Phase transition in agent-based epidemiological SIR models

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We explore the dynamics of the agent based SIR model and calculate the formula for the analog of reproduction number.

The SIR differential equation model

The classical susceptible, infectious and recovered (SIR) epidemiological model undergoes a phase transition when the reproduction number R_0 =1.
This will occur when the speed of infection is greater than zero.

```
i'[t] == (β s[t] / N - 1 / μ) i[t]
```

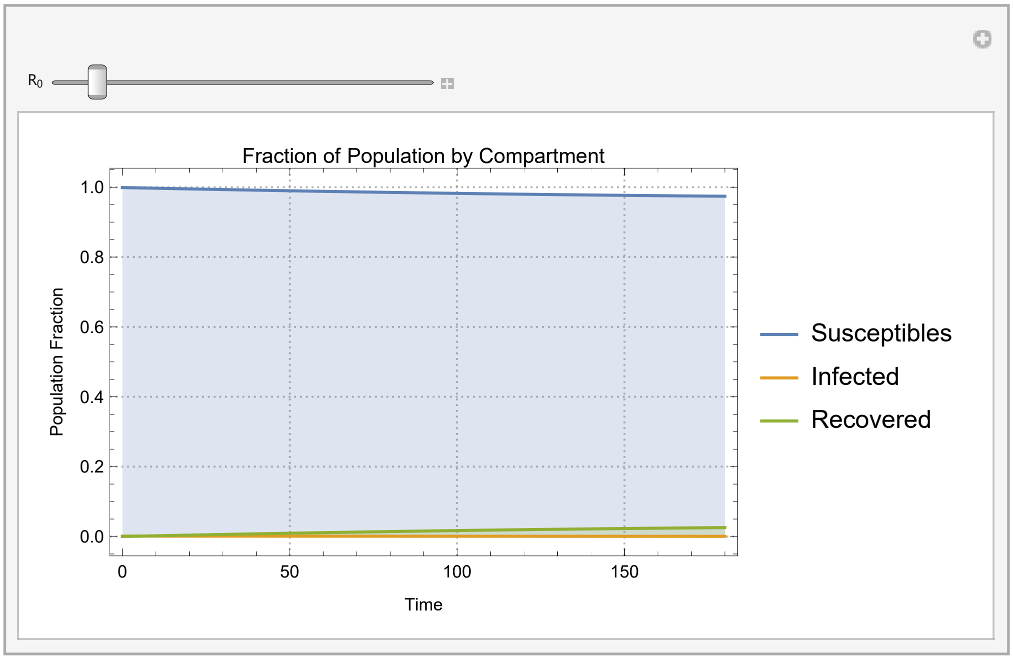
where β is the contact rate, s[t] is the number of susceptibles, N is the total population and μ is the infectious period. Assuming that i[t] ⟼ 0 then s[t] /N ⟼1, we obtain

```
β - 1 / μ ≥ 0
β μ ≥ 1
R0 = β μ ≥ 1
```

Visualizing the transition between a population free from infection and an epidemic. Making $\mu = 1$ then $R_0 == \beta$.

```
In[•]:= With[{μ = 5}, sirSoln = ParametricNDSolve[{sd'[t] == -β sd[t] × id[t] / population,
           id'[t] == β sd[t] × id[t] / population - id[t] / μ, rd'[t] == id[t] / μ, id[0] == 1,
           rd[0] == 0., sd[0] == population - 1}, {sd, id, rd}, {t, 0, maxTime}, β];
         Manipulate[
          Plot[Evaluate[({sd[R0 / μ][t], id[R0 / μ][t], rd[R0 / μ][t]} / population) /. sirSoln],
           ⋯ ], {{R0, .99}, 0.9, 2}, SaveDefinitions → True]]
```

Out[•]=



An agent based model approach to epidemiology

The agent based model approach allows the inclusion of different properties and interactions in the epidemiologic model, as each host is represented uniquely an can be assigned specific characteristics (such as its unique contact network, mobility, infection duration, etc.). In this essay, our agent based model is set up as follows:

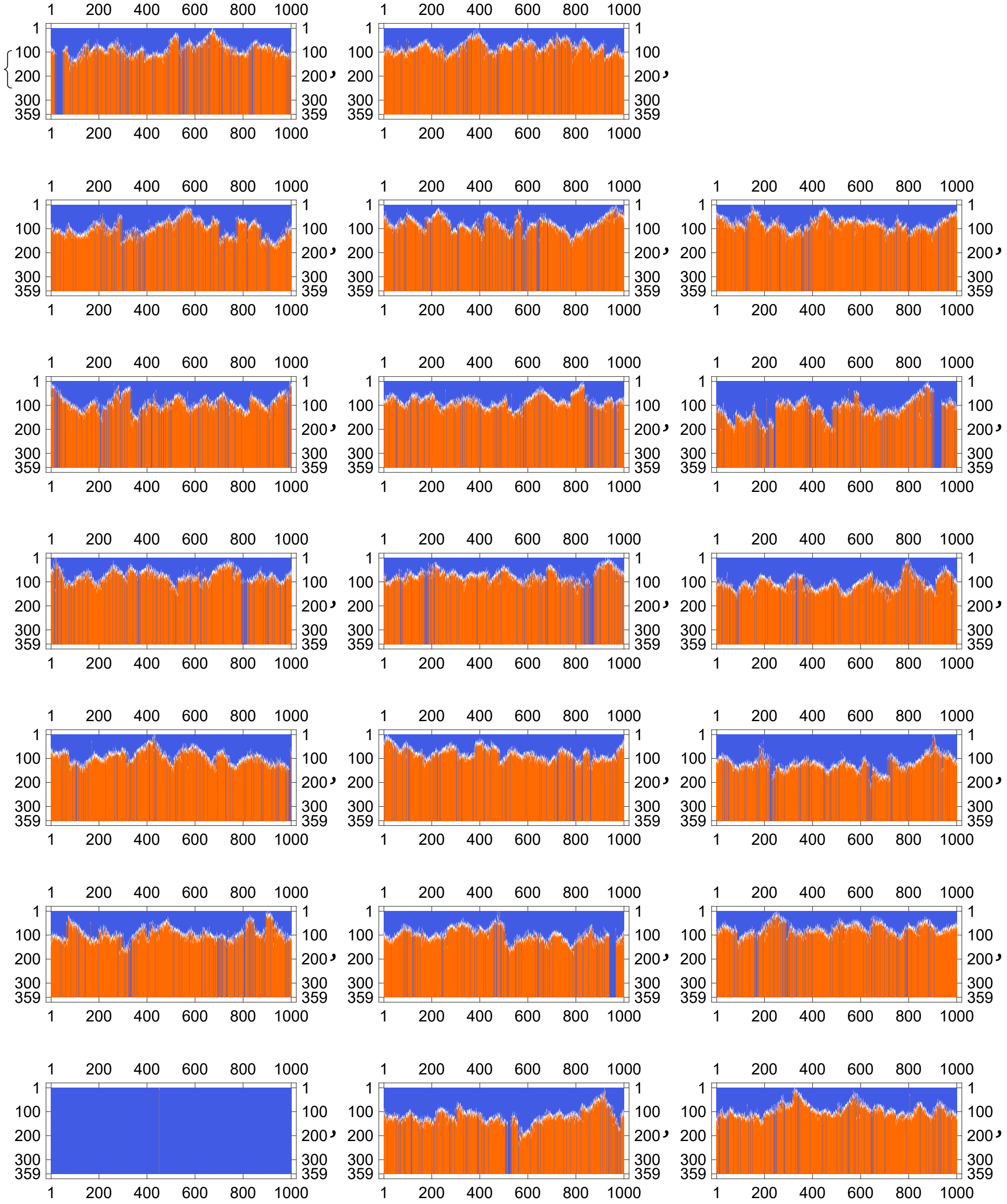
- Each agent belongs to a contact network, represented by a Watts Strogratz Random Graph of 1,000 nodes, a rewiring probability of 0.04 and a regular degree that spans in the experiments from 2 to 10.
- In each time tick, a susceptible agent might be infected by a compromised neighbor with probability "ContactRate". The range explores goes from x to y.
- The infectious period is distributed according to a log normal distribution of time spanning from x to y with a dispersion of 1.35.

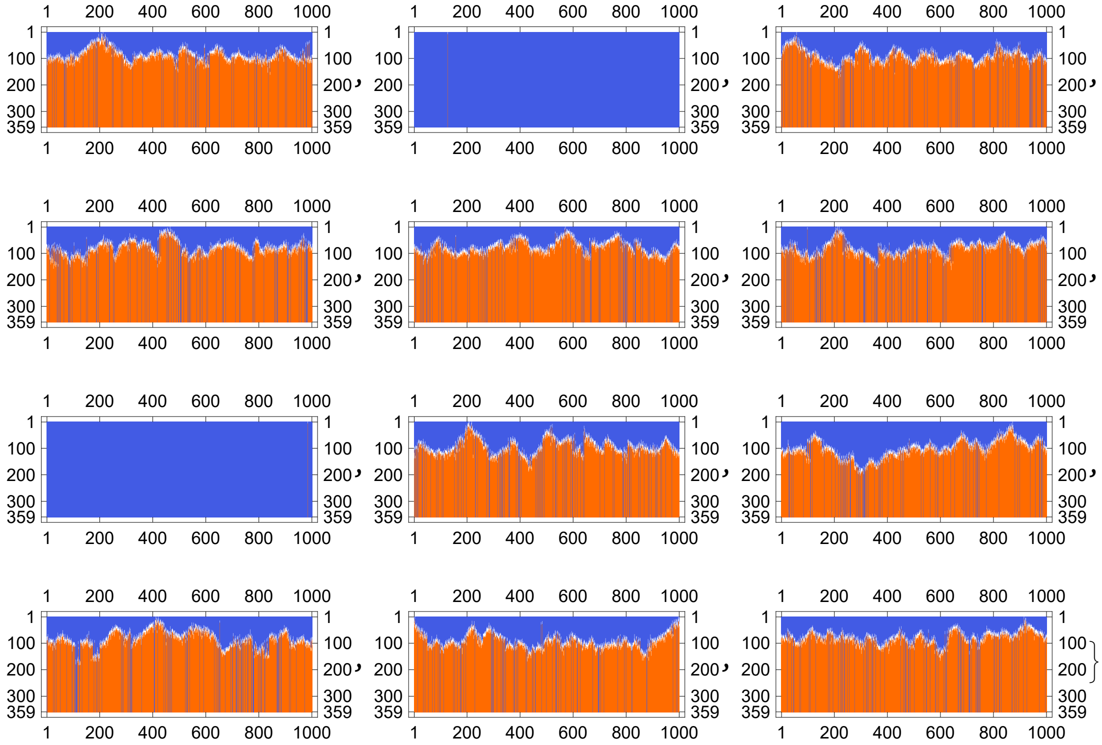
Run a set of 32 simulations on a network of regular degree 12, contact rate 0.012 and infectious period 12

```
In[∘]:= gr = RandomGraph[WattsStrogatzGraphDistribution[1000, 0.04, 9]];
        val = ParallelTable[simGraph[gr, 360, <|β[IP] → 0.012, aip → 12|>], {nbrSims, 32}];
```

It is interesting to visualize that in several scenarios the spread of the disease did not prosper, while in other scenarios, the pathogen distributed across the whole population.

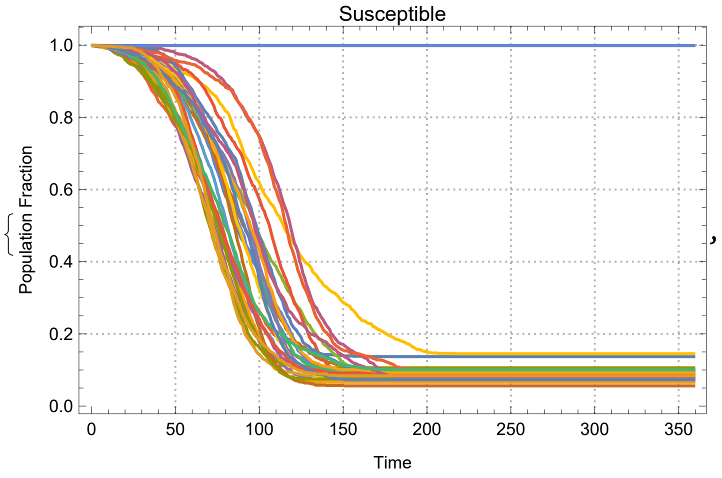
```
In[∘]:= MatrixPlot /@ val
Out[∘]=
```

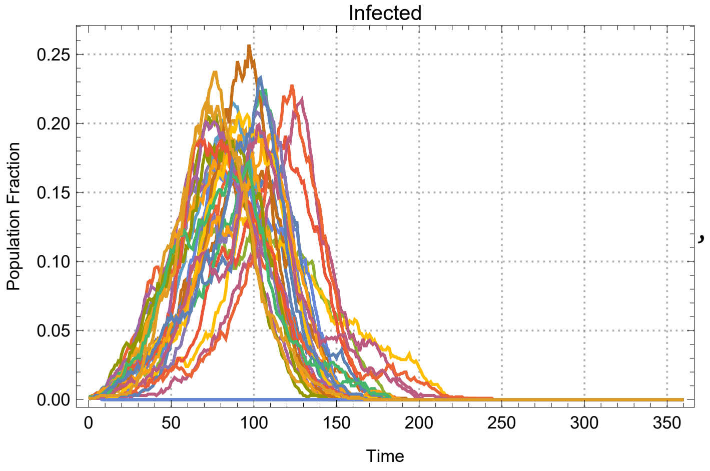


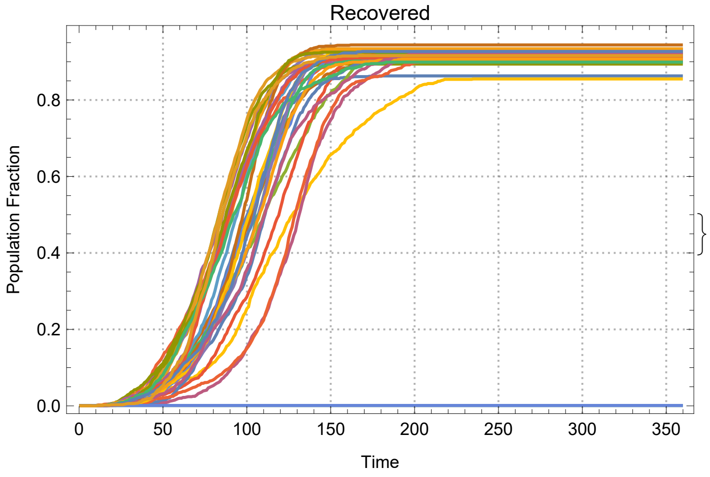


Visualizing the trend of each compartment across all simulations.

```
In[∘]:= With[{td = createTemporalData[val] / 1000.}, ListPlot[td[#], ⋯ +] & /@ Keys[td]]
Out[∘]=
```





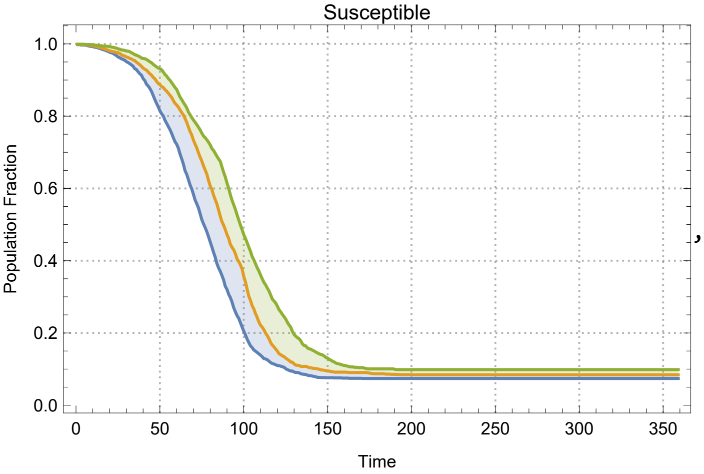


Data can be aggregated to show the 25%, 50% and 75% quartile.

```
In[•]:= With[{td = createAQuartiles[createTemporalData[val] / 1000.]},
         ListPlot[td[#], ⋯ ] & /@ Keys[td]]
```

Out[•]=

{



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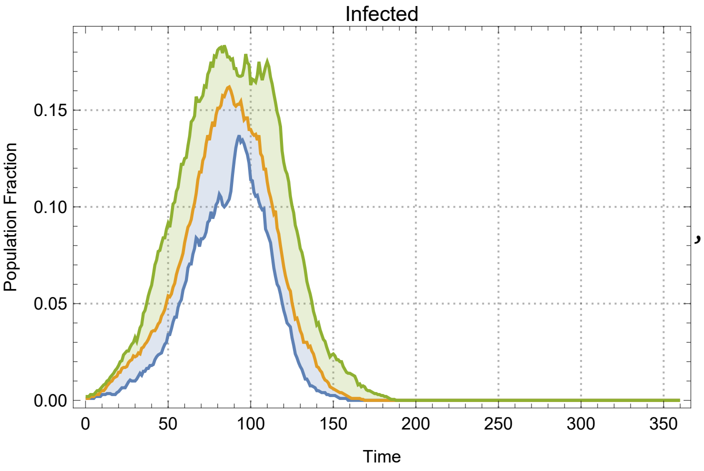

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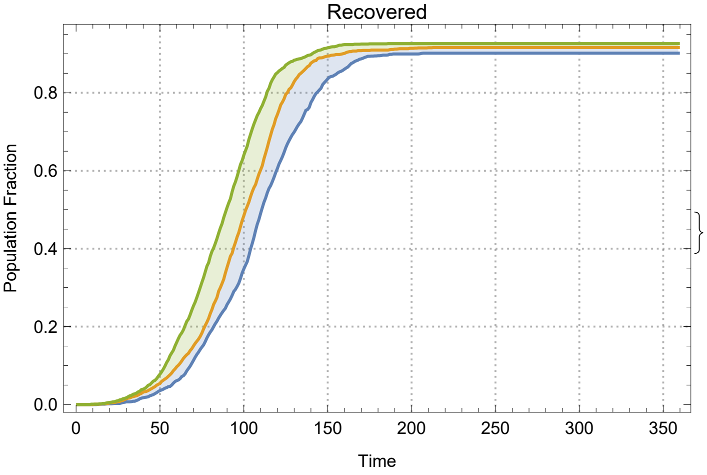


}

Exploring the parameter space

The following code was used to generate a whole simulation set across different parameter values.

```
In[∘]:= nbrSimulations = 32;
        maxTime = 180;
        kDegrees = Range[2, 10];
        betas = Table[Exp[n] / 100, {n, 0, 3.22, 0.064376`}];
        aips = Join[Range[0.5, 6, 0.25], {⋯} + ];
```

With the parameters established, the simulations can be performed.

```
In[∘]:= (*records={};
        Monitor[Do[
           gr=RandomGraph[WattsStrogatzGraphDistribution[1000,0.04,regularDegree]];
           val=ParallelTable[simGraph[gr,maxTime,<|β[IP]→b,aip→a|>],{nbrSims,nbrSimulations}];
           td=createTemporalData[val];
           qtl=createAQuartiles[td];
           assoc=Association["VertexCount"→1000,
             "RegularDegree"→regularDegree,"RewiringProbability"→0.04,"ContactRate"→b,
             "InfectiousPeriod"→a,"NbrSimulations"→nbrSimulations,"MaxTime"→maxTime,
             "Paths"→td,"Quartiles"→qtl,"VarianceSusceptibles"→variance[val]
            ];
           records=Join[records,{assoc}],{b,betas},{a,aips},{regularDegree,kDegrees}];,
          {b,a,regularDegree}]*)
```

The generated simulation results were saved for future analysis.

Analysis

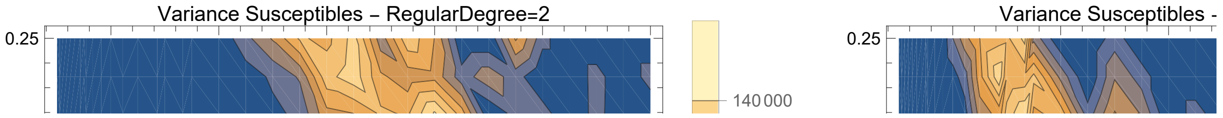
When the epidemiological model enters a transition phase, the number of susceptible at the end of the simulation can vary significantly between the different runs. We have saved the variance of the number of susceptible.

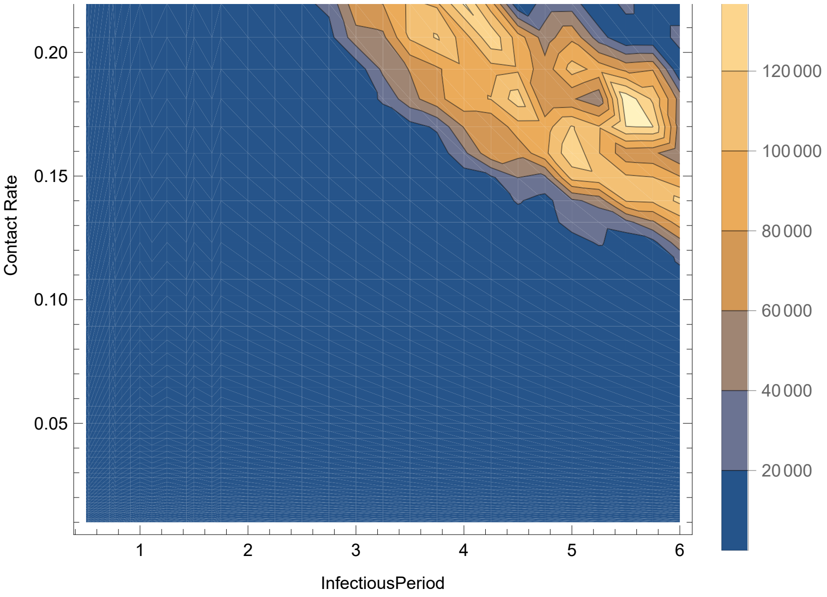
```
In[∘]:= dsVariance = CloudGet[
          CloudObject["https://www.wolframcloud.com/obj/287d6609-db53-4dfc-91c4-891d344ebdfe"]]
```

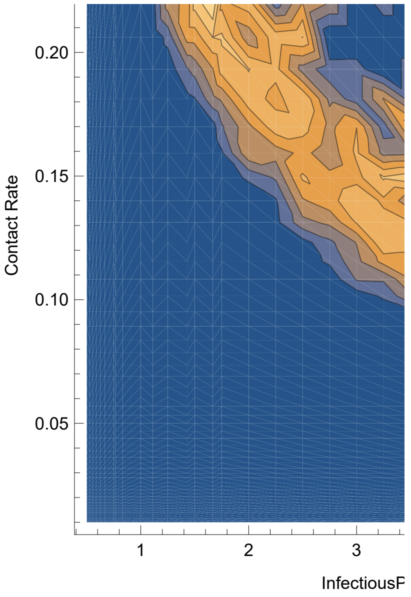
We can visualize the transition with the use of contour plots

```
In[∘]:= Grid[Partition[
          Table[ListContourPlot[dsVariance[Select[#"RegularDegree" == n &], {#"InfectiousPeriod",
               #"ContactRate", #"VarianceSusceptibles"} &], ⋯ + ], {n, 2, 10}], UpTo[3]]]
```

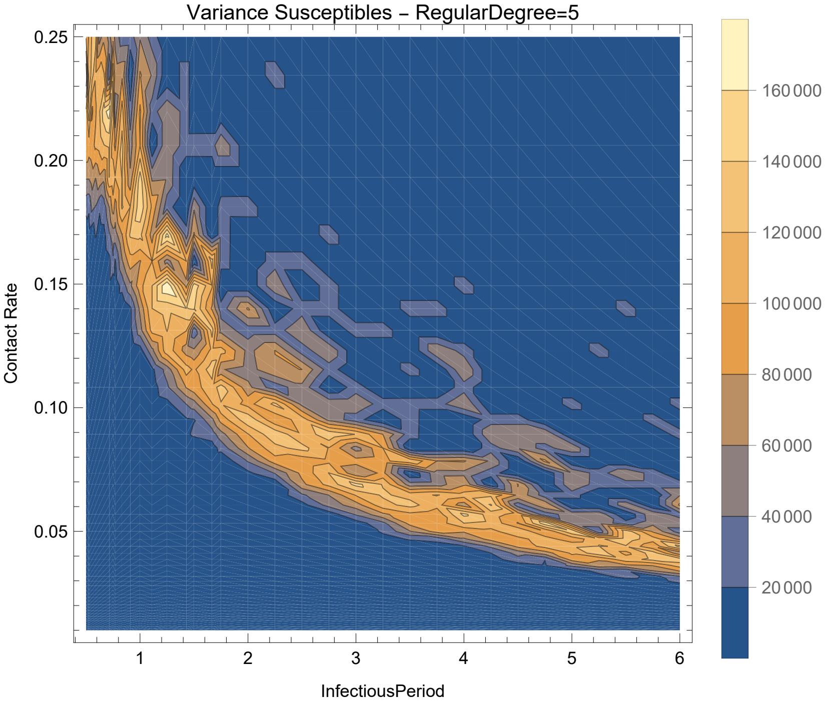
Out[∘]=



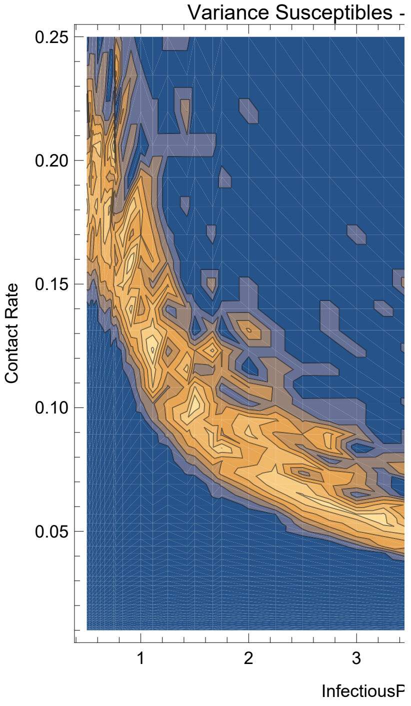




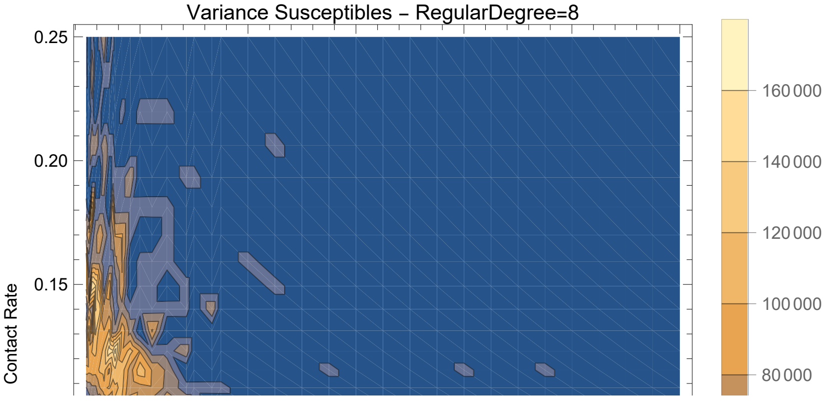
Variance Susceptibles – RegularDegree=5



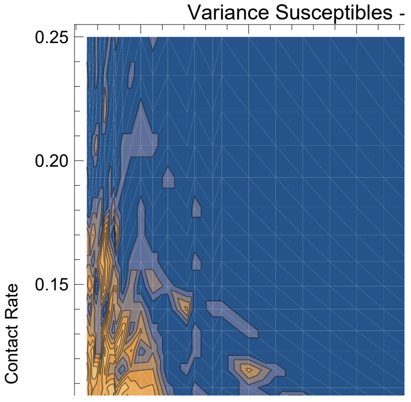
Variance Susceptibles -

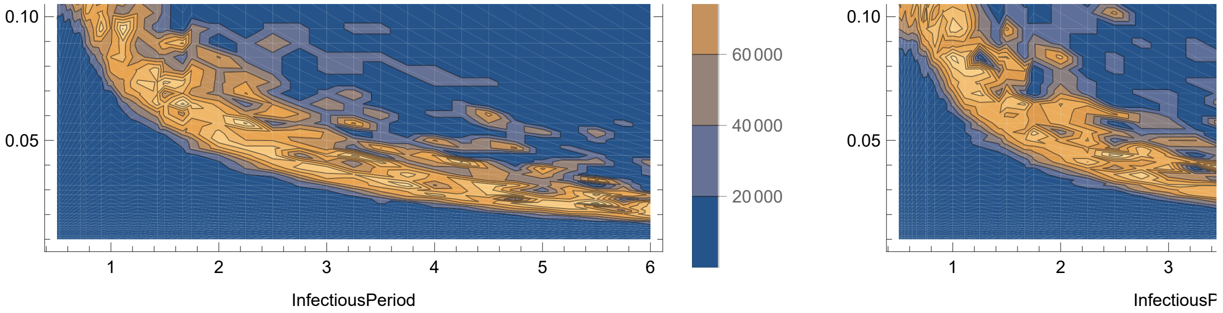


Variance Susceptibles – RegularDegree=8



Variance Susceptibles -

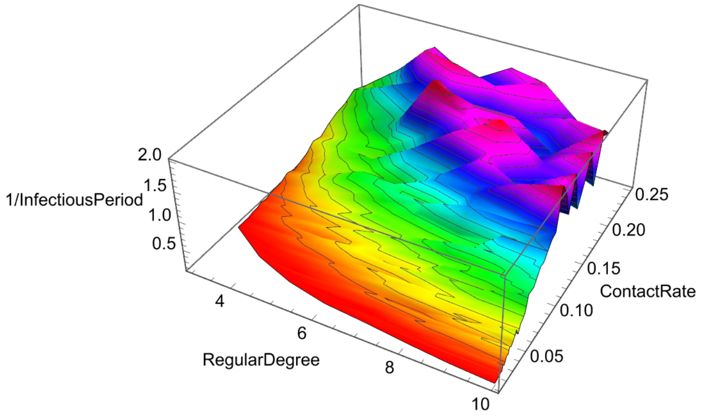




By identifying the maximum variance for each set of parameters:

In[∘]:=
```
max = Normal@dsVariance[
    GroupBy[KeyTake[{"RegularDegree", "ContactRate"}]] /*Normal/* (Association @@@ # &), <|
     "VarianceSusceptibles" → Query[Max, "VarianceSusceptibles"] |>];
ja = JoinAcross[max, Normal@dsVariance[All,
      {"RegularDegree", "ContactRate", "VarianceSusceptibles", "InfectiousPeriod"}],
    {"RegularDegree", "ContactRate", "VarianceSusceptibles"}] // Values;
jaFrontier = Flatten[Rest@
    Table[Cases[ja, {n, cr_, var_ /; var > 40000, ip_} → {n, cr, 1 / ip}], {n, 2, 10}], 1];
ListPlot3D[jaFrontier, ⋯ + ]
```

Out[∘]=



In[∘]:=
```
nlm = NonlinearModelFit[
   Cases[jaFrontier, {a_, b_, c_} → {b, c, a}], a (λ / β) ^b, {a, b}, {β, λ}]
```

Out[∘]=

FittedModel[$2.05576\left(\frac{\lambda}{\beta}\right)^{0.615128}$]

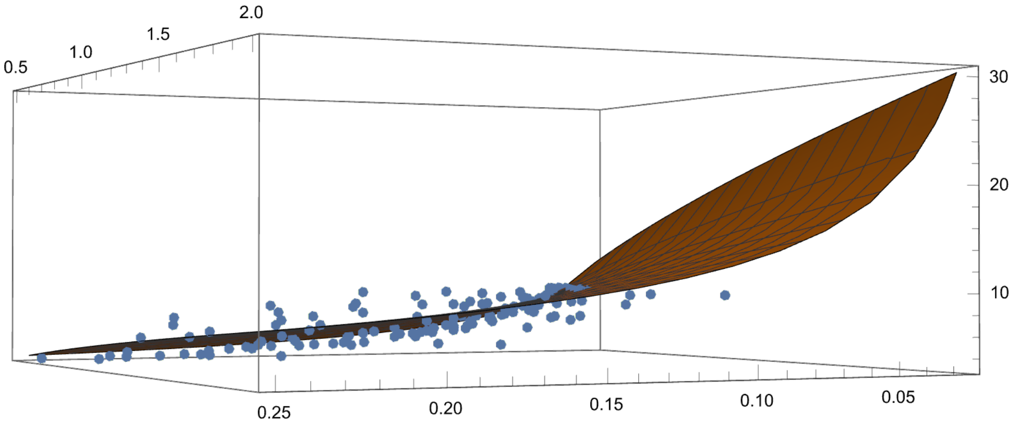
In[∘]:=
```
nlm["ParameterTable"]
```

Out[∘]=

	Estimate	Standard Error	t-Statistic	P-Value
a	2.05576	0.0884666	23.2377	1.46441×10^{-67}
b	0.615128	0.0196814	31.2543	9.20302×10^{-94}

```
In[•]:= nlm["AdjustedRSquared"]
Out[•]=
        0.983219
```

```
In[•]:= Show[Plot3D[nlm[x, y], {x, 0.025, 0.25}, {y, 0.5, 2}],
         ListPointPlot3D[Cases[jaFrontier, {a_, b_, c_} → {b, c, a}]]]
Out[•]=
```



The analog to the reproduction number in this case, has the following formula, where β is the contact rate, λ is the inverse of the infectious period and k is the regular degree of the network. When the value of $R_0 > 1$ the pathogen will most likely spread through the population.

```
In[•]:= Equal[R₀, k / nlm["Function"] /. {#1 → β, #2 → λ, Function → Sequence}]
Out[•]=
```

$$R_0 == \frac{0.486437\,k}{\left(\frac{\lambda}{\beta}\right)^{0.615128}}$$

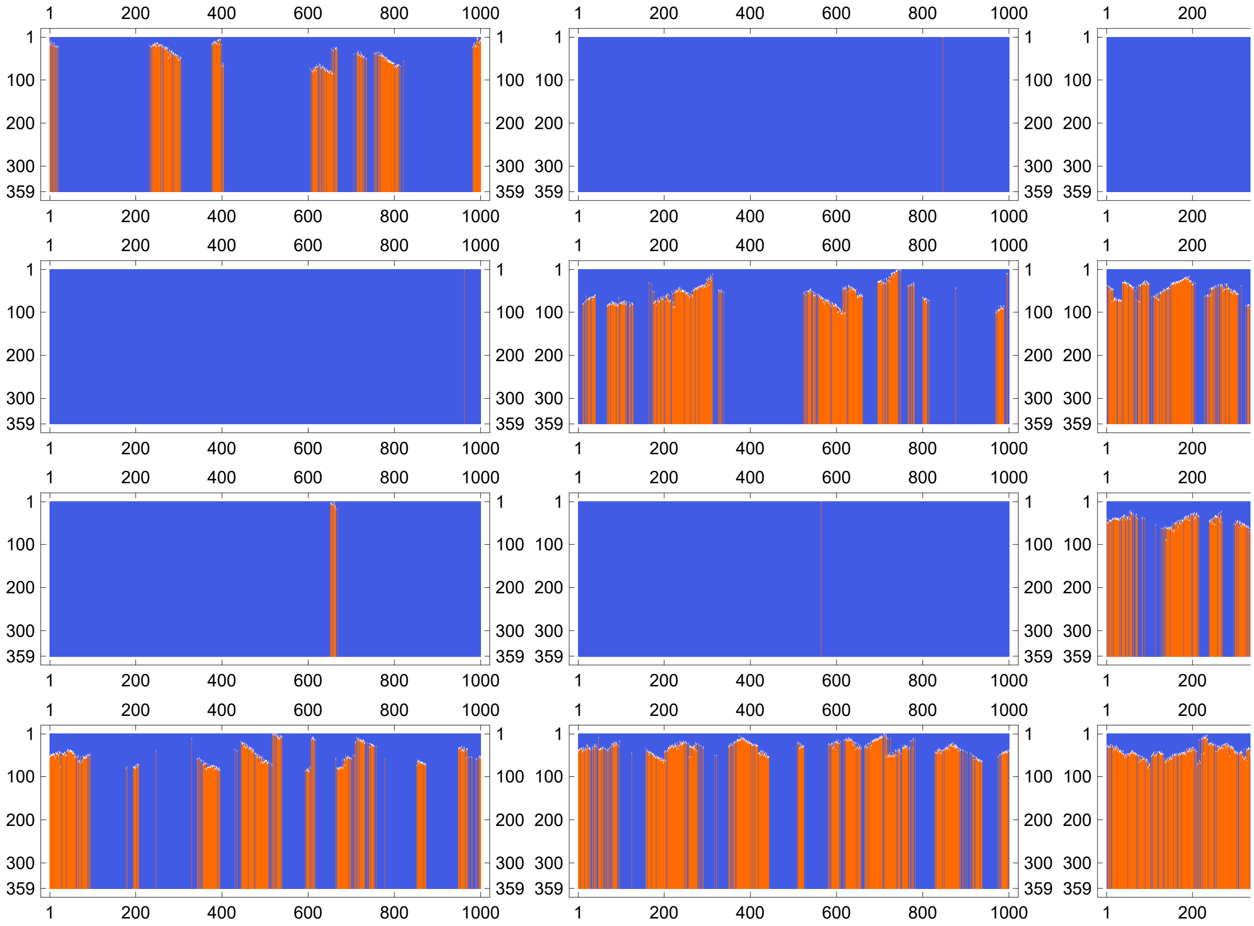
Examples

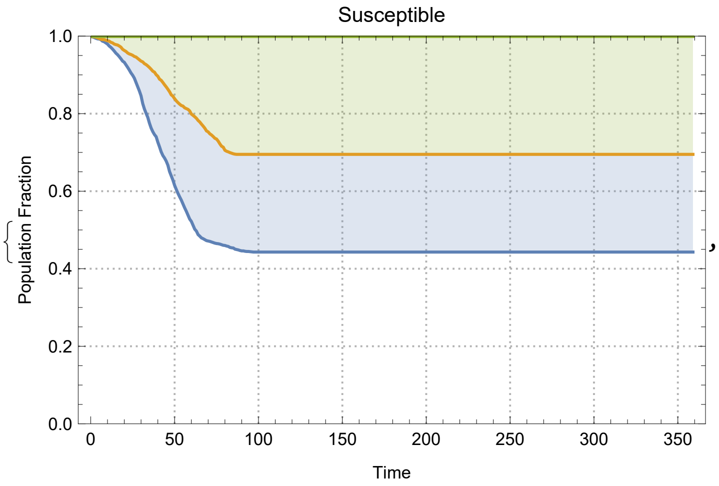
Find the regular degree in the transition for β=0.05 and infectious period = 3.

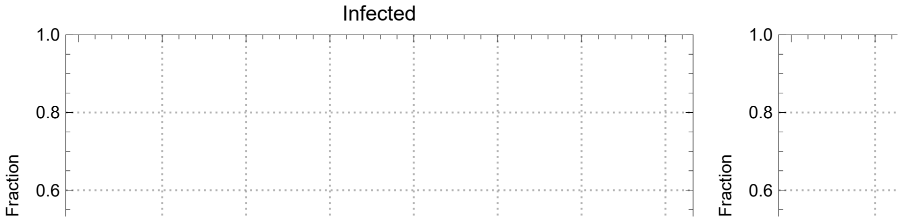
```
In[•]:= nlm[.05, 1 / 3]
Out[•]=
        6.60363
```

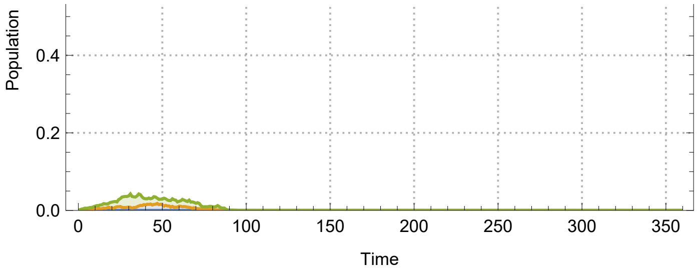
```
In[•]:= Column[{chart[6, .05, 3], chart[8, .05, 3]}]
Out[•]=
```

Regular Degree = 6









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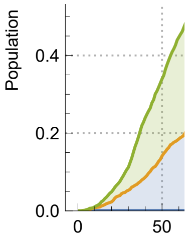
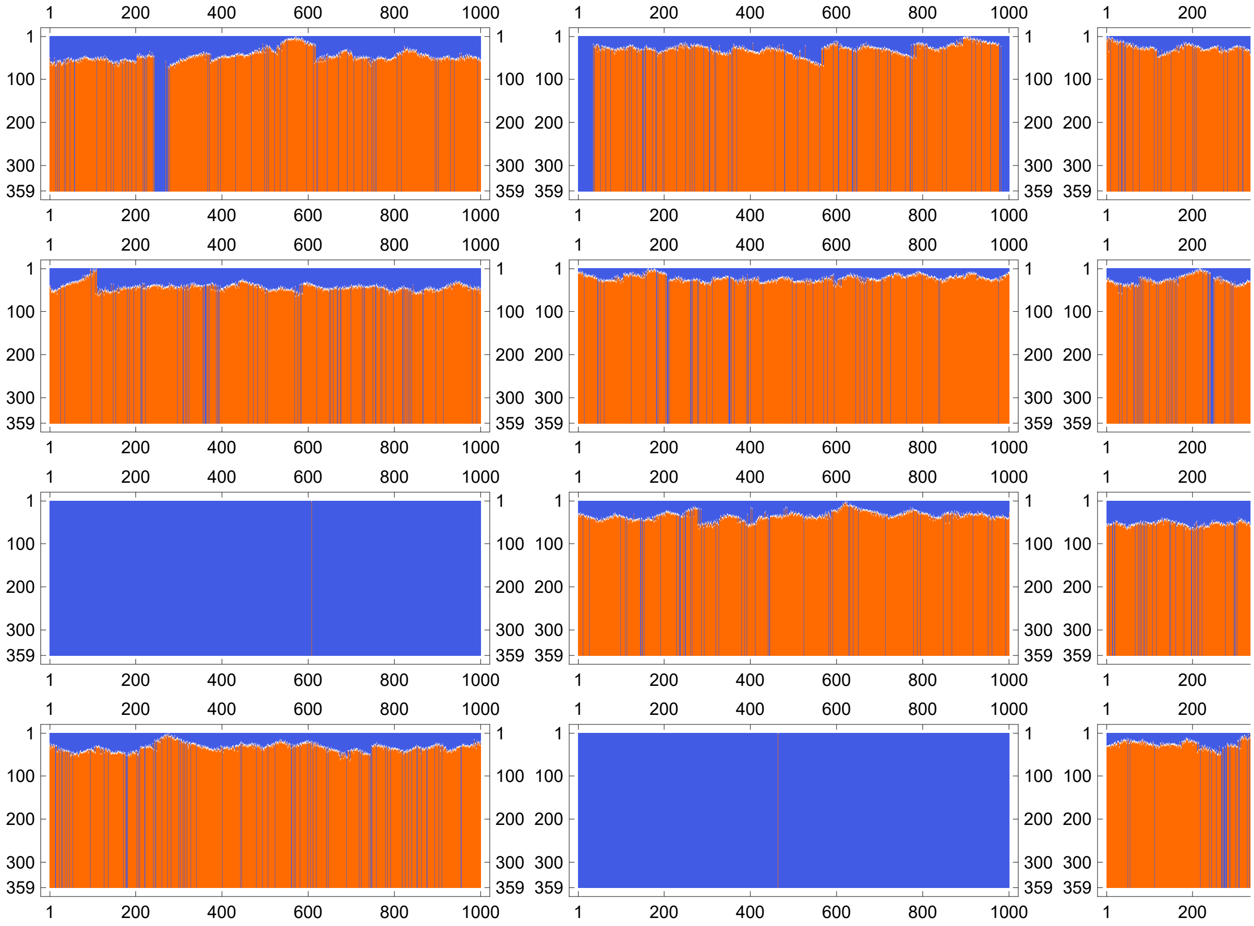
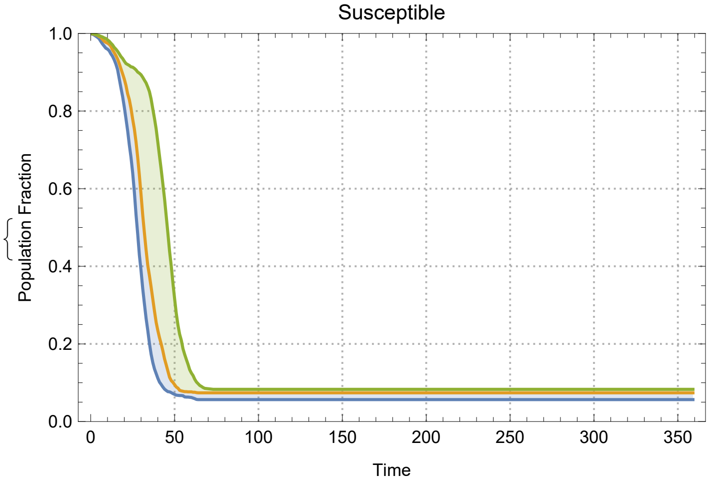


Regular Degree = 8





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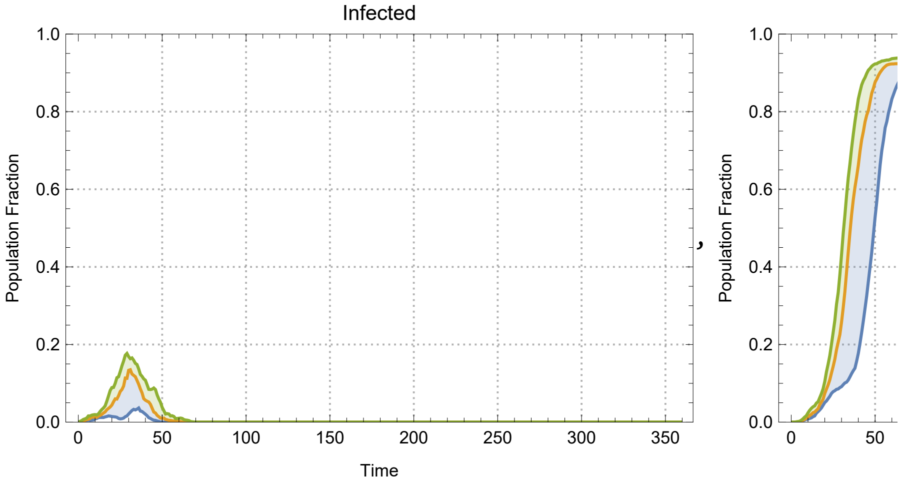
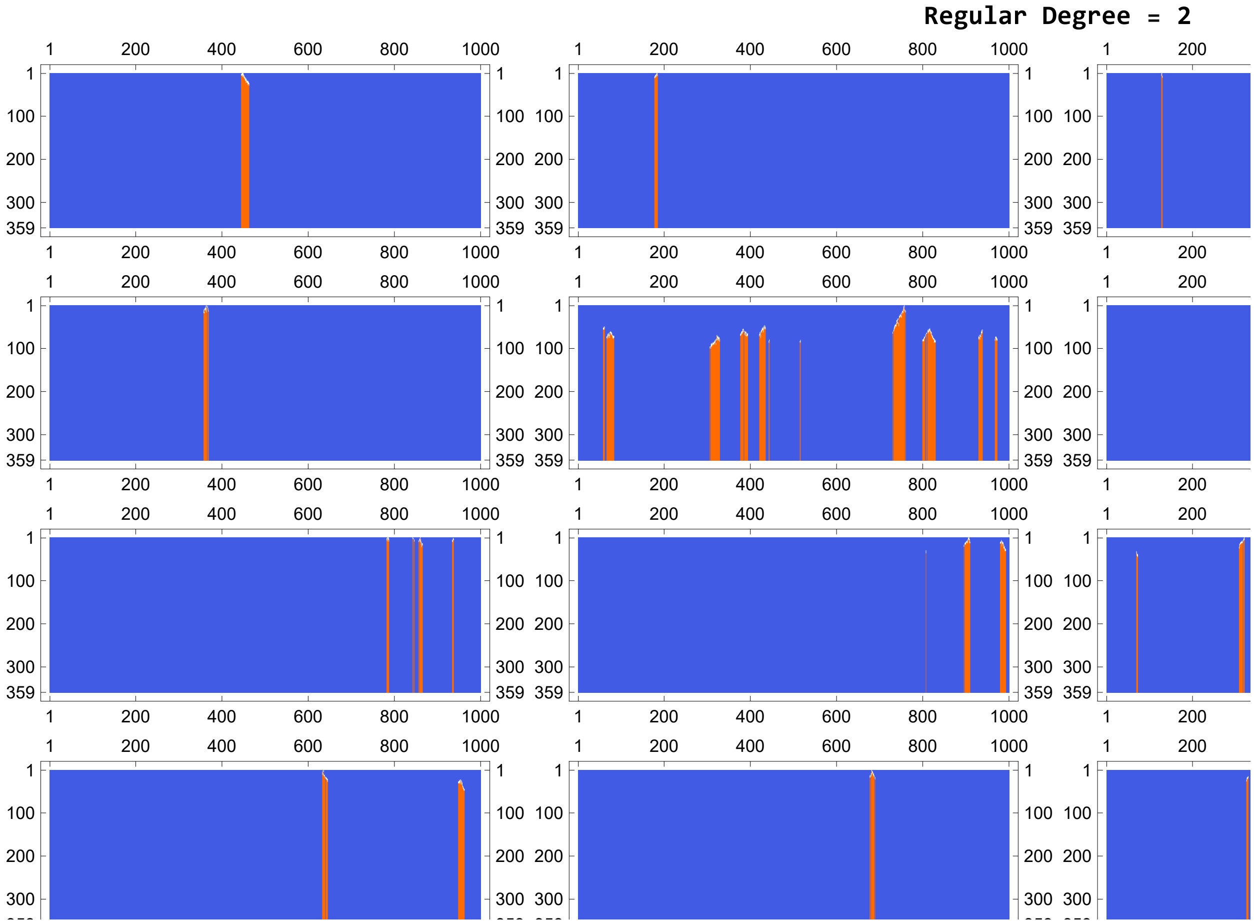
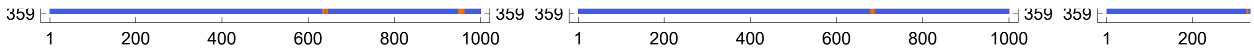


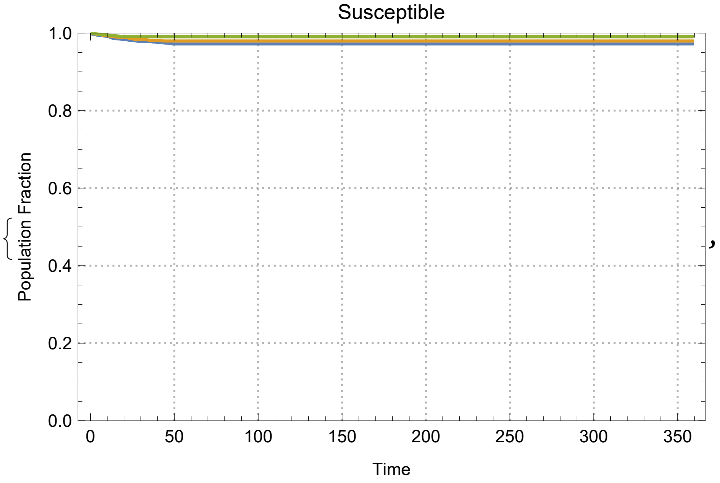
Similar test for β=0.12 and infectious period = 4.5.

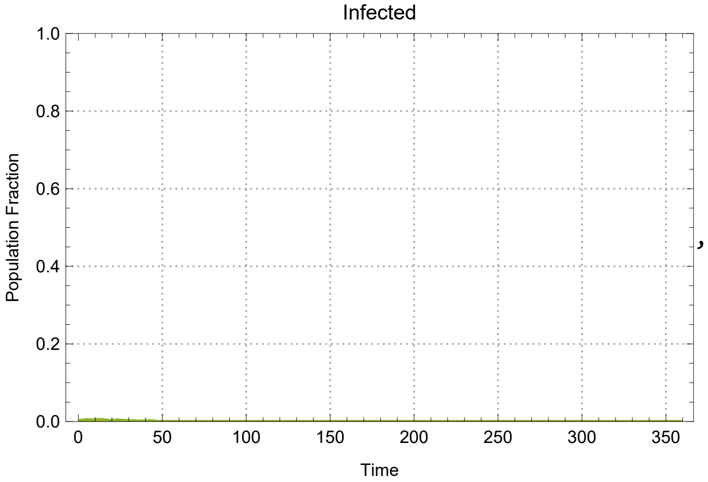
```
In[●]:= nlm[0.12, 1 / 4.5]
Out[●]=
        3.00321
```

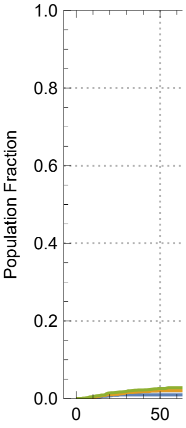
```
In[●]:= Column[{chart[2, .12, 4.5], chart[4, .12, 4.5]}]
Out[●]=
```



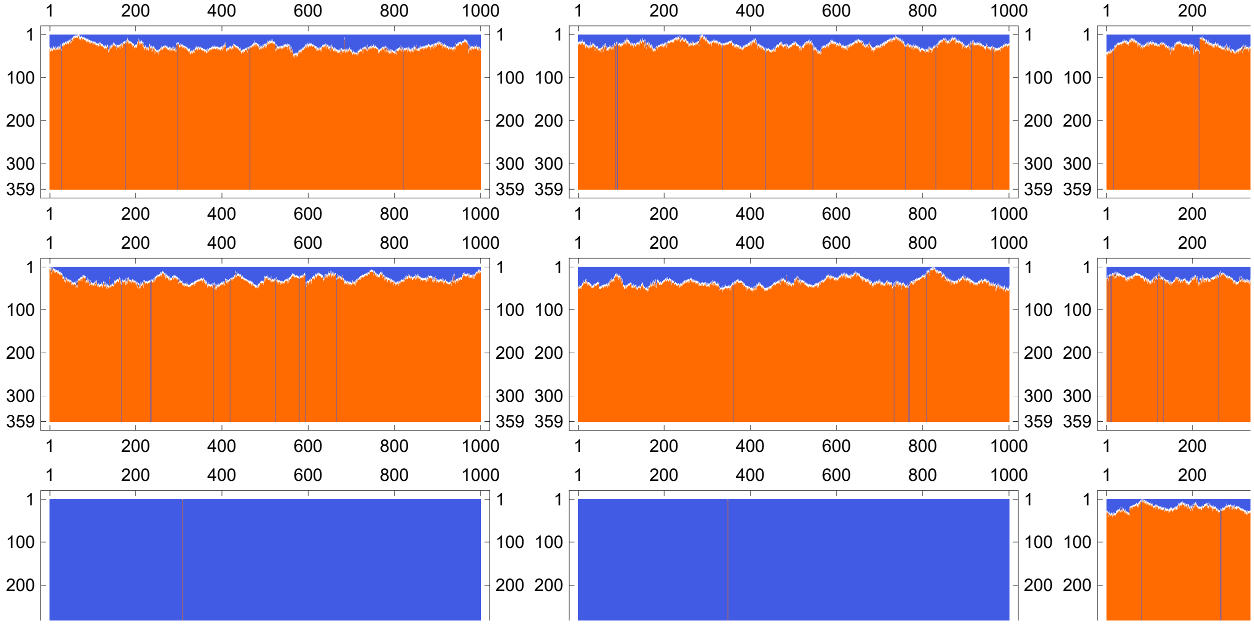


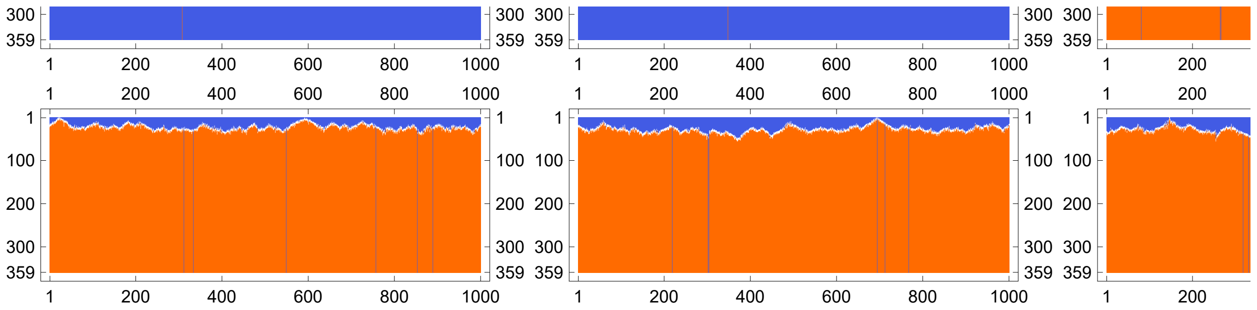


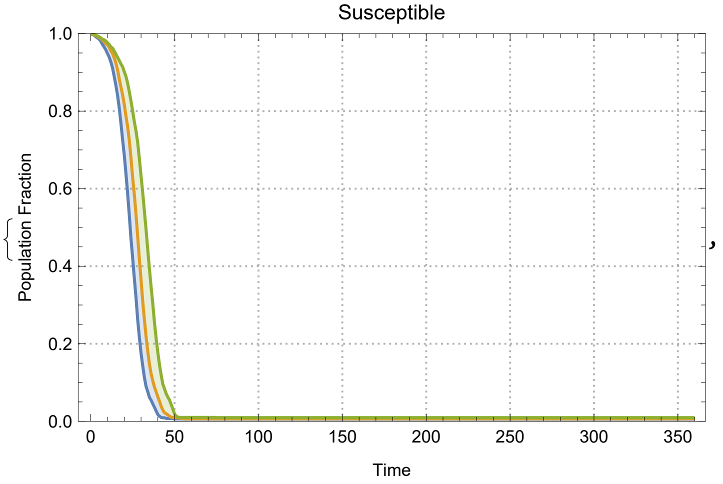


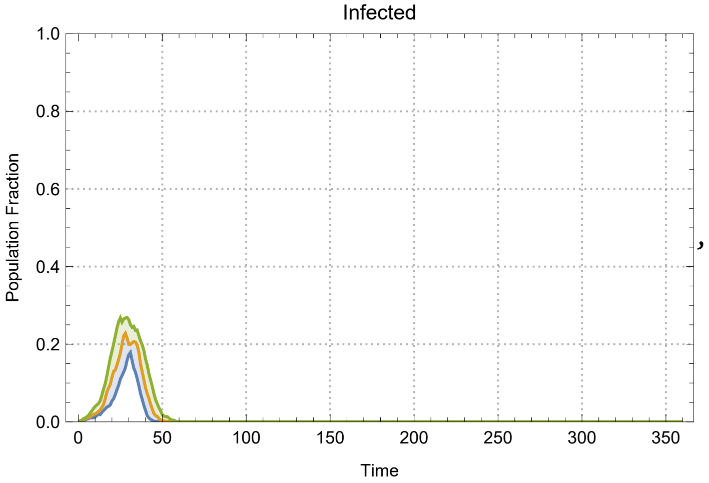


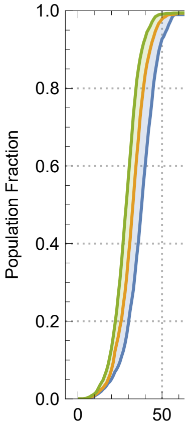
`Regular Degree = 4`











Conclusion

For the particular network configuration explored, and the infectious period distribution specified, we were able to obtain a formula estimate for the reproduction number for the agent based model. Values above one for this metric indicate that the pathogen simulated will spread through the network used as the contact network.

Initialization Cells