \mathcal{L}\left(a_k, c_k | \{Obs\}\right) = \begin{cases} \hat{a}_k = \frac{u_k}{t_k} \\ \hat{c}_k = \frac{d_k}{t_k} \end{cases}$$

 u_k (d_k) is the number of up (down) jumps from k, t_k is the time spent in k.

Is the approximation good?





t

how does that help?



Different network families produce different (k, a_k) curves!

Fit proposal

$$a_k \sim a_k^{\theta} = Ck^p (N-k)^q$$

MLE:

Examples:





3-d plot



We concatenated 10^4 epidemics on 10^2 realisations for each point!

2-d plot



Towards inference based on discrete observations of the epidemic

• We used the Birth-Death process approximation of epidemics to characterise different families in the C, p, q space

• Now we will see how this helps when only discrete observations (in time) are available

Bayesian inference

- Dataset: $D = \{I(t_1), I(t_2), \dots, I(t_n)\} = \{k_1, k_2, \dots, k_n\}$ discrete observations
- prior distributions using output from characterisation: $\operatorname{Rog} \rightarrow (C, n, q) \circ (\pi p)$

$$\begin{aligned} \operatorname{Reg} &\to (C, p, q) \sim \pi_{Reg} \\ \operatorname{E-R} \to (C, p, q) \sim \pi_{E-R} \\ \operatorname{B-A} \to (C, p, q) \sim \pi_{B-A} \end{aligned}$$
$$\mathcal{L}(C, p, q; D) = \prod_{i=2}^{n} \mathbb{P}(I(t_i - t_{i-1}) = k_i | I(0) = k_{i-1}, C, p, q) \end{aligned}$$

• Maximum Posterior Probability $\pi(type|D)$ requires to numerically evaluate this integral(costly!): $\pi(D|type) = \int \mathcal{L}(C, p, q; D) \pi_{type}(C, p, q) dC dp dq.$

Results



Output probabilities: $p_{Reg} = 0.01\%, \ p_{E-R} = 0.02\%, \ p_{B-A} = 99.7\%$

it is a Barabási-Albert network (very likely)

To summarise

1 We introduced the Birth-Death Process approximation for SIS on networks

2 We tested that it is a good approximation

3 We proposed a model for the rates that led to characterisation

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Inference based on discrete observations of the epidemic

Conclusions

- It is possible to infer the network family from discrete observations of an epidemic
- Many directions are worth investigating:
 - More complex network models (clustering, communities,...)
 - Can we infer something more? $(\langle k \rangle, \tau)$
 - Can we extend it to different dynamics? (SIR,SEIRS,...)
 - Is there a better parametric model to fit the a_k curves?
 - Scaling with the size?
 - Real data?
- We hope that this method will become a new useful tool in network inference.

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I: 506



