Towards a Multi-Subject Analysis of Neural Connectivity

C. J. Oates¹, L. Costa¹, S. Mukherjee², T. Nichols¹, J. Q. Smith¹, J. Cussens³

 ¹ Department of Statistics, University of Warwick, CV4 7AL, UK.
² MRC Biostatistics Unit and CRUK Cambridge Institute, University of Cambridge, CB2 0SR, UK.
³ Department of Computer Science and York Centre for Complex Systems Analysis, University of York, YO10 5GE, UK.

3rd September 2014

Workshop on Statistical Systems Biology

9th -11th December 2014

warwick.ac.uk/SSB

Keynote Speakers:

Prof. David Balding, Chair of the UCL Genetics Institute.

- Dr. Clive Bowsher, School of Mathematics, Bristol.
- Prof. Mustafa Khammash, Control Theory and Systems Biology, ETH Zurich.
- Prof. Walter Kolch, Director of the Conway Institute and Systems Biology Ireland, University College Dublin.
- Prof. John Lygeros, Head of the Automatic Control Laboratory, ETH Zurich.
- Dr. Sach Mukherjee, Group Leader at the Netherlands Cancer Institute.
- Prof. Simon Tavaré FRS, Director of Cancer Research UK Cambridge Institute.
- Prof. Darren Wilkinson, School of Mathematics and Statistics, Newcastle.

Call for Papers, Presentations and Posters

In partnership with Statistical Applications in Genetics and Molecular Biology (De Gruyter) we are soliciting high-quality research for joint journal submission and presentation at the workshop. In addition, we are encouraging the submission of contributed presentations and posters in relevant research areas.





Motivation: Uncovering neural connectivity

How are these brain regions interacting?







(a) Visual

(b) DMN

(c) Executive Control

< ロ > (同) (三) (三) 三) のへの

Motivation: Uncovering neural connectivity







(a) Visual



(c) Executive Control

How are these brain regions interacting?

Multiregression dynamical models (MDMs; Catriona Queen and Jim Smith, 1993):



Motivation: Uncovering neural connectivity



Figure: fMRI data; replicate data from the same subject. DAGs estimated from time series data using MDMs.

<u>Node Number</u>	Symmetry	Summary			
1	Bilateral	Motor:hand/face			
2	Bilateral	Sensory: All-but-face			
3	Bilateral	Motor:All-but-face			
4	Bilateral	UNKNOWN			
5	Left Dominant	Sensorimotor: L Hand+Arms			
6	Right Dominant	Sensorimotor: R Hand+Arms			
7	Bilateral	Sensory: Trunk-to-feet			
8	Bilateral	Sensory: Face			
9	Bilateral	Auditory			
10	Bilateral	Sensorimotor:All-but-face - Sensory:Face			

An ideal algorithm



Figure: fMRI data; joint learning of all DAGs simultaneously. [λ is a "regularity" parameter.]

э

An ideal algorithm



Figure: fMRI data; joint learning of all DAGs simultaneously. [λ is a "regularity" parameter.]

But how might this work? Seems challenging ...

◆□▶ ◆□▶ ◆三▶ ◆三▶ 三三 のへぐ



Figure: A Bayesian hierarchical model for multiple DAGs.

◆□▶ ◆□▶ ◆三▶ ◆三▶ 三三 のへぐ

Joint prior over multiple DAGs:

$$p(G^{(1:K)}|N) \propto \underbrace{\left(\prod_{(k,l) \in N} r(G^{(k)}, G^{(l)})\right)}_{\text{regularity}} \times \underbrace{\left(\prod_{k=1}^{K} m(G^{(k)})\right)}_{\text{multiplicity correction}}$$

◆□▶ ◆□▶ ◆臣▶ ◆臣▶ 臣 のへぐ

Joint prior over multiple DAGs:

$$p(G^{(1:K)}|N) \propto \underbrace{\left(\prod_{(k,l)\in N} r(G^{(k)}, G^{(l)})\right)}_{\text{regularity}} \times \underbrace{\left(\prod_{k=1}^{K} m(G^{(k)})\right)}_{\text{multiplicity correction}}$$

Structural Hamming distance:

$$\log(r(G^{(k)}, G^{(l)})) = -\lambda \sum_{(j,i)} \mathbb{I}\{j \in G_i^{(k)} \Delta G_i^{(l)}\}.$$

◆□▶ ◆□▶ ◆臣▶ ◆臣▶ 臣 のへぐ

Joint prior over multiple DAGs:

$$p(G^{(1:K)}|N) \propto \underbrace{\left(\prod_{(k,l)\in N} r(G^{(k)}, G^{(l)})\right)}_{\text{regularity}} \times \underbrace{\left(\prod_{k=1}^{K} m(G^{(k)})\right)}_{\text{multiplicity correction}}$$

Structural Hamming distance:

$$\log(r(G^{(k)},G^{(l)})) = -\lambda \sum_{(j,i)} \mathbb{I}\{j \in G_i^{(k)} \Delta G_i^{(l)}\}.$$

Binomial correction:

$$m(G^{(k)}) = \prod_{i=1}^{P} {\binom{P}{|G_i^{(k)}|}}^{-1} \mathbb{I}\{|G_i^{(k)}| \le d_{\max}\}.$$

◆□▶ ◆□▶ ◆三▶ ◆三▶ 三三 のへぐ

Joint prior over DAGs and the network N:

$$p(G^{(1:K)}, N) \propto p(G^{(1:K)}|N)p(N)$$

where η controls the density of the network N and

 $\log(p(N)) \stackrel{+C}{=} \eta \|N\|.$

Joint prior over DAGs and the network N:

$$p(G^{(1:K)}, N) \propto p(G^{(1:K)}|N)p(N)$$

where η controls the density of the network N and

 $\log(p(N)) \stackrel{+C}{=} \eta \|N\|.$

Then interest is in the "doubly joint" MAP

$$(\hat{G}^{(1:\mathcal{K})}, \hat{N}) := \arg \max_{G^{(1:\mathcal{K})}, N} p(\boldsymbol{Y}^{(1:\mathcal{K})} | G^{(1:\mathcal{K})}, N) p(G^{(1:\mathcal{K})}, N).$$



Design a local move that encourages more similar DAGs...

・ロト ・聞ト ・ヨト ・ヨト

э.



Pick an edge on which the two DAGs differ.

э.



Propose to add/remove this edge to the other DAG.

(日)、

э.



Check no cycles are created.

э



Delete an edge from each cycle.

(日) (同) (日) (日)

э



But these new DAGs are as different as when we started!

Clearly a different approach is needed.

・ロト ・聞ト ・ヨト ・ヨト

-

Inference for single DAGs is "easy":

Inference for single DAGs is "easy":

Consider a Bayesian network \mathbf{Y} with respect to a directed acyclic graph (DAG) model G. i.e.

$$p_{\mathbf{Y}}(\mathbf{y}|G) = \prod_{i=1}^{P} p(\mathbf{y}_{P}|\mathbf{y}_{G_{i}}, G_{i}).$$

◆□▶ ◆□▶ ◆臣▶ ◆臣▶ 臣 の�?

Inference for single DAGs is "easy":

Consider a Bayesian network \boldsymbol{Y} with respect to a directed acyclic graph (DAG) model G. i.e.

$$p_{\mathbf{Y}}(\mathbf{y}|G) = \prod_{i=1}^{P} p(\mathbf{y}_{P}|\mathbf{y}_{G_{i}}, G_{i}).$$

There is interest in the maximum a posteriori (MAP) estimate

$$\hat{G} := \arg \max_{G} p_{\mathbf{Y}}(\mathbf{y}|G)p(G).$$

< □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > <

Inference for single DAGs is "easy":

Consider a Bayesian network \boldsymbol{Y} with respect to a directed acyclic graph (DAG) model G. i.e.

$$p_{\mathbf{Y}}(\mathbf{y}|G) = \prod_{i=1}^{P} p(\mathbf{y}_{P}|\mathbf{y}_{G_{i}}, G_{i}).$$

There is interest in the maximum a posteriori (MAP) estimate

$$\hat{G} := \operatorname{arg\,max}_{G} p_{\mathbf{Y}}(\mathbf{y}|G)p(G).$$

◆□▶ ◆□▶ ◆三▶ ◆三▶ 三三 のへぐ

Choose a "nice" $p(G) = \prod_{i=1}^{P} p_{G_i}(G_i)$.

Cussens '10 and Jaakola *et al.* '10 cast the MAP estimator in a DAG model as an integer linear program (ILP):

 $\max \boldsymbol{f}^{\mathsf{T}} \boldsymbol{x}$ subject to $\boldsymbol{A} \boldsymbol{x} \leq \boldsymbol{b}, \quad \boldsymbol{C} \boldsymbol{x} = \boldsymbol{d}, \quad \boldsymbol{x} \in \mathbb{Z}^d$

・ロト・日本・モート モー うへぐ

Cussens '10 and Jaakola *et al.* '10 cast the MAP estimator in a DAG model as an integer linear program (ILP):

 $\max \boldsymbol{f}^{\mathsf{T}}\boldsymbol{x}$ subject to $\boldsymbol{A}\boldsymbol{x} \leq \boldsymbol{b}, \quad \boldsymbol{C}\boldsymbol{x} = \boldsymbol{d}, \quad \boldsymbol{x} \in \mathbb{Z}^d$

Objective function:

$$\begin{aligned} \boldsymbol{f}^{T} \boldsymbol{x} &= \log[p_{\boldsymbol{Y}}(\boldsymbol{y}|G)p(G)] &= \sum_{i=1}^{P} \log[p(\boldsymbol{y}_{i}|\boldsymbol{y}_{G_{i}},G_{i})p_{G_{i}}(G_{i})] \\ &= \sum_{i=1}^{P} \sum_{\pi \subseteq \{1:P\}} \log[p(\boldsymbol{y}_{i}|\boldsymbol{y}_{\pi},\pi)p_{G_{i}}(\pi)]x_{i,\pi} \end{aligned}$$

where $x_{i,\pi} = \mathbb{I}\{G_i = \pi\}$ and e.g. $\boldsymbol{x} = (0, 0, 1, 0, 0, 0, \dots, 1, 0, 0).$

Cussens '10 and Jaakola *et al.* '10 cast the MAP estimator in a DAG model as an integer linear program (ILP):

 $\max \boldsymbol{f}^{\mathsf{T}}\boldsymbol{x}$ subject to $\boldsymbol{A}\boldsymbol{x} \leq \boldsymbol{b}, \quad \boldsymbol{C}\boldsymbol{x} = \boldsymbol{d}, \quad \boldsymbol{x} \in \mathbb{Z}^d$

Objective function:

$$f^{T} \mathbf{x} = \log[p_{\mathbf{Y}}(\mathbf{y}|G)p(G)] = \sum_{i=1}^{P} \log[p(\mathbf{y}_{i}|\mathbf{y}_{G_{i}}, G_{i})p_{G_{i}}(G_{i})]$$
$$= \sum_{i=1}^{P} \sum_{\pi \subseteq \{1:P\}} \log[p(\mathbf{y}_{i}|\mathbf{y}_{\pi}, \pi)p_{G_{i}}(\pi)]x_{i,\pi}$$

where $x_{i,\pi} = \mathbb{I}\{G_i = \pi\}$ and e.g. $\boldsymbol{x} = (0, 0, 1, 0, 0, 0, \dots, 1, 0, 0).$

Q: How to ensure x corresponds to a well-defined DAG?

Convexity:

$$\sum_{\pi \subseteq \{1:P\}} x_{i,\pi} = 1 \hspace{1em} orall i \in \{1:P\}$$

No self-loops:

$$x_{i,\pi} = 0 \quad \forall \pi \in i$$

Acyclicity (version of Jaakola et al., '10):

$$\sum_{i \in C} \sum_{\substack{\pi \subseteq \{1:P\}\\ \pi \cap C = \emptyset}} x_{i,\pi} \ge 1 \quad \forall \emptyset \neq C \subseteq \{1:P\}.$$

These constraints together exactly characterise the space of DAGs.

< □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > <

Claim: $(\hat{G}^{(1:K)}, \hat{N})$ is characterised by an extended ILP.

Claim: $(\hat{G}^{(1:K)}, \hat{N})$ is characterised by an extended ILP. **Sketch:** Need to encode N in the state vector \boldsymbol{x} :

 $E^{(k,l)} := \mathbb{I}\{(k,l) \in \mathbb{N}\} \quad \forall k, l \text{ with } k < l$

・ロト・日本・モート モー うへぐ

Claim: $(\hat{G}^{(1:K)}, \hat{N})$ is characterised by an extended ILP. **Sketch:** Need to encode N in the state vector \boldsymbol{x} :

$$E^{(k,l)} := \mathbb{I}\{(k,l) \in \mathbb{N}\} \quad \forall k, l \text{ with } k < l\}$$

Now construct binary indicators of individual edges and disagreement between edges:

$$e_{j,i}^{(k)} = \sum_{\substack{\pi \subseteq \{1:P\}\\j \in \pi}} x_{i,\pi}^{(k)} \quad \forall i, j, k.$$

$$d_{j,i}^{(k,l)} = \mathbb{I}\{j \in G_i^{(k)} \Delta G_i^{(l)}\} \quad \forall i, j, k, l \text{ with } k < l$$

$$D_{j,i}^{(k,l)} = \mathbb{I}\{j \in G_i^{(k)} \Delta G_i^{(l)} \text{ and } (k, l) \in N\} \quad \forall i, j, k, l.$$

Claim: $(\hat{G}^{(1:K)}, \hat{N})$ is characterised by an extended ILP. **Sketch:** Need to encode N in the state vector \boldsymbol{x} :

$$E^{(k,l)} := \mathbb{I}\{(k,l) \in \mathbb{N}\} \quad \forall k, l \text{ with } k < l\}$$

Now construct binary indicators of individual edges and disagreement between edges:

$$e_{j,i}^{(k)} = \sum_{\substack{\pi \subseteq \{1:P\}\\j \in \pi}} x_{i,\pi}^{(k)} \quad \forall i, j, k.$$

$$d_{j,i}^{(k,l)} = \mathbb{I}\{j \in G_i^{(k)} \Delta G_i^{(l)}\} \quad \forall i, j, k, l \text{ with } k < l$$

$$D_{j,i}^{(k,l)} = \mathbb{I}\{j \in G_i^{(k)} \Delta G_i^{(l)} \text{ and } (k, l) \in N\} \quad \forall i, j, k, l.$$

XOR and AND constraints \equiv integer linear inequalities.

・ロト・4回ト・4回ト・4回ト・回・99(で)

Example: AND constraint A = AND(B, C)

$$\begin{array}{cccc} +A & -B & \leq & 0 \\ +A & -C & \leq & 0 \\ -A & +B & +C & \leq & 1 \end{array}$$

This linearisation of AND is **optimal**, in the sense that it describes all facets of the convex hull of feasible solutions for the AND constraint.

Some preliminary results...

<□ > < @ > < E > < E > E のQ @

Results: Simulation study



P = 5, K = 5

Figure: Simulated data; fixed N = complete, varying λ . [MCC = Matthews' correlation coefficient.]

Intuition: A modest amount of regularisation should help, but too much can lead to artefacts.

Results: Group analysis of fMRI data



Figure: fMRI data on two subjects; learning λ .

◆□ > ◆□ > ◆臣 > ◆臣 > ─ 臣 = ∽ 9 < ⊙

Results: Group analysis of fMRI data

Density hyperparameter	$\eta = 30$	$\eta = 40$	$\eta = 50$	$\eta = 60$	$\eta = 70$	$\eta = 80$
Ν	© 0 6 0 6	6 0 6 0 6 0	6 0 6 0 6 0			
Sub 1	Ŵ	Ŵ	Ŵ	Ŵ		
Sub 2						
Sub 3						
Sub 4						
Sub 5						
Sub 6						

Figure: fMRI data on six subjects; learning N. [$\lambda = 4$]

・ロト・日本・モート モー うへぐ

Summary

To do:

- Large-scale empirical study
- Informative group priors (e.g. based on demographic covariates or genealogy)
- Causal semantics for transfer learning

References:

 CJO, Lilia Costa, Tom Nichols (2014) Towards a Multi-Subject Analysis of Neural Connectivity.

To appear in Neural Computation.

arXiv:1404.1239.

 CJO, Jim Smith, Sach Mukherjee, James Cussens (2014) Exact Estimation of Multiple Directed Acyclic Graphs.

arXiv:1404.1238.

