PERCOLATION THEORY IN EPIDEMICS

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What is Percolation?

Movement and filtering of fluids through porous materials.

Example:

- Coffee percolation: Soluble compounds leave the coffee and join the water to form coffee. Insoluble compounds remain within the coffee filter.

Reference: https://images.app.goo.gl/e3YBt8vphP7kDKUa7

Diffusion vs Percolation in gases:

The spreading of perfume from one part of the room to other is by diffusion because there exists concentration gradient of perfume particles, so the molecules **naturally** spread out.

Gas molecules, adsorbed on the surface of a porous solid move through all pores large enough to admit them. Here, the **state of the medium** entirely determines the motion of the particle.

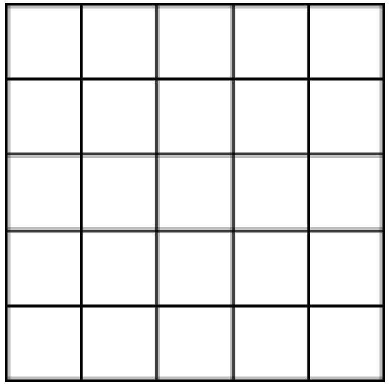
Percolation Theory:

- Percolation theory describes the behaviour of a network when nodes or links are removed.

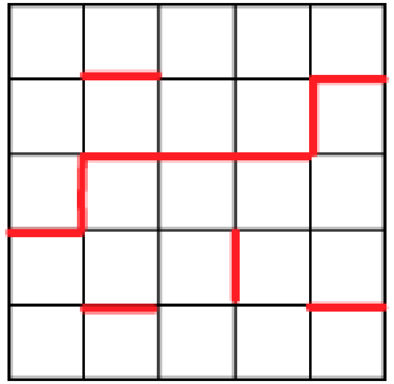
Example:

- Define p = Average degree of connectivity between sub-units of an arbitrary system.

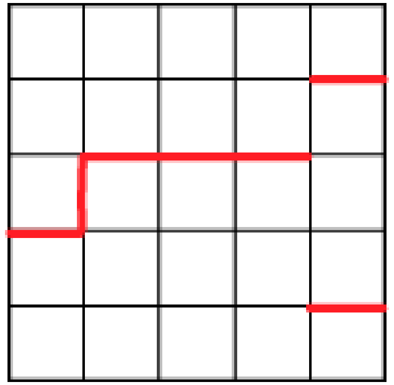
$p = 0$
• All sub-units are isolated from each other.



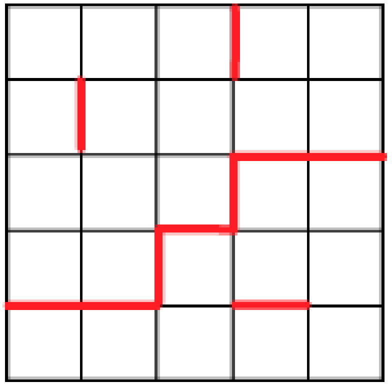
$p = 1$
• All sub-units are connected to some max neighbouring sub-units.



$p = 1\downarrow$
• At some $p = p_c$, there is **no longer** a connected path from one side to the other.



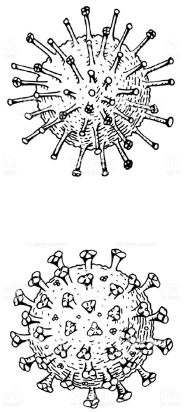
$p = 0\uparrow$
• At some $p = p_c$, the first connected path from one side to the other **appears**.

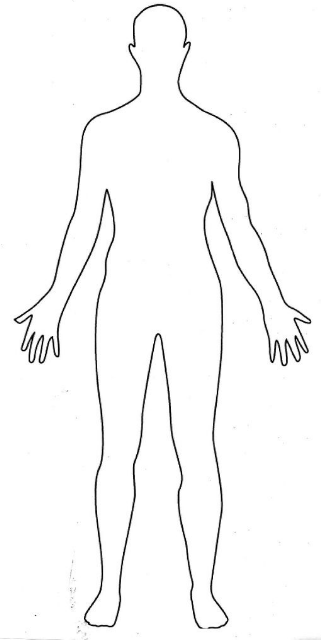


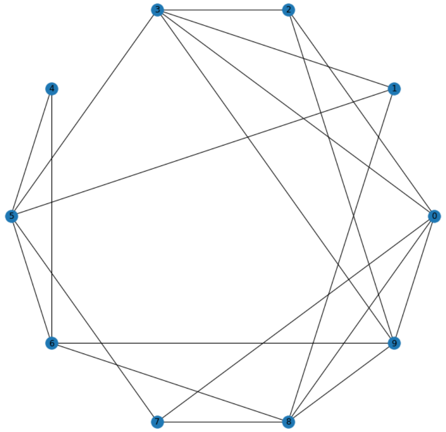
Epidemic spreading as a percolation model:

Model constituents:

Spreading agent: Virus → Medium or Host: Human body → Small-world network



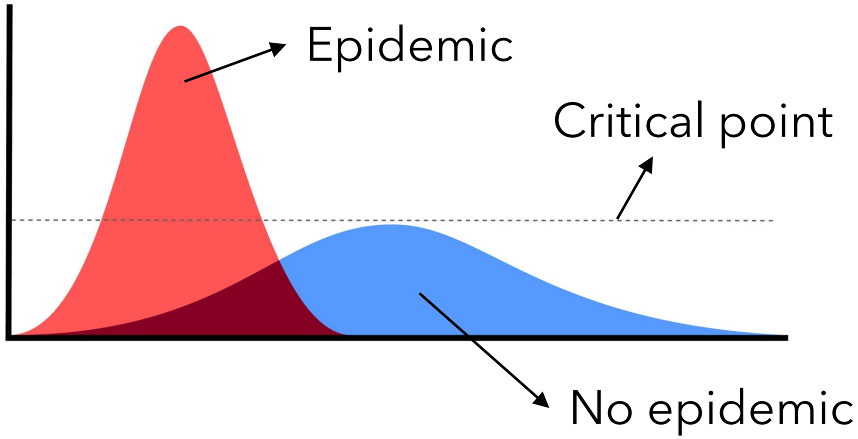




Reference: https://images.app.goo.gl/vqeS4X2YqwBFdA4L6

Percolation follows universality principle:

- Physical systems exhibit phase transitions: water to steam phase transition. The critical point of this transition in this system is 100℃.
- The universality corresponds to the **behaviour of systems** as they approach this critical point.
- In percolation, the phase transition is from 'no epidemic' to 'epidemic' at the critical point.

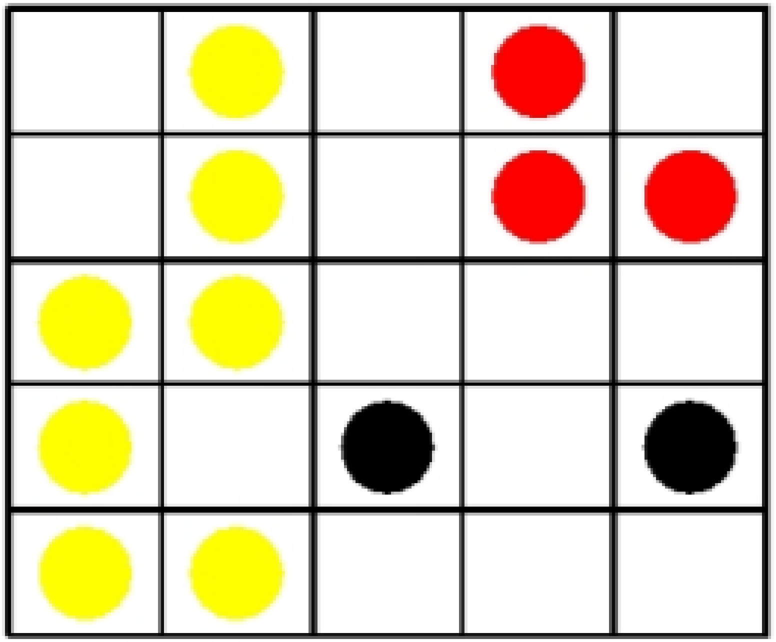


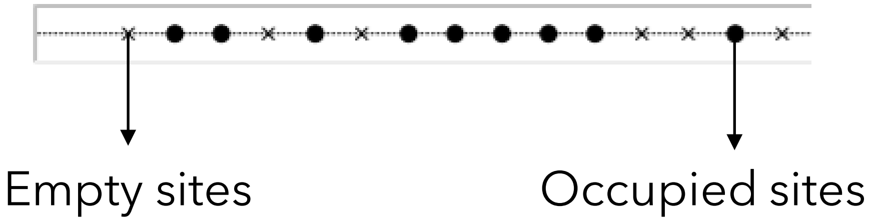
References: https://images.app.goo.gl/WPYmU4LByzu3LhDTA, https://images.app.goo.gl/LoKdoVJzk6EyE7Qu7

A simple model of disease transmission in small-world network:

- **Small-world network**: The number of degrees of separation between any two members of a given population is small by comparison with the size of the population itself.
- **Susceptibility**: The probability that an individual exposed to a disease will contract it.
- **Transmissibility**: The probability that contact between an infected individual and a susceptible one will result in the latter contracting the disease.

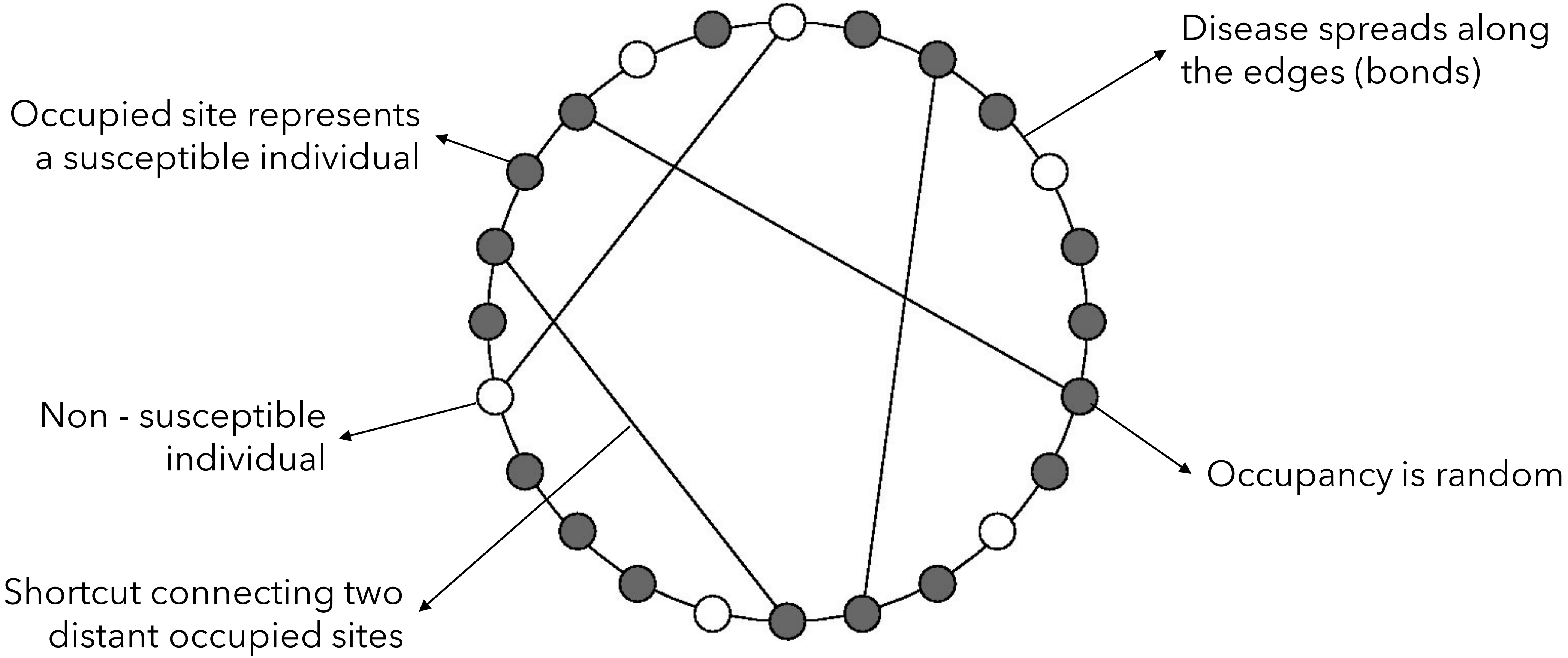
- **Cluster**: A cluster is a group of nearest neighbouring occupied sites.
- In the corresponding figure, we have one cluster of size 7, a cluster of size 3 and two clusters of size 1.
- Percolation in a 1d lattice: Infinite number of sites of equal spacing arranged in a line.
- In the corresponding figure, there is one cluster of size 5, one cluster of size 2, and two clusters of size 1.
- In a random graph, by contrast, the probability of there being a connection between any two people is uniform, regardless of which two you choose.





References: https://web.mit.edu/ceder/publications/Percolation.pdf

Model properties:



Analytical analysis of site percolation

What is the outcome of the models?

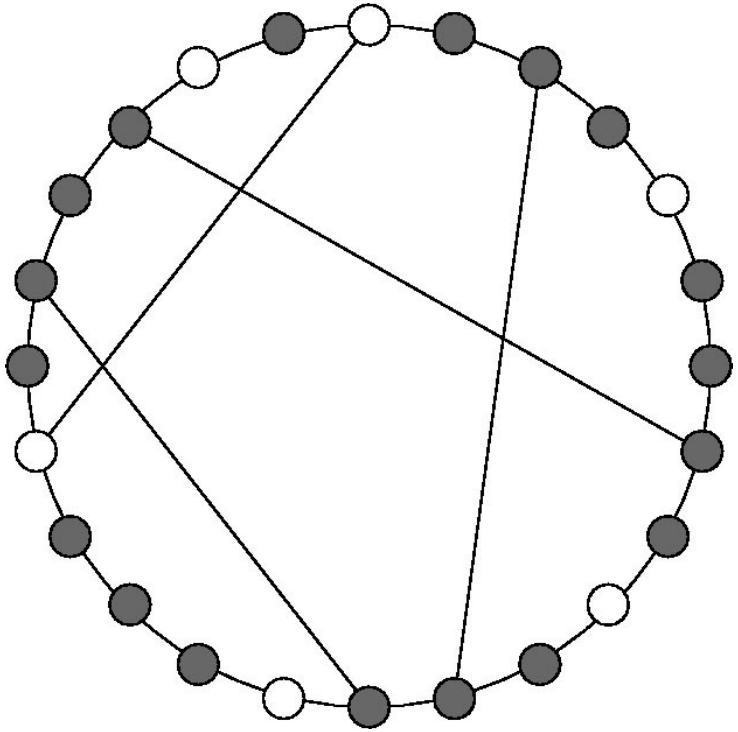
Stage I
- Disease begins with a single infected individual.

Stage II
- Spreads along the bonds and thus the clusters form.

Stage III
- Compute p_c where phase transition occurs.

I. Site Percolation Model:

- Every contact of a susceptible person with an infected person results in transmission i.e., **transmittivity is 1**.
- Less than 100% of the individuals are susceptible.
- In the site percolation [1]:
  - L = number of sites or bonds
  - p = fraction of shaded sites out of L
  - k = Number of next nearest neighbours
  - Shortcuts are added randomly between chosen pairs of sites
  - Occupancy of shaded sites is random



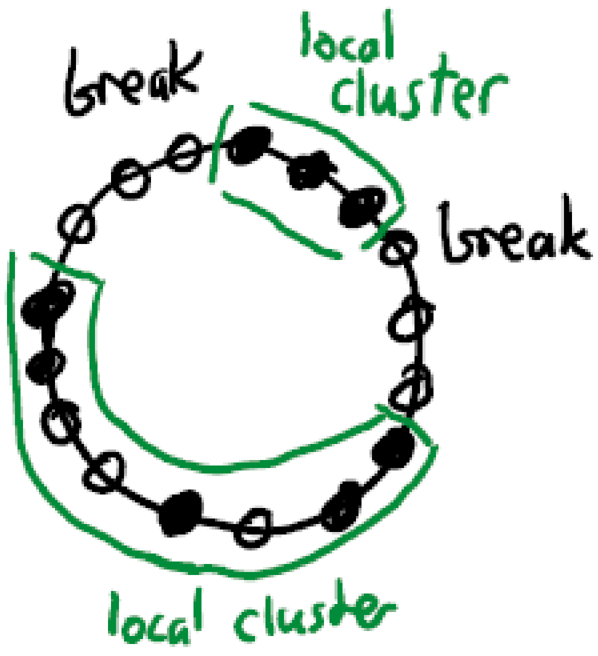
$L = 24, k = 1$
p = ¾ & 4 shortcuts.
[1]

- Φ = average number of shortcuts per bond.
- Now, the probability that two randomly chosen sites have a shortcut between them (ψ) is then:

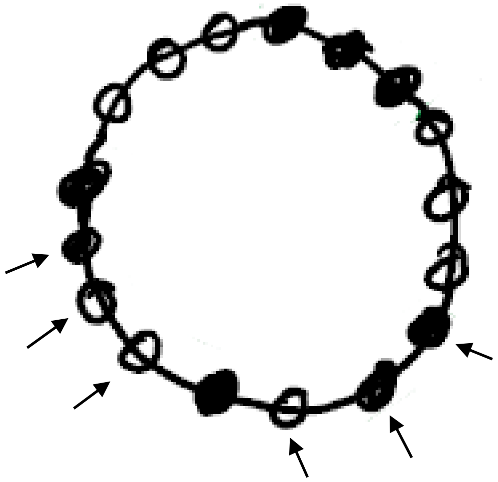
$$\psi = 1 - \left(1 - \frac{2}{L^2}\right)^{k\phi L} \approx \frac{2k\phi}{L}$$ [1]

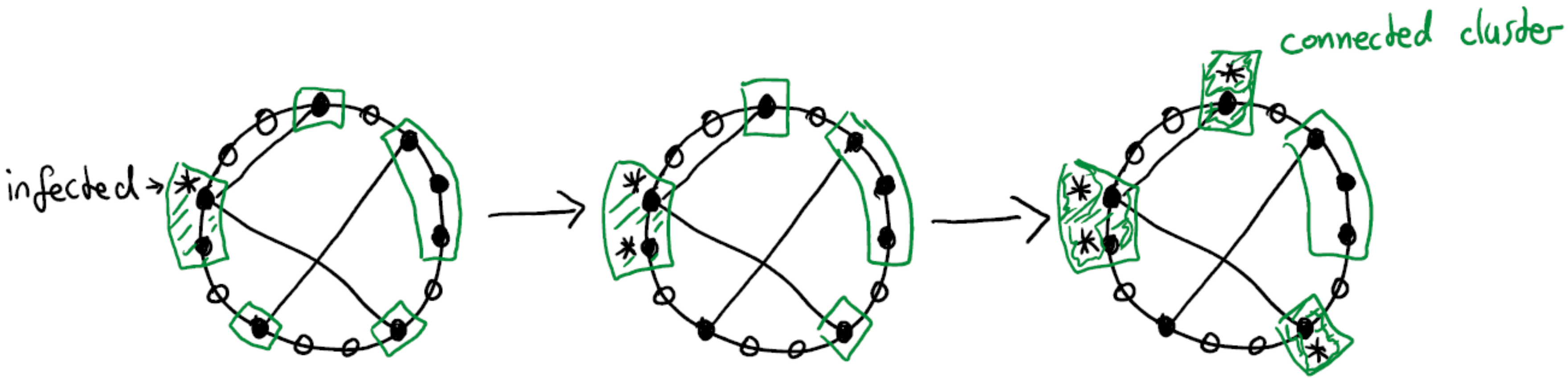
- Local clusters are defined as occupied sites that are connected together by the near neighbour bonds which are themselves connected together by shortcuts.
- For $k = 1$, the average number of local clusters of length i is:

$$N_i = (1-p)^2 p^{\mathrm{i}} L$$ [1]



$k = 3$





Connected cluster formation

- We define a vector $\vec{v}_n$ at each step in this process, whose components v_{ni} are equal to the probability of adding a local cluster of size i to the connected cluster. Now for $p \leq p_c$, the probability increases linearly with a transition matrix M:

$$\vec{v}_{n+1} = M\vec{v}_n \text{ where } M = N_i\left[1 - (1-\psi)^{\mathrm{i}j}\right]$$ [1]

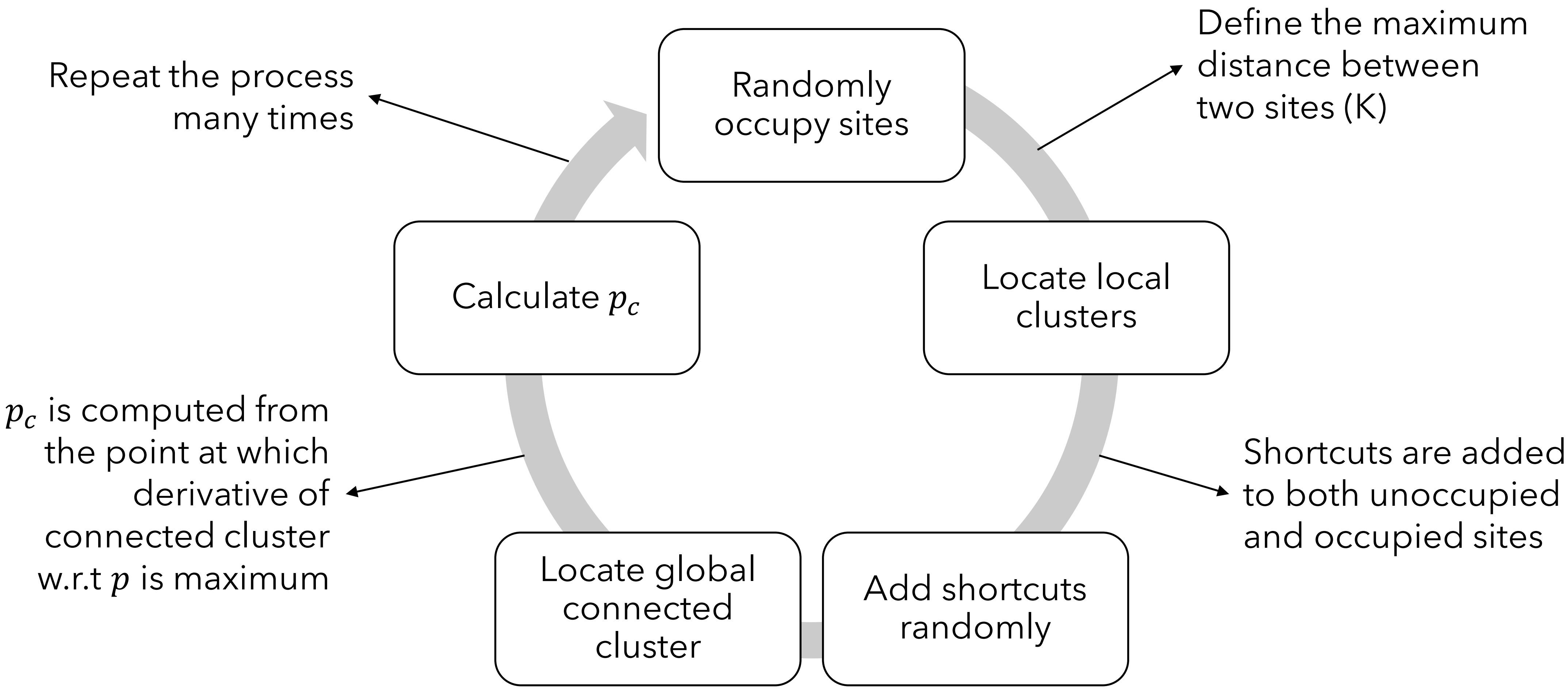
Here, M_{ij} = number of local clusters of size i connected to local clusters of size j

Consider the largest eigenvalue $\lambda_{\max}$ of M [1]:

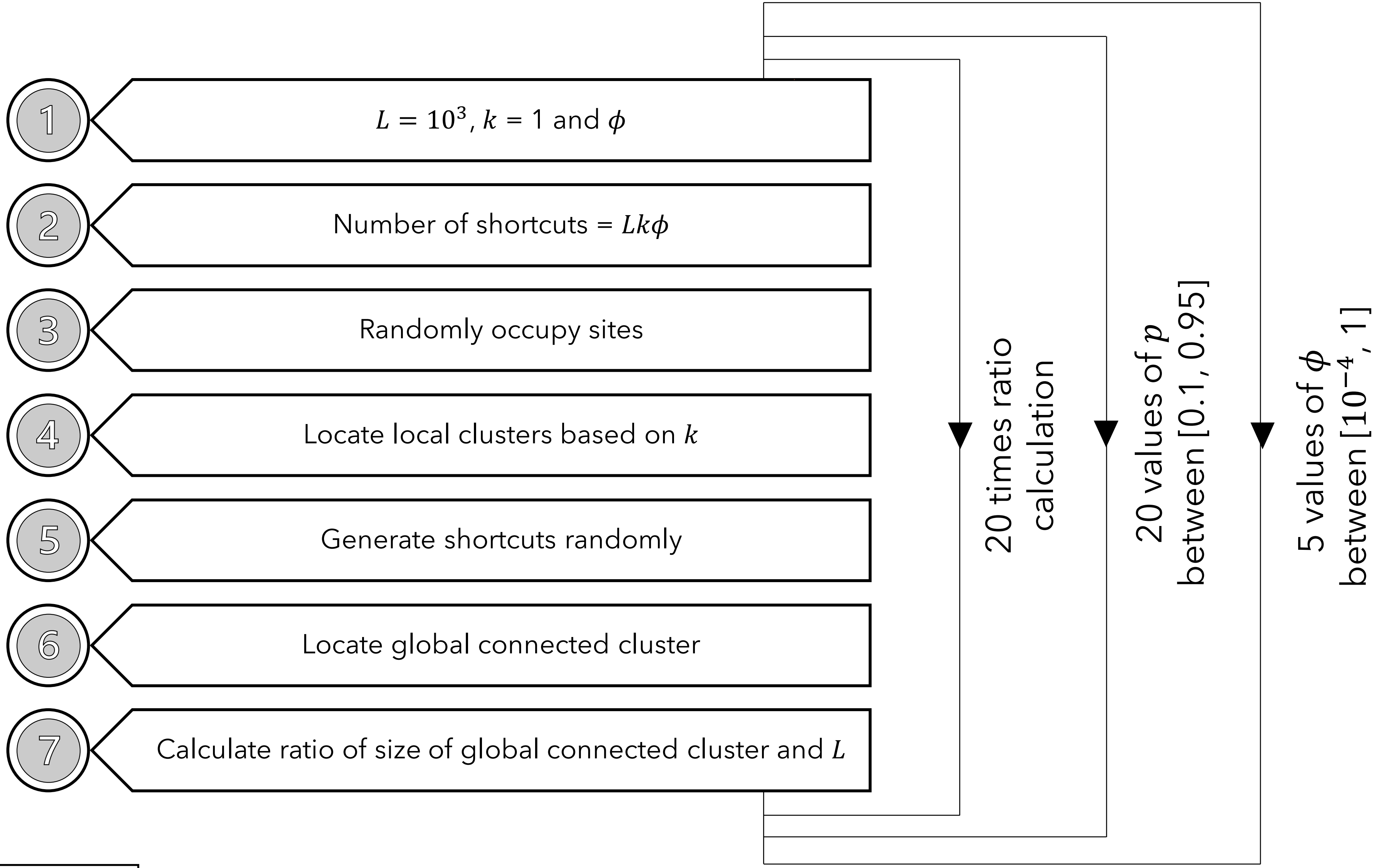
$\lambda_{\max} < 1$, no epidemic	$\lambda_{\max} > 1$, epidemic	$\lambda_{\max} = 1$, percolation threshold occurs
• $\vec{v}_{n+1} \longrightarrow 0$ i.e., the rate at which new local clusters are added falls off.	• $\vec{v}_{n+1}$ grows until the size of the cluster becomes limited by the size of the entire network.	• Percolation threshold that corresponds to the separation between an epidemic and no epidemic.

- We set $k = 1$ and $\lambda = 1$ to obtain $\phi = \frac{1-p_c}{2p_c(1+p_c)}$ [1]
- And solving for p_c gives: $\boldsymbol{p_c} = \frac{\sqrt{4\phi^2+12\phi+1}-2\phi-1}{4\phi}$ [1]

Numerical Simulation flow:



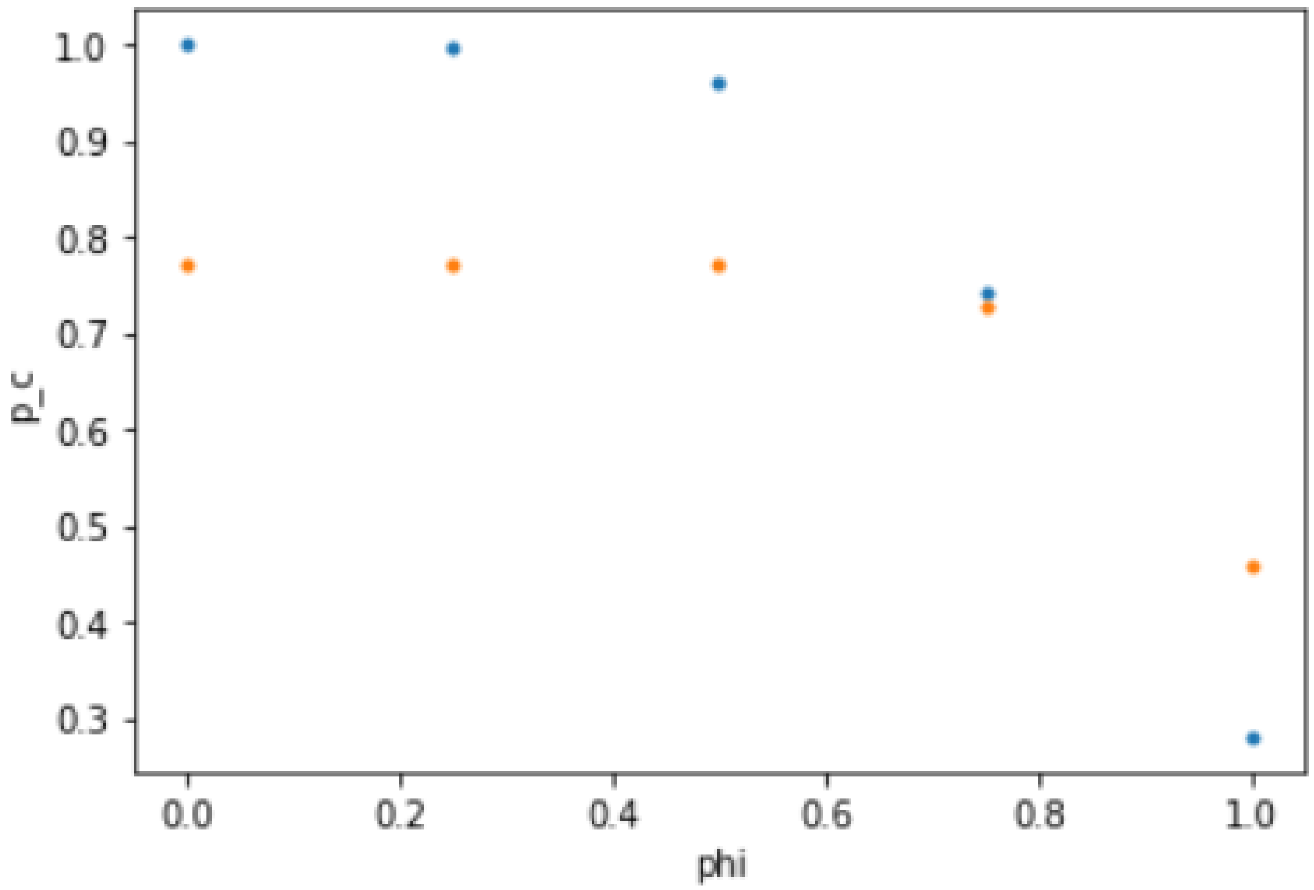
Numerical Simulation:



Numerical analysis of site percolation

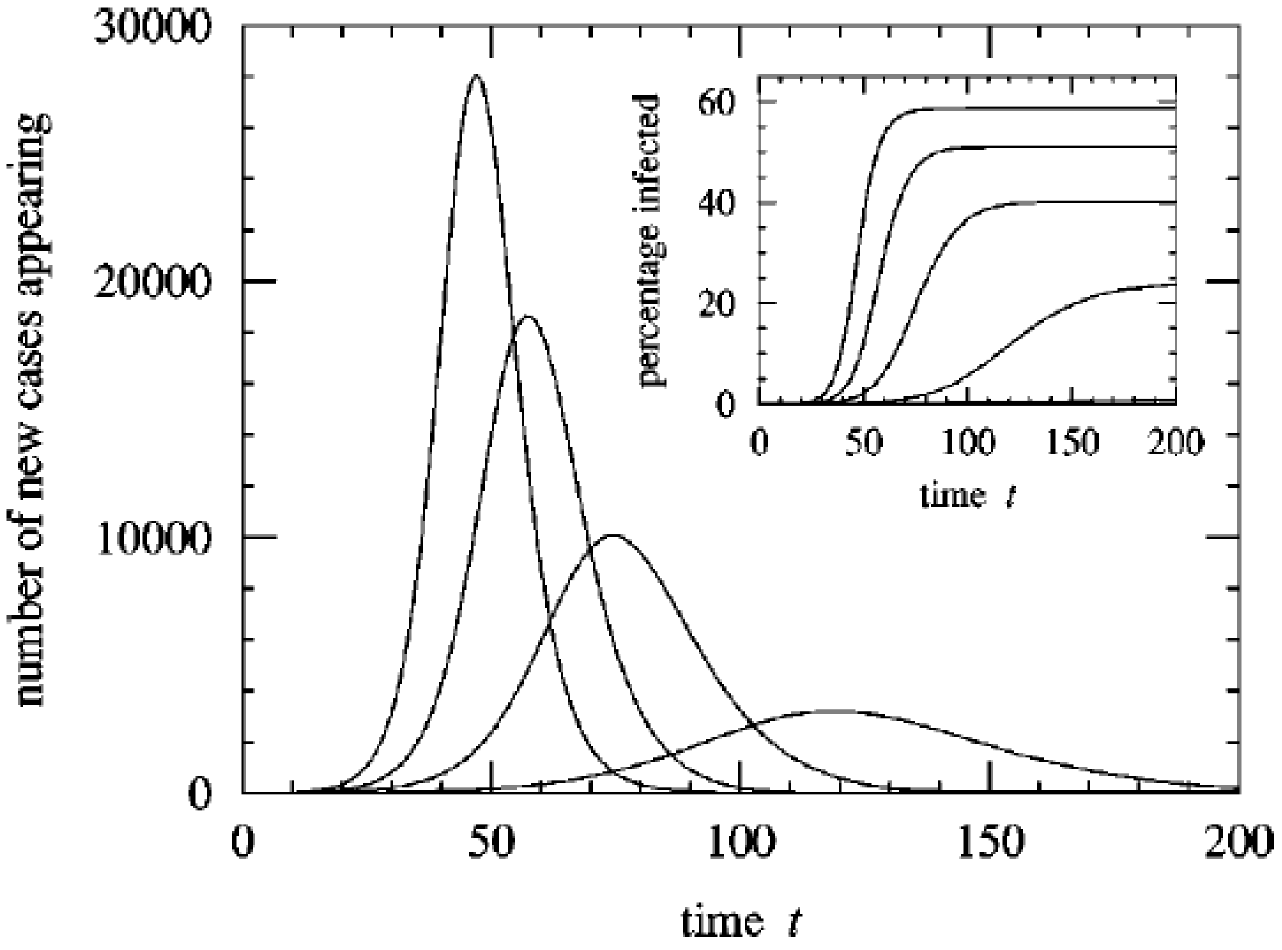
Analytical (blue) and Simulation (orange) results:

- Graph for the percolation threshold (p_c) as a function of shortcut density (ϕ).



Analytical and numerical results

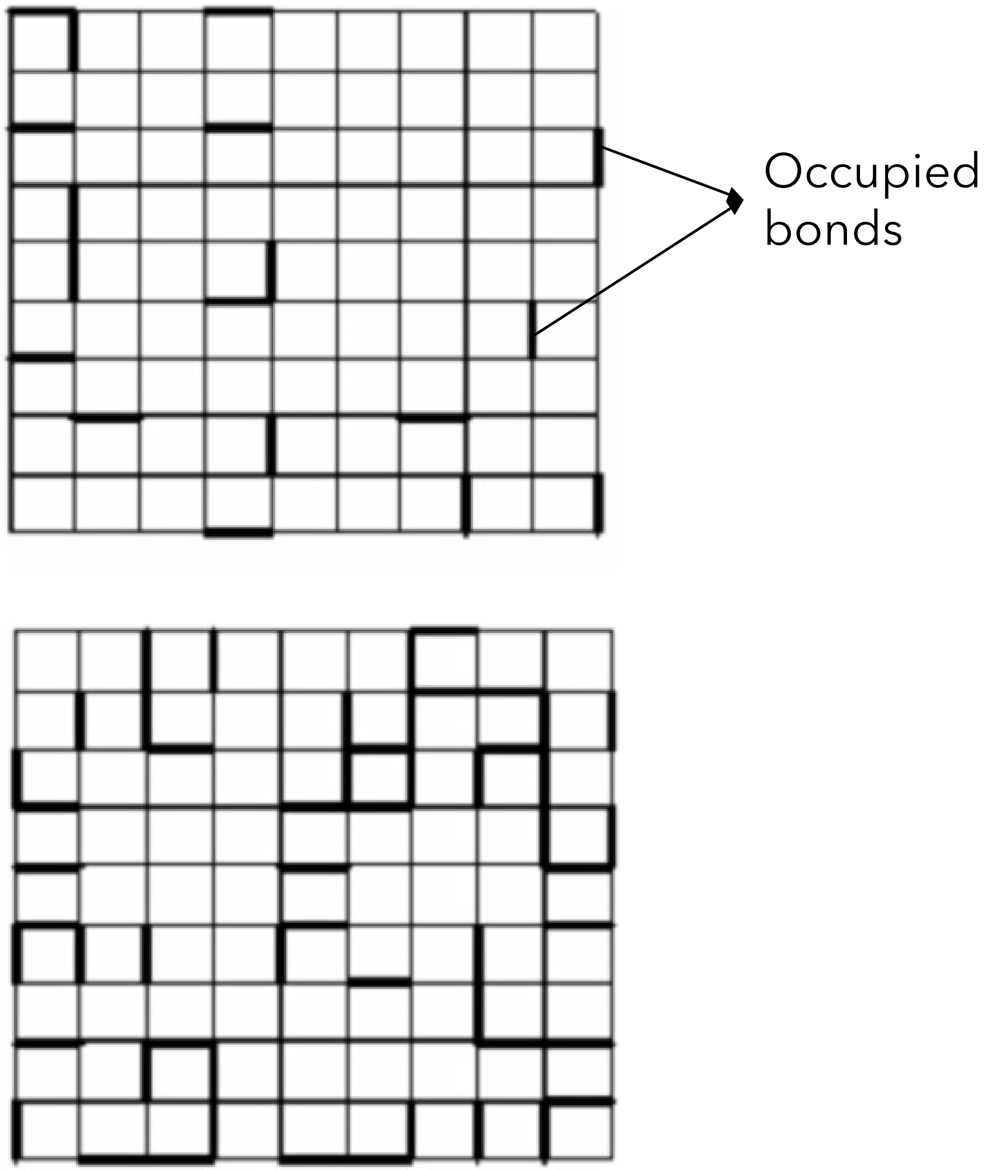
- $L = 10^6$, $k = 5$, and $\phi = 0.01$. The top four curves are for $p = 0.60, 0.55, 0.50$, and 0.45, all of which are above the predicted percolation threshold of $p_c = 0.401$ and show evidence of the occurrence of substantial epidemics [1].
- A fifth curve, for $p = 0.40$, is plotted but is virtually invisible next to the horizontal axis because even fractionally below the percolation threshold no epidemic behaviour takes place [1].



II. Bond Percolation:

- An alternative model of disease transmission is one in which all individuals are susceptible i.e., **susceptibility is 1** [1].
- Transmission takes place with less than 100% efficiency [1].
- An epidemic sets in when a sufficient fraction p_c of the bonds on the graph are occupied before a giant connected component forms whose size is comparable to the size of the network [1].
- In this model, the fraction p of occupied bonds is the transmissibility of the disease.

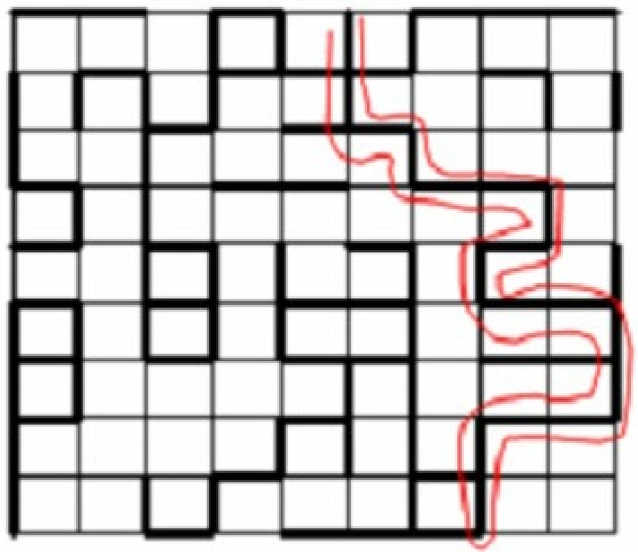
- Each bond (or site) in the lattice is occupied with probability p.
- At $p = 0$, all bonds are empty [2].
- For small p, there is a sparse population of bonds (top image) resulting in only small clusters [2].
- As p increases (bottom image), the mean size of the clusters grows.

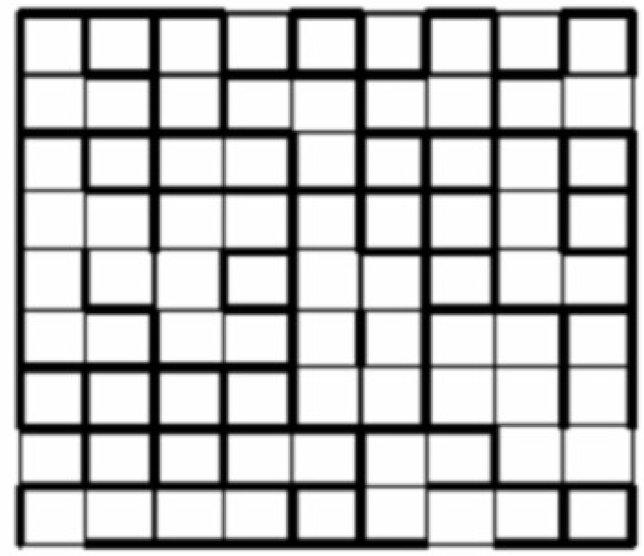


[2]

Bond percolation

- As p increases from 0 to 1, there is a specific value of $p = p_c$ (top image), at which a large cluster emerges providing full connectivity of the network from one side to the other for the first time.
- Beyond p_c, (bottom image) the number of fully connected paths increases [2].
- When $p = 1$, all bonds are occupied [2].





[2]

Bond percolation

- For k = 1, p_c for bond percolation = p_c of site percolation for the following reasons [1]:
  - a local cluster of i sites now consists of i -1 occupied bonds with two unoccupied ones at either end, so that the number of local clusters of i sites is:

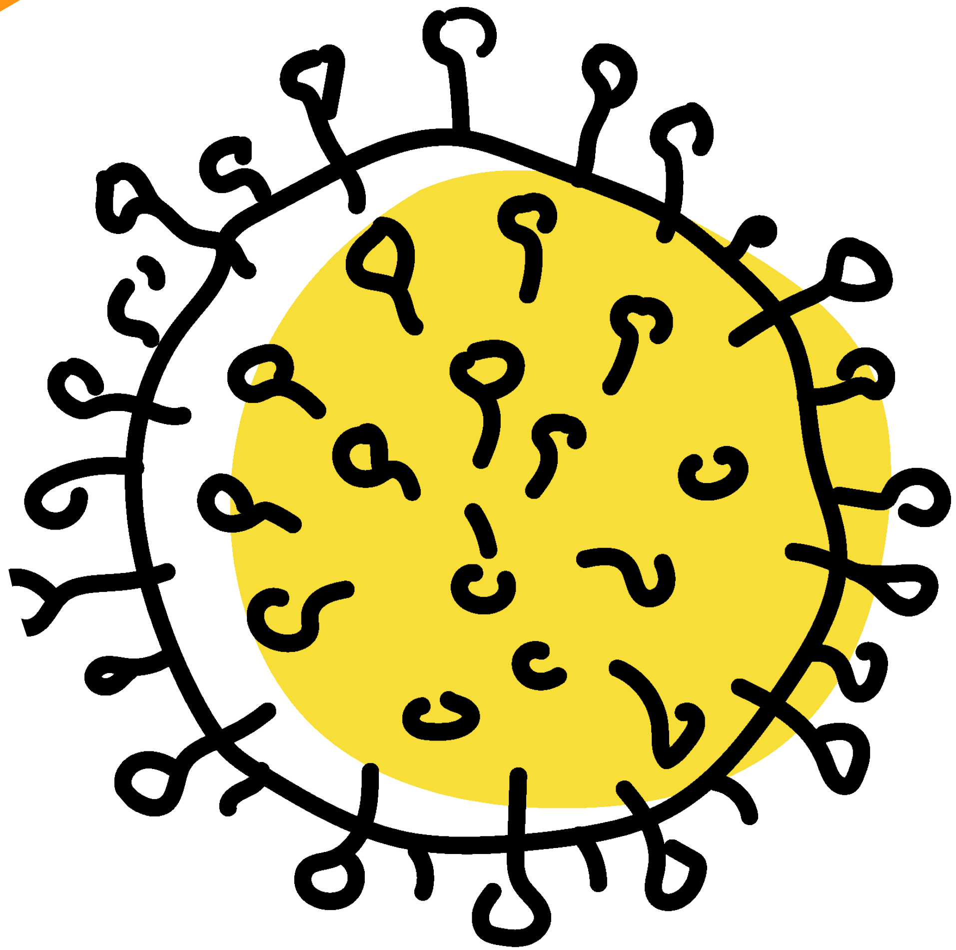
$$N_i = (1-p)^2 p^{\mathrm{i}-1} L$$ [1]

    which has one less factor of p than in the site percolation
  - The probability of a shortcut between two random sites now has an extra factor of p in it – it is equal to ψp instead of just ψ [1].
  - The two factors of p cancel and we end up with the same expression for the eigenvalue of M as before and the same threshold density (p_C).

COVID-19:

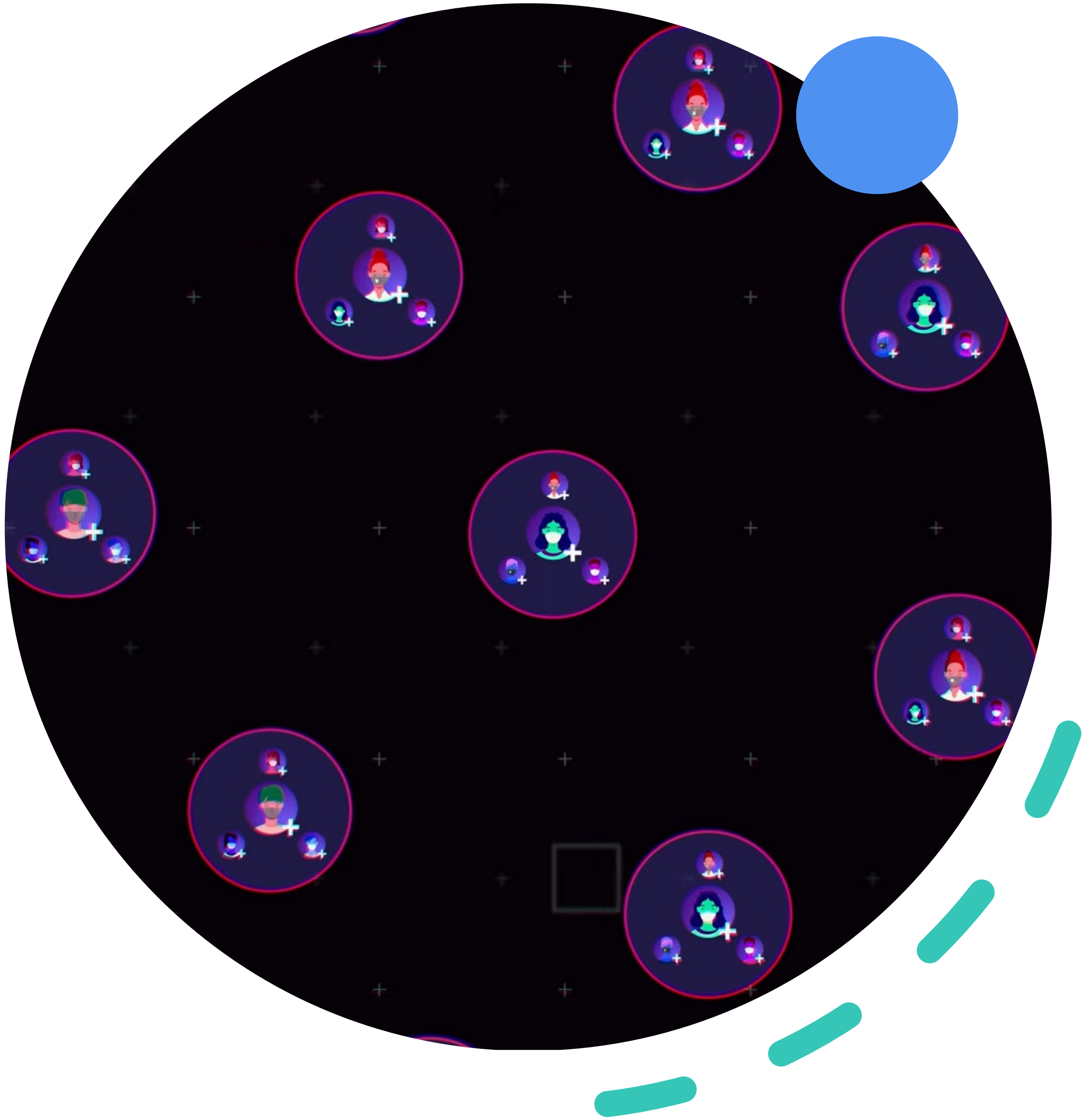
Timeline [3]**:**

- 31 Dec 2019 – Wuhan, China: First case of corona virus.
- 13 January 2020 - COVID-19 in Thailand, the first recorded case outside of China.
- 22 January 2020 - Evidence of human-to-human transmission in Wuhan.
- 30 January 2020 - WHO declared the novel coronavirus outbreak a PHEIC (Public Health Emergency of International Concern).
- 11 March 2020 – WHO declared the novel coronavirus outbreak a global pandemic.



How to model COVID-19?

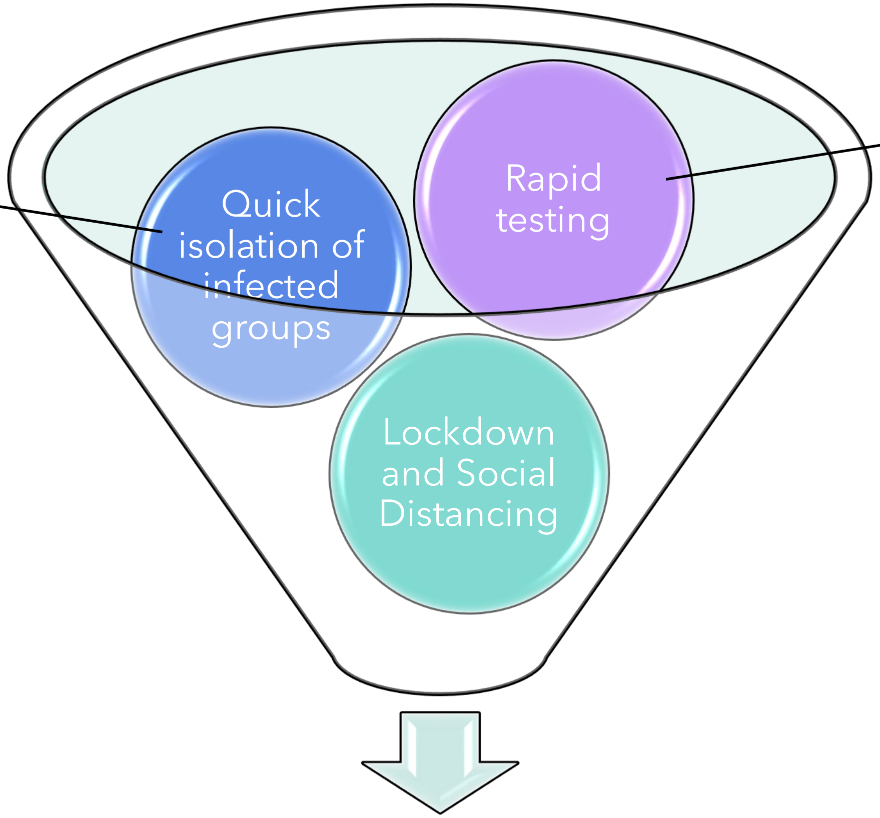
- **Contact tracing**: Finding each sick person and then figuring out who they recently interacted with.
- Apple and Google has rolled out a **contact tracing system** that automatically and autonomously notifies someone if they've been in contact with someone who's infected.
- So this system helps keep the infection within that **isolated** local group.



Reference: https://www.youtube.com/watch?time_continue=179&v=b7dxCRm5t5g&feature=emb_title

COVID-19 measures:

Infection dies out within local group, failing to spread to any other



Allows to identify infected individuals, thus leading to isolation

Elimination of shortcuts between local groups

References:

[1] Cristopher Moore, & M. E. J. Newman. (2000). Epidemics and percolation in small-world networks. *Physical Review E. Volume 61, Number 5*. Published 2000 Jan 07

[2] Suki B. The major transitions of life from a network perspective. *Front Physiol*. 2012;3:94. Published 2012 Apr 10. doi:10.3389/fphys.2012.00094

[3] https://www.who.int/news-room/detail/27-04-2020-who-timeline---covid-19