Predicting Covid-19 infections using multi-layer centrality measures

Master Thesis

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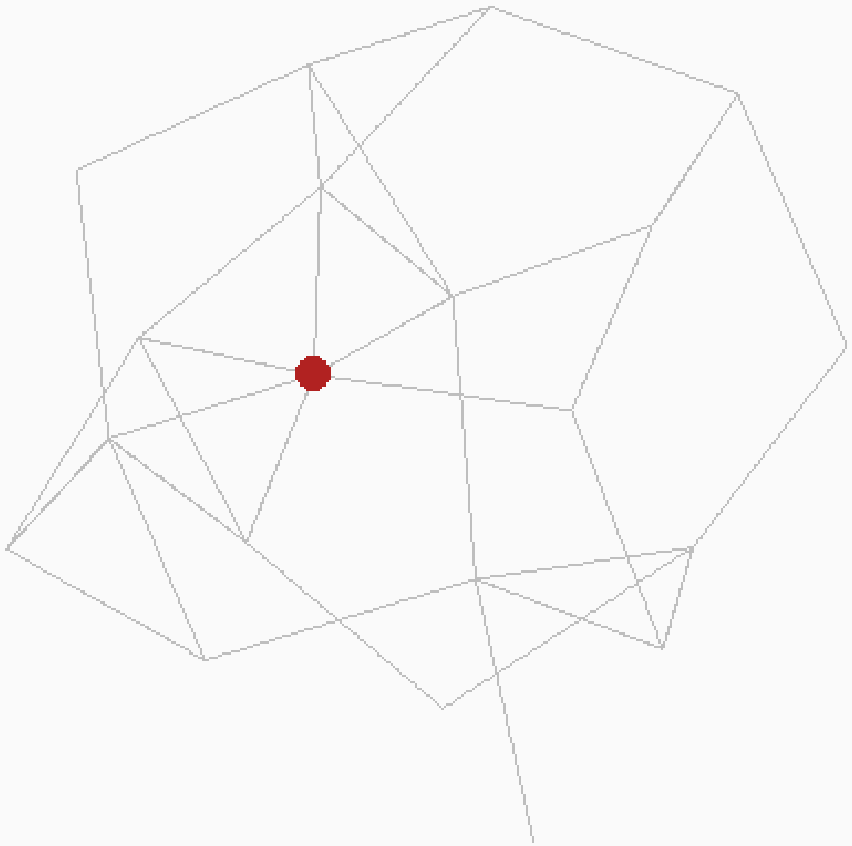
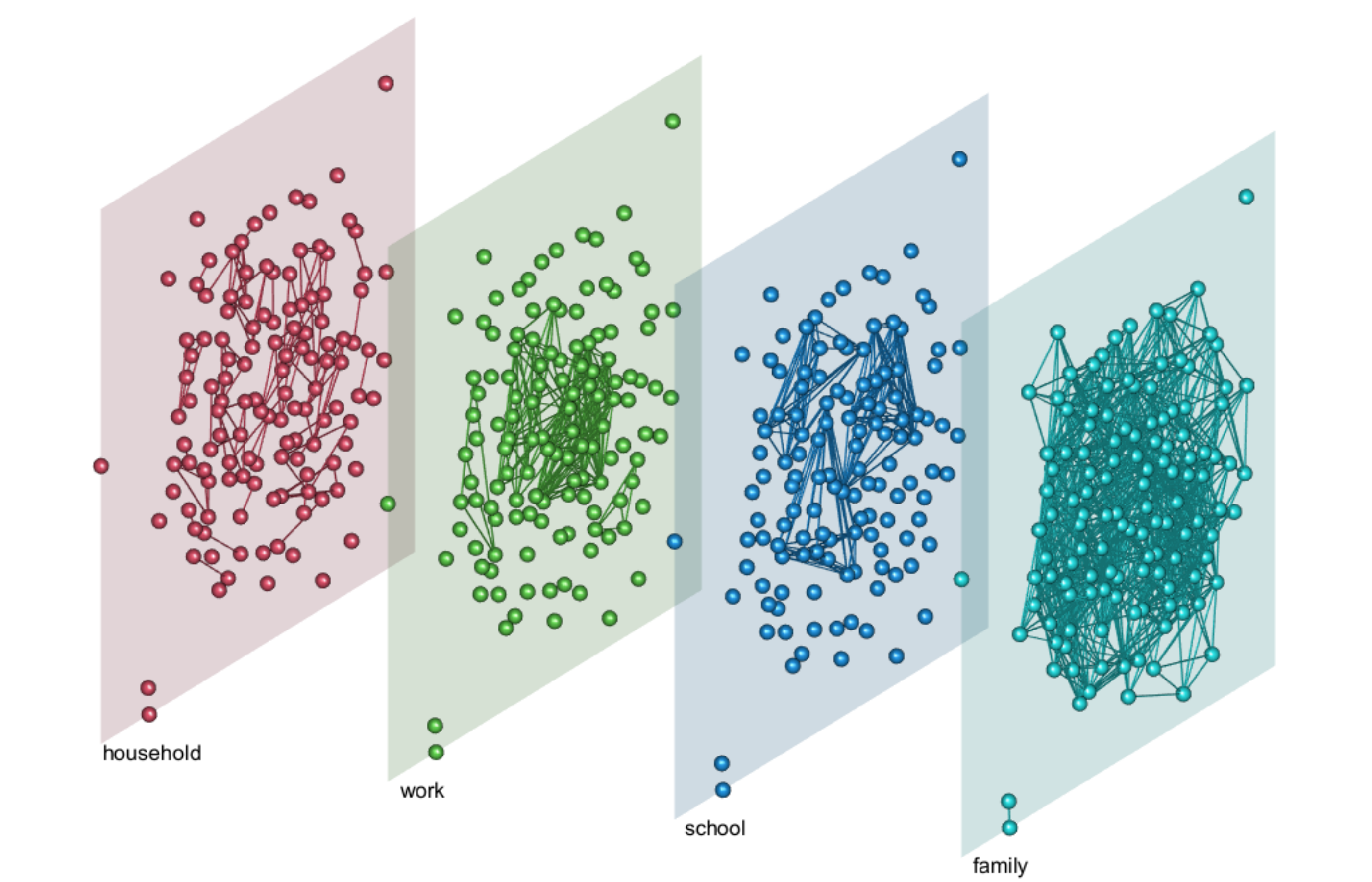


Model spread to inform policy decisions!

Who gets infected and **when**?

Predicting Covid-19 infections using **multi-layer** centrality measures

Our lives are multi-layered.



CBS micro-data allows to construct multi-layer network dataset.

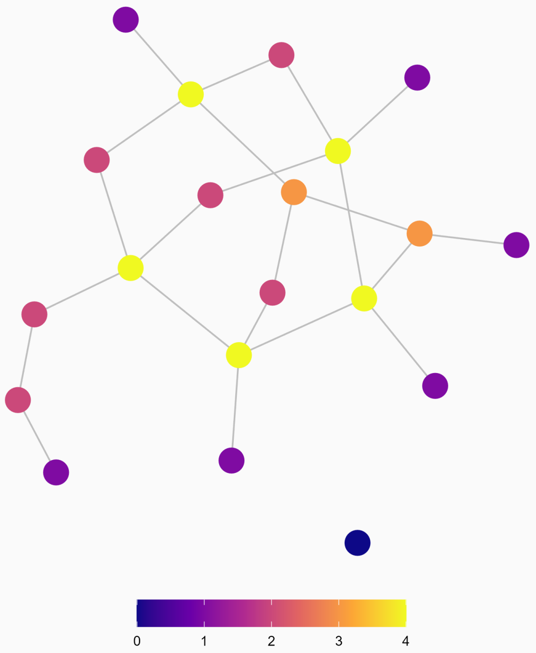
Micro-data can be linked to **PCR test data.**

Analyses conducted on regional **subset** of ~ 1m nodes.

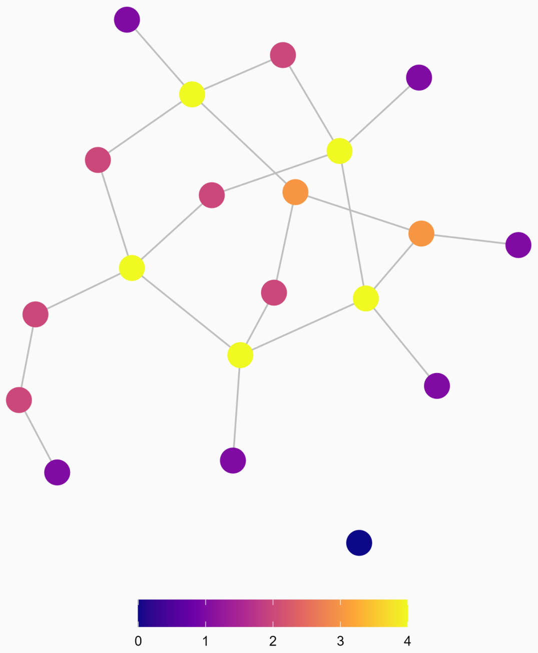
Predicting Covid-19 infections using multi-layer

centrality measures

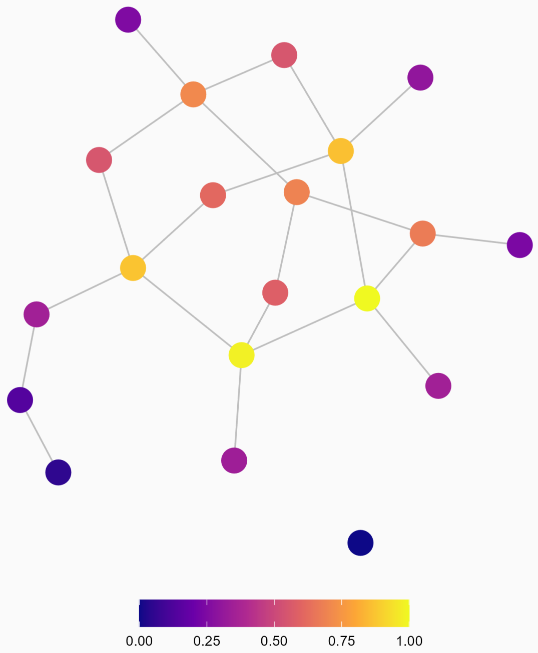
Degree

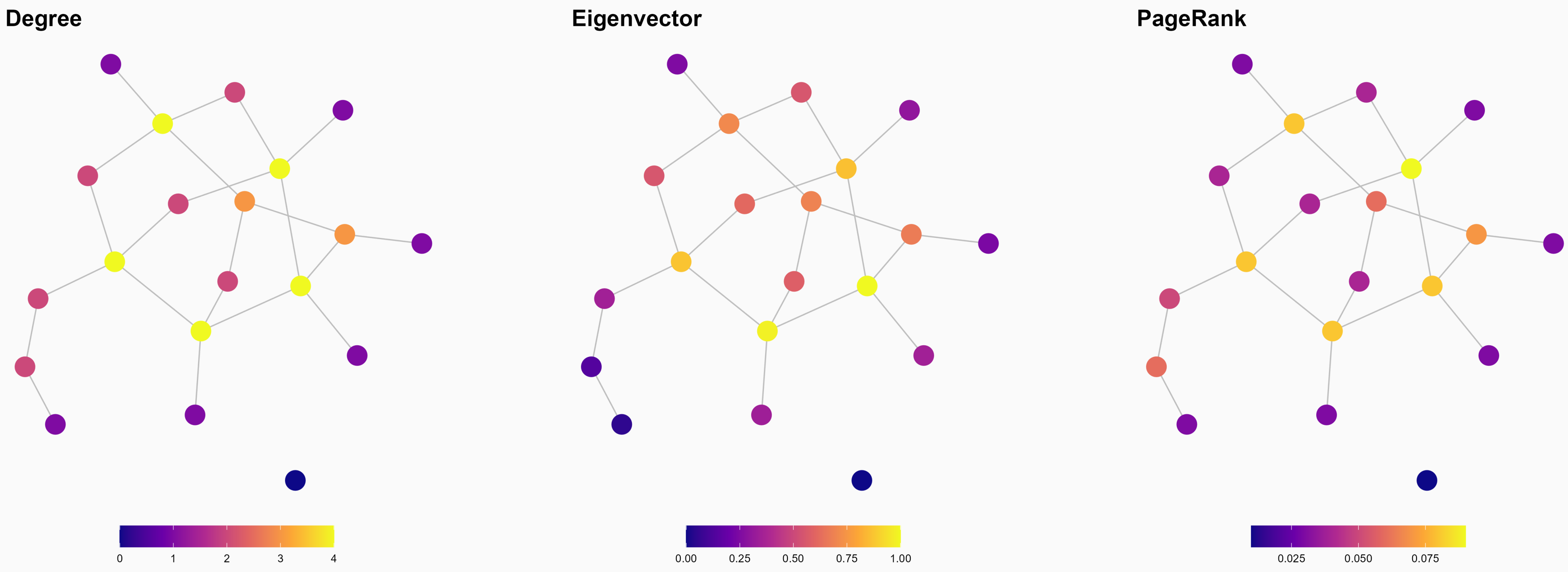


Degree



Eigenvector

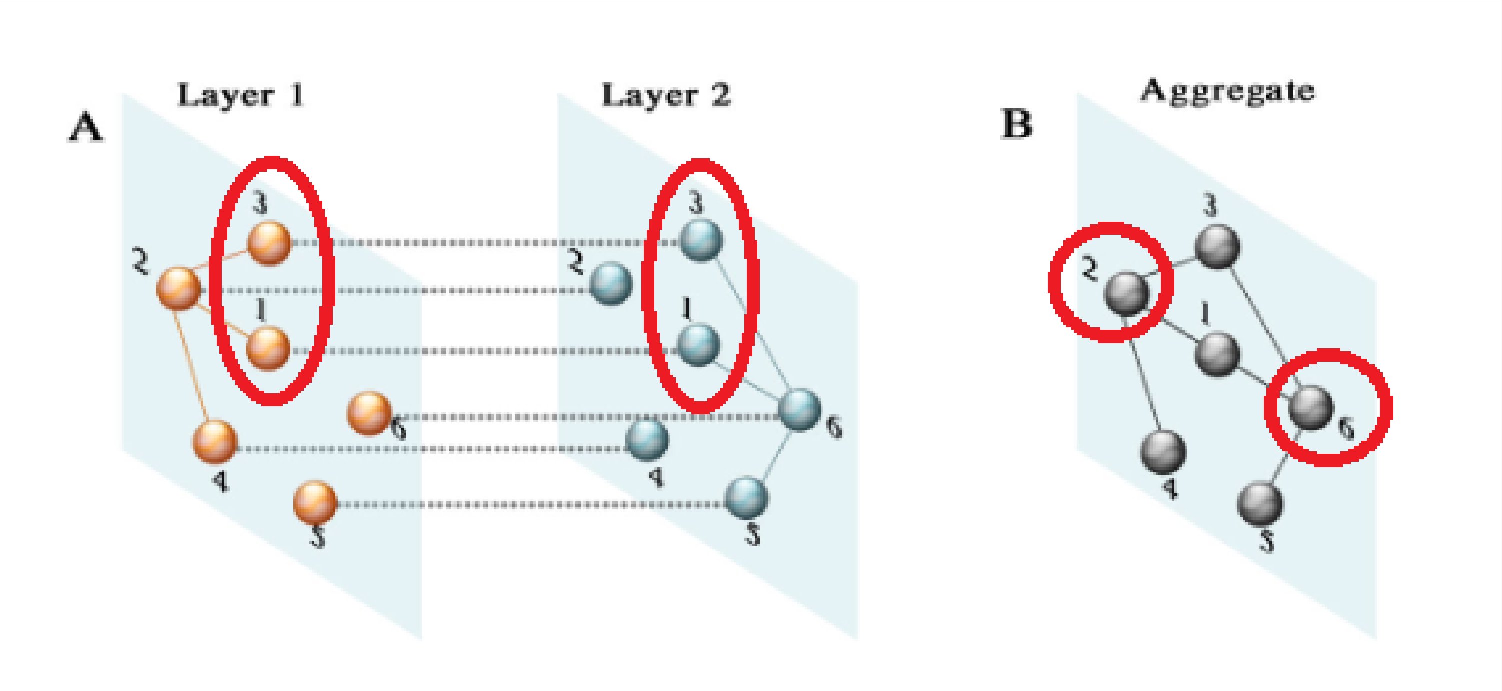



Degree
0
1
2
3
4
Eigenvector
0.00
0.25
0.50
0.75
1.00
PageRank
0.025
0.050
0.075

Single-layer centrality

≠

Multi-layer centrality



De Domenico et al. 2015, Supplementary Figure 1

De Domenico, M., Solé-Ribalta, A., Omodei, E., Gómez, S., & Arenas, A. (2015). Ranking in interconnected multilayer networks reveals versatile nodes. Nature Communications, 6(1), 6868. https://doi.org/10.1038/ncomms7868

Bringing it all together:

> How well can multi-layer centrality measures predict the infection of individuals with epidemic diseases like Covid-19?

Analytic Strategy

Outcome: **Time until infection**

Predictors: Degree, Eigenvector, PageRank

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   b. Uno's Concordance Index C of Cox models including linear combinations of centralities as predictors

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4. Average the estimates across simulations

Results

a. **Medium negative correlations** of all centrality measures with outcome

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Also: Only small differences between single-layer and multi-layer measures.

Is that it?

Multiple layers, multiple transmission rates.

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➔ **Weighted Degree centrality**

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...minimal performance increase

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$$R^2 \leq 0.01$$

Lessons learned

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Centrality measures could still **complement** prediction models

… **if** used with representative contact networks.

Backup slides

Behind the scenes: **Simulating an epidemic** on a large-scale network using a SIR model.

$$\frac{dS}{dt} = -\beta I S$$

$$\frac{dI}{dt} = \beta I S - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Each node can be in one of the **three states**, and **transitions stochastically** based on *network contacts*, *transmission rate*, and *recovery time*.

$$S \rightarrow I$$

$$I \rightarrow R$$

Where the transmission probabilities for the nodes in layer l at time t is given by:

$$\boldsymbol{\tau'}_{lt} = 1 - (1 - \tau_l)^{\mathbf{\Gamma_{t-1}}}$$

Do you have...

👩👴👶👦...many close relatives? (Degree Centrality)

👩👴👶👦 👭 👧👴👵👦...many close relatives and also a partner with a big family? (Eigenvector Centrality)

✈️🌍 👧👴👵👦... but that partner's family lives in a different country? (Betweenness Centrality)

... then you could be a **super-spreader**.

High centrality ⇝ High spreading capacity

But: High spreading capacity ≠ High infection risk