

Epidemics and Percolation

Computational Physics

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Introduction

- ▶ simulation of epidemic spreading: percolation
- ▶ SIR model → individual based approach
- ▶ focus on measures to control epidemics
- ▶ model needs an appropriate population
→ *clustering* and the *small world* property

Percolation

- ▶ flow of a fluid through a medium [1]
- ▶ geometrical problem on a lattice:
 - sites/bonds have probability p to be occupied
- ▶ analyze clusters of connected sites depending on p

For example the percolation threshold:

- ▶ infinite lattice sizes: critical p_c
 - $p > p_c$ exists a system spanning cluster [2]
 - $p < p_c$ no such cluster
 - ⇒ phase transition at p_c
- ▶ finite lattice sizes: less extreme transition at p_c

Cluster Identification

- ▶ *weighted union find with path compression*
→ sort sites or bonds in a tree structure
- ▶ checks every occupied site
- ▶ single neighboring site is occupied:
→ find its root, amend new site directly to root
- ▶ multiple neighboring sites are occupied:
→ find both roots, amend the smaller trees root site to the root of the larger (weighting)
- ▶ finding a root: the tree needs to be traversed from the node to the root
→ traversed nodes are directly amended to the root
⇒ keep the tree height as short as possible (path compression)
- ▶ possible to find all clusters in time $O(N)$
(N = number of sites in the network)

From Percolation to Epidemics

- ▶ think of a population as the medium and a disease as the fluid
- ▶ combine bond and site percolation
- ▶ individuals are the sites and their contacts are bonds
- ▶ disease can spread (flow) through physical contacts (bonds) and infect (occupy) individuals

Model Population

- ▶ clustering: individuals have common acquaintances
- ▶ small world property: number of intermittent links between any two individuals is low
- ▶ real world: only about 6 [3]
- ▶ 2D lattice in which only nearest neighbors can have contact
→ clustering
- ▶ add random bonds between people
→ small world property

SIR Realization

- ▶ start with single infected *Patient Zero*
- ▶ run time in discrete steps
- ▶ give disease a chance to spread to any individual who has a connection to an infected once per time step
- ▶ chance is determined by transmissibility p_{trans} and susceptibility p_{susc} → $p_{\text{tot}} = p_{\text{trans}} * p_{\text{susc}}$
- ▶ infected have a chance to recover from the disease, after which they cannot be infected again
- ▶ in our realization: p_{trans} is constant for entire population
- ▶ choose 2 distributions of p_{sus} , one where each individual is equally susceptible and one where there is an actual distribution depending on the age
- ▶ second distribution did not lead to much insights → focus on the first

SIR Realization

- ▶ infected recover after 6(2) time steps
- ▶ susceptibility is set to 0.7 for everyone at first
- ▶ after recovery susceptibility is set to 0, no chance for second infection
- ▶ also possible to 'vaccinate' a proportion r of the population at the beginning
- ▶ start with maximally transmissible disease $p_{\text{trans}} = 1$
- ▶ introduce a factor to p_{trans} that reduces the amount of contact between people

→ social distancing D

- ▶ e.g. $p_{\text{trans}}[\text{new}] = p_{\text{trans}}[\text{old}]/D = 0.5$
- ▶ $D = 2$ corresponds to everyone in the population cutting their contacts to others in half
- ▶ could do: in each time step test p_{susc} and $p_{\text{trans}}[\text{new}]$ against a uniform distribution
- ▶ but: p_{susc} and $p_{\text{trans}}[\text{new}]$ are independent of each other

→ test only against p_{tot}

Observables

- ▶ from the data obtained in the simulations it is possible to derive some quantities of interest
- ▶ $I(t)$ is the number of infected at time t
- ▶ I_{\max} is the maximum of concurrently infected individuals
- ▶ the size of an epidemic is the proportion of initially susceptible individuals who were affected by the disease at some point
- ▶ P_{ME} is the probability of a major outbreak, which we define as a size of ≥ 0.02 , which depends on the initial parameters chosen for each simulation

Error Estimation

- ▶ for each parameter set we run the simulation 100 times
- ▶ this is to account for the probabilistic differences and to be able to gauge the accuracy
- ▶ most of the values shown are means over these 100 runs
- ▶ since the values are not normally distributed we use bootstrapping to estimate the standard errors of these means
- ▶ to verify the bootstrapping works we visually checked the qqplots of the resulting distribution
- ▶ also checked that the biases are small compared to the standard error

Visual Propagation of a disease

$$(r = 0.14, D = 4)$$

red: currently infectious; black: recovered; white: not affected

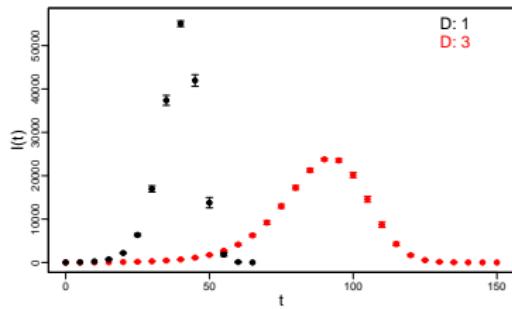
Visual Propagation of a disease

$$(r = 0.2, D = 4.7)$$

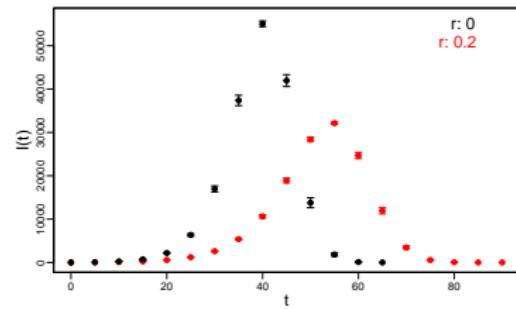
red: currently infectious; black: recovered; white: not affected

Concurrently Infected $I(t)$

- ▶ reduction in the maximal number of concurrently infected
- ▶ D : 'flattening' of the curve



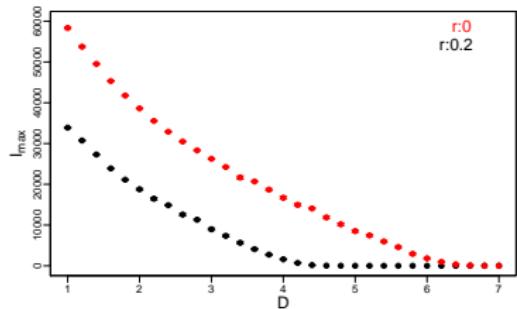
$$r = 0$$



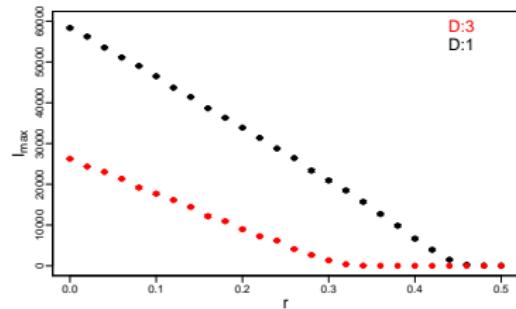
$$D = 1$$

Maximal concurrently Infected I_{\max}

- ▶ r & D : significant impact
- ▶ $D \in 1-2$: strong reduction
- ▶ $D > 2$: flattening reduction



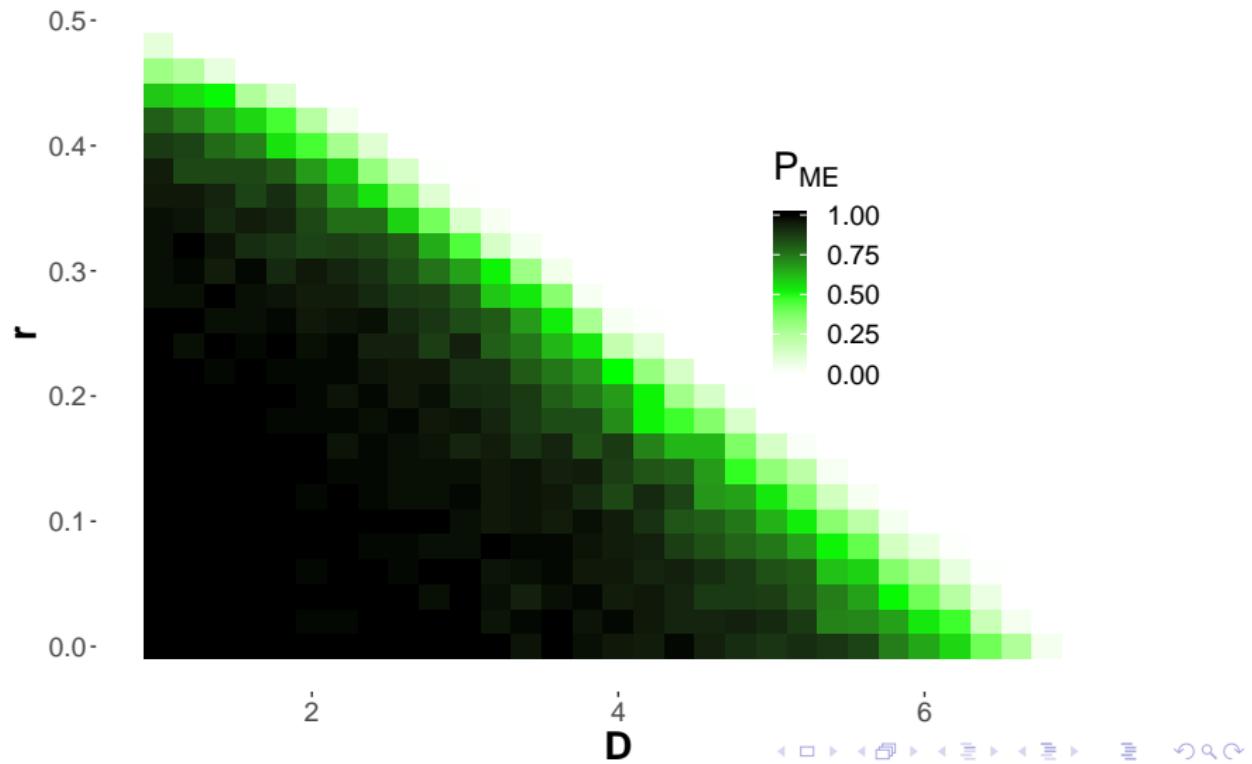
r fixed



D fixed

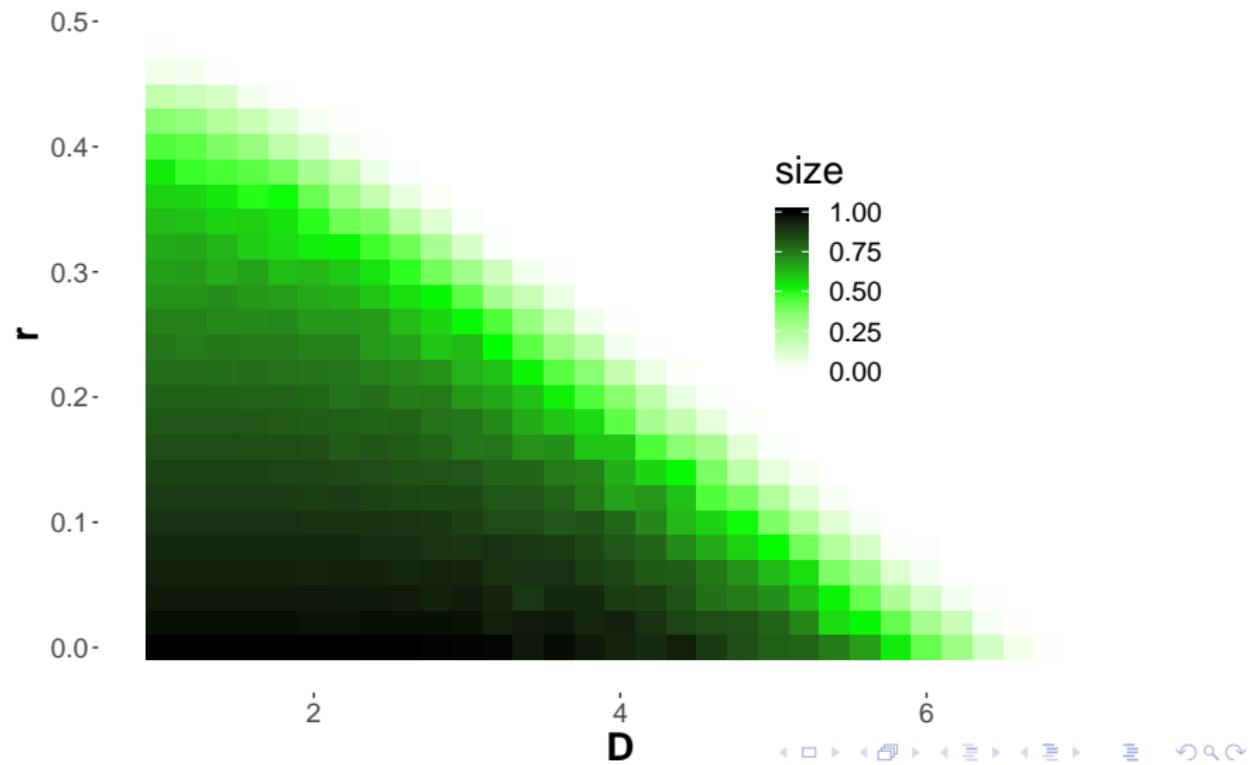
Epidemic Outcomes - P_{ME}

- ▶ phase transition from ME to minor epidemic
→ similar to percolation



Epidemic Outcomes - size

- ▶ r : decreasing size \rightarrow herd immunity visible
- ▶ D : size \approx const \rightarrow only prolonging the disease



Summary - Results

- ▶ SIR epidemics spread on small-world 2D lattice
- ▶ test impact: initial vaccination r & social distancing D
- ▶ r & D : reduction of the maximal concurrently infected I_{\max}
- ▶ r : reduction of the epidemic size (herd immunity)

Limitations:

- ▶ model chosen for the population
- ▶ arbitrarily set disease parameters

Outlook:

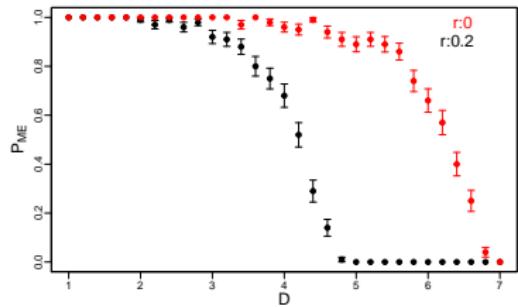
- ▶ higher dimensional lattice, next nearest neighbor interactions
- ▶ time delay for r & D
- ▶ recovered return to being susceptible after time
- ▶ clustering information

Sources

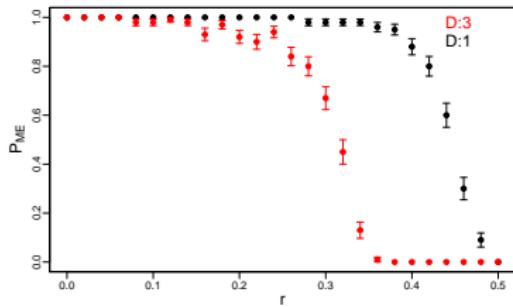
-  Muhammad Sahimi. *Applications of Percolation Theory*. 2009 (cit. on p. 3).
-  Dieter W. Heermann Kurt Binder. *Monte Carlo Simulation in Statistical Physics*. 2019 (cit. on p. 3).
-  Cristopher Moore and M. E. J. Newman. “Epidemics and percolation in small-world networks”. In: *Phys. Rev. E* 61 (5 May 2000), pp. 5678–5682. DOI: 10.1103/PhysRevE.61.5678. URL: <https://link.aps.org/doi/10.1103/PhysRevE.61.5678> (cit. on p. 6).

Backup - Heatmap Slices P_{ME}

fixed r :

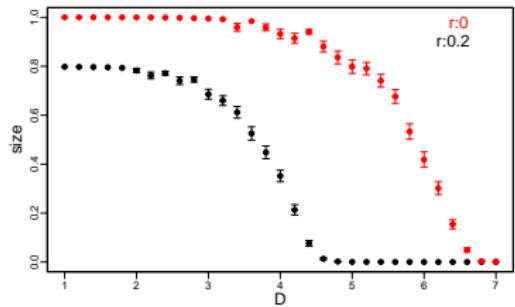


fixed D :

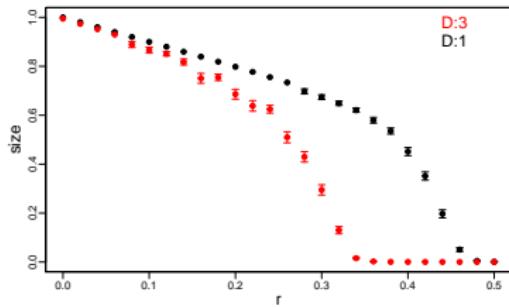


Backup - Heatmap Slices: size

fixed r :

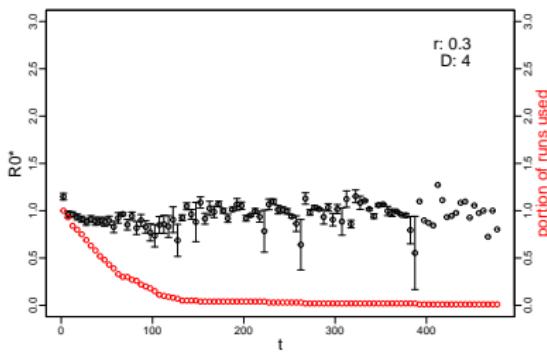
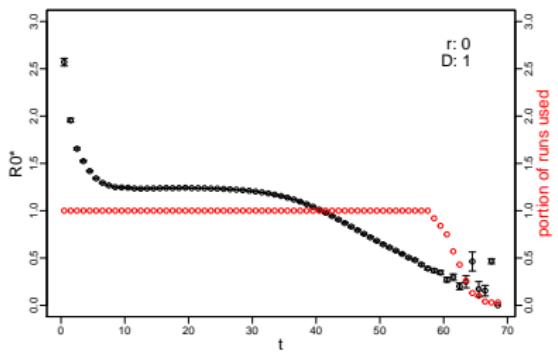


fixed D :



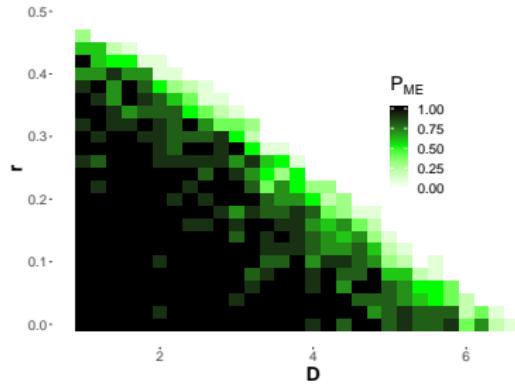
Backup - $R0^*$

- ▶ $R0^*$ for all time steps
- ▶ can only be computed from ongoing runs at time t (red)
- ▶ more than one patient 0 needed to show $> 1 / < 1$ prediction



Backup - Age Dependent Susceptibility Distribution

- ▶ repeated simulation for age dependent susceptibility



- ▶ overall distribution very similar
- ▶ not as smooth, less samples used for this overview

Backup - Visual Propagation of a disease

$$(r = 0.2, D = 4)$$

red: currently infectious; black: recovered; white: not affected