

Compartment epidemic model with retarded transition rates

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Outline :

Four compartment model of epidemic spreading via random walkers on a 2D lattice. Infected walkers infect susceptible walkers. Constant population, no mortality.

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Part I: Compartment epidemic model with retarded transition rates

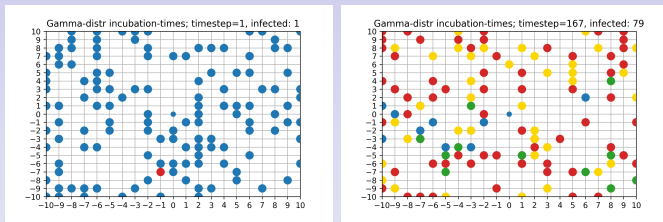


Figure: Colors of indicate health status **S** **C** **I** **R** of the walkers. Left: One infected walker at $t = 0$. Right: State of epidemic spreading $t > 0$.

- $Z \gg 1$ random walkers navigate independently on a $N \times N$ square-lattice, jumping with probability $1/4$ to any of four neighbor lattice points
- Each walker is in one of the states ('compartments')

S : susceptible (for infection)

C : incubated, infected but not infectious

I : infected and infectious

R : recovered and immune

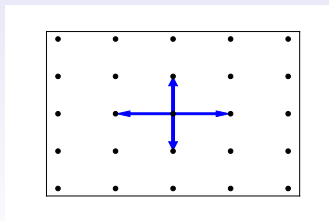
Simple random walk

Z walkers navigate *independently* on a periodic 2D lattice.
Position of walker j ($j = 1, \dots, Z$)

$$\begin{aligned}x_j(t) &= x_j(t-1) + \eta_x^{(j)}(t) \\y_j(t) &= y_j(t-1) + \eta_y^{(j)}(t)\end{aligned}, \quad t = 1, 2, \dots \quad (1)$$

random steps

$(\eta_x^{(j)}(t), \eta_y^{(j)}(t)) = (1, 0); (-1, 0); (0, 1); (0, -1)$ with probability $\frac{1}{4}$.



Microscopic model for Brownian motion (Feller1968).

Infection rule :

If **S** meets **I** , i.e. in a collision of an **I** with an **S** walker

the **S** walker gets infected with probability P_{inf}

performing the delayed transition pathway

S → **C** → **I** → **R** → **S**

with random sojourn times t_C, t_I, t_R in the compartments

drawn from probability density functions

$$\mathbb{P}(t_{C,I,R} \in [\tau, \tau + d\tau]) = K_{C,I,R}(\tau)d\tau$$

Population fractions

$$s = Z_S(t)/Z, c = Z_C(t)/Z, j = Z_I(t)/Z, r = Z_R(t)/Z$$

constant population $s(t) + c(t) + j(t) + r(t) = 1$

Macroscopic $S \rightarrow C \rightarrow I \rightarrow R \rightarrow S$ evolution equations:

$$\frac{d}{dt}s(t) = -\mathcal{A}(t) + \langle \mathcal{A}(t - t_C - t_I - t_R) \rangle$$

$$\frac{d}{dt}c(t) = \mathcal{A}(t) - \langle \mathcal{A}(t - t_C) \rangle$$

$$\frac{d}{dt}j(t) = \langle \mathcal{A}(t - t_C) \rangle - \langle \mathcal{A}(t - t_C - t_I) \rangle$$

$$\frac{d}{dt}r(t) = \langle \mathcal{A}(t - t_C - t_I) \rangle - \langle \mathcal{A}(t - t_C - t_I - t_R) \rangle.$$

$$t \geq 0$$

$\mathcal{A}(t)$ infection rate = collision rate \times probability of infection in a collision S and I (contains microscopic information on the type of random walk).

$t = 0$ begin of observation, $\mathcal{A}(t)$ causal

Averaging over random variable $t_{C,I,R}$:

$$\begin{aligned}\langle f(t_{C,I,R}) \rangle &= \int_0^\infty f(\tau) \mathbb{P}[t_{C,I,R} \in [\tau, \tau + d\tau]] \\ &= \int_0^\infty f(\tau) K_{C,I,R}(\tau) d\tau\end{aligned}$$

Average of retarded causal infection rate

$$\begin{aligned}\langle \mathcal{A}(t - t_{C,I,R}) \rangle &= \int_0^\infty \mathcal{A}(t - \tau) K_{C,I,R}(\tau) d\tau \\ \int_0^t \mathcal{A}(t - \tau) K_{C,I,R}(\tau) d\tau &= (K_{C,I,R} \star \mathcal{A})(t)\end{aligned}$$

Averages of causal randomly retarded infection rate

$t_{C,I,R}$ mutually independent random variables

$$\langle \delta(t - t_{C,I,R}) \rangle = K_{C,I,R}(t)$$

$$\langle \Theta(t - t_{C,I,R}) \rangle = \int_0^t K_{C,I,R}(\tau) d\tau$$

$$\langle \mathcal{A}(t - t_C - t_I) \rangle (K_C \star K_I \star \mathcal{A})(t)$$

$$\langle \mathcal{A}(t - t_C - t_I - t_R) \rangle (K_C \star K_I \star K_R \star \mathcal{A})(t)$$

Laplace-transform

$$\hat{K}_{C,I,R}(\lambda) = \langle e^{-\lambda t_{C,I,R}} \rangle = \int_0^\infty e^{-\tau\lambda} K_{C,I,R}(\tau) d\tau$$

$$\langle e^{-\lambda(t_C + t_I + t_R)} \rangle = \hat{K}_C(\lambda) \hat{K}_I(\lambda) \hat{K}_R(\lambda)$$

→ Evolution equations $s(t) + c(t) + j(t) + r(t) = 1$ (constant population without deaths) for arbitrary waiting time distributions

$$\frac{d}{dt}s(t) = -\mathcal{A}(t) + (\mathcal{A} \star K_C \star K_I \star K_R)(t)$$

$$\frac{d}{dt}c(t) = \mathcal{A}(t) - (\mathcal{A} \star K_C)(t)$$

$$\frac{d}{dt}j(t) = (\mathcal{A} \star K_C)(t) - (\mathcal{A} \star K_C \star K_I)(t)$$

$$\frac{d}{dt}r(t) = (\mathcal{A} \star K_C \star K_I)(t) - (\mathcal{A} \star K_C \star K_I \star K_R)(t)$$

$\mathcal{A}(t)$ infection rate, **assumption**: $\mathcal{A}(t) = \beta j(t)s(t)$ simplest form of **nonlinear** function of $j(t)$ and $s(t)$ describing probability of collision of I and S walkers.

SCIRS Eqs in Laplace domain with initial conditions $s(0) = 1 - j_0$, $c(0) = 0$, $j(0) = j_0$, $r(0) = 0$

$$\hat{s}(\lambda) = \frac{1 - j_0}{\lambda} - \hat{A}(\lambda) \frac{[1 - \hat{K}_C(\lambda)\hat{K}_I(\lambda)\hat{K}_R(\lambda)]}{\lambda}$$

$$\hat{c}(\lambda) = \hat{A}(\lambda) \frac{(1 - \hat{K}_C(\lambda))}{\lambda}$$

$$\hat{j}(\lambda) = \frac{j_0}{\lambda} + \hat{A}(\lambda)\hat{K}_C(\lambda) \frac{(1 - \hat{K}_I(\lambda))}{\lambda}$$

$$\hat{r}(\lambda) = \hat{A}(\lambda)\hat{K}_C(\lambda)\hat{K}_I(\lambda) \frac{(1 - \hat{K}_R(\lambda))}{\lambda}$$

Endemic equilibrium: $f(\infty) = \lim_{\lambda \rightarrow 0} \lambda \hat{f}(\lambda)$

with $\hat{A}(\lambda) \sim \frac{\beta J_e S_e}{\lambda}$, ($\lambda \rightarrow 0$)

For $\langle t_{C,I,R} \rangle < \infty$ we get for the endemic equilibrium

$$\begin{aligned}
 S_e(J_e) &= \frac{1 - j_0}{1 + \beta \langle T \rangle J_e} \\
 C_e(J_e) &= \frac{(1 - j_0) \beta \langle t_C \rangle J_e}{1 + \beta \langle T \rangle J_e} \\
 J_e &= j_0 + \beta \langle t_I \rangle J_e \frac{1 - j_0}{1 + \beta \langle T \rangle J_e} \\
 R_e(J_e) &= \frac{(1 - j_0) \beta \langle t_R \rangle J_e}{1 + \beta \langle T \rangle J_e}.
 \end{aligned} \tag{2}$$

The third relation in (2) is an implicit equation for J_e

$$J_e^2 - 2aJ_e - b = 0 \tag{3}$$

Only roots $J_e \in [0, 1]$ correspond to an endemic equilibrium.

Endemic equilibrium for waiting times with existing mean

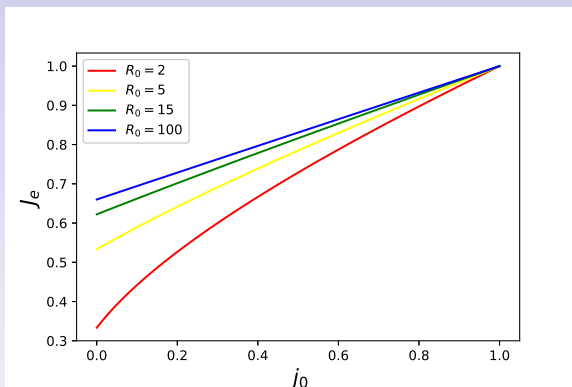


Figure: Endemic value $J_e(j_0, R_0)$ vs j_0 for different values of $R_0\beta\langle t_I \rangle > 1$ where in all curves $\langle t_C \rangle = \langle t_R \rangle = 5$, $\langle t_I \rangle = 20$.

Monotonic increase of J_e with j_0 and R_0 especially $J_e(j_0 = 1, R_0) = 1$ is a stable endemic equilibrium point.

For globally healthy state $j_0 = 0$ and $s_0 = 1$ initial condition the endemic equilibrium yields

$$S_e = \frac{1}{R_0}$$

$$C_e = \frac{R_0 - 1}{R_0} \frac{\langle t_C \rangle}{\langle T \rangle}$$

$$J_e = \frac{R_0 - 1}{R_0} \frac{\langle t_I \rangle}{\langle T \rangle}$$

$$R_e = \frac{R_0 - 1}{R_0} \frac{\langle t_R \rangle}{\langle T \rangle}$$

$$\langle T \rangle = \langle t_C + t_I + t_R \rangle, \quad R_0 = \beta \langle t_I \rangle$$

and exists solely for $R_0 > 1$ depending only from R_0 and the mean waiting times $\langle t_{C,I,R} \rangle$.

Epidemic spreading requires:

(i) Unstable globally healthy state (unstable fixpoint)

(ii) stable endemic equilibrium (stable focus) → Stability analysis:

$$s(t) = S_e + ue^{\mu t}, \quad c(t) = C_e + ve^{\mu t},$$

$$j(t) = J_e + we^{\mu t}, \quad r(t) = R_e + xe^{\mu t}$$

u, v, w, x 'small' time independent constants.

Instability of globally healthy state

Solvability condition

$$\tilde{\mu} = R_0 e^{-\tilde{\mu} t_1} [1 - e^{-\tilde{\mu}}]$$

If there is an $\Re \mu > 0$ then healthy state is unstable.

This is the case for $R_0 > 1$ which is the condition that a SCIRS epidemics starts to spread.

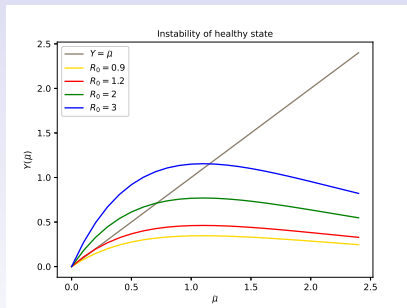


Figure: We depict $g(\tilde{\mu}, R_0) = R_0 e^{-\tilde{\mu} t_1} (1 - e^{-\tilde{\mu}})$ for different values of R_0 . For $R_0 = 0.9$ (lower curve) the healthy state is stable. In the other curves $R_0 > 1$ the healthy state is unstable. In all plots we chose $t_1 = t_c/t_i = 0.5$.

Interpretation of $R_0 = \beta \langle t_I \rangle$ as basic reproduction number:

Average number of new infections caused by the first infected walker during his illness period $\langle t_I \rangle$.

Heuristic deduction:

Consider initial condition $j_0 = \frac{1}{Z}$ and $s_0 = 1 - j_0$ of one infected individual $Z_I(0) = j_0 Z = 1$ in a healthy, i.e. susceptible population $Z_S(0) = s_0 Z = Z - 1$ the the rate of new infections caused by the first infected walker is

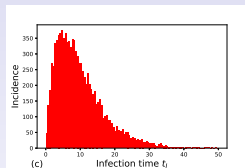
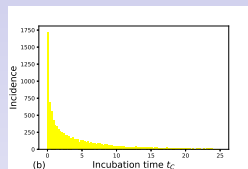
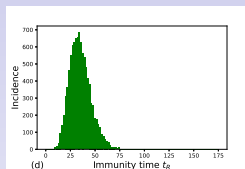
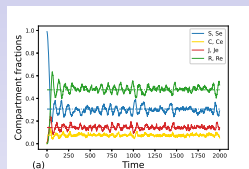
$$\left. \frac{dZ_c(t)}{dt} \right|_{t=0} = Z \beta s(t) j(t) \Big|_{t=0} = \frac{\beta}{Z} Z_S(t) Z_I(t) \Big|_{t=0} = \beta \frac{Z-1}{Z} \rightarrow \beta,$$

which is the number of new infections per time unit at $t = 0$.

During the average time $\langle t_I \rangle$ of his disease, this walker causes

$$R_0 \approx \left. \frac{dZ_c(t)}{dt} \right|_{t=0} \langle t_I \rangle = \beta \langle t_I \rangle \text{ new infections.}$$

Implementation of SCIRS random walkers – (PYTHON) simulations

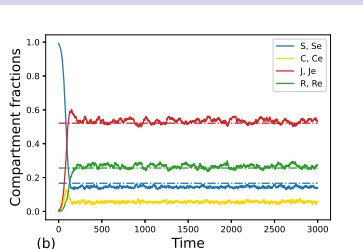
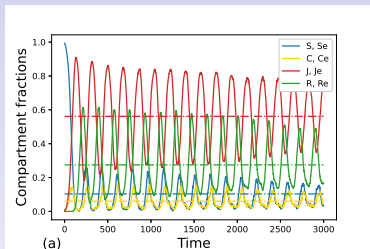


Average population fractions over 10 random walk realizations with $Z = 100$, $N = 11$ (density $Z/N^2 \approx 0.83$), $P_{inf} = 0.9$ and Gamma distributed waiting times having the means $\langle t_C \rangle = 5$, $\langle t_I \rangle = 10$, $\langle t_R \rangle = 35$, $\xi_C = 0.1$, $\xi_I = 0.2$, $\xi_R = 0.3$.

Animation 1

Implementation of SCIRS random walkers – (PYTHON) simulations

Compartment fractions averaged over 10 random walk realizations



(a) δ -distributed, (b) exponentially distributed waiting times
with $Z = 150$, $N = 21$ (density $Z/N^2 \approx 0.34$), $P_{inf} = 0.9$, mean incubation time $\langle t_C \rangle = 10$, $\langle t_I \rangle = 100$, $\langle t_R \rangle = 50$.

Endemic states (dashed lines) for (a) δ -distributed waiting times: $S_e \approx 0.10$ ($R_0 \approx 9.68$), $C_e \approx 0.06$, $J_e \approx 0.56$, $R_e \approx 0.27$, and $r_C \approx 0.07$, $r_I \approx 1.00$, $r_R = 0.98$.

Endemic states (dashed lines) for (b) exponential waiting times: $S_e \approx 0.16$ ($R_0 \approx 6.01$), $C_e \approx 0.06$, $J_e \approx 0.52$, $R_e \approx 0.26$ and $r_C \approx 1.07$, $r_I \approx 1.00$, $r_R \approx 0.98$

In all simulations excellent agreement of S_e , C_e , J_e , R_e with Eqs. (12)!

Animation 2

Animations of SCIRS epidemic evolution

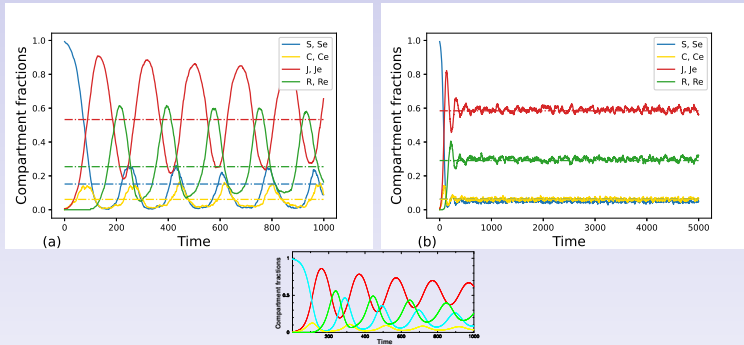


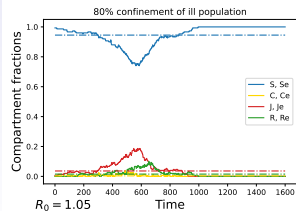
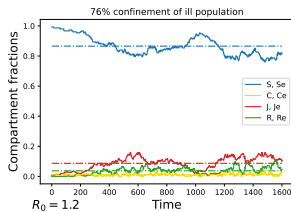
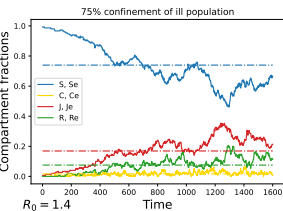
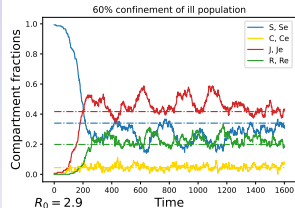
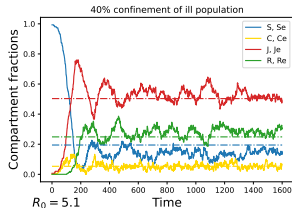
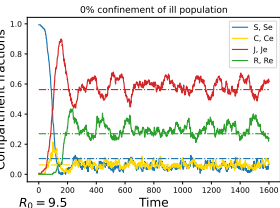
Figure: (a) δ -distributed waiting times with Hopf unstable oscillatory behavior
(b): All waiting times are Gamma distributed where means are identical with those of (a).
(c) Numerical solution of the macroscopic SCIRS Eqs. with same parameters as in (a).

Animation 3

Good agreement with the averaged microscopic behavior.

Effect of confinement measures

Confinement of a fraction of I walkers during 90% of their illness time ($t_{conf} = 0.9t_I$)



References:

- [1] W.O. Kermack, A.G. McKendrick, A contribution to the mathematical theory of epidemics, Proc. Roy. Soc. A 115, 700–721 (1927)
- [2] M. Bestehorn, T. M Michelitsch, B. A. Collet, A. P. Riascos, A. F. Nowakowski, Phys. Rev. E, 105, 024205, (2022).
- [3] T. Granger, T.M. Michelitsch, M. Bestehorn, A. P. Riascos, B. A. Collet, Four-compartment epidemic model with retarded transition rates, Phys. Rev. E 107, 044207 (2023).

- For animated simulations, further details and download of these slides consult:



<https://sites.google.com/view/scirs-model-supplementaries/accueil>

Thank you very much!