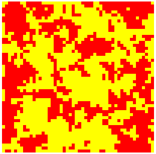
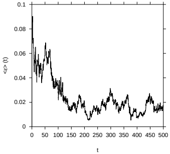
Evolution of n-species Kimura/Voter Model towards Criticality, a surrogate for General Models in a system of accidental pathogens





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Theory of accidental pathogens

infection with pathogens in different strains:

harmless infected with resident strain I

infected with mutant strain Y

mutant can cause disease case X accidentally

with transition probability ε

Y strain has disadvantage against I strain due to the accident

$\Longrightarrow$ for $\varepsilon \longrightarrow 0$ criticality

$\Longrightarrow$ evolution towards small ε

specific example: meningococcal disease (bacterial meningitis and septicaemia)

Kimura/Voter Model

consider two phenotypes Y and I, each dieing and leaving space, then space taken by neighbour offspring

$$I_i + Y_j \xrightarrow{v} Y_i + Y_j$$

$$Y_i + I_j \xrightarrow{\iota} I_i + I_j$$

at lattice site $i \in \{1, ..., N\}$ an type $Y_i = 1$, or not $Y_i = 0$, hence $I_i := 1 - Y_i = 1$,

Spatially extended Version!

Stochastic dynamics given for variables $Y_i \in \{0, 1\}$ for $i \in \{1, ..., N\}$

with the constraint that an individual belongs to one of the two classes I or Y meaning: $I_i + Y_i = 1$

the Master Equation for the probability $p(Y_1, Y_2, ..., Y_N; t)$ for the spatial system for N individuals

$$\frac{d}{dt} \quad p \quad (Y_1, Y_2, \ldots, Y_N, t)$$

$$= \sum_{i=1}^{N} \upsilon \left(\sum_{j=1}^{N} J_{ij} Y_j \right) Y_i \;\; p(Y_1, \ldots, 1 - Y_i, \ldots, Y_N, t)$$

$$+ \sum_{i=1}^{N} \iota \left(\sum_{j=1}^{N} J_{ij} (1 - Y_j) \right) (1 - Y_i) \;\; p(Y_1, \ldots, 1 - Y_i, \ldots, Y_N, t)$$

$$- \sum_{i=1}^{N} \left[\upsilon \left(\sum_{j=1}^{N} J_{ij} Y_j \right) (1 - Y_i) + \iota \left(\sum_{j=1}^{N} J_{ij} (1 - Y_j) \right) Y_i \right] \cdot p(Y_1, \ldots, Y_i, \ldots, Y_N, t)$$

Adjacency matrix $J_{ij} \in \{0, 1\}$ contains 0 for no contribution and 1 for a connection between sites i and j.The Term $\sum_{j=1}^{N} J_{ij} Y_j$ is the Infection-Force (Replacement-Force) of the neighbouring sites imposed on a site i.

Dynamics of Global Mean Value and Mean Field Approximation

global mean value dynamics contains pairs

$$\frac{d}{dt}\langle Y\rangle = (\upsilon - \iota)\left(Q\langle Y\rangle - \langle YY\rangle_1\right)$$

mean field approximation gives from pairs

$$\langle \mathbf{YY} \rangle_1 \approx \frac{\mathbf{Q}}{\mathbf{N}} \cdot \langle \mathbf{Y} \rangle^2$$

giving in the dynamics of the mean a closed ODE

$$\frac{d}{dt} \langle Y \rangle \;=\; (\upsilon - \iota)\frac{Q}{N} \langle Y \rangle \left(N - \langle Y \rangle \right)$$

"neutral" for symmetry between Y and I, i.e. $\upsilon = \iota$

Toy model for Evolution or Kimura Model

including mutations

$$\begin{aligned} I_i &\xrightarrow{\nu} Y_i \\ Y_i &\xrightarrow{\mu} I_i \end{aligned}$$

giving in mean field approximation

$$\frac{d}{dt}\langle Y\rangle = (\upsilon-\iota)\frac{Q}{N}\langle Y\rangle\left(N-\langle Y\rangle\right)+(\nu-\mu)\langle Y\rangle$$

**"neutral" for symmetry between Y and I,
i.e. $\upsilon=\iota$ and $\nu=\mu$**

Transition rates for classical SIR model

for one strain only

Transition rates for classical SIR model for one strain only

The SIR model was introduced by W.O. Kermack and A.G. McKendrick in 1927.

In this model a population is divided into three classes:

The susceptibles S: Those who are not infected and not immune.

The infectives I: Those who are infected and can transmit the disease.

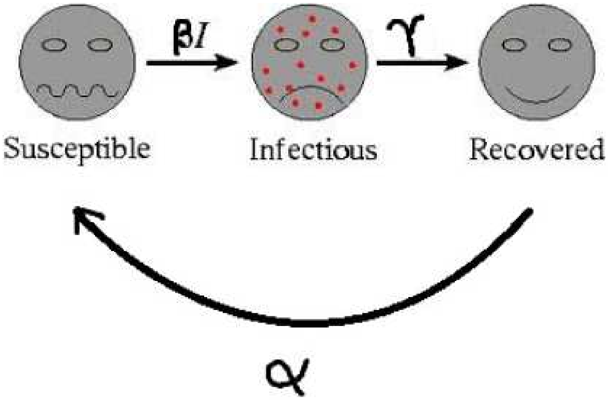
The recovered R: Those who have been infected and are immune (recovered or dead).

In simple models we assume:

Ignore natural births and deaths during epidemics

No Subdivisions of the population by age, sex, mobility, ...

constraint $\mathbf{N = S + I + R = const.}$


βI
γ
Susceptible
Infectious
Recovered
α

Transition rates for classical SIR model

for one strain only

$$R \xrightarrow{\alpha} S$$

$$S + I \xrightarrow{\beta} I + I$$

$$I \xrightarrow{\gamma} R$$

Transition rates for classical SIR model

with mutations into other strain Y

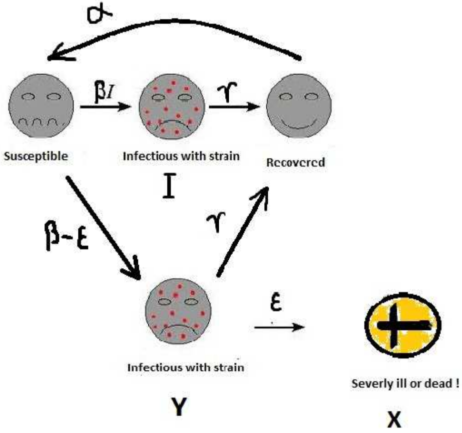
$$
\begin{array}{rcl}
\mathbf{R} & \xrightarrow{\alpha} & \mathbf{S} \\
\mathbf{S}+\mathbf{I} & \xrightarrow{\beta-\mu} & \mathbf{I}+\mathbf{I} \\
 & \xrightarrow{\mu} & \mathbf{Y}+\mathbf{I} \\
\mathbf{I} & \xrightarrow{\gamma} & \mathbf{R}
\end{array}
$$

Transition rates for classical SIR model

... and Y dynamics ...

$$
\begin{array}{rcl}
R & \xrightarrow{\alpha} & S \\
S+I & \xrightarrow{\beta-\mu} & I+I \\
 & \xrightarrow{\mu} & Y+I \\
I & \xrightarrow{\gamma} & R \\
S+Y & \xrightarrow{\beta-\nu} & Y+Y \\
 & \xrightarrow{\nu} & I+Y \\
 & & \\
Y & \xrightarrow{\gamma} & R
\end{array}
$$

Transition rates for the SIRYX model including pathogenicity ε



Transition rates for the SIRYX model

including pathogenicity ε

$$
\begin{array}{rcl}
R & \xrightarrow{\alpha} & S \\
S + I & \xrightarrow{\beta - \mu} & I + I \\
 & \xrightarrow{\mu} & Y + I \\
I & \xrightarrow{\gamma} & R \\
S + Y & \xrightarrow{\beta - \nu - \varepsilon} & Y + Y \\
 & \xrightarrow{\nu} & I + Y \\
 & \xrightarrow{\varepsilon} & X + Y \\
Y & \xrightarrow{\gamma} & R \\
X & \xrightarrow{\varphi} & S
\end{array}
$$

Epidemic model

Master equation

$$\frac{dp(\underline{n})}{dt} = \sum_{\underline{\tilde{n}} \neq \underline{n}} w_{\underline{n},\underline{\tilde{n}}} \; p(\underline{\tilde{n}}) - \sum_{\underline{\tilde{n}} \neq \underline{n}} w_{\underline{\tilde{n}},\underline{n}} \; p(\underline{n}) \quad .$$

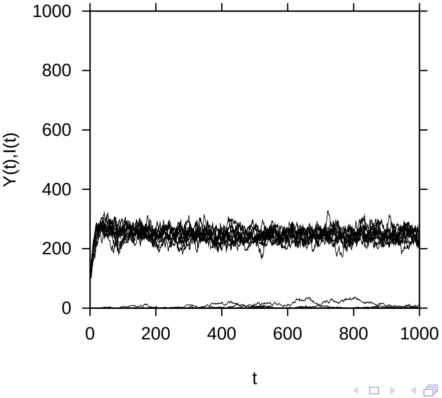
with transition rates $w_{\underline{n},\underline{\tilde{n}}}$ defined by the transitions between host classes S, I, R, Y and X :

Transition rates of the SIRYX model explicitly

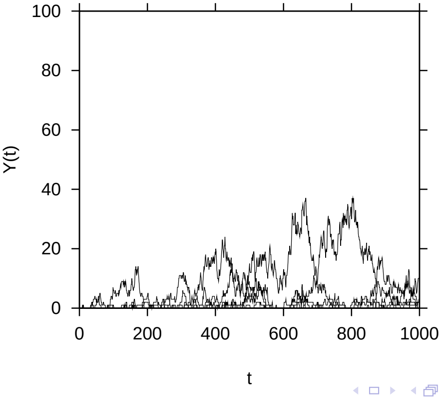
$$
\begin{array}{rcl c rcl}
w_{(R-1,S+1),(R,S)} & = & \alpha \cdot R & , & R & \xrightarrow{\alpha} & S \\
w_{(S-1,I+1),(S,I)} & = & (\beta-\mu) \cdot \frac{I}{N}\, S & , & S+I & \xrightarrow{\beta-\mu} & I+I \\
w_{(S-1,Y+1),(S,Y)} & = & \mu \cdot \frac{I}{N}\, S & , & & \xrightarrow{\mu} & Y+I \\
w_{(I-1,R+1),(I,R)} & = & \gamma \cdot I & , & I & \xrightarrow{\gamma} & R \\
w_{(S-1,Y+1),(S,Y)} & = & (\beta-\nu-\varepsilon) \cdot \frac{Y}{N}\, S & , & S+Y & \xrightarrow{\beta-\nu--\varepsilon} & Y+Y \\
w_{(S-1,I+1),(S,I)} & = & \nu \cdot \frac{Y}{N}\, S & , & & \xrightarrow{\nu} & I+Y \\
w_{(S-1,X+1),(S,X)} & = & \varepsilon \cdot \frac{Y}{N}\, S & , & & \xrightarrow{\varepsilon} & X+Y \\
w_{(Y-1,R+1),(Y,R)} & = & \gamma \cdot Y & , & Y & \xrightarrow{\gamma} & R \\
w_{(X-1,S+1),(X,S)} & = & \varphi \cdot X & , & X & \xrightarrow{\varphi} & S
\end{array}
$$

SIRYX model:

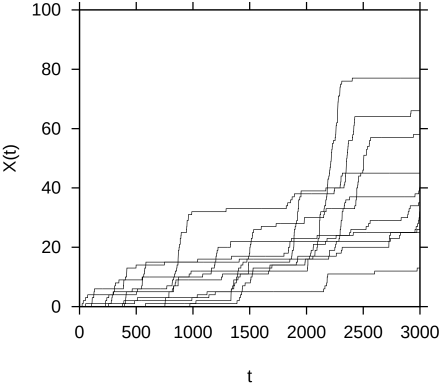
Simulation of epidemics in time



SIRYX model: Simulation of epidemics in time

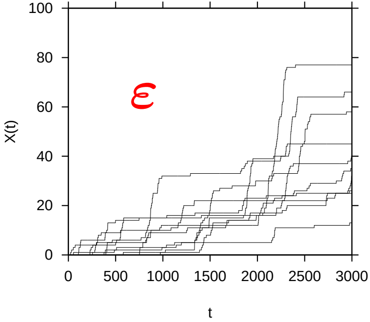


SIRYX model: Simulation of epidemics in time



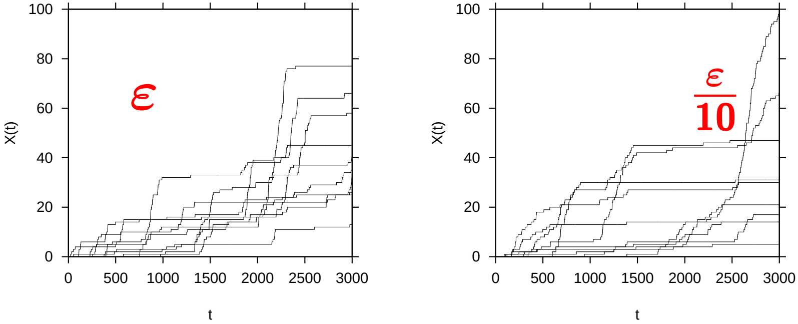
cumulative disease cases

SIRYX model:

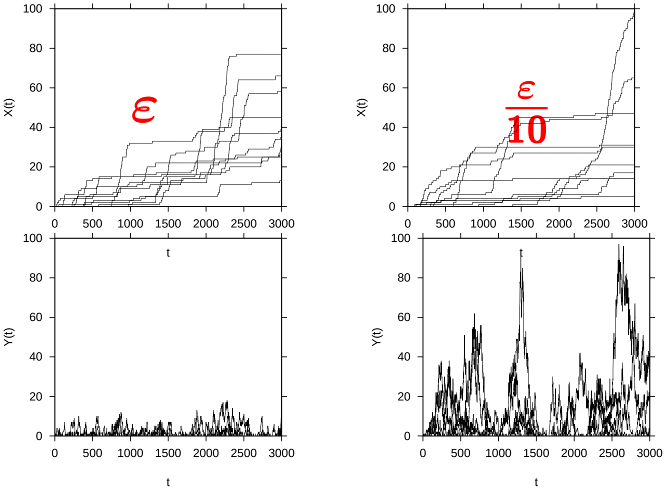


$$\frac{\varepsilon}{10}$$

SIRYX model:


100
80
60
40
20
0
X(t)
0
500
1000
1500
2000
2500
3000
t
ε
$\frac{\varepsilon}{10}$

SIRYX model:


ε
$\frac{\varepsilon}{10}$
X(t)
Y(t)
t
0
20
40
60
80
100
0
500
1000
1500
2000
2500
3000

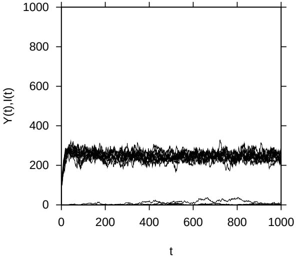
Transition rates of the SIRYX model explicitly

$$\begin{array}{rclcrcl}
w_{(R-1,S+1),(R,S)} & = & \alpha \cdot R & , & R & \xrightarrow{\alpha} & S \\
w_{(S-1,I+1),(S,I)} & = & (\beta-\mu)\cdot \frac{I}{N}\, S & , & S+I & \xrightarrow{\beta-\mu} & I+I \\
w_{(S-1,Y+1),(S,Y)} & = & \mu \cdot \frac{I}{N}\, S & , & & \xrightarrow{\mu} & Y+I \\
w_{(I-1,R+1),(I,R)} & = & \gamma \cdot I & , & I & \xrightarrow{\gamma} & R \\
w_{(S-1,Y+1),(S,Y)} & = & (\beta-\nu-\varepsilon)\cdot \frac{Y}{N}\, S & , & S+Y & \xrightarrow{\beta-\nu-\varepsilon} & Y+Y \\
w_{(S-1,I+1),(S,I)} & = & \nu \cdot \frac{Y}{N}\, S & , & & \xrightarrow{\nu} & I+Y \\
w_{(S-1,X+1),(S,X)} & = & \varepsilon \cdot \frac{Y}{N}\, S & , & & \xrightarrow{\varepsilon} & X+Y \\
w_{(Y-1,R+1),(Y,R)} & = & \gamma \cdot Y & , & Y & \xrightarrow{\gamma} & R \\
w_{(X-1,S+1),(X,S)} & = & \varphi \cdot X & , & X & \xrightarrow{\varphi} & S
\end{array}$$

Transition rates of the SIRYX model

SIR-sub-system stationary

$$
\begin{array}{rclcrcl}
w_{(R-1,S+1),(R,S)} & = & \alpha \cdot R & , & R & \xrightarrow{\alpha} & S \\
w_{(S-1,I+1),(S,I)} & = & (\beta - \mu) \cdot \frac{I}{N}\, S & , & S + I & \xrightarrow{\beta-\mu} & I + I \\
w_{(S-1,Y+1),(S,Y)} & = & \mu \cdot \frac{I}{N}\, S & , & & \xrightarrow{\mu} & Y + I \\
w_{(I-1,R+1),(I,R)} & = & \gamma \cdot I & , & I & \xrightarrow{\gamma} & R \\
w_{(S-1,Y+1),(S,Y)} & = & (\beta - \nu - \varepsilon) \cdot \frac{Y}{N}\, S & , & S + Y & \xrightarrow{\beta-\nu-\varepsilon} & Y + Y \\
w_{(S-1,I+1),(S,I)} & = & \nu \cdot \frac{Y}{N}\, S & , & & \xrightarrow{\nu} & I + Y \\
w_{(S-1,X+1),(S,X)} & = & \varepsilon \cdot \frac{Y}{N}\, S & , & & \xrightarrow{\varepsilon} & X + Y \\
w_{(Y-1,R+1),(Y,R)} & = & \gamma \cdot Y & , & Y & \xrightarrow{\gamma} & R \\
w_{(X-1,S+1),(X,S)} & = & \varphi \cdot X & , & X & \xrightarrow{\varphi} & S
\end{array}
$$



stationary values of SIR-sub-system for harmless resident strain

$$S^* = N\frac{\gamma}{\beta} \quad , \qquad I^* = N\frac{\alpha}{\beta}\left(\frac{\beta-\gamma}{\alpha+\gamma}\right) \quad , \qquad R^* = N - S^* - I^*$$

master equation for YX-sub-system

stationary values of SIR-sub-system for harmless resident strain

$$\mathsf{S}^* = \mathsf{N}\frac{\gamma}{\beta} \quad , \qquad \mathsf{I}^* = \mathsf{N}\frac{\alpha}{\beta}\left(\frac{\beta-\gamma}{\alpha+\gamma}\right) \quad , \qquad \mathsf{R}^* = \mathsf{N}-\mathsf{S}^*-\mathsf{I}^*$$

gives transition rates approximated

$$\begin{array}{lcll}
w_{(S^*,Y+1),(S^*,Y)} & = & \mu\cdot\frac{S^*}{N}\,I^* & =: \quad c \\
w_{(S^*,Y+1),(S^*,Y)} & = & (\beta-\nu-\varepsilon)\cdot\frac{S^*}{N}\,Y & =: \quad b\cdot Y \\
w_{(S^*,X+1),(S^*,X)} & = & \varepsilon\cdot\frac{S^*}{N}\,Y & =: \quad g\cdot Y \\
w_{(Y-1,R^*),(Y,R^*)} & = & \gamma\cdot Y & =: \quad a\cdot Y \\
w_{(X-1,S^*),(X,S^*)} & = & \varphi\cdot X \quad . &
\end{array}$$

master equation for YX-sub-system

$$\begin{aligned}\frac{d}{dt}p(Y,X,t) \;&=\; (b\cdot(Y-1)+c)\;p(Y-1,X,t)\;+\\ &+a\cdot(Y+1)\;p(Y+1,X,t)\;+\\ &+g\cdot Y\;p(Y,X-1,t)\;-\\ &-(bY+aY+gY+c)\;p(Y,X,t)\end{aligned}$$

hence

$$p(X) = \frac{\tilde{g}^X \cdot \tilde{a}}{\Gamma(X+1)} \sum_{\mu=0}^{\infty} \frac{\Gamma(X+1+2\mu)}{\Gamma(\mu+2)} \cdot \frac{(\tilde{a}\ \tilde{b})^\mu}{\mu!}$$

and with Gauss hypergeometric function

$$_2F_1(u, v; w; x) := \sum_{\nu=0}^{\infty} \frac{(u)_\nu \cdot (v)_\nu}{(w)_\nu} \cdot \frac{x^\nu}{\nu!}$$

with $\eta := \frac{\varepsilon}{\beta} \sim \varepsilon$ **resulting in**

$$p_\eta(X) = \eta^X \cdot 2^{-(X+1)} \cdot \quad {}_2F_1\left(\frac{X+1}{2}, \frac{X+2}{2}; 2; 1-\eta\right)$$

gives conditioned on at least one case

$p_\eta(X|X \geq 1) = \frac{p_\eta(X)}{1-p_\eta(X=0)}$ (using Bayes' rule)

$$\begin{aligned} p_\eta(X|X \geq 1) &= (1+\sqrt{\eta}) \cdot 2^{-(X+1)} \cdot \quad {}_2F_1\left(\frac{3-X}{2}, \frac{2-X}{2}; 2; 1-\eta\right) \\ &\rightarrow \; {}_2F_1\left(\frac{3-X}{2}, \frac{2-X}{2}; 2; 1\right) \\ &= 2^{-(X+1)} \cdot \; \frac{\Gamma(2)\Gamma(x-\frac{1}{2})}{\Gamma(\frac{1+X}{2})\Gamma(\frac{1+X}{2}+\frac{1}{2})} \end{aligned}$$

for $\eta \rightarrow 0$

Scaling for large X

after limit of $\eta \to 0$ hence

$$p_\eta(X|X \geq 1) \quad \to \quad \underbrace{2^{-(X+1)} \cdot \frac{\Gamma(X-\frac{1}{2})}{\Gamma(1+X)\cdot\sqrt{2\pi}\cdot 2^{-(X+1)+\frac{1}{2}}}}_{\text{for } \eta\to 0}$$

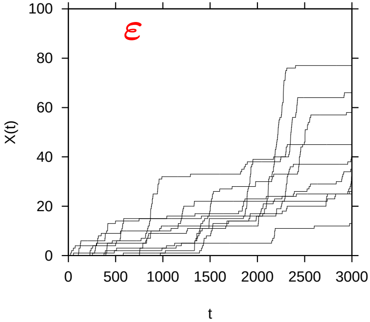
$$= \quad \frac{\Gamma(X-\frac{1}{2})}{2\sqrt{\pi}\cdot\Gamma(1+X)}$$

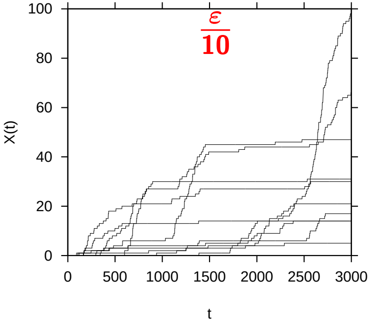
$$\sim \quad \underbrace{\frac{e^{\frac{3}{2}}}{2\sqrt{\pi}} \cdot \frac{(X-\frac{1}{2})^{(X-\frac{1}{2})}}{(X+1)^{(X+1)}}}_{\text{for } X\to\infty} \sim \frac{1}{2\sqrt{\pi}} \cdot X^{-\frac{3}{2}}$$

or keeping track of the limits undertaken

$$\lim_{X\to\infty} \lim_{\eta\to 0} \lim_{\tau\to\infty} \left(\frac{p_\eta(X,\tau|X\geq 1)}{X^{-\frac{3}{2}}} \right) = \text{const.} = \frac{1}{2\sqrt{\pi}}$$

SIRYX model:

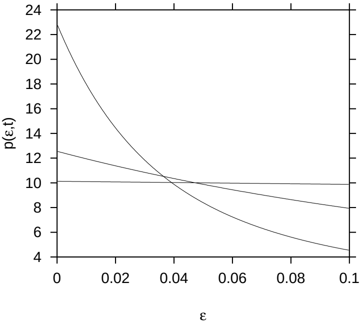




$$p(X) \sim X^{-\frac{3}{2}} \qquad \text{for } \varepsilon \longrightarrow 0$$

Evolution towards criticality:

Mutations generate different pathogenicity values



t=0

t=20

t=100

$$\mathbf{p}(\varepsilon, \mathbf{t}) = \frac{\frac{1}{\varepsilon}\left(1 - \mathbf{e}^{-\varepsilon\frac{\gamma}{\beta}\mathbf{t}}\right)}{\sum_{\nu=1}^{\infty}(-1)^{\nu+1}\cdot\frac{\left(\varepsilon_{\mathrm{m}}\frac{\gamma}{\beta}\mathbf{t}\right)^{\nu}}{\nu\cdot\nu!}} \quad .$$

Domination of the system by small ε without tuning
$=>$ self-organized criticality

Stollenwerk, Jansen, 2003, Phys. Lett. A

Simulation for 3 Mutant Systems I, Y and Z

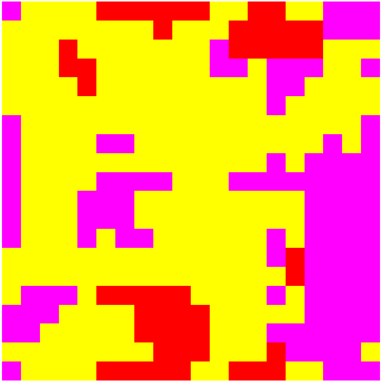


Figure: The three voter model for a lattice 20 by 20 for maximal time $t = 40$, including mutations of the transition rates with "pathogenicities" ϵ between 0.5 and 0.

We expand the SIRYX model by including a new strain mutated Bacteria labeled by Z.

The Reaction schemes will be expand by including the pathogenicity of the 3 strains $\epsilon_1, \epsilon_2, \epsilon_3$:

$$\begin{aligned} S + I &\xrightarrow{\beta-\epsilon_1} I + I & \qquad I &\xrightarrow{\alpha} S \\ S + Y &\xrightarrow{\beta-\epsilon_2} Y + Y & \qquad Y &\xrightarrow{\alpha} S \\ S + Z &\xrightarrow{\beta-\epsilon_3} Z + Z & \qquad Z &\xrightarrow{\alpha} S \end{aligned}$$

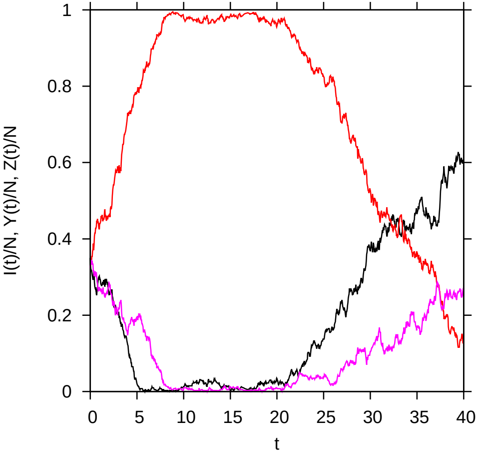


Figure: Evolution of the three Strains I , Y and Z in detail.

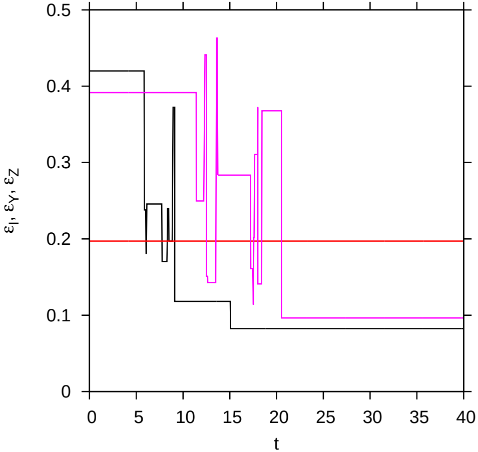
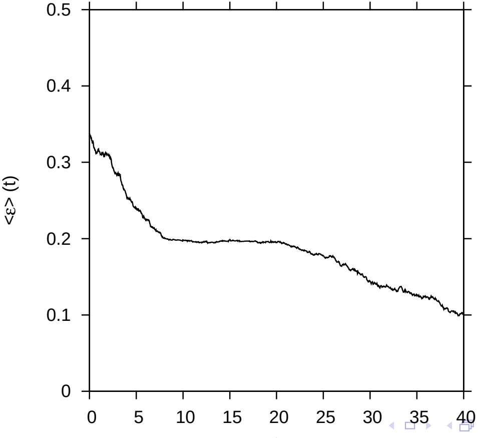


Figure: Changes of ε_1 , ε_2 and ε_3 with time.

$$< \varepsilon > := \sum_{i=1}^{3} \varepsilon_i . \frac{I_i}{N}$$



Thanks for your Attention!!!