Simulations and analysis of Covid-19 spread

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Aim

- Building an open source simulation interface for Estonia using the aforementioned SPG:
  - Underlying graph is dynamic and represents the connections between people that can carry the virus
  - Connections can be made to depend on the day/weather/governmental policies like vaccinations and lockdowns/etc.
  - Simulations run using a stochastic SIR model

- Understanding better how viruses spread in populations.
  - This includes testing the so-called superspreader effect, the idea that infection spread in the early stages of the pandemic are dictated by supercarriers

Estonia's Synthetic Population Generator → Stochastic SIR model
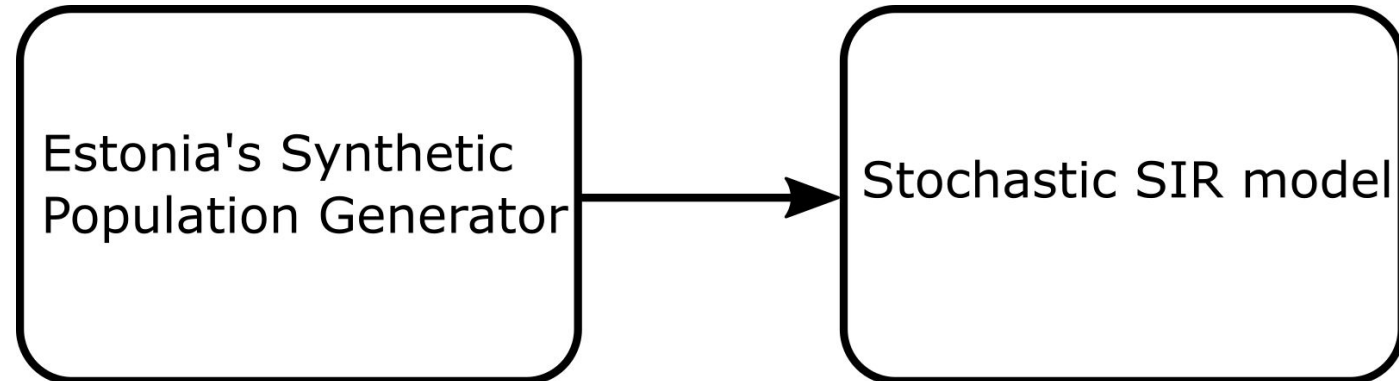
Technical details

- Underlying Graph used for the simulation:
  - Node – a person (~1.3 million nodes in total)
  - Edge – connection between two people, the weight of which denotes the likelihood of virus transmittion
  - Weight is a function of the current day, climate conditions, the type of connection at hand
  - Types of connections: intra-household, -workplace, -school, -supermarket..

Technical details

- Simulation is performed using the stochastic SIR model
  - Infection is iterated day-by-day
  - Each node is either susceptible (S), infected (I) or recovered (R)
  - Each day, infected nodes infect neighbouring susceptible nodes with some probability (given by the weight). Each infected node will recover with some probability depending on how long they've been infected for.
  - Recovered nodes are effectively cut out of the graph, as they don't influence the virus spread

Susceptible → Infected → Recovered
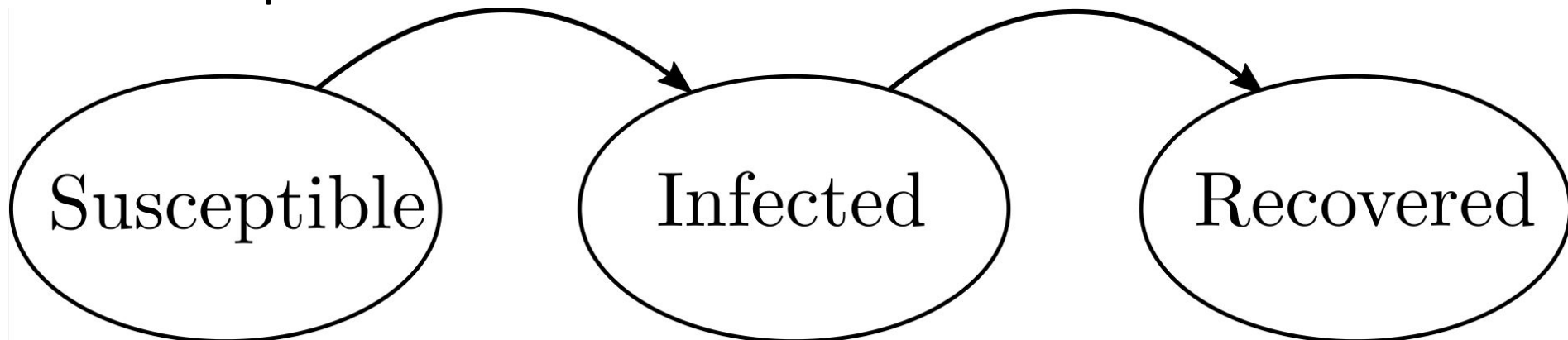
Technical details

- Probability of infected node recovering each day as a function of the infection duration
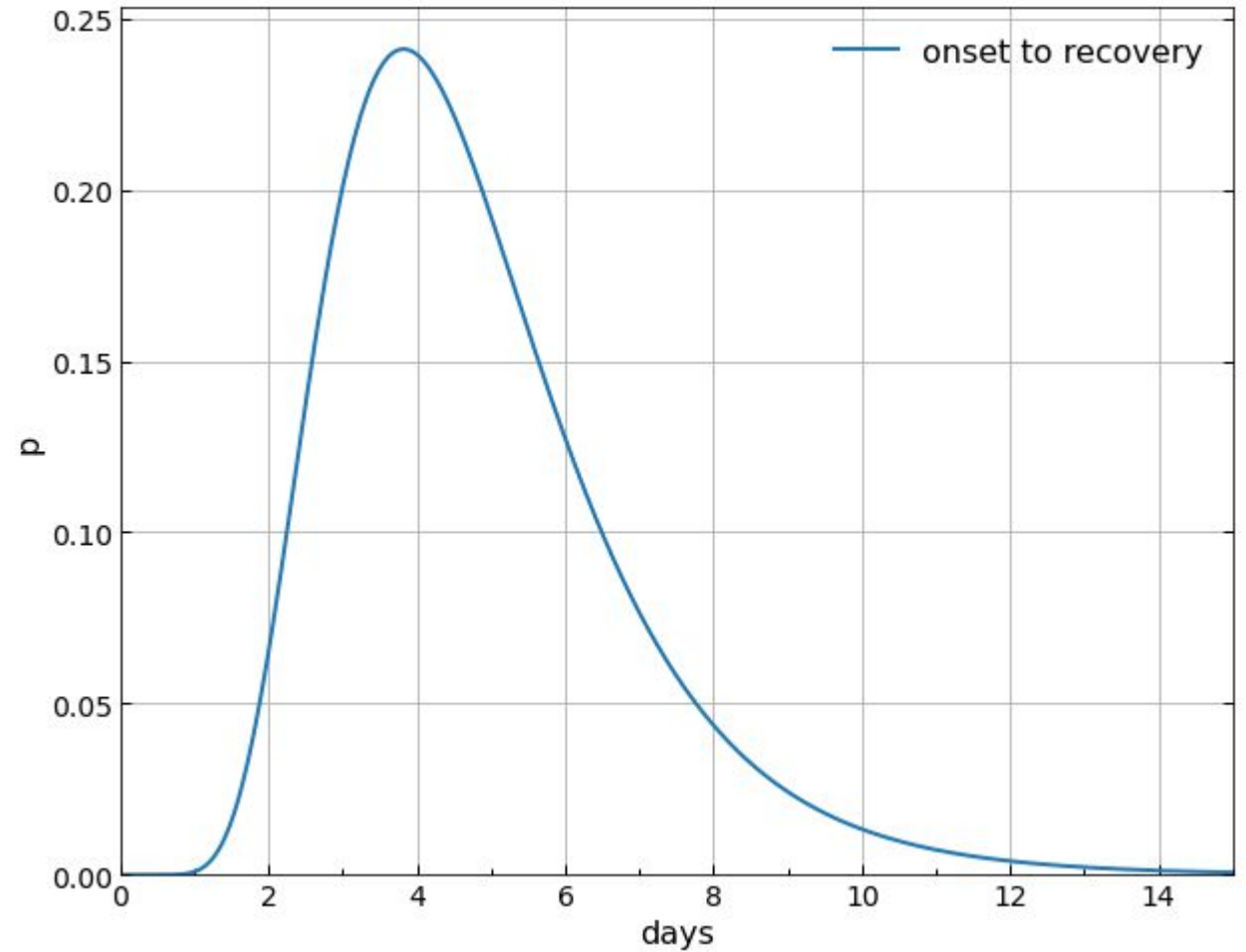
Preliminary simulations

- We have performed some preliminary analysis before finishing Estonia's simulation interface.

- Analysis done in as simple of a system as possible
  - Iteration is week-by-week and people are assumed to be infectious for 1 week
  - Graph is time-independent and weight p=0.10, N=500 000
  - We use a scale-free network for the graph

Scale-free network

- A network whose degree distribution $P(m)$ follows a power law $m^{-\kappa}$, where κ is a parameter of the graph

- Good descriptor for how human population interactions are distributed

- For $N = 500\ 000$, there are few people with ~1000 connections

Random retwork
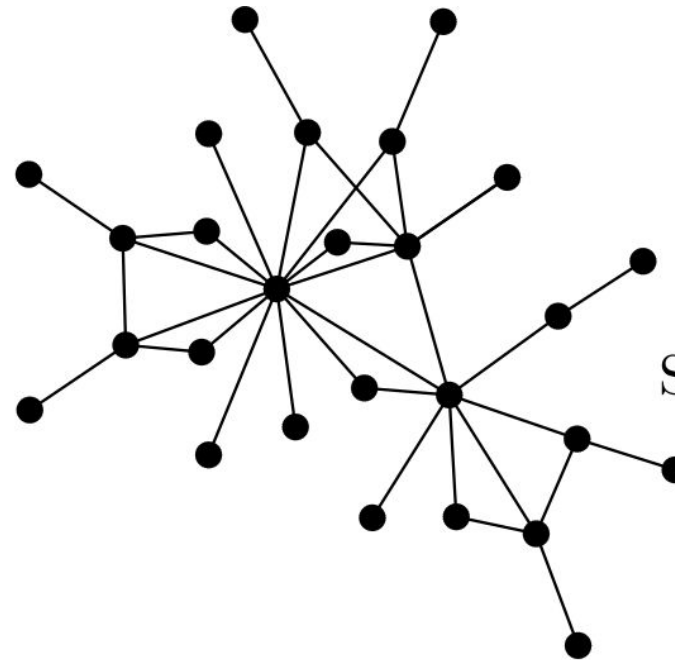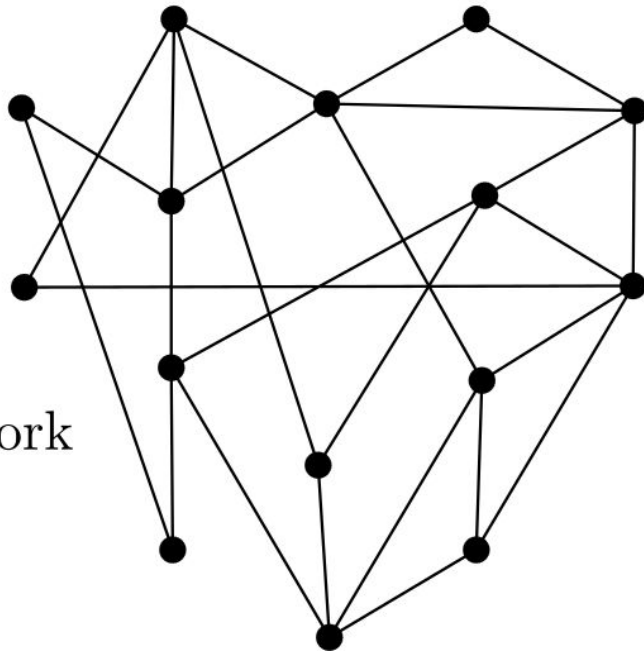
Scale-free network

- We expect higher degree nodes (people with more connections) to get infected earlier -> virus is expected to be more infectious in the earlier stages
  - Investigating the effective value of R_E as a function of the fraction of people infected
  - R_E = average number of people that a currently infectious person infects
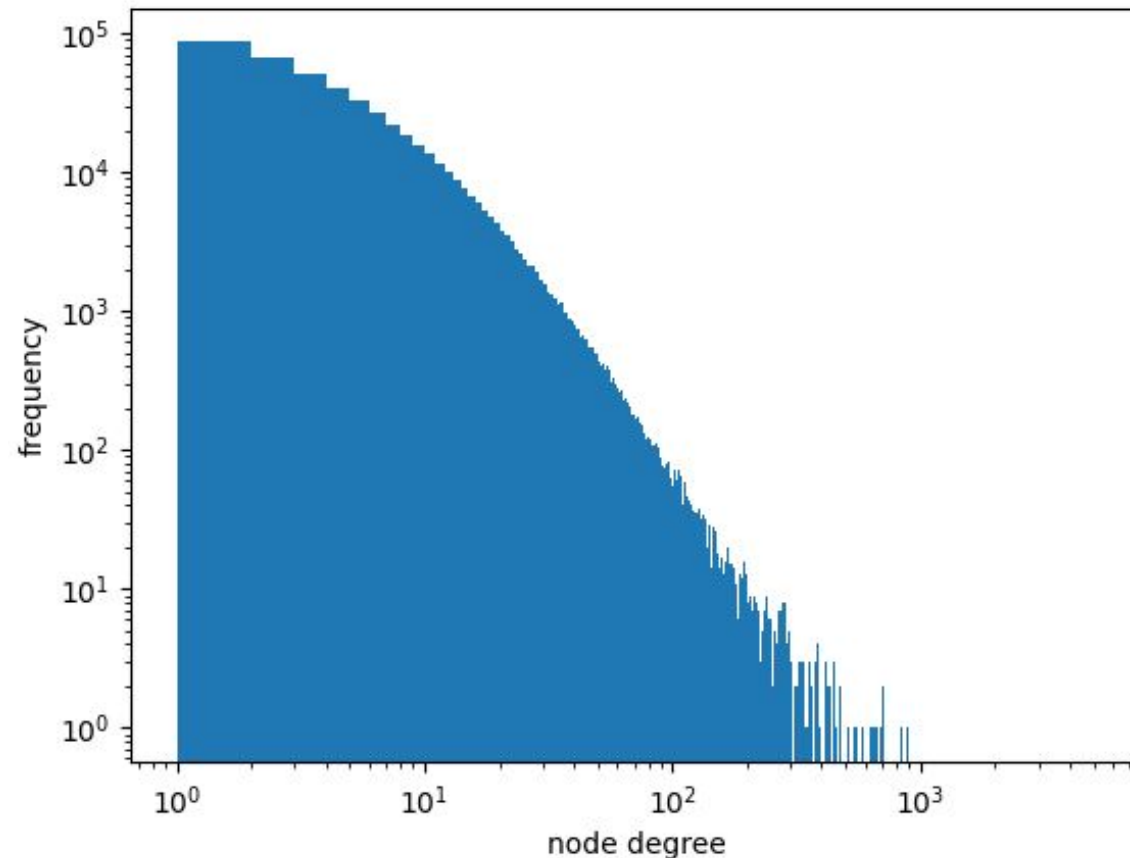
Random network results
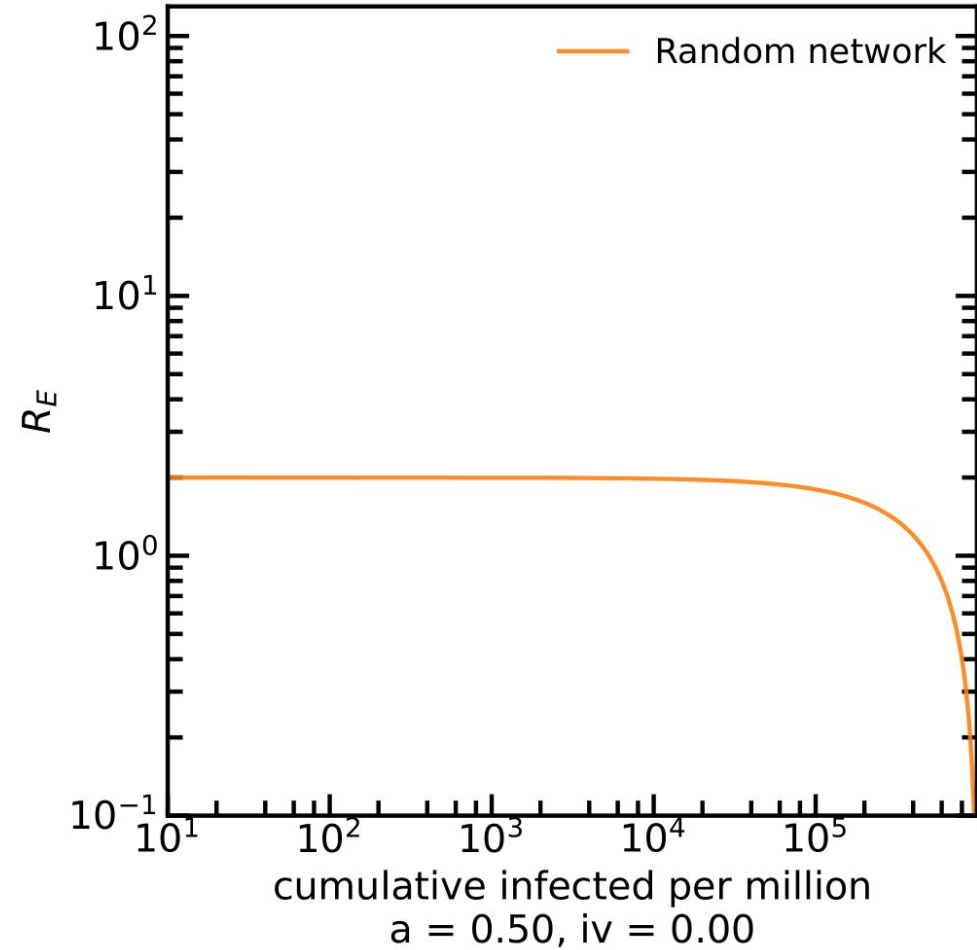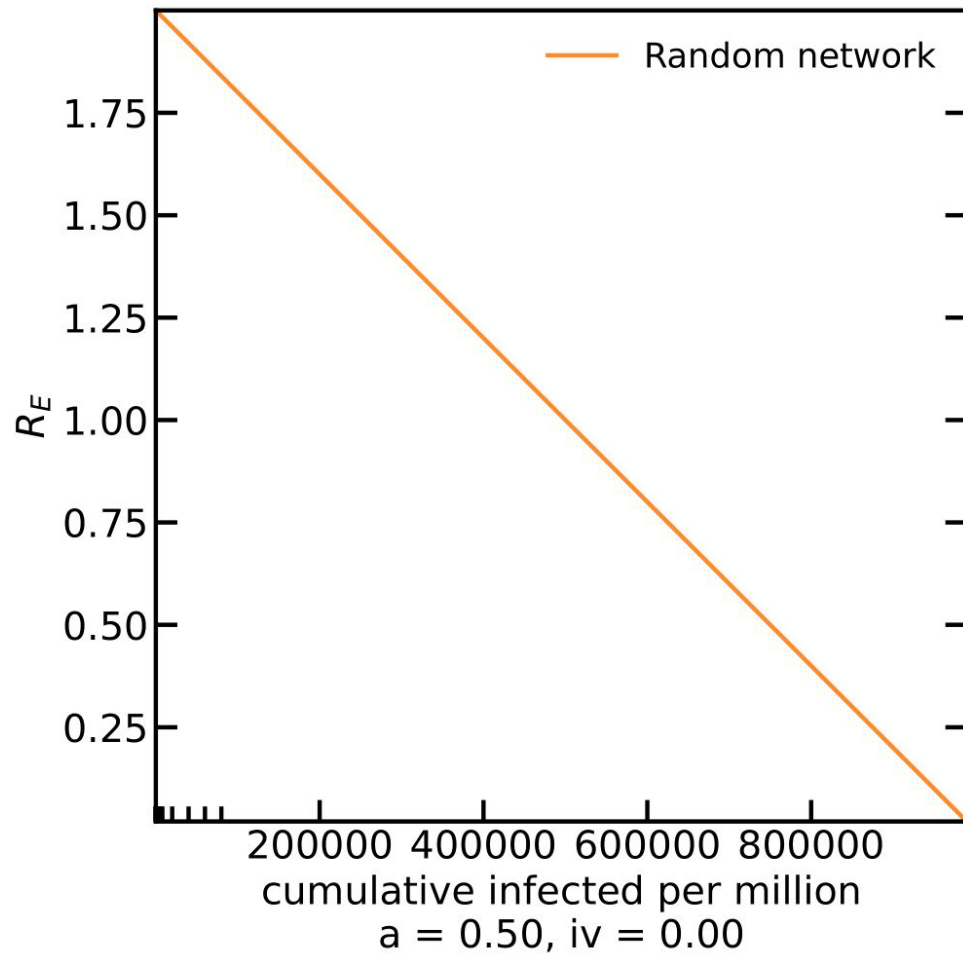
Preliminary results

- Simulations indicate a steady drop-off in R_E as more people are infected, regardless of the parameters of the graph, or the number of vaccinated people
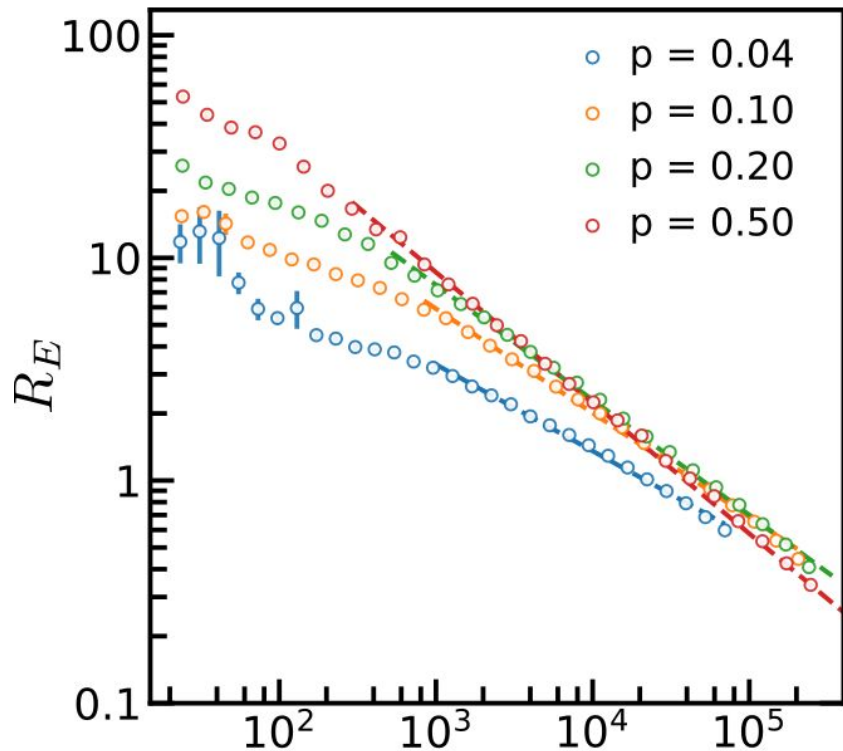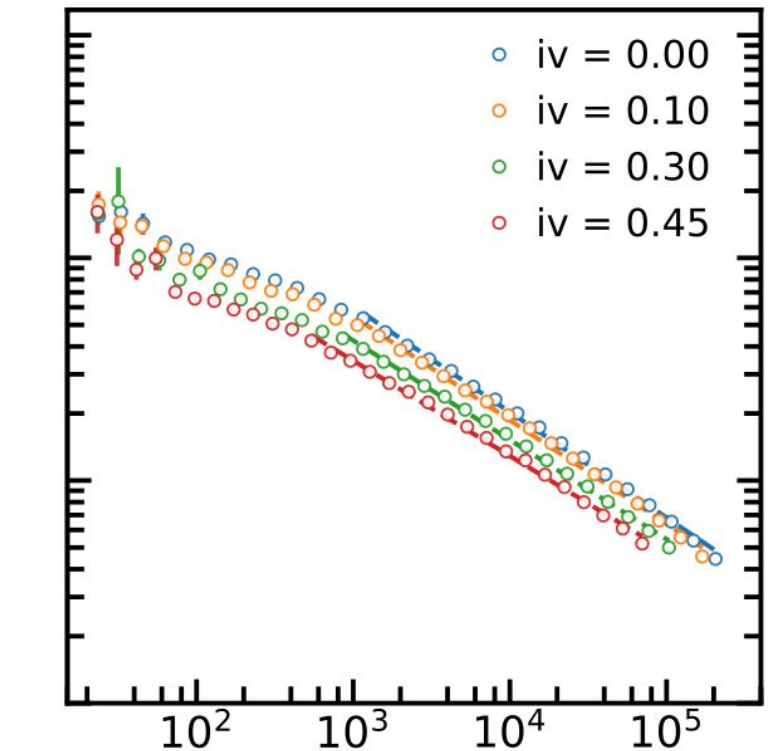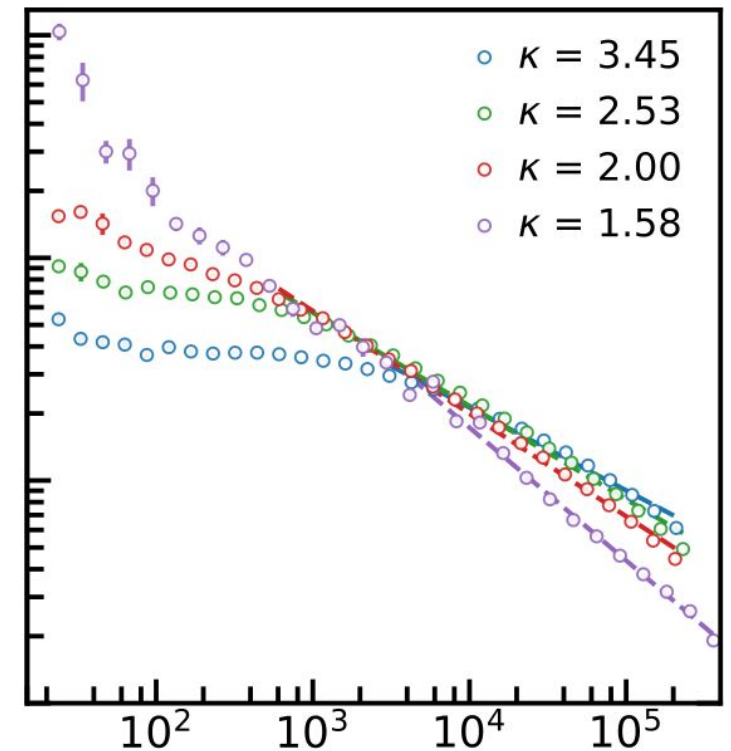
Intuition

- The higher the degree of a person is, the more likely it is to get infected.

- Hence, as the pandemic starts and gets going, the distribution of infected people heavily favours people with higher degrees

- As the pandemic keeps going, the high degree nodes recover and are effectively removed from the graph.

- Assuming only the highest degree people are infected, the power law for R_E vs f is reproduced

Real world data comparison

- Noisy because of the uncertainty of measurements during early stages

- However, similar power law trend can still be observed

- Open source data from https://github.com/CSSEGISandData/COVID-19
- Includes daily case reports per country and sometimes per county
- Updated daily

Country/Region	Lat	Long	1/22/20	1/23/20	1/24/20	1/25/20	1/26/20	1/27/20	1/28/20	1/29/20	1/30/20	1/31/20	02/01/2020	02/02/2020	02/03/2020	02/04/2020
Jamaica	18.1096	-77.2975	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Japan	36.204824	138.252924	2	2	2	2	4	4	7	7	11	15	20	20	20	22
Jordan	31.24	36.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Kazakhstan	48.0196	66.9237	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Kenya	-0.0236	37.9062	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Kiribati	-3.3704	-168.734	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Korea, South	35.907757	127.766922	1	1	2	2	3	4	4	4	4	11	12	15	15	16
Kosovo	42.602636	20.902977	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Kuwait	29.31166	47.481766	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Kyrgyzstan	41.20438	74.766098	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Laos	19.85627	102.495496	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Latvia	56.8796	24.6032	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lebanon	33.8547	35.8623	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lesotho	-29.61	28.2336	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Liberia	6.428055	-9.429499	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Libya	26.3351	17.228331	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Liechtenstein	47.14	9.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lithuania	55.1694	23.8813	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Luxembourg	49.8153	6.1296	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MS Zaandam	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Madagascar	-18.766947	46.869107	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Malawi	-13.2543	34.3015	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Malaysia	4.210484	101.975766	0	0	0	3	4	4	4	7	8	8	8	8	8	10
Maldives	3.2028	73.2207	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Analysis

- The behaviour of the scale-free model can be seen in real world data. Haven't yet been reproduced using Estonia's SPG (WIP)

- Isolating superspreaders is of outmost importance, as they dictate the spread in the early stages of the pandemic

- Vaccination policies could account for superspreaders.
    - A possible way would be using the amount of pre-existing antibodies in the body that have been picked up in earlier epidemics as an indicator when to vaccinate somebody

Questions?