

Disease Propagation

using CIM model

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What the app does?

This is an application which models disease propagation in a network of 31 people using the Conditional Influence Model. It has the following properties:

- The disease is contagious.
- People influence each other due to physical contact.
- The disease is fatal.
- There is immunization. If someone gets immunization, he/she will not get the disease again.

The following code shows the

How to find who gets the disease?

I have applied the following code for calculating the probabilities for getting sick in the next step:

```
C <- matrix(0, N, N)
for (i in 1:N) {
  for (j in 1:N) {
    if(i==j){
      C[i,j] <- 1
    }else
      # Node i gets influenced by node j iff i is H and j is I.
      C[i,j] <- S[3*(i-1)+1]*S[3*(j-1)+2]
  }
}

# transpose of E (E_t): Refer to the paper for the formula.
E_t <- t(D) * t(C) + diag(1,N,N) * (D %*% (matrix(1,N,N)-t(C)))

H <- A_0 + kronecker(E_t - (diag(1, N,N)*E_t), input$DI)

P <- S %*% H
```

Input

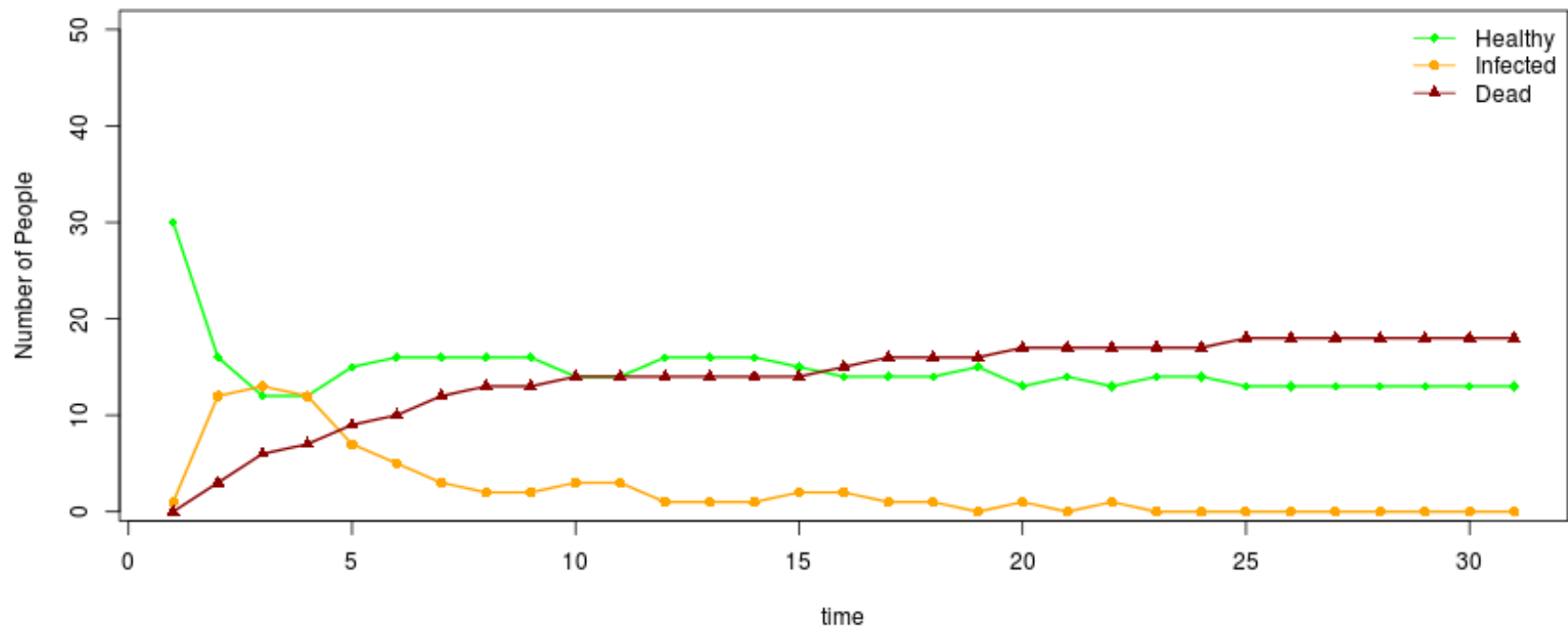
Users can input the number of people infected and also the amount of influences between nodes by changing the Markov chain matrices. A full explanation of this is provided in the DOcumentation tab. Users can also select whether they want to see the result for only one random run or the result for an average of a long run (average over 50 random runs).

	H	I	D
Healthy	1	0	0
Infected	0.5	0.4	0.1
Dead	0	0	1

	H	I	D
Healthy	0.55	0.3	0.15
Infected	0.3	0.4	0.3
Dead	0	0	1

Output

The App produces a table and a plot. These represent the number of healthy, infected and dead people for a time period of 30 steps.



	Healthy	Infected	Dead
1	30.00	1.00	0.00
2	16.00	12.00	3.00
3	12.00	13.00	6.00
4	12.00	12.00	7.00