Contact Processes and SIR model simulations: different percolation universality classes

Physics of Complex Systems

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Introduction

Overview

Contact processes (SIS) and SIR model are two kind of epidemic models.
Three possible states for each node:

- **S**, susceptible.
- **I**, infected.
- **R**, recovered (not present in SIS).

In this work:

- (1+1) dimensional SIS $\rightarrow$ **Directed Percolation** (DP);
- (2+1) dimensional SIR $\rightarrow$ **Dynamical Percolation** (DyP):
  - Simulation with perfect immunization.
  - Quick discussion on partial immunization.

Goal: determine critical point and critical exponents.

Non-equilibrium phase-transitions

Active phase: at least one active site (infected individual).

Absorbing phase: all sites are inactive (no infected individuals).

The sistem evolution is governed by transition rates (infection rate and recovery rate in our case):

- There exists a threshold for the transition rates wich defines a phase a transition between the active phase and the absorbing one.

The system is not at equilibrium: detailed balance does not hold.

Contact Process

Description

N individuals in a one-dimensional lattice with periodic boundary conditions.

- S $\rightarrow$ I with transition rate $\lambda n_i/2$.
- I $\rightarrow$ S, spontaneously with recovery rate $\mu = 1$.

where $\lambda =$ infection rate and $n_i/2$ is the fraction of infected neighbors.

Monte Carlo algorithm

Let $c = 1/(1+\lambda)$, the steps for the simulation are:

1. Pick an infected node I randomly.
2. Generate $u \in (0,1)$ uniformly distributed.
   - if u $<$ c (recovery rate), then let I become S;
   - otherwise, pick a random neighbor of I: if it is S, then let it go I.
3. repeat 1 and 2 as long as there are N_I infected nodes (Monte Carlo step).

Initial conditions

Two possibilities for the initial conditions of the lattice [1]:

- **Homogeneous**, with an high percentage of initial infected.
  - Critical exponents: δ, $\nu_\parallel$, β, z, $\nu_\perp$.
- **Localized**, with a single infected node.
  - Critical exponents: θ, δ.

Homogeneous I. C.

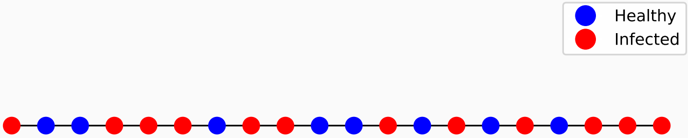

Figure 1: Example of initial lattice with 60% infected nodes.

Density of infected nodes over time as order parameter [1]. At criticality:

- $\langle \rho(t) \rangle \sim t^{-\delta}$, where $\langle ... \rangle$ is an **ensemble average**.

This can be exploited in order to determine the critical point and the δ exponent.

Critical point and δ

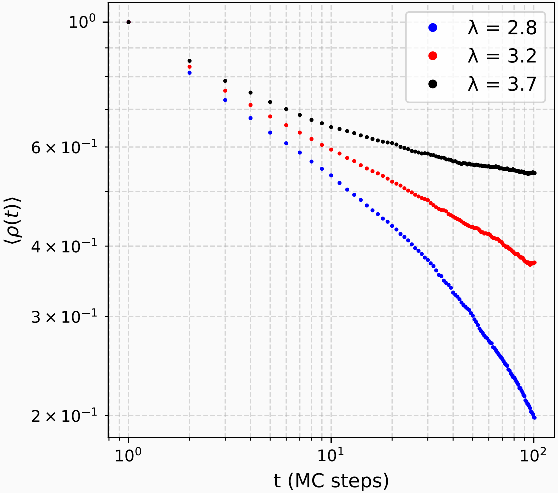

Figure 2: Density of infected nodes as function of time steps for a lattice of $N = 100$ individuals. The averages are done over 10^3 different realizations.

Critical point and δ

A rough estimation of λ_c can be obtained with the following procedure:

- Take reasonable lower and upper bounds for λ, (e.g. 2.8 and 3.7).
- Take n rates between the lower and the upper (included).
- For each λ in the range, do a linear regression of the average density.
- Keep the λ that generates the best fit.

Note that the slope of the linear fit is the δ exponent.

For our computations we use $\lambda_i = [3.29, 3.2975, 3.305, 3.3125, 3.32]$.

Results for λ_c and δ (finite-size)

For each λ in the chosen interval we run 10^4 simulations for 10^3 time steps.

N	20
λ_c	3.2975
δ	~ 0.861
R^2	~ 0.901

N	50
λ_c	3.2975
δ	~ 0.235
R^2	~ 0.963

N	100
λ_c	3.305
δ	~ 0.154
R^2	~ 0.999

Table 1: Results for the critical point and δ exponent obtained with $\mathrm{N} = 20, 50, 100$. The best regression is the one obtained with $\mathrm{N} = 100$. The regression is performed on all the points of the average except the first 50. Computational time for $\mathrm{N} = 100$: ~ 4 min.

Actual values of λ_c and δ [1]:

- $\lambda_c = 3.29785(2)$.
- $\delta = 0.159464(6)$.

Other exponents

Estimation of $\nu_{\parallel}$ and β:

- Plotting $\rho(t)t^{\delta}$ vs. $t|\lambda - \lambda_c|^{\nu_{\parallel}}$ for different λ, one can determine $\nu_{\parallel}$ tuning its value such that all curves collapse [1].
- The exponent β is then $\beta = \delta\nu_{\parallel}$.

Estimation of z and $\nu_{\perp}$:

- The exponent z can be determined in a similar way plotting $\rho(t)t^{\delta}$ vs. t/N^{z} [1].
- The exponent $\nu_{\perp}$ is then $\nu_{\perp} = \nu_{\parallel}/z$.

In the next slides we show the plots for various $\nu_{\parallel}$ and z in order to observe the behaviour of data collapsing.

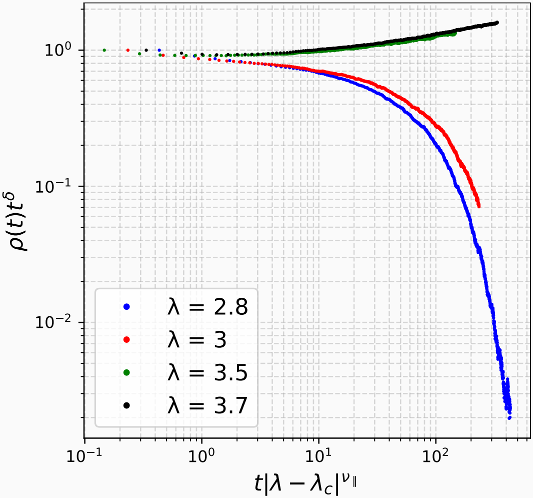

Figure 3: Data collapse with $\nu_\parallel = 1.2$ for a lattice of 100 nodes starting from a fully occupied situation. The number of steps is 10^3 and averages are done over 10^3 trajectories as well.

$\nu_\parallel = 2.2$

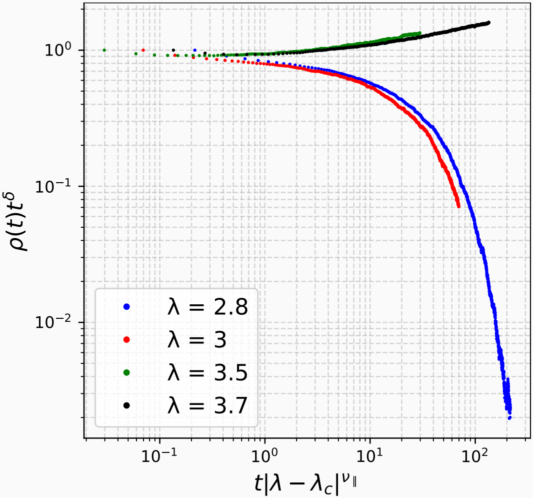

Figure 4: Data collapse with $\nu_\parallel = 2.2$ for a lattice of 100 nodes starting from a fully occupied situation. The number of steps is 10^3 and averages are done over 10^3 trajectories as well.

$\nu_\parallel = 1.7$

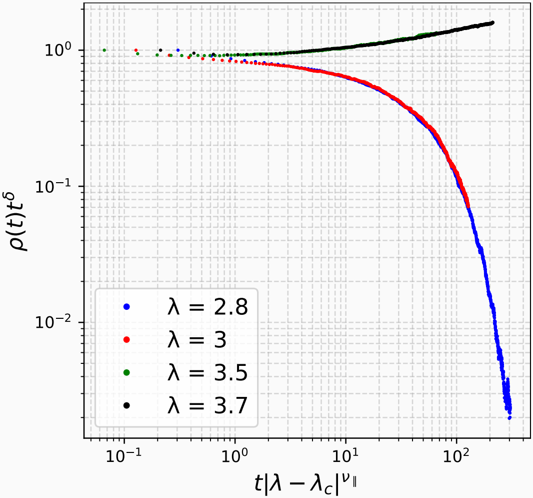

Figure 5: Data collapse with $\nu_\parallel = 1.7$ for a lattice of 100 nodes starting from a fully occupied situation. The number of steps is 10^3 and averages are done over 10^3 trajectories as well. From [1], $\nu_\parallel = 1.73$.

$z = 1.1$

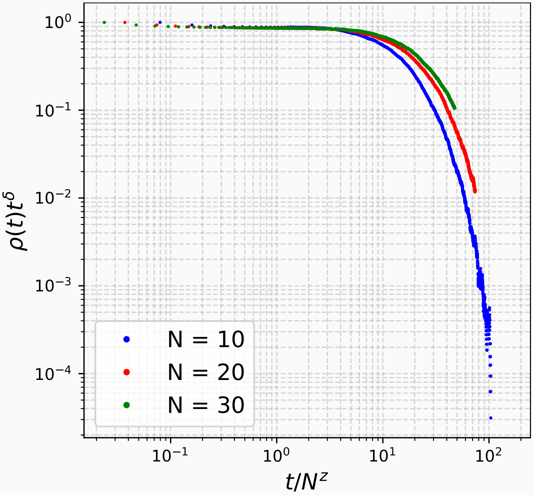

Figure 6: Data collapse with $z = 1.1$ for different lattice sizes starting from a fully occupied situation. The number of steps is $2 \cdot 10^3$ and averages are done over 10^4 trajectories as well.

$z = 2.1$

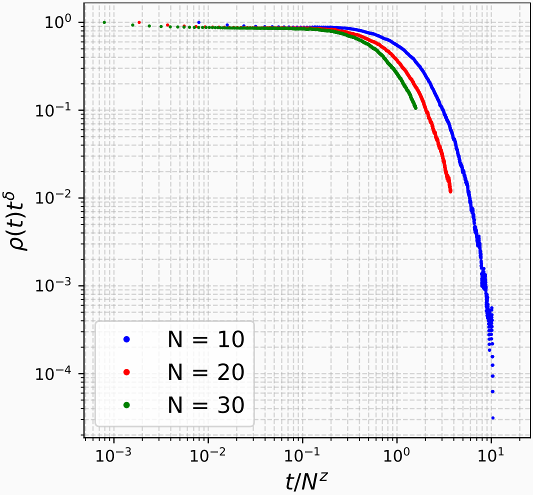

Figure 7: Data collapse with $z = 2.1$ for different lattice sizes starting from a fully occupied situation. The number of steps is $2 \cdot 10^3$ and averages are done over 10^4 trajectories as well.

$z = 1.5$

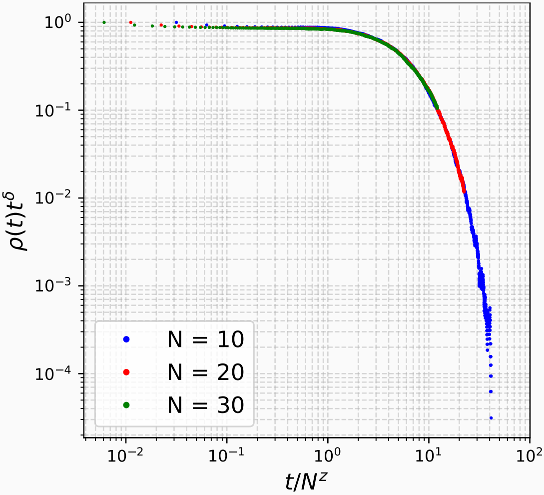

Figure 8: Data collapse with $z = 1.5$ for different lattice sizes starting from a fully occupied situation. The number of steps is $2 \cdot 10^3$ and averages are done over 10^4 trajectories as well. From [1], $z = 1.58$.

Summary (Homogeneous I. C.)

Exponent	Estimated	Actual value (DP)
δ	~ 0.154	0.159464(6)
$\nu_{\parallel}$	~ 1.7	1.733847(6)
β	~ 0.262	0.276486(8)
z	~ 1.5	1.580745(10)
$\nu_{\perp}$	~ 1.133	1.096854(4)

Table 2: Summary of critical exponents (DP [1]) estimated with homogeneous initial conditions. The δ exponent present in this table refers to the one obtained with $N = 100$.

Localized I. C.

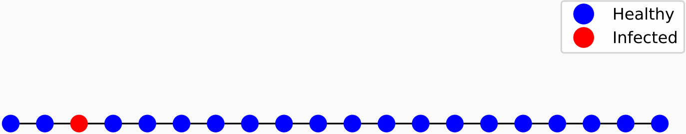

Figure 9: Example of initial lattice with one infected node.

At criticality [1]:

- $\langle n(t) \rangle \sim t^{\theta}$, number of infected nodes over time steps.
- $P(t) \sim t^{-\delta}$, the survival probability i.e. the fraction of the ensemble that at time t has not reached the absorbing phase [6], [1].

Critical point and θ

We can repeat the same procedure of the homogeneous initial conditions in order to find the λ_c and θ.

N	10^3
λ_c	3.2975
θ	~ 0.306
R^2	~ 0.9995

N	$5 \cdot 10^3$
λ_c	3.31255
θ	~ 0.337
R^2	~ 0.9993

N	10^4
λ_c	3.2975
θ	~ 0.310
R^2	~ 0.9994

Table 3: Results for the critical point and θ exponent obtained with $\mathrm{N} = 10^3, 5 \cdot 10^3, 10^4$. The regression is performed on all the points of the average but the first 50. Computational time for $\mathrm{N} = 10^4$: ~ 5 min.

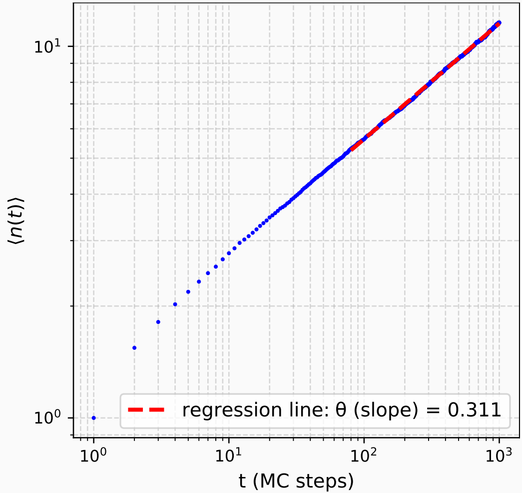

Figure 10: Estimation of θ for a lattice with $N = 10^4$ individuals. The critical point considered is $\lambda = 3.29785$ and the averages are done over $2 \cdot 10^4$ different realizations (trajectories). For the regression $R^2 = 0.9995$

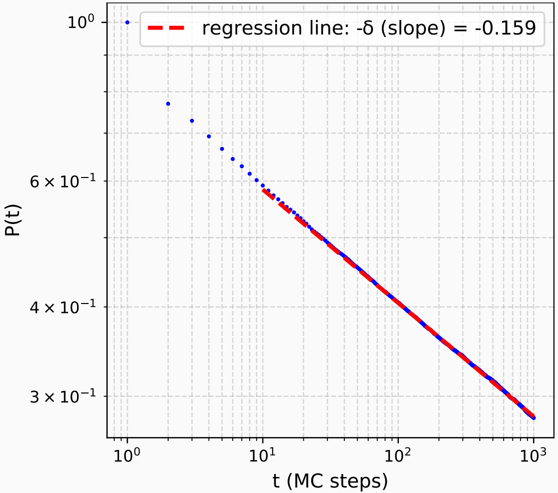

Figure 11: Estimation of δ for a lattice with $N = 10^4$ individuals. The critical point considered is $\lambda = 3.29785$ and the averages are done over $2 \cdot 10^4$ different realizations (trajectories). For the regression $R^2 = 0.9997$.

Summary (Localized I. C.)

Exponent	Estimated	Actual value (DP)
θ	~ 0.311	0.313686(8)
δ	~ 0.159	0.159464(6)

Table 4: Summary of critical exponents (DP [1]) obtained with localized initial conditions.

SIR model

Description

N individuals in a square lattice of size L with periodic boundary conditions.

- S $\rightarrow$ I with probability $\lambda n_i/4$;
- I $\rightarrow$ R, spontaneously with recovery probability c;
- R $\rightarrow$ S spontaneously, with probability $p_2 = 0$ (perfect immunization) or $p_2 > 0$ (partial immunization);

Monte Carlo algorithm similar to the one of CP: the only difference is the presece of the state R.

Infinite possible absoring phases: any combination of N_S and N_R [6].

We'll focus on simulation with perfect immunization in order to determine the exponents: τ, γ, $\nu_\perp$ and β.

Plot of one simulation

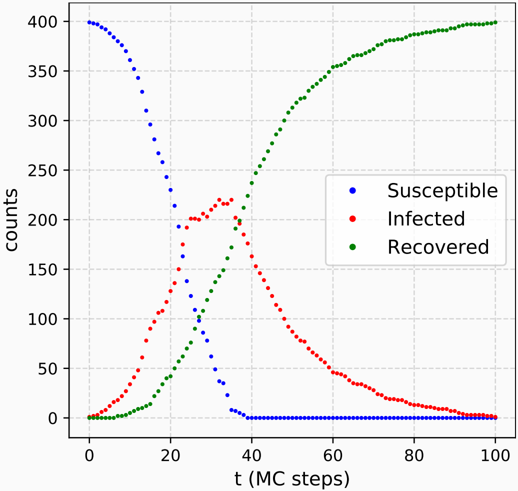

Figure 12: Single simulation of the system evolution (linear size $L = 20$) starting from one infected individual and all the other being susceptible ($c = 0.05$). In red we can distinguish the so called "peak" of infection.

SIR dynamics

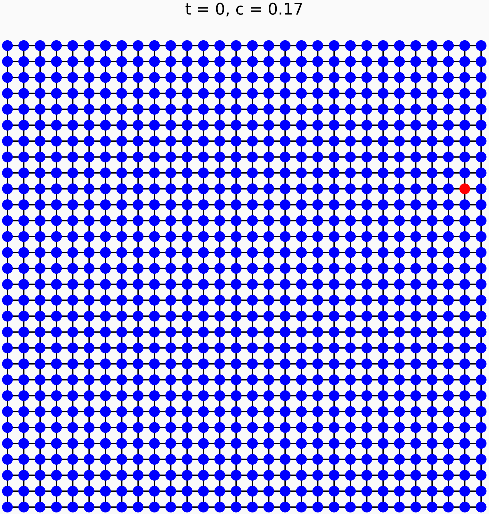

Figure 13: Animation of SIR model simulation with infected in red, susceptible in blue and recovred in grey.

Order parameter

The order parameter is given by the cluster size distribution of recovered sites. At criticality [2], [3]:

$$n_s \sim s^{-\tau}$$

where n_s is the number of cluster of size s. Thus, following [2], the probability of having a cluster of size greater than s obeys to:

$$P_{\geq s} \sim s^{2-\tau}$$

The exponent τ (**Fisher exponent**) is known exactly in 2-d [4]:
$\tau = 187/91 \simeq 2.055$

$P_{\geq s}$

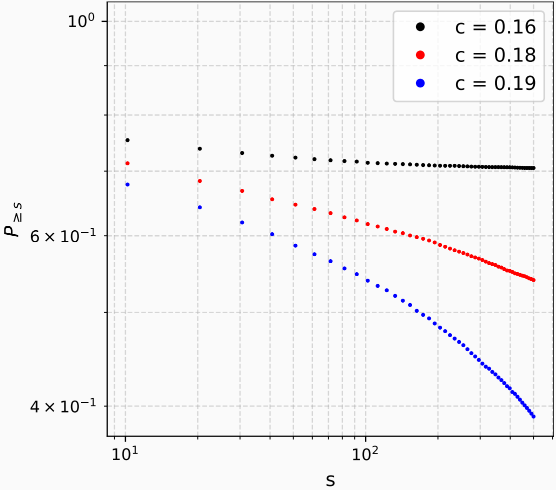

Figure 14: Plot of $P_{\geq s}$ for a lattice of linear size $L = 40$. Averages are done over 10^4 clusters. In this plot can be distinguished the subcritical and the supercritical regions.

Results for c_c and τ

For this computation we use $c_i = [0.17, 0.1725, 0.175, 0.1775, 0.8]$.

L	20
c_c	0.175
τ	~ 2.053
R^2	~ 0.9996

L	30
c_c	0.175
τ	~ 2.054
R^2	~ 0.9996

L	50
c_c	0.175
τ	~ 2.053
R^2	~ 0.9985

Table 5: Results for the critical point and τ exponent obtained with L = 20, 30, 50. The regression is performed on all the points of the average but the first. Computational time for L = 50: $\sim$ 5 min.

Restricted set of c_i

Now, one possibility could be to use a new set of c_i with bounds closer to 0.175:

- $c_i = [0.175, 0.1755, 0.176, 0.1765, 0.177]$.

With this new set we find:

L	20
c_c	0.1765
τ	~ 2.054
R^2	~ 0.9996

Table 6: Results for the critical point obtained with a restricted set of c_i with $L = 20$.

Plot of $P_{\geq s}$

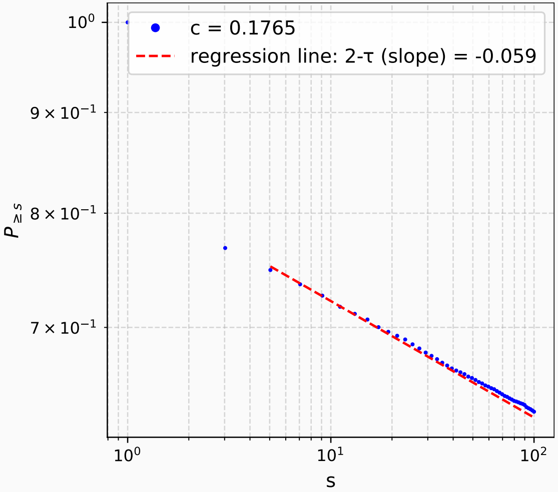

Figure 15: Plot of the order parameter at the critical point $c_c = 0.1765$ for a lattice of linear size $L = 20$. The slope is equal to $2 - \tau$. For the regression $R^2 = 0.9997$.

Other exponents (γ and $\nu_\perp$)

Estimation of $\gamma/\nu_\perp$ [4]:

- The stationary mean cluster size $S = \langle N_R \rangle$ can be exploited to estimate the ratio $\gamma/\nu_\perp$. At criticality []:

$$S \sim L^{\gamma/\nu_\perp},$$

Estimation of $\nu_\perp$ [4]:

- Plotting $SL^{\gamma/\nu_\perp}$ vs. $(c - c_c)L^{1/\nu_\perp}$ for different values of L, the $\nu_\perp$ exponent is the one for which all curves collapse.

In the following slides we're going to show the plots for the determination of $\gamma/\nu_\perp$ and for $\nu_\perp$ respectively.

$\gamma/\nu_\perp$

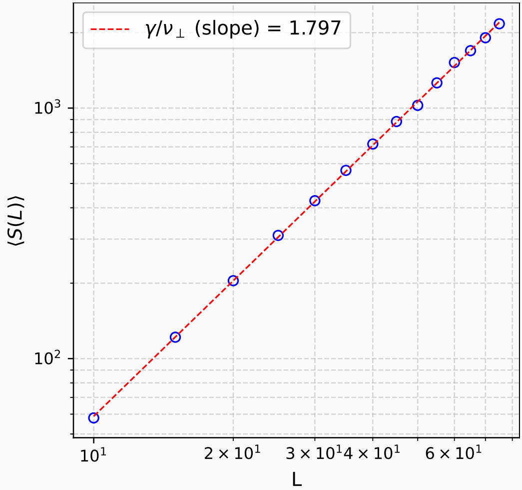

Figure 16: Plot of S vs. linear size. Averages are done over 10^3 trajectories and the critical point considered is $c_c = 0.1765$. For the regression $R^2 = 0.9997$.

$\nu_\perp = 0.7$

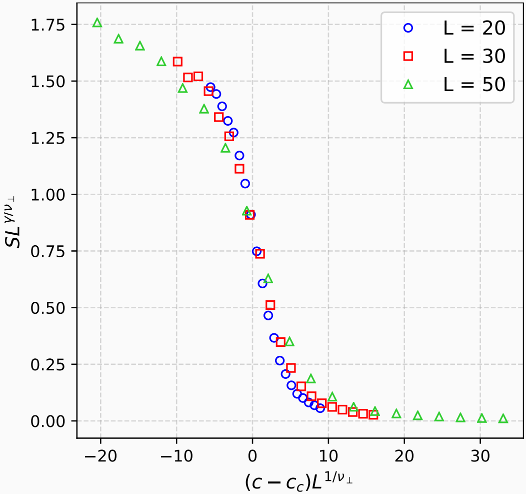

Figure 17: Data collapse with $\nu_\perp = 0.7$ for different lattice sizes. The critical point considered is $c_c = 0.1765$. Here it seems that the chosen $\nu_\perp$ is not the optimal one.

$\nu_\perp = 2$

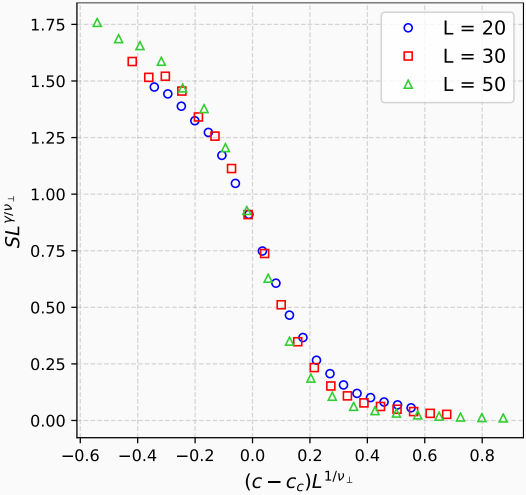

Figure 18: Data collapse with $\nu_\perp = 2$ for different lattice sizes. The critical point considered is $c_c = 0.1765$. Here, again, it seems that the chosen $\nu_\perp$ is not the optimal one.

$\nu_\perp = 1.33$

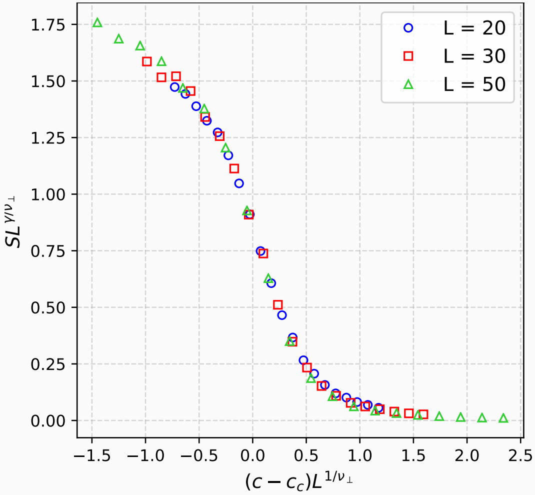

Figure 19: Data collapse with $\nu_\perp = 1.33$ for different lattice sizes. The critical point considered is $c_c = 0.1765$. From [4] $\nu_\perp = 1.333$. Here all curved collapsed.

Other exponents (β)

Finally, having determined γ and $\nu_\perp$, we can exploit the following scaling relation [4] at c_c in order to find β:

$$M \sim L^{(\beta+2\gamma)/\nu_\perp},$$

where $M = \langle N_R^2 \rangle$.

$(\beta + 2\gamma)/\nu_\perp$

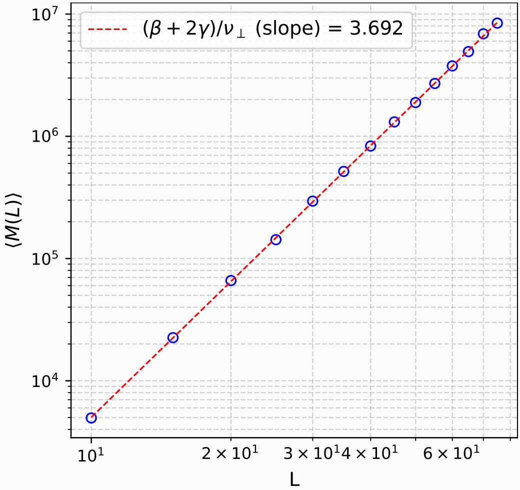

Figure 20: Plot of M vs. L. Averages are done over 10^3 different realizations and the critical point considered is $c_c = 0.1765$. For the regression $R^2 = 0.9999$.

Summary (SIR)

Exponent	Estimated	Value (DyP)
τ	~ 2.054	$187/91 \simeq 2.055$
$\nu_\perp$	~ 1.33	$4/3 \simeq 1.333$
γ	~ 2.39	$43/18 \simeq 2.388$
β	~ 0.131	$5/36 \simeq 0.1389$

Table 7: Summary of critical exponents (DyP [4], [5]) obtained with the SIR model.

SIRS ($p_2 > 0$)

We introduce the possibility of re-becoming susceptible after being recovered R $\rightarrow$ S [6].

- For $p_2 > 0$ but small enough, the SIRS is still in the DyP.
- Otherwise, the model belongs again to DP.

Different Monte Carlo algorithm: simulation are much more computational demanding.

As suggested in [5], since here we have the possibility of R $\rightarrow$ S, one possible analysis could exploit the statistics followed by the number of infected:

$$\langle n(t) \rangle \sim t^{\eta}, \qquad P(t) \sim t^{-\delta}.$$

Critical point of SIR (more rigorous method)

In this work we provided just a very rough estimation of the critical point. Following [2], here we explain the idea for a much more rigorous method:

- Plot $s^{\tau-2}P_{\geq s}$ against s^{σ} for different c_i close to a reasonable critical value.
- Do a linear regression of the plots for large s.
- Put the slopes found in a new plot and do a new linear regression in order to find the intercept with the x-axis.

Conclusion

Summary

- In this work we provide results of Monte Carlo simulations for the SIS and the SIR models.
- We exploit several scaling behaviours in order to find the critical point and some critical exponents for both models.
  - Critical exponents of SIS $\rightarrow$ Directed Percolation.
  - Critical exponents of SIR $\rightarrow$ Dynamical Percolation.
- Due to computational requirement, we just show a quick and rough estimation for the critical points.
- The critical exponents found are in agreement with the ones present in the scientific literature.

Source code

The code for the simulations is written in `Python` and it involves **Numba** in order to speed-up computations.

[1] H. Hinrichsen, "Non-equilibrium critical phenomena and phase transitions into absorbing states," *Advances in Physics*, vol. 49, no. 7, pp. 815–958, 2000. DOI: 10.1080/00018730050198152. eprint: https://doi.org/10.1080/00018730050198152. [Online]. Available: https://doi.org/10.1080/00018730050198152.

[2] T. Tomé and R. M. Ziff, "Critical behavior of the susceptible-infected-recovered model on a square lattice," *Physical Review E*, vol. 82, no. 5, 2010, ISSN: 1550-2376. DOI: 10.1103/physreve.82.051921. [Online]. Available: http://dx.doi.org/10.1103/PhysRevE.82.051921.

[3] G. Santos, T. Alves, G. Alves, A. Macedo-Filho, and R. Ferreira, "Epidemic outbreaks on two-dimensional quasiperiodic lattices," *Physics Letters A*, vol. 384, no. 2, p. 126 063, 2020, ISSN: 0375-9601. DOI: https://doi.org/10.1016/j.physleta.2019.126063. [Online]. Available: https://www.sciencedirect.com/science/article/pii/S0375960119309533.

[4] D. R. de Souza, T. Tomé, and R. M. Ziff, "A new scale-invariant ratio and finite-size scaling for the stochastic susceptible–infected–recovered model," *Journal of Statistical Mechanics: Theory and Experiment*, vol. 2011, no. 03, P03006, 2011, ISSN: 1742-5468. DOI: 10.1088/1742-5468/2011/03/p03006. [Online]. Available: http://dx.doi.org/10.1088/1742-5468/2011/03/P03006.

[5] D. R. de Souza and T. Tomé, “Stochastic lattice gas model describing the dynamics of the sirs epidemic process,” *Physica A: Statistical Mechanics and its Applications*, vol. 389, no. 5, pp. 1142–1150, 2010, ISSN: 0378-4371. DOI: https://doi.org/10.1016/j.physa.2009.10.039. [Online]. Available: https://www.sciencedirect.com/science/article/pii/S0378437109009091.

[6] R. Livi and P. Politi, *Nonequilibrium Statistical Physics: A Modern Perspective*. Cambridge University Press, 2017. DOI: 10.1017/9781107278974.