

Agent-based network random walks for modelling the spread of a pandemic

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1 Introduction

Though the aim of this was to model the spread of SARS-CoV-2 virus, no special parameters for that have been added. Hence, this random walk can be considered to be any epidemic/pandemic.

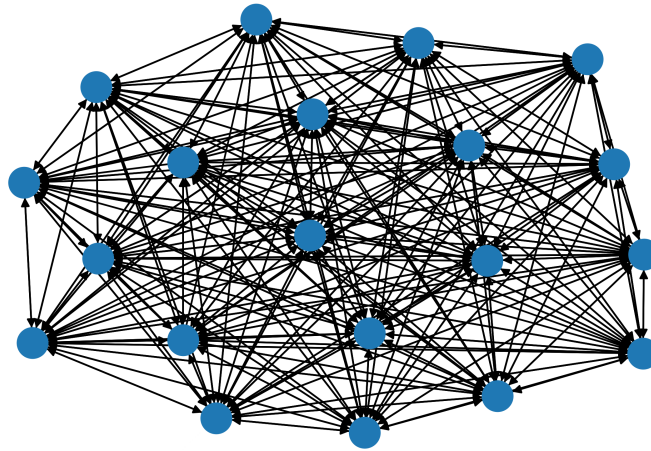


Figure 1: A network of maximum 20 clusters

Source code: https://github.com/p-j-r/covid-19/blob/master/Network_Walks.py
Other implemented models like SIR can also be found here.

Cluster:

Any population (big, small, city or even village) can be modelled as a lattice cluster of $m \times n$ nodes of some population density per node. A node can be thought of as a point in the cluster where the random walkers are free to go! (shops, malls, etc...). Density means the initial average number of people per node.

This class is just a more complicated version of `corona_walk` which can be found in the same

repository. Once formalised, it can be used as a Python package.

Exit Policy:

So an object (cluster)'s place function initialises the walkers at random positions on the lattice. If a walker is already at an **exit_node**, it stays there. However, any new walker coming to the *exit_node* is jumped to a new cluster! Each cluster has a unique *exit_node*. So, the graph of clusters G , has a unique one-on-one correspondence to a node!

Remove Policy:

When a walker is moved to a new node of G i.e., a new cluster, his (her) infect status is upgraded to 3 (removed from cluster). *0-initial, not infected; 1-infected, sick; 2-dead;*

2 Results

2.1 No Measures taken:-

An epidemic-causing virus is left uninterrupted without any precautionary measures.

```
max_clusters=20;                                //Maximum possible Clusters
max_size=250                                     // Values of m,n  $\in (max\_size/2, max\_size)$ 
lifetime = 14                                    //Lifetime – parameter
density  $\in (0.4, 1.6)$                           //Averagenodedensity
```

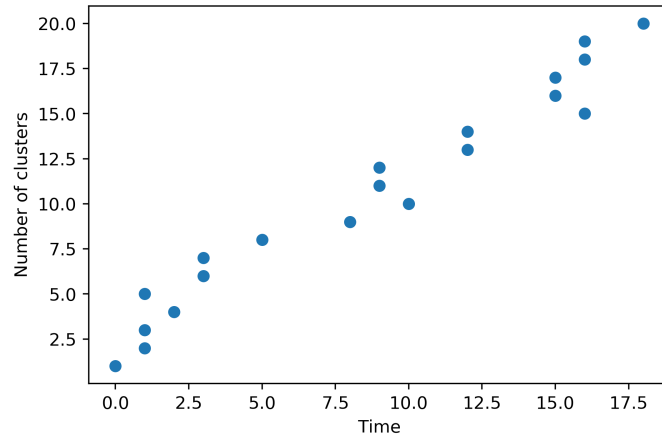


Figure 2: The rate of clusters spawning.

The plot has a linear fit. At the same iteration, 1-5 clusters are formed.

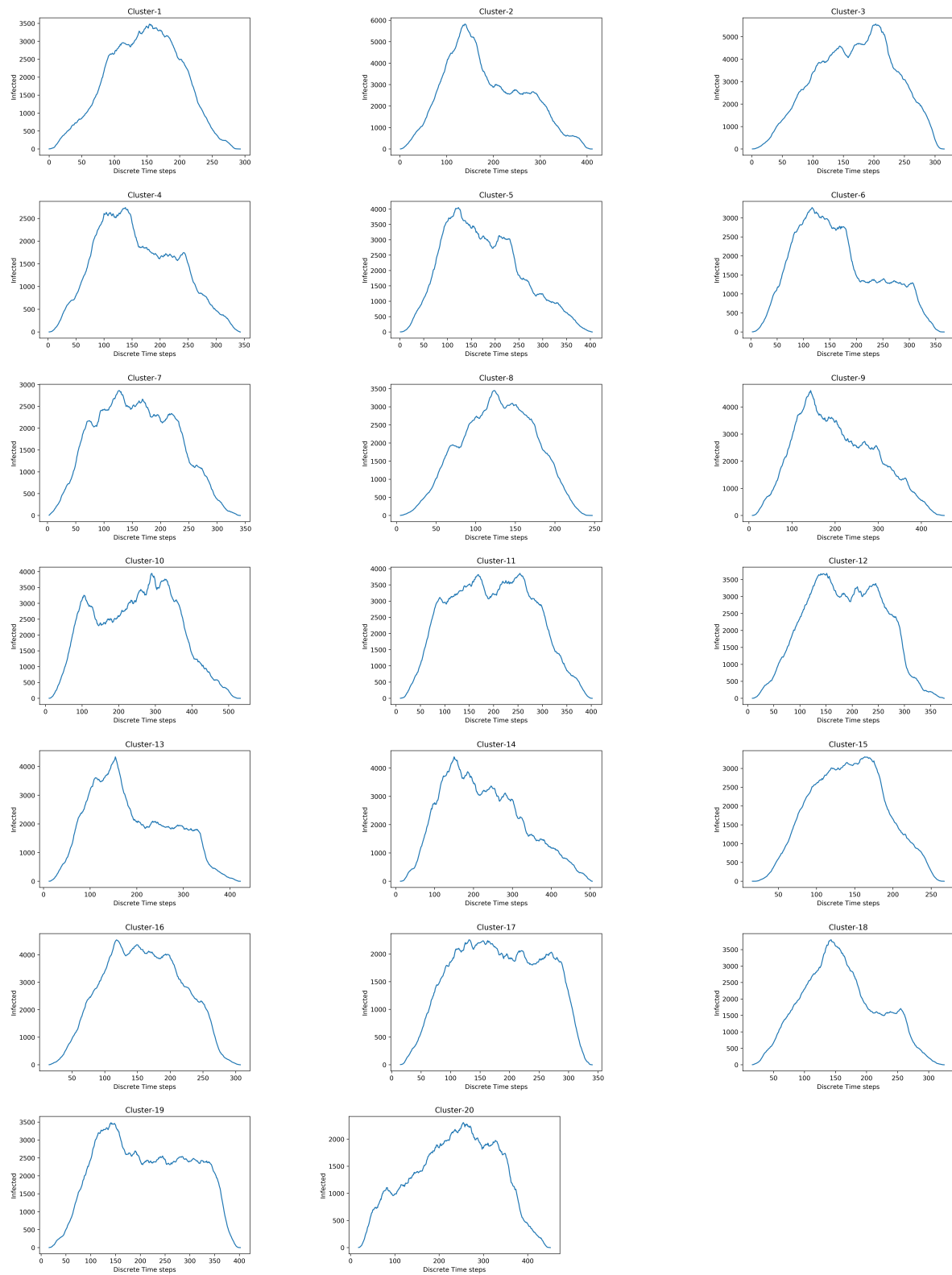


Figure 3: The infected graphs of the each individual cluster

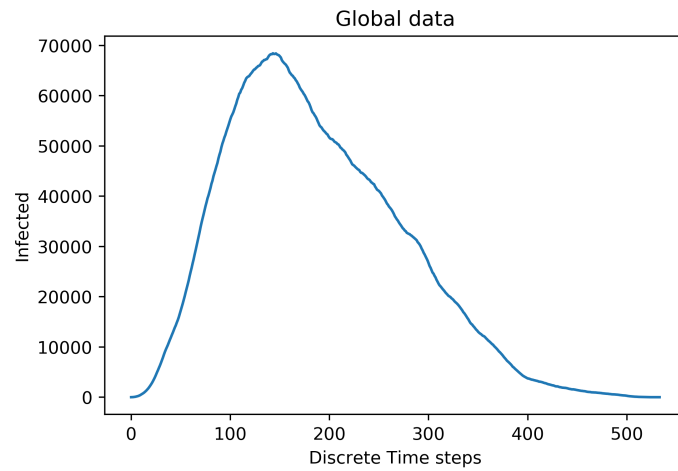


Figure 4: The global infection graph

The infection peaks very quickly, but the falling down is gradual!

2.2 Measures taken:-