Simplicity and Complexity of Belief-Propagation #2

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A simple Mathematical model for Phylogentic reconstruction

- Consider broadcast process on trees for h levels X_h and $d = 2$.
- Unknown permutation $\sigma \in S_{2^d}$.
- Input: i.i.d samples from $Y_s \sim \tilde{X}_h, 1 \leq s \leq m$, where $\tilde{X}_h(i) = X_h(\sigma(i))$.
- Goal: recover T, i.e. $\sigma \mod \Gamma$, where $\Gamma =$ ways to draw.
- E.G: 3 possible trees on when $h = 2$ and $7 \times 5 \times 3 \times 3$ when $h = 3$.

An inference procedure

- Estimate the covariance $r_{i,j} = Cov[\tilde{X}_h(i), \tilde{X}_h(j)]$.
- Identify siblings as maximizing correlation.
- For each sample i, let Z_i be a 2^{d-1} dimensional vector where

$$Z_i(w) = maj(Y_v : v \text{ descendant of } w)$$

- Repeat.
- Let $p(m, h) :=$ probability of recovering the tree from m samples.
- Exercise: If $2\theta^2 > 1$, and $m \geq C_\theta h$, then $p(m, h) \geq 0.9$.
- Exercise: If $2\theta^2 < 1$, then $p(m, h) \leq m c_\theta^h$, where $c_\theta < 1$.

$2\theta^2 < 1 \implies$ need $\exp(Ch)$ samples to recover the tree

- Exercise: $\|P_T^+ - P_T^-\|_{TV} \le 2E_T[|M_h|] \le 2 \times (2\theta^2)^{h/2}$
- $\implies$ If two $h+2$-level trees T, T' have the same topology in the last h levels then:

$$\|X_{h+2} - X'_{h+2}\|_{TV} \le 8 \times (2\theta^2)^{h/2} \implies$$

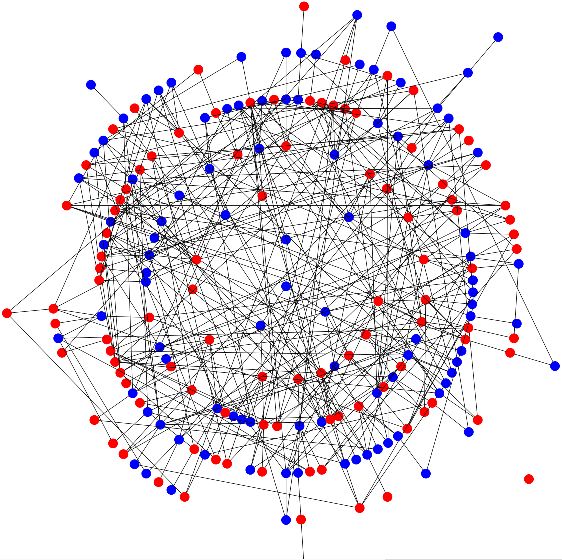
- $$\|(X_{h+2})^{\otimes m} - (X'_{h+2})^{\otimes m}\|_{TV} \le 8m \times (2\theta^2)^{h/2} \implies$$
- To distinguish between two topologies need at least $m = \Omega((2\theta^2)^{-h/2})$ samples.

Application 2: The Block Model

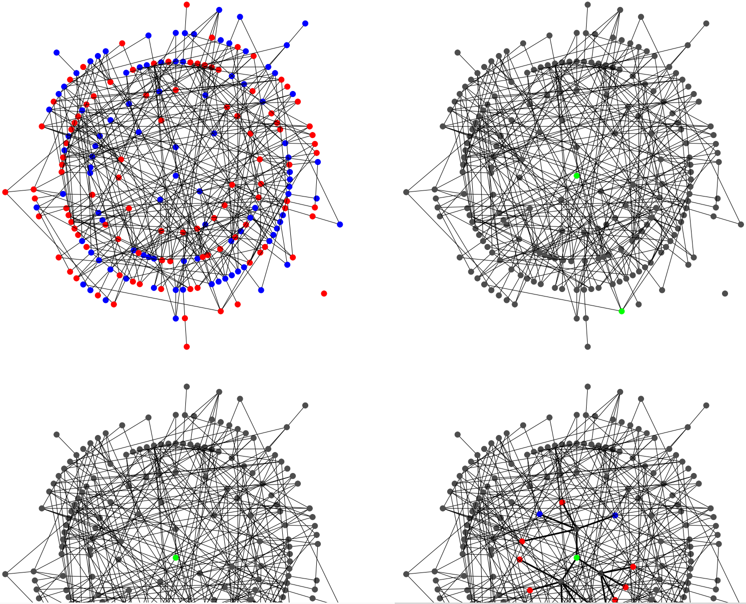
- Random graph $G = (V, E)$ on n nodes.
- Half blue / half red ($\pm$).
- Two nodes of the same color are connected with probability $2d\theta/n + d(1-\theta)/n$.
- Two nodes with different colors are connected with probability $d(1-\theta)/n$.
- Note: average degree is d and if $u \sim v$ then $E[X_u X_v] = \theta$.
- Inference: which nodes are likely red/blue ?
- Conjecture (Decelle, Krzakala, Moore and Zdeborova, 11): "Belief-Propagation" is the optimal algorithm.
- and ... possible to do better than random iff $d\theta^2 > 1$.

The Block Model in pictures

A sample from the model



The easier direction ...



The Conjecture is Correct

Theorem (M-Neeman-Sly, Massoulie 14)

If $d\theta^2 > 1$ *then possible to detect (infer better than random).*

BP and a New Type of Random Matrix

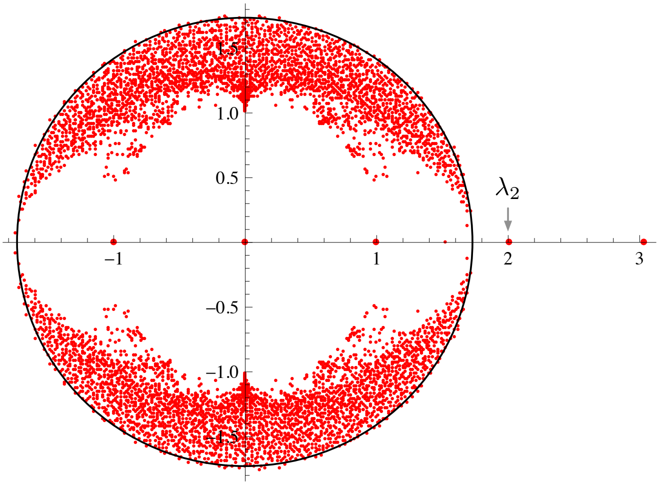
- **Thm** If $d\theta^2 > 1$ then possible to detect.
- **Conj:**(Krzakala,Moore,M,Neeman,Sly, Zdebrovoa,Zhang 13): If A is the adjacency matrix, then w.h.p the second eigenvector of

$$N = \begin{pmatrix} 0 & D - I \\ -I & A \end{pmatrix}, \quad D = diag(d_{v_1}, \ldots, d_{v_n}),$$

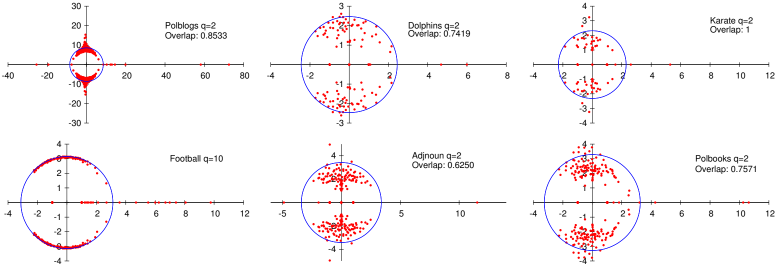
is correlated with the partition and the second eigenvalue is $d(1 - 2\varepsilon) + o_n(1)$.
- No orthogonal structure! N is not symmetric or normal. Singular vector of N are useless.
- KMMNSZZ derived N by Linearizing Belief Propagation and applying a number-theory identity by Hashimoto (89).
- Note: conjectured linear algebra algorithm is deterministic.
- Conjecture established by Bordenave-Lelarge-Massoulie 15.

The Eigenvalues of N

$$d = 3, \quad d(1-2\varepsilon) = 2, \quad \sqrt{d} = 1.732...$$



The spectrum on real networks



Part 2: NON-LINEAR THEORY
Large q

Generalizations for large q

- Claim: For all q if $d\theta^2 > 1$ then:
  - For the tree broadcast model, can distinguish.
  - Can detect the in the block model.
  - Recover phylogenies from sequences of length $O(\log n)$.
- Pf (for q even): Divide q colors to two sets of size $q/2$. Call one $+$ and the other $-$. $\square$
- More generally, this is true for broadcast process with Markov chains M on edges where

$$\theta = \max(|s| : s \in \sigma(A) \setminus \{1\})$$

- Pfs:
  - For tree broadcast models: Kesten-Stigum 66.
  - For block models: Bordenave, Lelarge, Massouile-15, Abbe-Sandon-15..
  - For phylogeny, M-Roch-Sly-15.

Doing Better for large q?

Thm: For large q, $\exists\theta_q$ with $d\theta_q^2 < 1$ and such that for $\theta > \theta_q$:

- For the tree broadcast model, can distinguish (M-01,Sly-09 ...)
- But not using linear or robust estimators (M-Peres-03, Janson-M-04)
- Can detect the in the block model.
- But believed to have computational/statistical gap (Abbe-Sandon-15, Banks-Moore-Neeman-Netrapalli-16)
- Recover phylogenies from sequences of length $O(\log n)$.
- Not written (Conjecture: cannot be done robustly).

Linear reconstruction for large q

Theorem (Count Reconstruction, Robust Reconstruction (Mossel-Peres, Janson-Peres))

For all q and d-ary tree, $d\theta^2 = 1$ is the threshold for:

- *Count reconstruction : inference of root better than random, based only on the census of $c_h \in Z^q$.*

$$c_h(a) = \left|\{v \in L_h : X_v = a\}\right|, \quad Var[\mathbb{E}[X_0|c_h]] \to 0 \textbf{ iff } d\theta^2 \leq 1$$

- *Robust Reconstruction : inference given noisy versions of the leaves $(Y_v : v \in L_h)$, where $Y_v = X_v$ with probability η and $Y_v \sim U[q]$ with probability $1 - \eta$ for some fixed $\eta > 0$.*

$$Var[\mathbb{E}[X_0|Y_{L_h}]] \to 0 \textbf{ iff } d\theta^2 \leq 1$$

A *Double* phase transition for large q

Theorem (Count Reconstruction, Robust Reconstruction (Mossel-Peres, Janson-Peres))

For all q and d-ary tree, $d\theta^2 = 1$ is the threshold for: census and robust reconstruction.

Theorem (Reconstruction for large q (Mossel 00))

If $d\theta > 1$ then for $q > q_\theta$ can distinguish the root better than random:

$$\lim_{h\to\infty} Var[\mathbb{E}[X_0|X_{L_h}]] > 0$$

$\Longrightarrow$ Non-linear estimators are superior.

Pf: Shows fractal nature of information.