Deep learning of contagion dynamics on complex networks

Murphy, Laurence and Allard

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Key Contributions

- A training procedure and appropriate GNN architecture.
- Assessing validity of the approach.
- Providing predictions for unseen network structures.



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Goal: Build a model $\hat{\mathcal{M}}$, parameterised by tunable Θ , such that

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Therefore, the outcomes from the GNN will be

$$\hat{y}_i = \hat{f}(x_i, \Phi_i, x_{\mathcal{N}_i}, \Phi_{\mathcal{N}_i}, \Omega_{i\mathcal{N}_i}; \Theta) ..$$

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$$\mathcal{L}(\Theta) = \sum_{t \in \mathcal{T}'} \sum_{v_i \in \mathcal{V}'(t)} rac{w_i(t)}{Z'} \mathcal{L}(y_i(t), \hat{y}_i(t)).$$

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$$w_i(t) \propto
ho \left(k_i, x_i, \Phi_i, x_{\mathcal{N}_i}, \Phi_{\mathcal{N}_i}, \Omega_{i\mathcal{N}_i}\right)^{-\lambda},$$

where k_i is the degree of node v_i in G.

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- III Interacting contagion dynamics (with two diseases): $S = \{S_1S_2, I_1S_2, S_1I_2, I_1I_2\} = \{0, 1, 2, 3\}.$

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- III Interacting contagion dynamics (with two diseases): $S = \{S_1S_2, I_1S_2, S_1I_2, I_1I_2\} = \{0, 1, 2, 3\}.$
- IV *Metapopulation* dynamics: status of individuals are gathered by geographical regions. E.g. Deterministic metapopulation dynamics with constant population size, and have S, I or R for each individual.

Performance

- We compare GNN predictions ŷ_i(t) with corresponding target y_i(t).
- ► Use Pearson correlation coefficient r between predictions and targets. Compute error as 1 r for each degree class k.

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 The GNN outperforms the MLE on Erdos-Renyi and Barabasi-Albert networks.

Performance

- We compare GNN predictions ŷ_i(t) with corresponding target y_i(t).
- ► Use Pearson correlation coefficient r between predictions and targets. Compute error as 1 r for each degree class k.
- The GNN outperforms the MLE on Erdos-Renyi and Barabasi-Albert networks.

A **Barabasi-Albert** network is one in which we begin with m_0 nodes fully connected to each other. Nodes are then added one at a time, and are each connected to $m \le m_0$ existing nodes. A connection with an existing node *i* is made with probability

$$p_i = rac{k_i}{\sum_j k_j}.$$

So we tend to see certain nodes become "hubs" and others become relatively isolated.

Performance

A Graphical Interlude



First transform state of every node, x_i , with shared multilayer perceptron using

$$\hat{f}_{in}: \mathcal{S} \to \mathbb{R}^d$$

 $x_i \mapsto \hat{f}_{in}(x_i) =: \xi_i$

or alternatively, if the attributes Φ_i are available

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The outcome of each node is

$$\hat{y}_i = \hat{f}_{out}(\nu_i).$$

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$$a_{ij} = \sigma \left[\mathcal{A} \left(\xi_i \right) + \mathcal{B} \left(\xi_j \right) + \mathcal{C} \left(\psi_{ij} \right) \right],$$

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$$u_i = \hat{f}_{att}(\xi_i, \xi_{\mathcal{N}_i}) = \xi_i + \sum_{v_j \in \mathcal{N}_i} a_{ij}\xi_j.$$

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Other important details

- The rectified Adam algorithm was used to optimise the hyperparameters.
- When S is discrete and countable, can simplify inputs to ρ(.), which we estimate as

$$\rho(k,x,l) = \frac{1}{|\mathcal{V}|T} \sum_{i=1}^{|\mathcal{V}|} \mathbb{1} \left(k_i = k\right) \times \sum_{t=1}^{T} \mathbb{1} \left(x_t(t) = x\right) \mathbb{1} \left(l_i(t) = l\right).$$

When we have continuous states, we cannot estimate ρ directly, and so we instead use

$$w_i(t) = [P(k_i)\Sigma(\Phi_i,\Omega_i|k_i)\Pi(\bar{x}(t))]^{-\lambda}$$