

Controlling the Spread of Disease With Network-Based Models of Influence

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Overview

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3 Results

4 Discussion and Future Work

Background

Motivation

- Public health resources are limited
- COVID mutations continue to appear
- Need to optimize response
- flatten the curve

SIR Model

- Predicts infection dynamics
- Commonly used public health model
- Susceptible, Infected, Removed/Recovered

SIR Model

Susceptible

Susceptible population decreases at a rate of $\frac{dS}{dt} = -bSI$

Infected

Infected population evolves at a rate of $\frac{dI}{dt} = bSI - kI$

Removed

Removed population increases at a rate of $\frac{dR}{dt} = kI$

SIR II

- S , I , R refer to concentrations of susceptible, infected, removed respectively
- b , k are rate constants
- transmission rates proportional to concentrations at a given time point

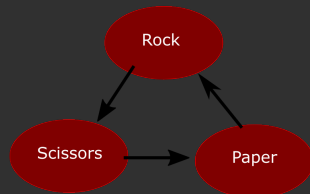
Network

Connections represented as $n \times n$ adjacency matrix

Nodes denote individuals, edges denote connections

Weights denote relative strength of connections between nodes

	Rock	Paper	Scissors
Rock	0	-1	1
Paper	1	0	-1
Scissors	-1	1	0



Haslemere Data

- Haslemere: small town in England pop. approx 10000
- Collected for BBC documentary
- Real world social network interaction data via GPS

Covid-HM Model (Firth et al., 2020)

- Simulates outbreak across network
- Incorporates network's structure

COVID-HM II

- Network structure is input
- each node can be S,I,R
- Nodes can be quarantined, isolated
- Outside infection probability

COVID-HM III

- Simulates 70 days/steps of an outbreak
- 468 total nodes in Haslemere data
- Subset of nodes infected at outset
- Infected nodes fixed across all trials

COVID-HM parameters

- No preemptive isolation among contacts
- Primary contact tracing
- Testing rate
- False positive rate
- Infectiousness
- Low outside infection rate (.001)

Motivation

- Can PRINCE predict influential nodes?
- How much isolation to see effect?
- Can PRINCE outperform random isolation?

Methods

PRioritization and Complex Network Elucidation (PRINCE) algorithm (Vanunu et al., 2010)

- Identifies and ranks high priority nodes
- Iteratively computes

$$F' = \alpha W' F^{t-1} + (1 - \alpha)Y$$

F'	vector of updated weights
α	$\alpha \in [0, 1]$ that controls network/weight interaction term
W	$n \times n$ adjacency matrix
F^{t-1}	Previous weights vector
Y	Vector of prior knowledge of i^{th} node

Idea

- Use PRINCE to isolate nodes in simulation
- Arrange nodes by PRINCE score
- Isolate highest scoring nodes
- Compare with benchmarks

Experimental Setup

- 468 total nodes
- Model simulates 70 days of an outbreak
- Each trial was repeated for 100 iterations
- Isolate initially infected, Susceptible, mixed cases
- PRINCE vs. no isolation baseline and random isolation null models

Results

Isolating Initially Infected Nodes

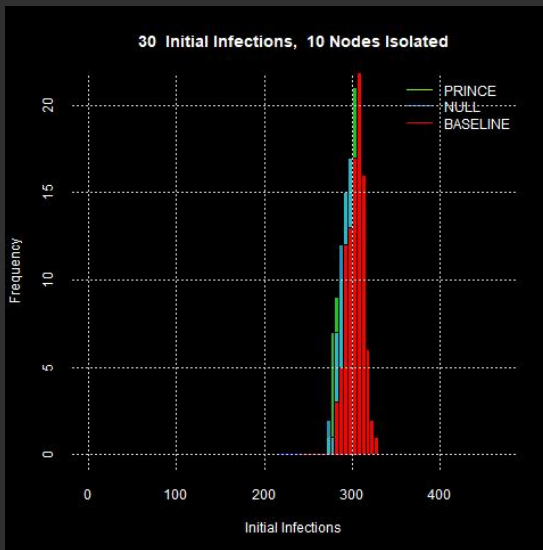


Figure: 30 Initial Infections, 10 Nodes Isolated

Isolating Initially Infected Nodes

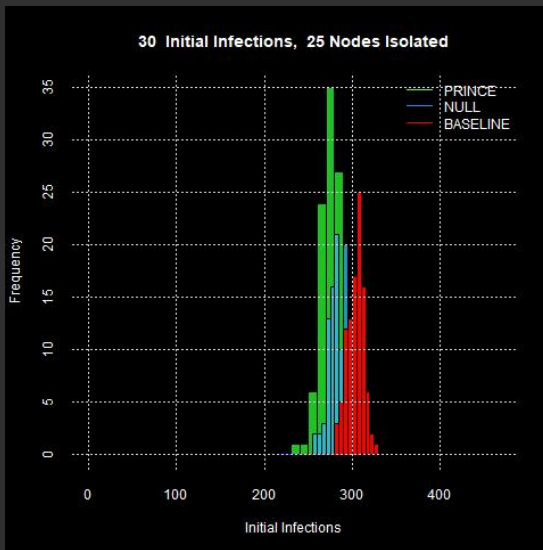


Figure: 30 Initial Infections, 25 Nodes Isolated

Isolating Initially Infected Nodes

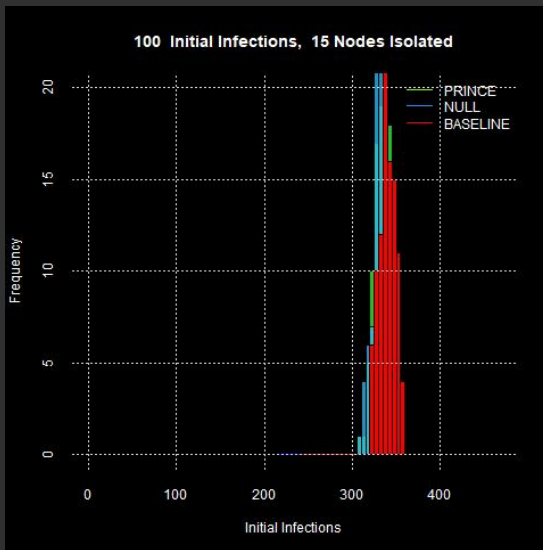


Figure: 100 Initial Infections, 15 Nodes Isolated

Isolating Initially Infected Nodes

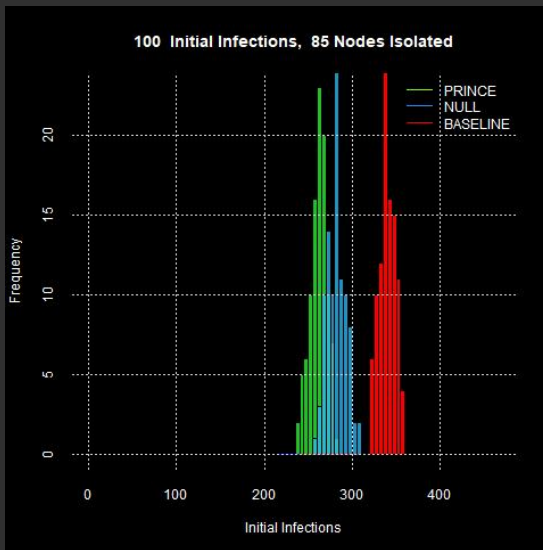


Figure: 100 Initial Infections, 85 Nodes Isolated

Isolating Initially Infected Nodes

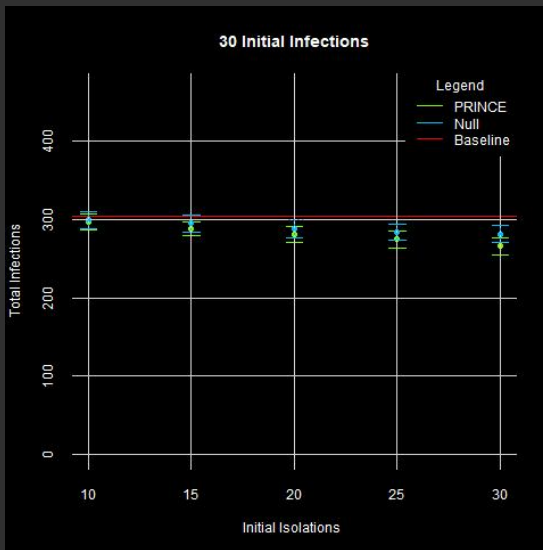


Figure: 30 Initial Infections

Isolating Initially Infected Nodes

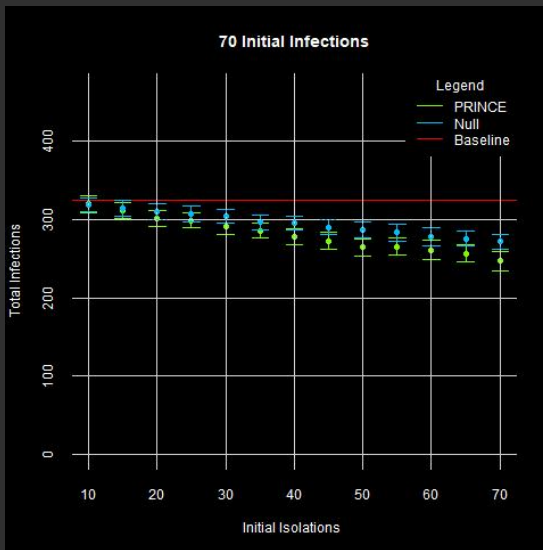


Figure: 70 Initial Infections

Isolating Initially Infected Nodes

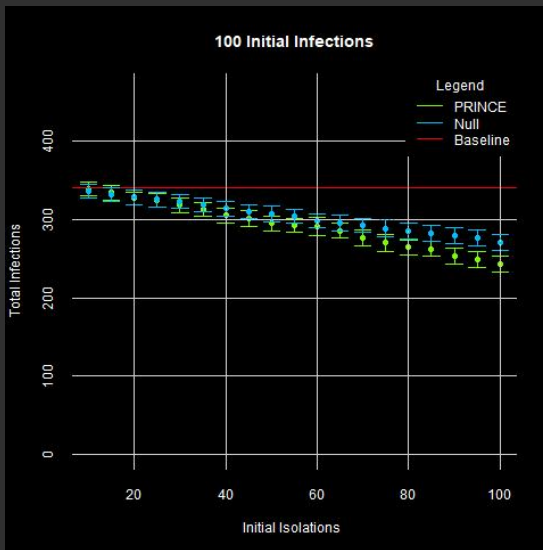


Figure: 100 Initial Infections

Isolating Susceptible Nodes

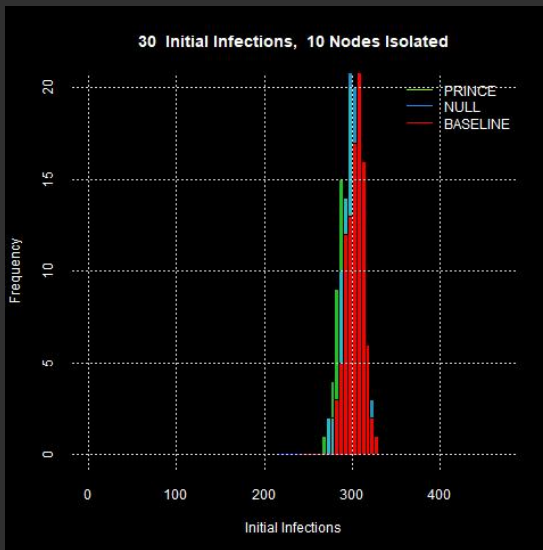


Figure: 30 Initial Infections, 10 Isolations

Isolating Susceptible Nodes

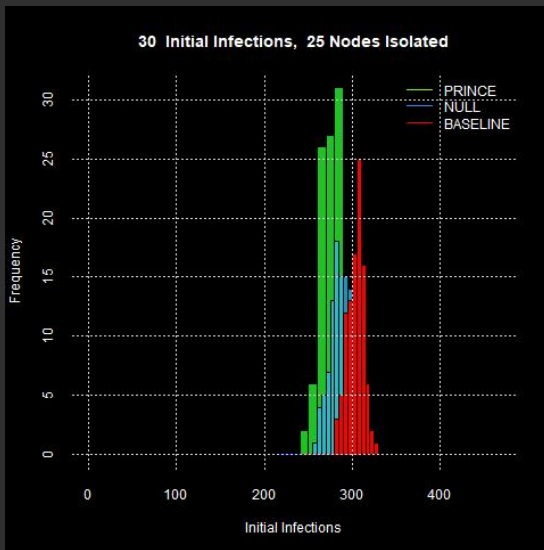


Figure: 30 Initial Infections, 25 Isolations

Isolating Susceptible Nodes

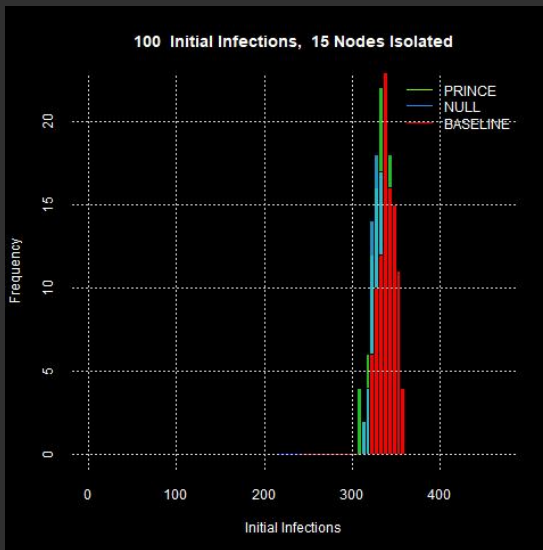


Figure: 100 Initial Infections, 15 Isolations

Isolating Susceptible Nodes

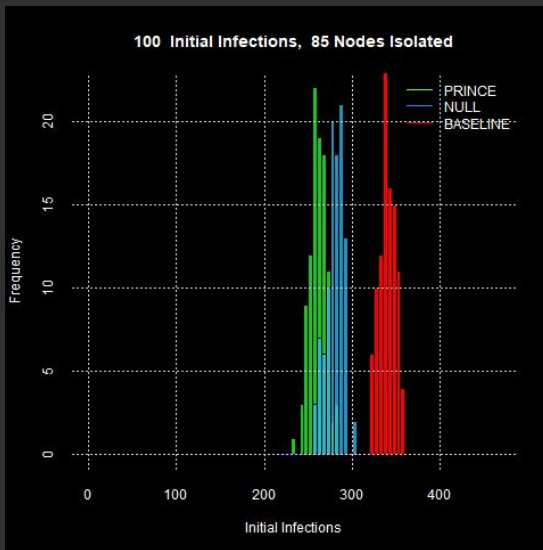


Figure: 100 Initial Infections, 15 Isolations

Isolating Susceptible Nodes

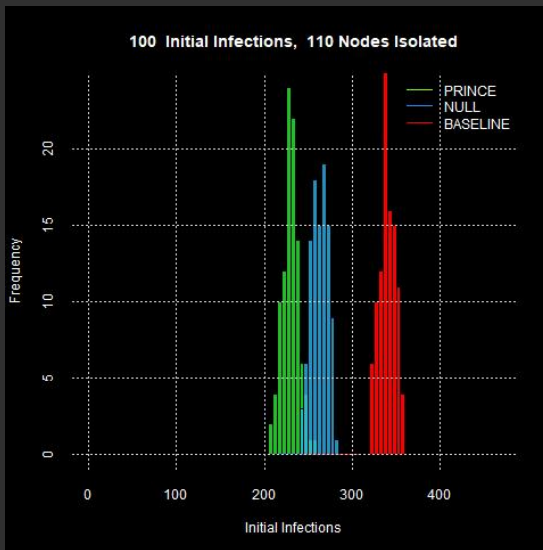


Figure: 100 Initial Infections, 110 Isolations

Isolating Susceptible Nodes

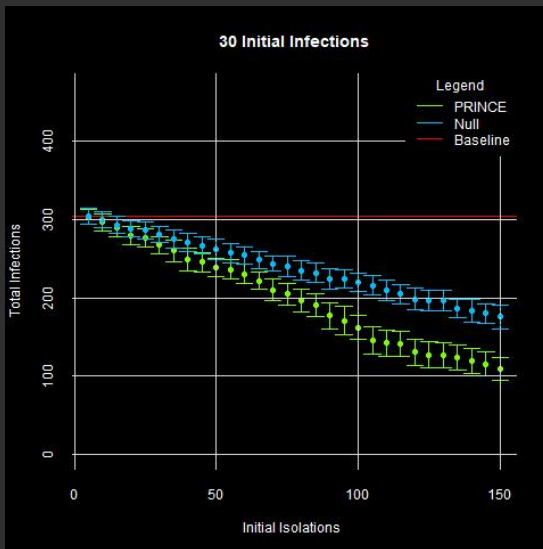


Figure: 30 Initial Infections

Isolating Susceptible Nodes

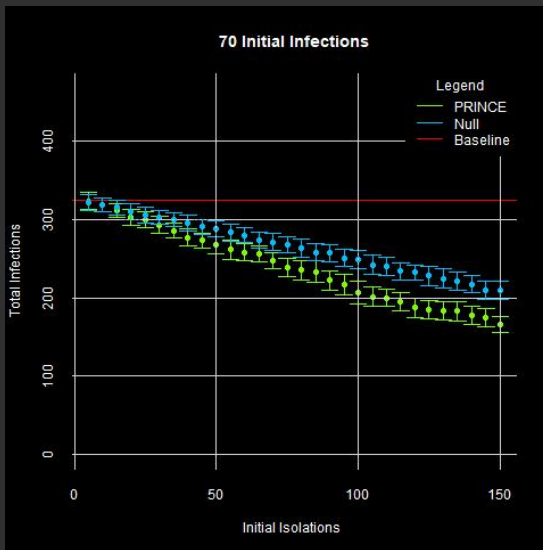


Figure: 70 Initial Infections

Isolating Susceptible Nodes

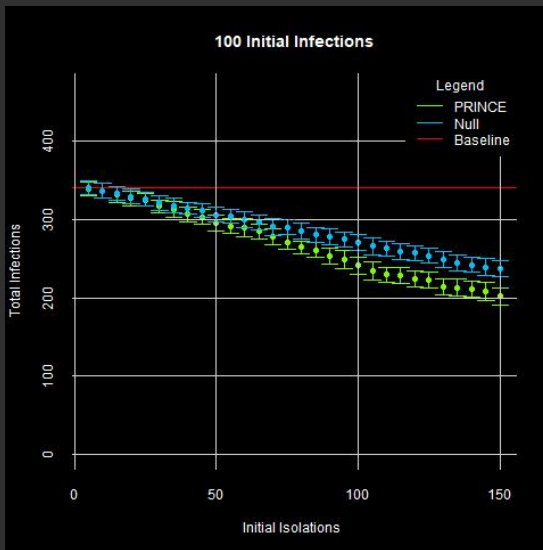


Figure: 100 Initial Infections

Mixed Case

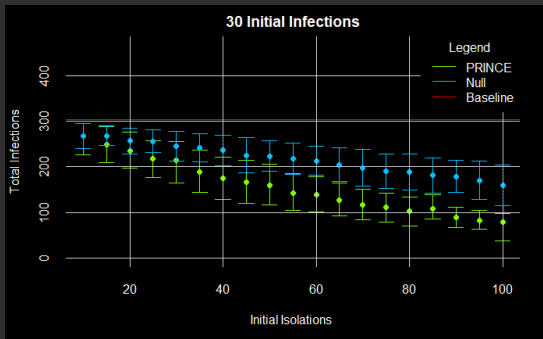


Figure: 30 Susceptible Nodes Isolated, All Infected Nodes Isolated

Mixed Case

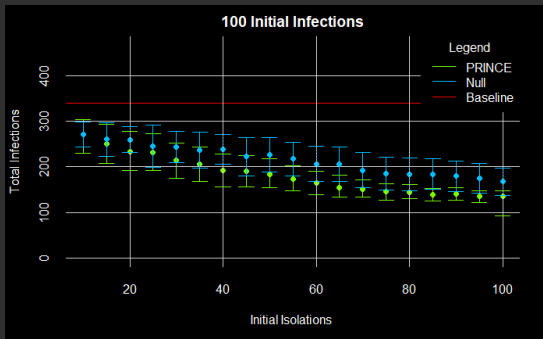


Figure: 190 Susceptible Nodes Isolated, All Infected Nodes Isolated

Discussion and Future Work

Discussion

- PRINCE effectively identifies high priority nodes
- Greater differential effect when isolating susceptible nodes
- Significantly lower disease transmission and disease burden
- Enhanced effectiveness of public health resources

Future Work

- Test different network structures
- Further investigate tuning parameters

The End