# ICS - Graphs

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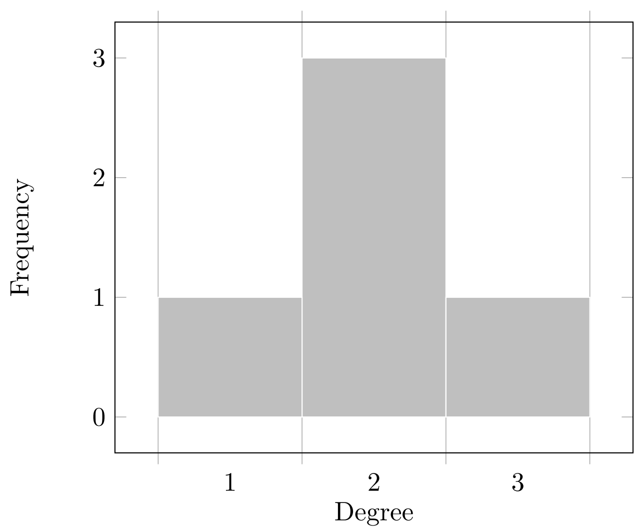
1. (a)




(b)

$$\begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \end{bmatrix}$$

(c) Degree centrality is calculated using:

$$C_{deg}(i) = \frac{k_i}{N-1}$$

betweenness centrality is calculated using:

$$C_{bet}(i) = \sum_{j,k \neq i} \frac{p_i(j,k)}{p(j,k)}$$

Where $p(j,k)$ is the amount of shortest paths between $j$ and $k$ and $p_i(j,k)$ is the amount of shortest paths between $j$ and $k$ through $i$.

| **Node** | **Betweenness centrality** | **Degree centrality** |
|---|---|---|
| 1 | 0 | $frac14$ |
| 2 | $\frac{1}{2}$ | $frac12$ |
| 3 | $\frac{2}{3}$ | $frac34$ |
| 4 | 0 | $frac12$ |
| 5 | 0 | $frac12$ |

(d)

$$\begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \end{bmatrix} \begin{pmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{pmatrix} = \begin{pmatrix} 1 \\ 2 \\ 3 \\ 2 \\ 2 \end{pmatrix}$$

This matrix-vector operation simply takes each row of the matrix, multiplies each value by 1 and sums these resulting ones and zero's together into an entry in the resulting vector. Since each 1 in each row corresponds to a connection between the respective node and its neighbour, counting these ones will result in the degree of this particular node.

(e) Only having directed edges, obviously implies that for a single edge only traversal in one way is possible. This means that vertices with only a degree of 1 can't reach its neighbour and be reachable by said neighbour. In this particular graph for example, there are two options with regards to the edge between vertex 1 and 2:

- The edge is directed from vertex 1 to 2, in which case vertex 1 can't be reached from any other vertex and, thus, not every vertex is reachable from any other.
- The other option is direction this edge from 2 to 1. In this case no vertex is reachable from 1 to 2, so the aforementioned characteristic doesn't hold true either.

(f) The local clustering coefficient for undirected graphs is computed using the following equation:

$$C_i = \frac{2|e_{jk} : v_j, v_k \in N_i, e_{jk} \in E|}{k_i(k_i - 1)}$$

For this particular network, the LCC's are:

| Vertex | LLC |
|---|---|
| 1 | 0 |
| 2 | 0 |
| 3 | $\frac{1}{3}$ |
| 4 | 1 |
| 5 | 1 |

(g) For any connected graph, such as this one, in order for every vertex to have a LLC of 1, the graph needs to be complete. If this were not the case, any vertex $v_i$ with non-interconnected neighbours $v_j$ and $v_k$ would have a LLC less than 1, as the number of possible edges interconnecting neighbours is not equal to the number of present edges interconnecting neighbours. This directly results from the aforementioned equation. So the minimum number of edged which have to be added is 4.

2. (a)

$$p(k) = \binom{N-1}{k} p^k (1-p)^{N-1-k}$$

This is true since the chance of making $k$ connections is $p^k$ and the chance of not making the remaining connections is $p^{N-1-k}$. The final piece of the aforementioned product, $\binom{N-1}{k}$, is the amount of possible combinations of connections for a given node with which it achieves a degree of $k$.

(b)

$$C_i = \frac{2e_i}{k_1(k_1 - 1)} = t$$

where $e_i$ is the number of inter-neighbour edges

$$e_i \in [0, k_1(k_1 - 1)]$$

(c)

(d)

(e) The expected degree is $(N-1)p$, since there are $(N-1)$ possible neighbours, each with a chance $p$ of forming an edge.

## Epidemics 1

(a) Not infected: $1 - i^r$
infected: $1 - (1 - i)^r$

(b)

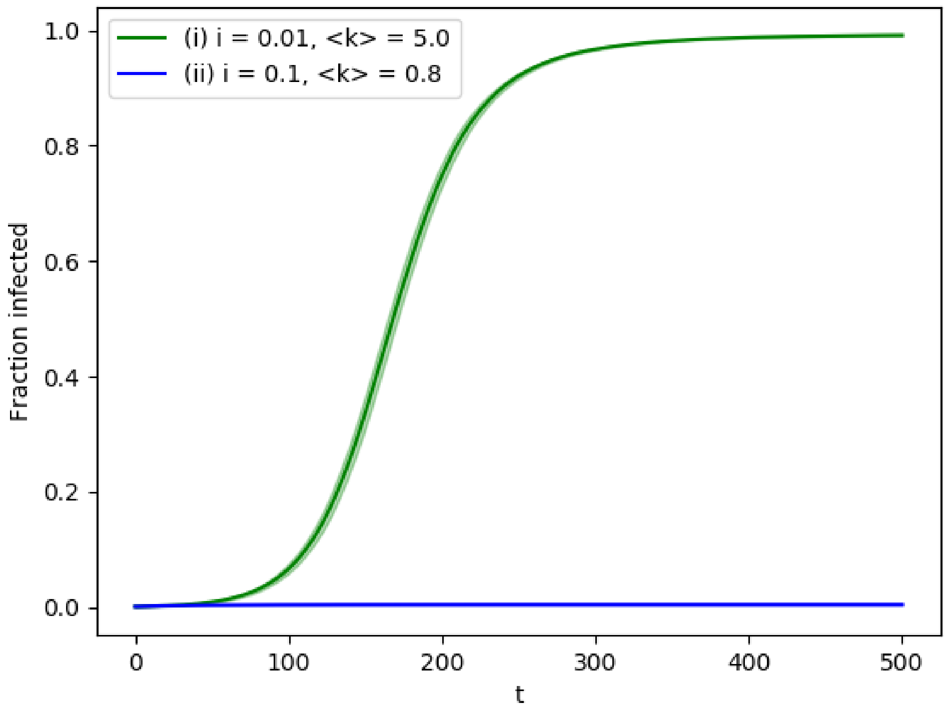



Figure 1: Mean $\frac{I}{N}$ for networks $i$ and $ii$ for 500 time steps with lighter regions showing the error.

(c) Yes, due to the higher $i$ (infection chance), the infection has a higher chance of spreading to a neighbouring vertex from an infected vertex in case ($ii$), compared to case ($i$). This phenomenon is most significant in the beginning of the simulation since, at this point, there are still a lot of non-infected nodes, so these can get infected in a relatively short amount of time steps. This does mean that $\langle k \rangle$ needs to be sufficiently large for there to be connections. Since, if $\langle k \rangle$ were to be 0, no new infections would take place.

(d) The chance that no neighbour is infected is equal to $1 - i^{\langle k \rangle}$, so the chance of at least one infection is equal to $1 - (1 - i)^{\langle k \rangle}$

(e) The graph clearly shows case ($ii$) having a steeper lope compared to case ($i$). This is in accordance with the computed probabilities in table 1

| Case | Computed chance |
|---|---|
| ($i$) | 0.049 |
| ($ii$) | 0.081 |

Table 1: Computed chance

(f) Since this is binomially distributed with $\langle k \rangle$ as the max number of infections and $i$ as the infection chance, the expectations is $\langle k \rangle i$.
$R_{0_{(i)}} = 0.05$
$R_{0_{(ii)}} = 0.08$

(g) Based on the values from the previous question, one can conclude that for the first time step case ($i$) grows $\frac{5}{8}$ times as fast as case ($ii$).

(h) As shown by figure 2, the ratio 5 : 8 corresponds rather well in the beginning. Case ($i$) starts somewhere around 0.05 and ($ii$) around 0.08.

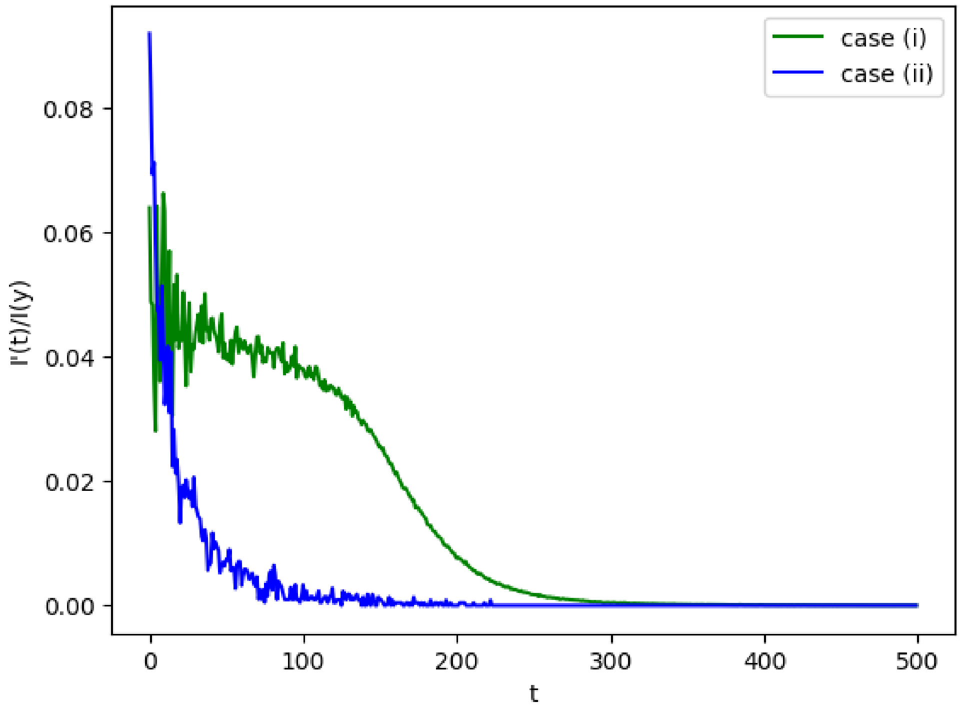



Figure 2: $\frac{I'(t)}{I(t)}$ as a function of $t$ for cases ($i$) and ($ii$)

(i) They both drop off to (almost) zero because after a while there is no increase in the amount of infected nodes anymore. Case ($ii$) drops off to 0 earlier because the graph is less connected and therefore less nodes can be reached to be infected after a certain amount of time, compared to case ($i$).

(j) Due to the less connected nature of the graph in case ($ii$), compared to case ($i$), not all susceptible nodes can be reached from the initially infected nodes. Thus after all reachable nodes have been infected, the amount of infected nodes settles on a constant value.

(k) For both cases the final outbreak size grows linearly as $N \to \infty$.

## Epidemics 2

(a) Important to note is that with this ODE, you don't look at the per node infection change, as you would with the simulation of the previous exercise, so the mean trend is observed—the graph is fully connected. Thus, an overall chance must be formulated based on the entire population of infected nodes infecting a subset of new nodes as opposed to individual nodes infecting their neighbours.

(b)

$$\begin{aligned}(1-(1-b)^I)\cdot S &= (1-(1-i)^{\frac{\langle k\rangle}{N}I})\cdot S \\ (1-b)^I &= (1-i)^{\frac{\langle k\rangle}{N}I} \\ 1-b &= (1-i)^{\frac{\langle k\rangle}{N}} \\ b &= 1-(1-i)^{\frac{\langle k\rangle}{N}}\end{aligned}$$

(c) $b$ for case $(i)$: $b = 1 - (1 - 0.01)^{\frac{\langle 5.0 \rangle}{10^5}} = 5.03 \cdot 10^{-7}$
$b$ for case $(ii)$: $b = 1 - (1 - 0.1)^{\frac{\langle 0.8 \rangle}{10^5}} = 8.43 \cdot 10^{-7}$

## Epidemics 3

(a)

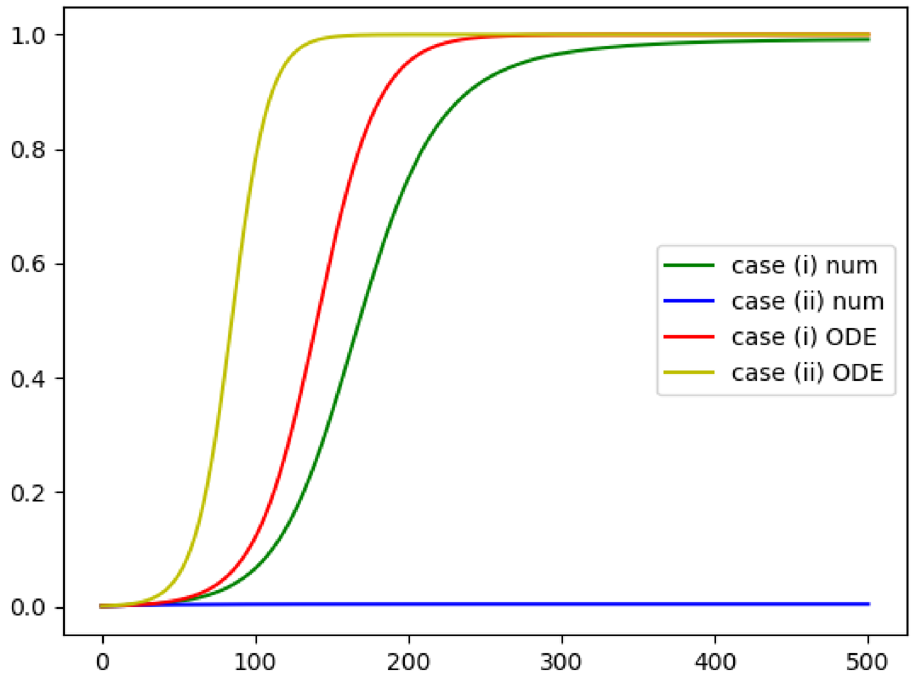



Figure 3: Numerical simulations vs. ODE approximations.

(b) This difference is caused by the fact that the ODE assumes the network is complete, and thus, won't take into account the effects caused by parts of the network not being reachable from any of the infected nodes. Thus, it most closely resembles case $i$.

(c) This is exponential growth. This can be explained by the fact that initially an infected node infects approximately $\langle k \rangle i$ neighbours, after which, in the next time step, these $\langle k \rangle i$ infected neighbours infect $\langle k \rangle i$ of their neighbours in turn. This effect causes initial exponential growth.

## Epedemics 4

(a)

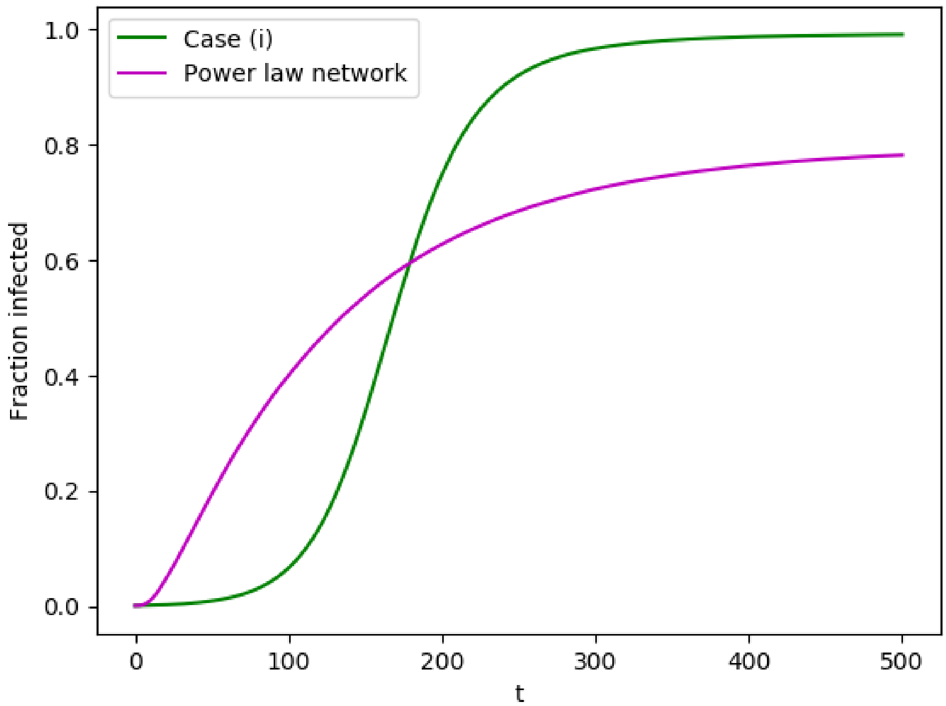



Figure 4: Scale free vs. random

(b) The infection initially spreads quicker in the scale free network due to the existence of hubs. If a hub gets—or is initially—infected, the infection is able to spread to significantly more new nodes because of the high amount of neighbours.

(c)

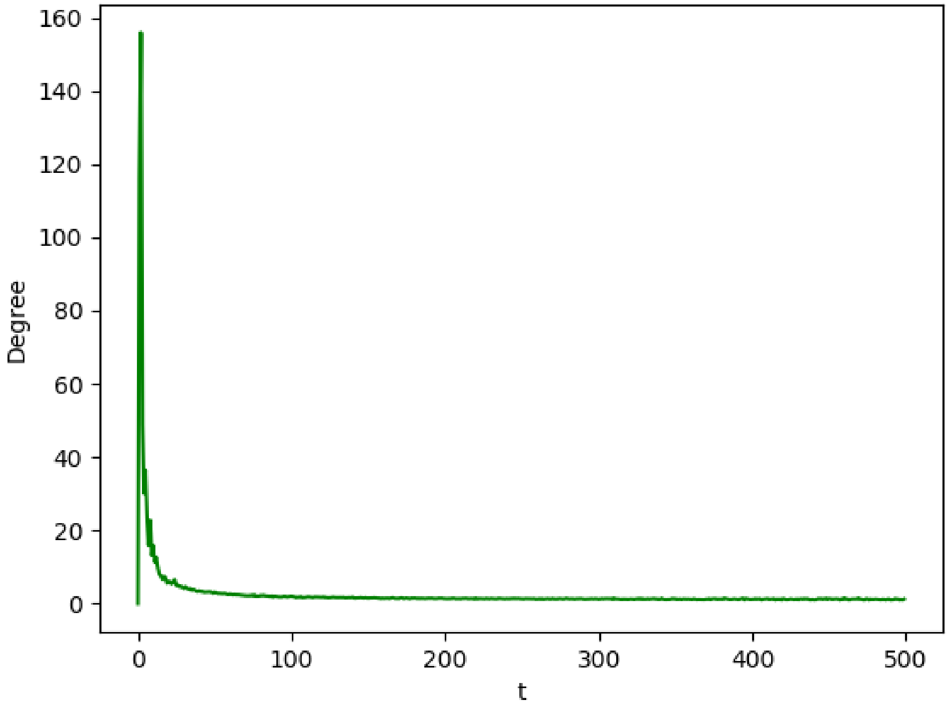



Figure 5: The average degree of newly infected nodes.

(d) The infection initially spreads to hubs and afterwards starts infecting the rest of the network.