# **Bayesian Spillover Graphs for Dynamic Networks: Supplementary Material**

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# A MOVING AVERAGE REPRESENTATION OF VAR(1)

We can rewrite a VAR(1) model with a moving average representation [Tsay, 2013] using the mean-adjusted model, which is useful for computing variances of forecast errors.

We define the **mean-adjusted model**  $\tilde{\mathbf{z}}_t = \mathbf{z}_t - \mu$ , where  $\mu = (I_d - \phi_1)^{-1} \phi_0$ .

Then,

$$\begin{aligned} \tilde{\mathbf{z}}_{t} &= \mathbf{a}_{t} + \phi_{1} \tilde{\mathbf{z}}_{t-1} \\ &= \mathbf{a}_{t} + \phi_{1} (\mathbf{a}_{t-1} + \phi_{1} \tilde{\mathbf{z}}_{t-2}) \\ &= \mathbf{a}_{t} + \phi_{1} \mathbf{a}_{t-1} + \phi_{1}^{2} (\mathbf{a}_{t-2} + \phi_{1} \tilde{\mathbf{z}}_{t-3}) \\ &= \mathbf{a}_{t} + \phi_{1} \mathbf{a}_{t-1} + \phi_{1}^{2} \mathbf{a}_{t-2} + \phi_{1}^{3} \mathbf{a}_{t-3} + \dots \end{aligned}$$

Hence,

$$\begin{aligned} \mathbf{z}_t &= \mu + \tilde{\mathbf{z}}_t \\ &= \mu + \mathbf{a}_t + \phi_1 \mathbf{a}_{t-1} + \phi_1^2 \mathbf{a}_{t-2} + \phi_1^3 \mathbf{a}_{t-3} + \dots \\ &= \mu + \mathbf{a}_t + \psi_1 \mathbf{a}_{t-1} + \psi_2 \mathbf{a}_{t-2} + \dots \\ &= \mu + \sum_{i=0}^{\infty} \psi_i \mathbf{a}_{t-i} \end{aligned}$$

where  $\psi_i = \phi_1^i$  for  $i \ge 0$ .

# **B PROOF OF THEOREM 1**

**Theorem 1.** If  $\phi_1$  is a DAG, then (1) no autocorrelation exists, (2)  $\phi_1$  can be specified by a strictly triangular matrix, (3) all eigenvalues of  $\phi_1$  are 0 and hence  $z_t$  is stationary.

**Proof:** By definition of DAG, no cycles can exist in the adjacency matrix, in this case,  $\phi_1$ . Hence, the diagonal entries which indicate dependency of  $z_{it}$  on  $z_{i,t+1}$  is necessarily 0, and thereby proving point (1).

Note that by definition, there exists a topological ordering on the vertices if and only if a graph has no directed cycles. Because  $\phi_1$  is a DAG, we can relabel the *d* vertices (time series components) as  $v_1, v_2, ..., v_d$ . If  $v_i v_{i'}$  is a directed edge into *i* from *i'* (indicating Granger-causality), then i > i'. Hence, all entries above the main diagonal are also 0 because these are entries for which i < i'. Combined with point (1) where main diagonal entries are also 0, this satisfies the definition of a strictly lower-triangular matrix (2).

We've shown that the adjacency matrix of a DAG is strictly lower-triangular via permutation, and note that the order of individual time series components does not matter, although in this case the *d* vertices are ordered from source to sink nodes.

The eigenvalues of any lower-triangular matrix is just its diagonal components [Axler, 1997], meaning that all eigenvalues for  $\phi_1$  is just 0. Since these are strictly less than 1 in magnitude, we can conclude that  $z_t$  is stationary (3).

# C EVALUATING ACCURACY FOR SOURCE & SINK NODE IDENTIFICATION

First, define Discounted Cumulative Gain (DCG) at position d, for d nodes arranged in a particular order:

$$DCG_{d} = \sum_{i=1}^{d} \frac{rel_i}{\log_2(i+1)}$$

where  $rel_i$  is the graded precision score of node at position *i*, e.g. {1, 0.5, 0} for {source, intermediary, sink} nodes respectively. Greater penalty is given for source or sink nodes ranked in lower positions. NDCG [Valizadegan et al., 2009] then equals DCG divided by Ideal Discounted Cumulative Gain (IDCG):

NDCG<sub>d</sub> = 
$$\frac{DCG_d}{IDCG_d}$$
, IDCG<sub>d</sub> =  $\sum_{i=1}^{|rel_d|} \frac{rel_i}{\log_2(i+1)}$ 

and  $|rel_d|$  represents the optimal order of nodes, which is given by the ground truth labels of each node.

# D BSG FOR IDENTIFYING SINK AND SOURCE NODES

#### **D.1** ABLATION EXPERIMENT - ERROR COVARIANCE $\Sigma_a$

Table	1: Average	NDCG (Accuracy	y) for Identif	ying Sink &	& Source Node	s with Depend	lent Errors, 5 Rep	ρ.
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Directed Acyclic	A. Weak Dependency $\sigma_{jk} = 0.1$		B. Moderate I	Dependency $\sigma_{jk} = 0.5$	C. Strong Dependency, $\sigma_{jk} = 0.9$	
	NDCG@24	NDCG@24	NDCG@24	NDCG@24	NDCG@24	NDCG@24
Method	Source Nodes	Sink Nodes	Source Nodes	Sink Nodes	Source Nodes	Sink Nodes
BSG, $h = 1$	$0.938 \pm 0.04$	$1\pm 0$	$0.951 \pm 0.004$	$1\pm 0$	$0.925 \pm 0.016$	$1\pm 0$
BSG, $h = 5$	$0.995\pm0.006$	$0.999\pm0.001$	$\textbf{0.993} \pm 0.004$	$0.997\pm0.002$	$0.961\pm0.011$	$\textbf{0.993} \pm 0.001$
<b>BSG</b> , $h = 10$	$\textbf{0.99} \pm 0.004$	$0.994\pm0.002$	$0.989\pm0.006$	$0.991\pm0.003$	$\textbf{0.975} \pm 0.01$	$0.988 \pm 0.004$
VAR-Between	$0.778 \pm 0.068$	$0.796 \pm 0.068$	_	_	—	_
VAR-Closeness	$0.648\pm0.024$	$0.926\pm0.024$	_	_	_	_
VAR-Degree	$0.8\pm0.045$	$0.868\pm0.053$	_	_	_	_
VAR-Eigen	$0.71\pm0.063$	$0.864\pm0.063$		—	—	—
DBN-Between	$0.75\pm0.036$	$0.825\pm0.036$	$0.747 \pm 0.085$	$0.827 \pm 0.085$	$0.721 \pm 0.075$	$0.853\pm0.075$
DBN-Closeness	$0.842 \pm 0.07$	$0.733 \pm 0.07$	$0.827\pm0.071$	$0.747\pm0.071$	$0.801\pm0.114$	$0.773\pm0.114$
DBN-Degree	$0.85\pm0.06$	$0.82\pm0.05$	$0.834 \pm 0.08$	$0.849 \pm 0.031$	$0.827 \pm 0.092$	$0.879 \pm 0.05$
DBN-Eigen	$0.752\pm0.031$	$0.822\pm0.031$	$0.73\pm0.081$	$0.845\pm0.081$	$0.713\pm0.071$	$0.862\pm0.071$
GVAR-Between	$0.729 \pm 0.066$	$0.845\pm0.066$	$0.684 \pm 0.078$	$0.891 \pm 0.078$	$0.729 \pm 0.04$	$0.845\pm0.04$
GVAR-Closeness	$0.685\pm0.037$	$0.89\pm0.037$	$0.632\pm0.04$	$0.943 \pm 0.04$	$0.689 \pm 0.062$	$0.885\pm0.062$
GVAR-Degree	t	t	†	t	†	t
GVAR-Eigen	$0.935\pm0.016$	$0.639\pm0.016$	$0.953\pm0.039$	$0.621\pm0.039$	$0.89\pm0.04$	$0.685\pm0.04$

- indicates retrieved NGC graph is degenerate, e.g., only edges are self-directed.

† indicates network measure cannot distinguish between nodes, e.g., all in/out degrees are equal.

### D.2 MULTISPECIES LOTKA-VOLTERRA - NONLINEAR DYNAMIC SYSTEMS

### **E** EVALUATING KINCADE FIRE SPILLOVERS

Multi-species LV	d = 20, T = 50		d = 20, T = 200		d = 20, T = 1000	
Method	NDCG@20 Source (Predator)	NDCG@20 Sink (Prey)	Source (Predator)	Sink (Prey)	Source (Predator)	Sink (Prey)
BSG, h = 1 BSG, h = 5 BSG, h = 10	$\begin{array}{c} 0.995 \pm 0.004 \\ \textbf{0.995} \pm 0.002 \\ 0.989 \pm 0.01 \end{array}$	$\begin{array}{c} 0.865 \pm 0.045 \\ 0.905 \pm 0.046 \\ \textbf{0.946} \pm 0.015 \end{array}$		$\begin{array}{c} \textbf{0.939} \pm 0.039 \\ 0.931 \pm 0.047 \\ 0.907 \pm 0.056 \end{array}$		$\begin{array}{c} \textbf{0.811} \pm 0.069 \\ 0.755 \pm 0.035 \\ 0.711 \pm 0.074 \end{array}$
VAR-Between VAR-Closeness VAR-Degree VAR-Eigen	$\begin{array}{c} 0.71 \pm 0.058 \\ 0.781 \pm 0.093 \\ 0.768 \pm 0.091 \\ 0.812 \pm 0.087 \end{array}$	$\begin{array}{c} 0.84 \pm 0.058 \\ 0.768 \pm 0.093 \\ 0.748 \pm 0.071 \\ 0.738 \pm 0.087 \end{array}$	$\begin{array}{c} 0.721 \pm 0.145 \\ 0.78 \pm 0.09 \\ 0.679 \pm 0.084 \\ 0.881 \pm 0.037 \end{array}$	$\begin{array}{c} 0.828 \pm 0.145 \\ 0.769 \pm 0.09 \\ 0.737 \pm 0.077 \\ 0.669 \pm 0.037 \end{array}$		  
DBN-Between DBN-Closeness DBN-Degree DBN-Eigen	$\begin{array}{c} 0.796 \pm 0.125 \\ 0.796 \pm 0.075 \\ 0.801 \pm 0.072 \\ 0.753 \pm 0.086 \end{array}$	$\begin{array}{c} 0.753 \pm 0.125 \\ 0.754 \pm 0.075 \\ 0.756 \pm 0.101 \\ 0.797 \pm 0.086 \end{array}$		$\begin{array}{c} 0.742 \pm 0.091 \\ 0.743 \pm 0.074 \\ 0.724 \pm 0.112 \\ 0.75 \pm 0.111 \end{array}$	$ \begin{vmatrix} 0.892 \pm 0.107 \\ 0.854 \pm 0.086 \\ 0.891 \pm 0.061 \\ 0.797 \pm 0.067 \end{vmatrix} $	$\begin{array}{c} 0.657 \pm 0.107 \\ 0.696 \pm 0.086 \\ 0.704 \pm 0.072 \\ 0.748 \pm 0.073 \end{array}$
GVAR-Between GVAR-Closeness GVAR-Degree GVAR-Eigen	$\begin{array}{c} 0.736 \pm 0.077 \\ 0.744 \pm 0.093 \\ \dagger \\ 0.791 \pm 0.129 \end{array}$	$\begin{array}{c} 0.814 \pm 0.077 \\ 0.806 \pm 0.093 \\ \dagger \\ 0.758 \pm 0.129 \end{array}$		$\begin{array}{c} 0.733 \pm 0.111 \\ 0.72 \pm 0.114 \\ & \dagger \\ 0.803 \pm 0.098 \end{array}$		$\begin{array}{c} 0.809 \pm 0.063 \\ 0.554 \pm 0.01 \\ \dagger \\ 0.734 \pm 0.077 \end{array}$

Table 2: Average NDCG (Accuracy) for Identifying Sink & Source Nodes with Nonlinear Systems, 5 Rep.

- indicates retrieved NGC graph is degenerate, e.g., only edges are self-directed.

† indicates network measure cannot distinguish between nodes, e.g., all in/out degrees are equal.



Multispecies Lotka-Volterra Population

Figure 1: Example Multi-species Lotka-Volterra Population with d = 20 and T = 1000. Warm colors refer to the 10 predator species and cool colors refer to the 10 prey species. Each predator hunts 2 prey and each prey is hunted by 2 predators.



Figure 2: Hourly PM 2.5 Concentration (FOD) by County During Kincade Fire - Oct. 22 to Nov. 7, 2019.



# Kincade Wildfire - 12 Hour Spillover Effects

Figure 3: County Ranking by BSG Importance and Vulnerability Scores, h = 12.



Figure 4: From left to right: Lower 95% HPDI Bound, Posterior Mean, and Upper 95% HPDI Bound. BSG for Kincade Fire, h=12 hours ahead. Note the strong variability in spillovers (edge weights) originating from Sonoma County and tighter intervals for indirect spillovers between San Francisco, Contra Costa, and Alameda counties.

### References

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