Markov-modulated interactions in SIR epidemics

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Presentation based on the paper Markov-modulated interactions in SIR epidemics, by E. Almaraz and A. Gómez-Corral.

Introduction

- Our model: stochastic susceptible-infectious-recovered (SIR) model in a Markov-modulated context to incorporate correlated events in a closed finite community.
- We work with non-exponential distributional assumptions on the contacts between an I and a S individual, and the duration of infectiousness, but keeping the dimensionality of the underlying Markov chain model tractable.

- The epidemic SIR model has been widely applied to infectious diseases (measles, chickenpox, mumps...), among other situations where infection confers (typically lifelong) immunity.
- SIR-models (deterministic and stochastic perspectives) have been studied by some authors like Allen (2003, 2007), Andersson and Britton (2000), Bailey (1975) and Keeling and Rohani (2008).
- The SIR-model was first analyzed in depth by Kermack and McKendrick in 1927.
- Britton (2010) and Isham (2005) made a review of the existing literature and some results about SIR model.

Stochastic perspective$\rightarrow$ there are four important quantities of the SIR-model

- the quasi-stationary distribution.
- the final size distribution of an epidemic.
- the expected duration of an epidemic.
- the basic reproduction number $\mathcal{R}_0$

Some authors have studied these quantities, for example:

- Allen (2008).
- Artalejo and López-Herrero (2010).
- Gani and Purdue (1984).
- Neuts and Li (1996).
- Grasman (1998).

The basic SIR-model

In the SIR-model, individuals develop an immunity to the disease. At time t, the population consists of:

- $I(t) = i$ infectives.
- $S(t) = s$ susceptibles.
- $R(t) = r$ removed individuals.

Events:

- Contacts between an infective and a susceptible.
- Removal of an infective.

Transitions	Events	Rates
$i \to i+1,\ s \to s-1,\ r \to r,$ for $i, s \in \mathbb{N}$	An infection	$\lambda_{i,s}$
$i \to i-1,\ s \to s,\ r \to r+1,$ for $i \in \mathbb{N}, s \in \mathbb{N}_0$	A removal	μ_i

Table: Stochastic transitions, events and rates in the basic SIR-model

Rates $\lambda_{i,s}$ and μ_i can be specified in many ways:

- $\lambda_{i,s} = \beta is$ and $\mu_i = \eta i$ (Bailey, 1975, Gani and Purdue, 1984).
- $\lambda_{i,s} = \beta i^{\alpha} s$ and $\lambda_{i,s} = \beta i \min\{s, \epsilon n\}$, $\alpha \in (0, 1)$ (Neuts and Li, 1996).
- $\lambda_{i,s} = (i + s)^{-1/2}$ (Saunders, 1980).

In the case of:

- closed population that is homogeneously mixed.
- two state variables.
- initial numbers of $m > 0$ infectives and $n > 0$ susceptibles.

the SIR-model is formulated as a time-homogeneous continuous-time Markov chain (CTMC)

$$\mathcal{X} = \{X(t) = (I(t), S(t)) : t \geq 0\}$$

defined on a finite state space

$$\mathcal{S}(m,n) = \{(i,s) \in \mathbb{N}_0 \times \mathbb{N}_0 : 0 \leq i \leq m+n,\ 0 \leq s \leq \min\{n, m+n-i\}\}$$

The process $\mathcal{X}$, which is from now on termed *basic*, is uniquely specified by the transition rates $\lambda_{i,s}$ and μ_i.

- states in $\mathcal{C}_0(n) = \{(0,0),(0,1),...,(0,n)\}$ are absorbing and are associated with the ultimate extinction of the epidemic.
- the irreducible class $\mathcal{C}(m,n) = \{(i,s) \in \mathbb{N}_0 \times \mathbb{N}_0 : 1 \leq i \leq m+n,\ 0 \leq s \leq \min\{n, m+n-i\}\}$ consists of transient states. This class can be expressed in terms of *levels* as $\cup_{s=0}^{n} l(s)$, where the sth level corresponds to states with s susceptibles present, that is, $l(s) = \{(i,s) \in \mathbb{N}_0 \times \mathbb{N}_0 : 1 \leq i \leq m+n-s\}$, for $0 \leq s \leq n$.

If states are labeled so that states in $I(s)$ precede states in $I(s-1)$, and transient states precede absorbing states, then the infinitesimal generator $\mathbf{Q}$ of $\mathcal{X}$ is given by

$$\mathbf{Q} = \begin{pmatrix} \mathbf{Q}_{\mathcal{C}(m,n),\mathcal{C}(m,n)} & \mathbf{Q}_{\mathcal{C}(m,n),\mathcal{C}_0(n)} \\ \mathbf{0}_{(n+1)\times J(m,n)} & \mathbf{0}_{(n+1)\times(n+1)} \end{pmatrix}, \tag{1}$$

where $J(m,n) = 2^{-1}(n+1)(2m+n)$ is the cardinality of the class $\mathcal{C}(m,n)$.

The matrices $\mathbf{Q}_{\mathcal{C}(m,n),\mathcal{C}(m,n)}$ and $\mathbf{Q}_{\mathcal{C}(m,n),\mathcal{C}_0(n)}$ in (1) take the form

$$\mathbf{Q}_{\mathcal{C}(m,n),\mathcal{C}(m,n)} = \begin{pmatrix} \mathbf{A}(n) & \mathbf{B}(n) & & & \\ & \mathbf{A}(n-1) & \mathbf{B}(n-1) & & \\ & & \ddots & \ddots & \\ & & & \mathbf{A}(1) & \mathbf{B}(1) \\ & & & & \mathbf{A}(0) \\ & & & & \mathbf{0}_{(n+1)\times(m+n)} \end{pmatrix}$$

where the sub-matrices $\mathbf{A}(s)$ and $\mathbf{B}(s)$ record transition rates related to jumps of $\mathcal{X}$ from states of the sth level to states of $l(s)$ and $l(s-1)$, respectively.

$$\mathbf{Q}_{\mathcal{C}(m,n),\mathcal{C}_0(n)} = \begin{pmatrix} \mathbf{t}(n) & & & & & \\ & \mathbf{t}(n-1) & & & & \\ & & \ddots & & & \\ & & & \mathbf{t}(1) & & \\ & & & & \mathbf{t}(0) & \\ & & & & & \mathbf{0}_{(n+1)} \end{pmatrix},$$

the column vector $\mathbf{t}(s)$ contains transition rates related to jumps of $\mathcal{X}$ from states of the sth level to the absorbing state $(0, s)$.

$$\mathbf{A}(s) = \begin{pmatrix} -q_{m+n-s,s} & \mu_{m+n-s} & & & \\ & -q_{m+n-s-1,s} & \mu_{m+n-s-1} & & \\ & & \ddots & \ddots & \\ & & & -q_{2,s} & \mu_2 \\ & & & & -q_{1,s} \end{pmatrix}, \tag{2}$$

$$\mathbf{B}(s) = \begin{pmatrix} \lambda_{m+n-s,s} & & & \\ & \lambda_{m+n-s-1,s} & & \\ & & \ddots & \\ & & & \lambda_{1,s} \quad 0 \end{pmatrix}. \tag{3}$$

Some extensions of the SIR classic model:

- SIR model with general distributed infection period (Clancy, 2014).
- PH, MAP general perspective: when there are "i" infected individuals we should consider "i" MAPs. As a result, the resulting problem is not tractable from a numerical perspective due to the underlying dimensionality.

Markov-modulated events in the SIR epidemic model

The dynamics in the SIR-model can be explained in terms of *scheduled* events.

The process $\mathcal{X}$ enters state $(i,s) \in \mathcal{C}(m,n)$ at time t. The next transition $(i,s) \to (i',s')$ is triggered by two scheduled events:

- $E_{(i,s)}(1,-1)$: infection of a susceptible.
- $E_{(i,s)}(-1,0)$: removal of an infective.

The occurrence instants of $E_{(i,s)}(1,-1)$ and $E_{(i,s)}(-1,0)$:

- are independent and exponentially distributed.
- with mean values $\lambda_{i,s}^{-1}$ and μ_i^{-1}, respectively.
- they are also independent of the story of $\mathcal{X}$ up to time t.

The basic process $\mathcal{X}$:

- spends in (i, s) an exponentially distributed period of time, with expected length $(\lambda_{i,s} + \mu_i)^{-1}$.
- it then moves to state $(i', s') = (i + z_1, s + z_2)$ with probability:
  - $(\lambda_{i,s} + \mu_i)^{-1}\lambda_{i,s}$ if $(z_1, z_2) = (1, -1)$: a new infection.
  - $(\lambda_{i,s} + \mu_i)^{-1}\mu_i$ if $(z_1, z_2) = (-1, 0)$: the removal of an infective.

$\Longrightarrow$ the basic state $(i, s) \in \mathcal{C}(m, n)$ is actualized with the information of the observed value (z_1, z_2) of a bivariate vector (Z_1, Z_2):

$$(i', s') = f((i, s), (Z_1, Z_2))$$

with

$$f((i, s), (z_1, z_2)) = (i + z_1, s + z_2)$$

for pairs $(z_1, z_2) \in \{(1, -1), (-1, 0)\}$.
Distributional assumptions for (Z_1, Z_2) are inherently linked to the superposition of two independent Poisson streams with arrival rates $\lambda_{i,s}$ and μ_i.

Basic process $\mathcal{X}$ replaced by *augmented* version $(\mathcal{X}, \mathcal{Y})$ allowing a Markovian dependence on a finite number of phases. To do that:

- every basic state $(i, s) \in \mathcal{C}(m, n)$ replaced by a set of augmented states (i, s, y_1, y_2) with $1 \leq y_k \leq L_k$ for predetermined values $L_k \in \mathbb{N}$ and $k \in \{1, 2\}$.
- we construct the superposition from two independent MAP's of orders L_1 and L_2 instead of Poisson processes.
- we introduce a third pair $(z_1, z_2) = (0, 0)$ that reflects a transition between phases, but it does not imply any transition in the basic state (i, s).

$\rightarrow$ Result: regular, time-homogeneous CTMC $(\mathcal{X}, \mathcal{Y})$, where the *phase* process $\mathcal{Y} = \{Y(t) = (Y_1(t), Y_2(t)) : t \geq 0\}$ can be thought of as a SD marked Markovian arrival process with two categories of *marked* events-type-(z_1, z_2)-:

- $(z_1, z_2) = (1, -1)$ if the infection of a susceptible individual is observed.
- $(z_1, z_2) = (-1, 0)$ if the removal of an infective is registered.

The state space $\mathcal{S}^*$ of $(\mathcal{X}, \mathcal{Y})$ can be partitioned into:

- $\mathcal{C}_0(n)$: set of absorbing states.
- $\mathcal{C}^*(m,n)$: class of transient states, where:
  - $\mathcal{C}^*(m,n) = \cup_{s=0}^{n} I^*(s)$.
  - $I^*(s)$: sth augmented level consists of states (i, s, y_1, y_2) with $1 \leq i \leq m+n-s$ and $1 \leq y_k \leq L_k$ for $k \in \{1,2\}$.

We use two *scaled* MAP's specified by characteristic matrices:

- $(\mathbf{C}^*_{0,(i,s)}, \mathbf{C}^*_{1,(i,s)})$ for the occurrence of an infection.
- $(\mathbf{D}^*_{0,(i,s)}, \mathbf{D}^*_{1,(i,s)})$ for the removal of an infective.

with

$$\begin{aligned} \mathbf{C}^*_{k,(i,s)} &= \hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_k, \\ \mathbf{D}^*_{k,(i,s)} &= \hat{\lambda}^{-1}(2)\mu_i\mathbf{D}_k, \end{aligned}$$

for $k \in \{1, 2\}$, where $(\mathbf{C}_0, \mathbf{C}_1)$ and $(\mathbf{D}_0, \mathbf{D}_1)$ are the characteristic matrices of two independent MAP's of orders L_1 and L_2, respectively, and fundamental arrival rates $\hat{\lambda}(1)$ and $\hat{\lambda}(2)$.

$\Longrightarrow$ The infinitesimal generator $\mathbf{Q}^*$ of $(\mathcal{X}, \mathcal{Y})$ has the structured form of $\mathbf{Q}$ in (1) with $\mathbf{A}(s)$, $\mathbf{B}(s)$, and $\mathbf{t}(s)$ in (2)-(3) replaced by suitably defined sub-matrices $\mathbf{A}^*(s)$ and $\mathbf{B}^*(s)$, and vectors $\mathbf{t}^*(s)$.

For every basic state $(i, s) \in \mathcal{C}(m, n)$, the fundamental arrival rate of type-(z_1, z_2) marks is given by

$$\bar{\lambda}_{(i,s)}(z_1, z_2) = \begin{cases} \lambda_{i,s}, & \text{if } (z_1, z_2) = (1, -1), \\ \mu_i, & \text{if } (z_1, z_2) = (-1, 0), \end{cases} \tag{4}$$

and the fundamental arrival rate $\bar{\lambda}_{(i,s)}$ of the SD MMAP is given by

$$\bar{\lambda}_{(i,s)} = q_{i,s}, \tag{5}$$

regardless of the initial MAPs with matrices $(\mathbf{C}_0, \mathbf{C}_1)$ and $(\mathbf{D}_0, \mathbf{D}_1)$.

The exact reproduction number $R_{exact,0}$

In the SIR-model defined by the rates $\lambda_{i,s} = \beta is$ and $\mu_i = \eta i$ with $\beta = N^{-1}\beta'$, the basic reproductive ratio $\mathcal{R}_0 = \eta^{-1}\beta'$ separates the growing and shrinking behaviors and, consequently, it marks the epidemic *threshold* between regimes in which the disease either increases or dies out in the long run.

Based on works of Artalejo et. al (2013), we define $R_{exact,0}$ as:

- the exact number of secondary cases generated by a typical infective individual during its infectious period.

Important:

- $\mathcal{R}_0$ is related to the *time of invasion* (i.e., for a community with $(I(0), S(0)) = (1, N-1)$ and $R(0) = 0$).
- $R_{exact,0}$ can be appropriately defined at every time instant.

In the Markov-modulated SIR-model:

- the basic state $(1, N-1)$ is replaced by the set of augmented states $(1, N-1, y_1, y_2)$ with phases $1 \leq y_k \leq L_k$ and $k \in \{1, 2\}$.
- *conditional* probability mass function $\mathbf{x}_{(1,N-1,y_1,y_2)} = \{x_{(1,N-1,y_1,y_2)}(j) : 0 \leq j \leq N-1\}$ of $R_{exact,0}$, provided that $(1, N-1, y_1, y_2) \in \mathcal{C}^*(m, n)$ is the initial state of $(\mathcal{X}, \mathcal{Y})$, is defined by the probabilities

$$P\left(R_{exact,0} = j \middle| \left(I(0), S(0), Y_1(0), Y_2(0)\right) = (1, N-1, y_1, y_2)\right),$$

$$0 \leq j \leq N-1.$$

We may define conditional probability mass functions $\mathbf{x}_{(i,s,y_1,y_2)}$ of $R_{exact,0}$ in terms of probabilities $x_{(i,s,y_1,y_2)}(j)$ for $0 \leq j \leq s$ and phases $1 \leq y_k \leq L_k$ with $k \in \{1,2\}$, when initial basic states $(i,s) \in \mathcal{C}(m,n)$ are observed.
For every basic state $(i,s) \in \mathcal{C}(m,n)$ and values $0 \leq j \leq s$, we let $\mathbf{x}_{(i,s)}(j)$ be the column vector of order $L_1 L_2$ with entries $(\mathbf{x}_{(i,s)}(j))_{(y_1-1)L_2+y_2} = x_{(i,s,y_1,y_2)}(j)$ for $1 \leq y_k \leq L_k$ and $k \in \{1,2\}$.
By conditioning on the first transition of the augmented process $(\mathcal{X},\mathcal{Y}) \rightarrow$ entries of $\mathbf{x}_{(i,s)}(j)$ satisfy

$$
\begin{aligned}
- & \left(\left(\hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_0\right) \oplus \left(\hat{\lambda}^{-1}(2)\mu_i\mathbf{D}_0\right)\right)\mathbf{x}_{(i,s)}(j) \\
= & \ \delta_{0,j}\left(\mathbf{e}_{L_1} \otimes \left(\hat{\lambda}^{-1}(2)\eta\mathbf{D}_1\mathbf{e}_{L_2}\right)\right) + \\
& + \left(\mathbf{I}_{L_1} \otimes \left(\hat{\lambda}^{-1}(2)\eta(i-1)\mathbf{D}_1\right)\right)\mathbf{x}_{(i-1,s)}(j) \\
& + (1-\delta_{0,j})\left(\left(\hat{\lambda}^{-1}(1)\lambda^*_{i,s}\mathbf{C}_1\right) \otimes \mathbf{I}_{L_2}\right)\mathbf{x}_{(i+1,s-1)}(j-1) \\
& + (1-\delta_{s,j})\left(\left(\hat{\lambda}^{-1}(1)\tilde{\lambda}_{i-1,s}\mathbf{C}_1\right) \otimes \mathbf{I}_{L_2}\right)\mathbf{x}_{(i+1,s-1)}(j), \quad (6)
\end{aligned}
$$

$0 \leq j \leq s$ and $(i,s) \in \mathcal{C}(m,n)$

where:

- $\lambda^*_{i,s}$: gives the individual rate at which a typical infective contacts with susceptibles.
- $\tilde{\lambda}_{i-1,s}$: reflects the superposition of the contact processes of the remaining $i-1$ infectives.

in the special case $\lambda_{i,s} = \beta is$ with $\beta = N^{-1}\beta'$, they are given by:

- $\lambda^*_{i,s} = N^{-1}\beta' s$.
- $\tilde{\lambda}_{i-1,s} = N^{-1}\beta'(i-1)s$.

Starting from $\mathbf{x}_{(i,0)}(0) = \mathbf{e}_{L_1 L_2}$ for $1 \leq i \leq m+n$, the triangular system of equations (6) can be efficiently solved in the natural order $j \geq 0$, $j \leq s \leq n$ and $1 \leq i \leq m+n-s$, and moments of $R_{exact,0}$ are then derived in an straightforward manner.
The role of $\mathcal{R}_0$ may be replaced by the *unconditional* expected value

$$\overline{R}_{exact,0} = \sum_{j=1}^{N-1} j \left(\eta(1) \otimes \eta(2)\right) \mathbf{x}_{(1,N-1)}(j),$$

where $\eta(1) \otimes \eta(2)$ is the stationary probability vector of the phase process $\mathcal{Y}$

The population transmission number R_p

R_p counts the exact number of secondary cases produced by all currently infective individuals prior to the first removal.
For a fixed augmented state $(i, s, y_1, y_2) \in \mathcal{C}^*(m, n)$, we define the conditional probabilities $y_{(i,s,y_1,y_2)}(j)$ by

$$P\left(R_p = j \middle| \left(I(0), S(0), Y_1(0), Y_2(0)\right) = (i, s, y_1, y_2)\right), \quad 0 \leq j \leq s,$$

from which we introduce vectors $\mathbf{y}_{(i,s)}(j)$ with entries $\left(\mathbf{y}_{(i,s)}(j)\right)_{(y_1-1)L_2+y_2} = y_{(i,s,y_1,y_2)}(j)$ for $1 \leq y_k \leq L_k$ and $k \in \{1, 2\}$.

An appeal to a first-step argument yields

$$-\left(\left(\hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_0\right)\oplus\left(\hat{\lambda}^{-1}(2)\mu_i\mathbf{D}_0\right)\right)\mathbf{y}_{(i,s)}(j)=$$
$$=\delta_{0,j}\left(\mathbf{e}_{L_1}\otimes\left(\hat{\lambda}^{-1}(2)\mu_i\mathbf{D}_1\mathbf{e}_{L_2}\right)\right)$$
$$+(1-\delta_{0,j})\left(\left(\hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_1\right)\otimes\mathbf{I}_{L_2}\right)\mathbf{y}_{(i+1,s-1)}(j-1), \quad (7)$$

for values $0\leq j\leq s$ and basic states $(i,s)\in\mathcal{C}(m,n)$, which can be routinely solved by starting from $\mathbf{y}_{(i,0)}(0)=\mathbf{e}_{L_1L_2}$. The *unconditional* expected value of R_p is then evaluated as

$$\overline{R}_p = \sum_{j=1}^{N-1} j\left(\eta(1)\otimes\eta(2)\right)\mathbf{y}_{(1,N-1)}(j),$$

Numerical experiments and discussion

We assume:

- $\lambda_{i,s} = \beta is$ with $\beta = N^{-1}\beta'$, $\beta' > 0$.
- $\mu_i = \eta i$ with $\eta = 1.0$,
- sizes $N \in \{10, 50, 100, 150\}$.
- Eight scenarios (see next table) defined in terms of standard Poisson processes, and positively and negatively correlated Markovian events, which are appropriately specified from two predetermined MAP's of order $L_1 = L_2 = 3$ with values $\rho_1 = 0.35016$ and -0.35016 for their correlation coefficients; in this setting, the basic SIR-model corresponds to scenario I.

Scenario	Occurrence of an infection	Occurrence of a removal
A	$\hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_1^+$	μ_i
B	$\hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_1^-$	μ_i
C	$\lambda_{i,s}$	$\hat{\lambda}^{-1}(2)\mu_i\mathbf{C}_1^+$
D	$\lambda_{i,s}$	$\hat{\lambda}^{-1}(2)\mu_i\mathbf{C}_1^-$
E	$\hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_1^+$	$\hat{\lambda}^{-1}(2)\mu_i\mathbf{C}_1^-$
F	$\hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_1^-$	$\hat{\lambda}^{-1}(2)\mu_i\mathbf{C}_1^+$
G	$\hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_1^+$	$\hat{\lambda}^{-1}(2)\mu_i\mathbf{C}_1^+$
H	$\hat{\lambda}^{-1}(1)\lambda_{i,s}\mathbf{C}_1^-$	$\hat{\lambda}^{-1}(2)\mu_i\mathbf{C}_1^-$
I	$\lambda_{i,s}$	μ_i

Table: Eight scenarios defined in terms of the matrices $\mathbf{C}^*_{1,(i,s)}$ and $\mathbf{D}^*_{1,(i,s)}$ for the occurrence of an infection and the removal of an infective, respectively

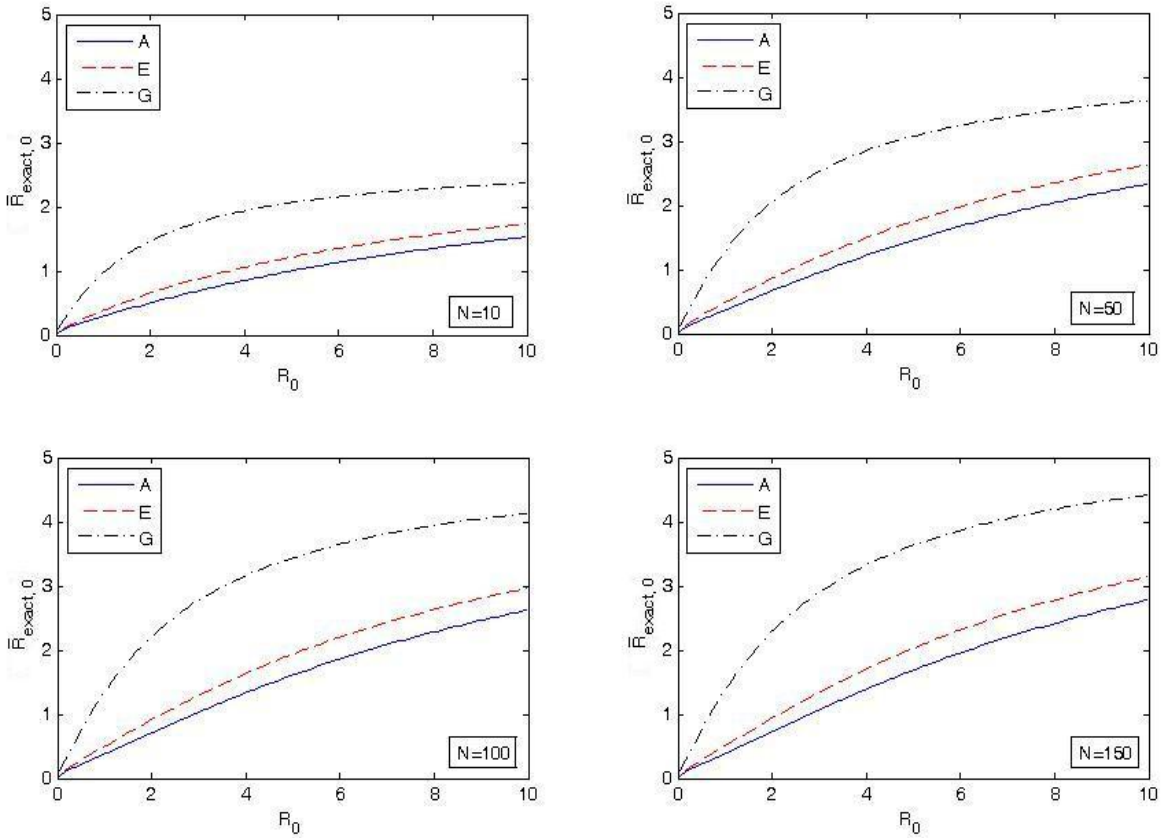

Figure: 1 The expected value $\overline{R}_{exact,0}$ versus the basic reproduction number $\mathcal{R}_0$ for scenarios A, E and G and sizes $N \in \{10, 50, 100, 150\}$

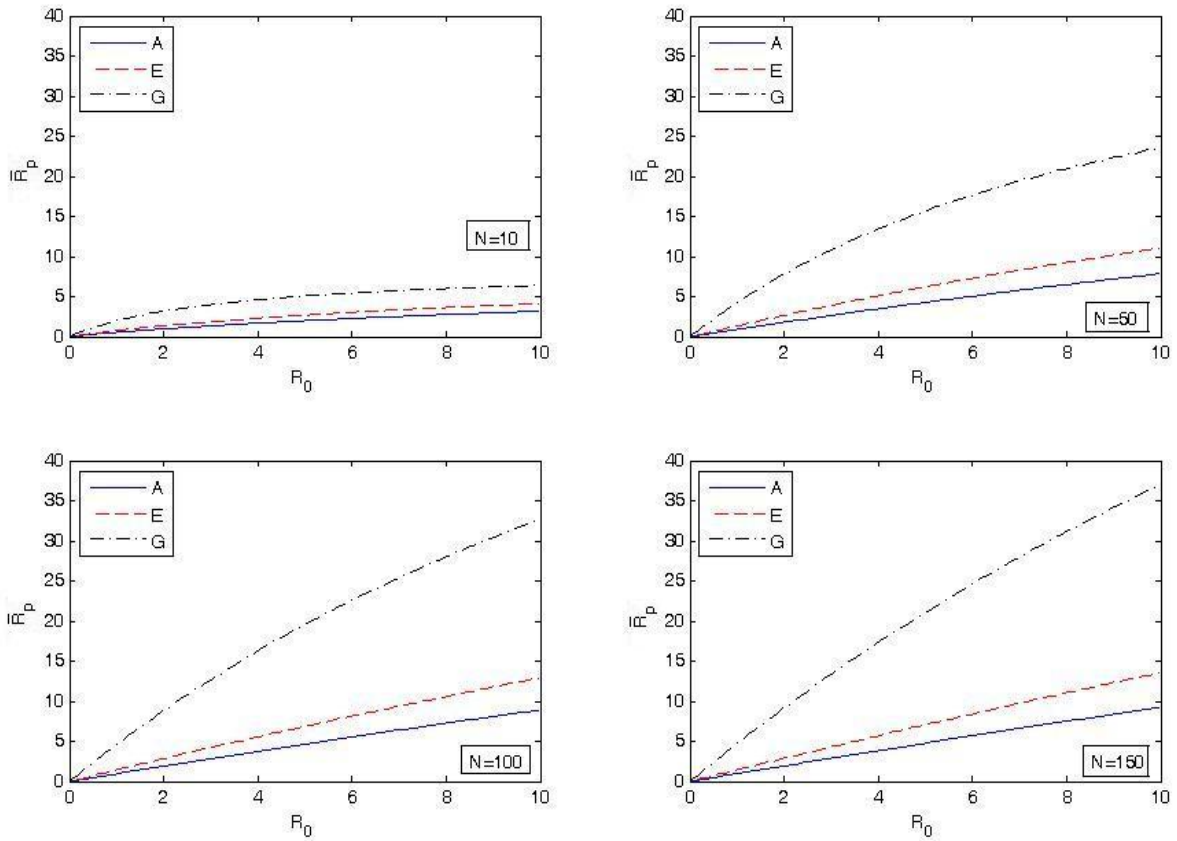

Figure: 4 The expected value $\overline{R}_p$ versus the basic reproduction number $\mathcal{R}_0$ for scenarios A, E and G and sizes $N \in \{10, 50, 100, 150\}$

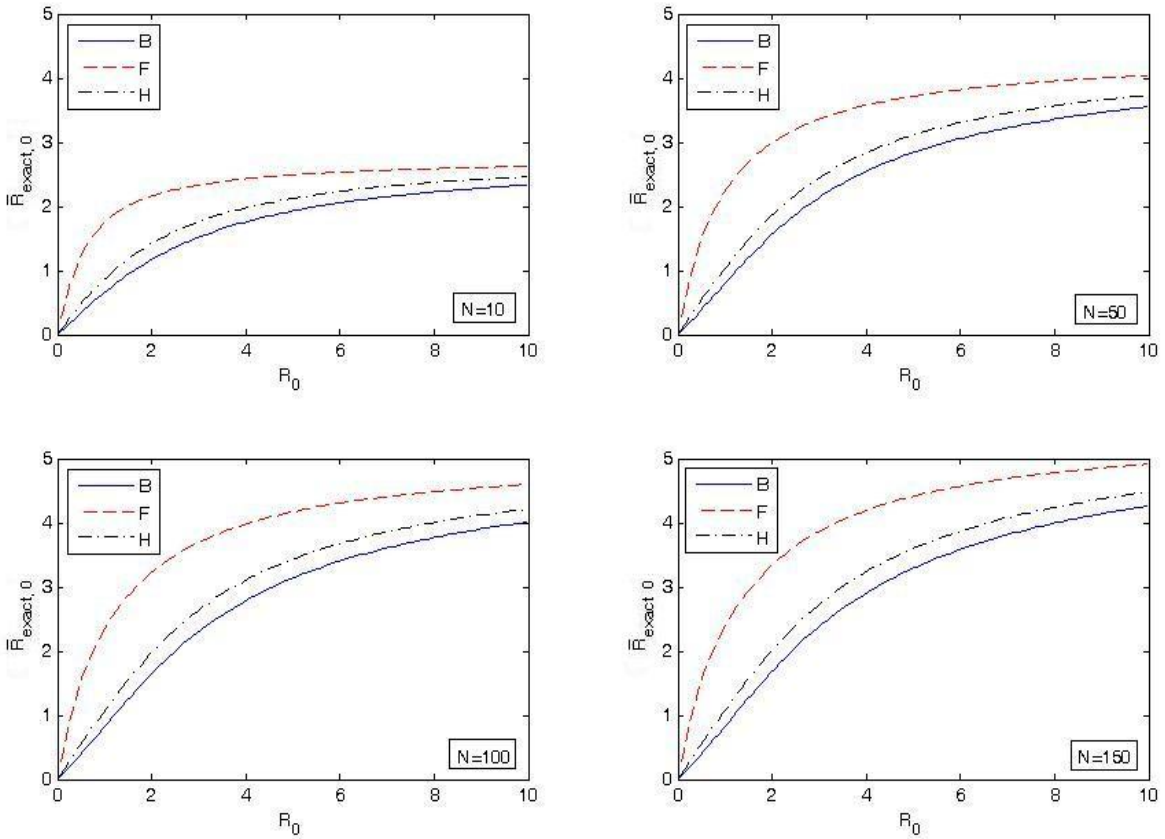

Figure: 2 The expected value $\overline{R}_{exact,0}$ versus the basic reproduction number $\mathcal{R}_0$ for scenarios B, F and H and sizes $N \in \{10, 50, 100, 150\}$

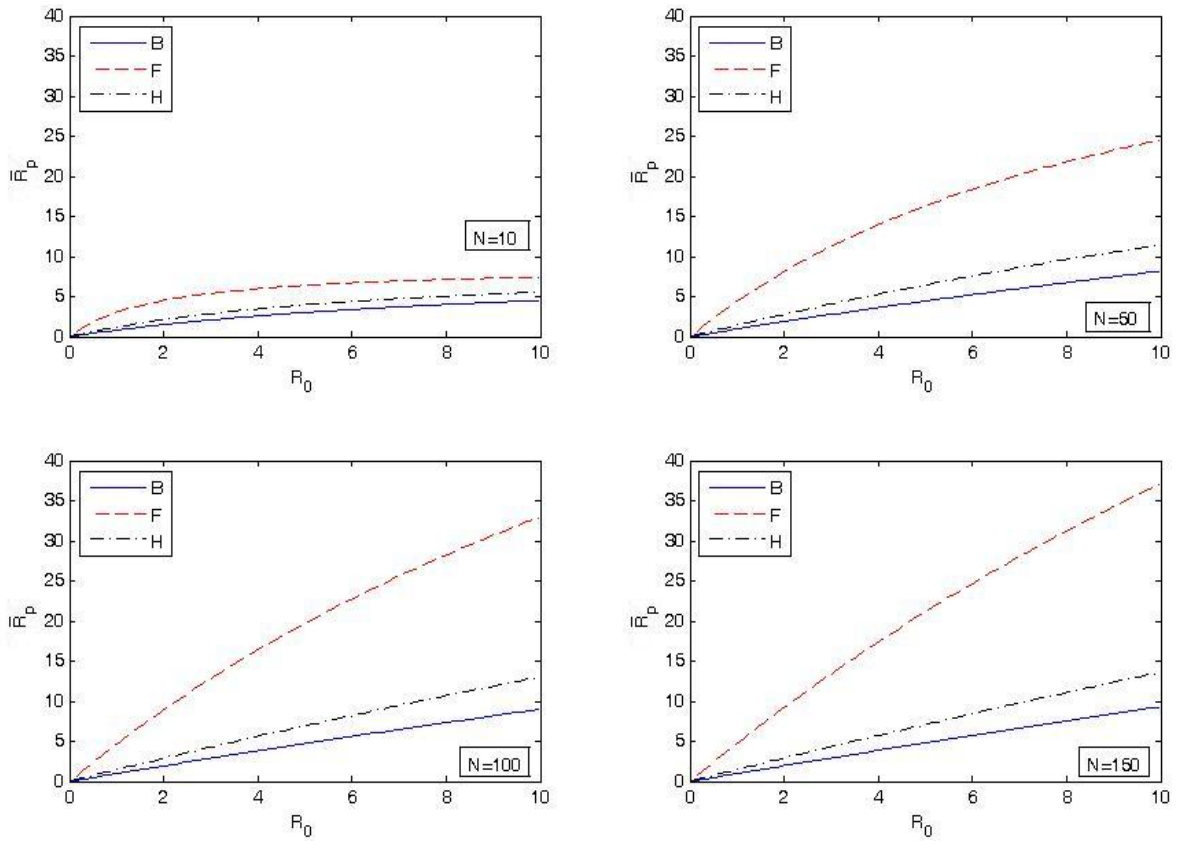

Figure: 5 The expected value $\overline{R}_p$ versus the basic reproduction number $\mathcal{R}_0$ for scenarios B, F and H and sizes $N \in \{10, 50, 100, 150\}$

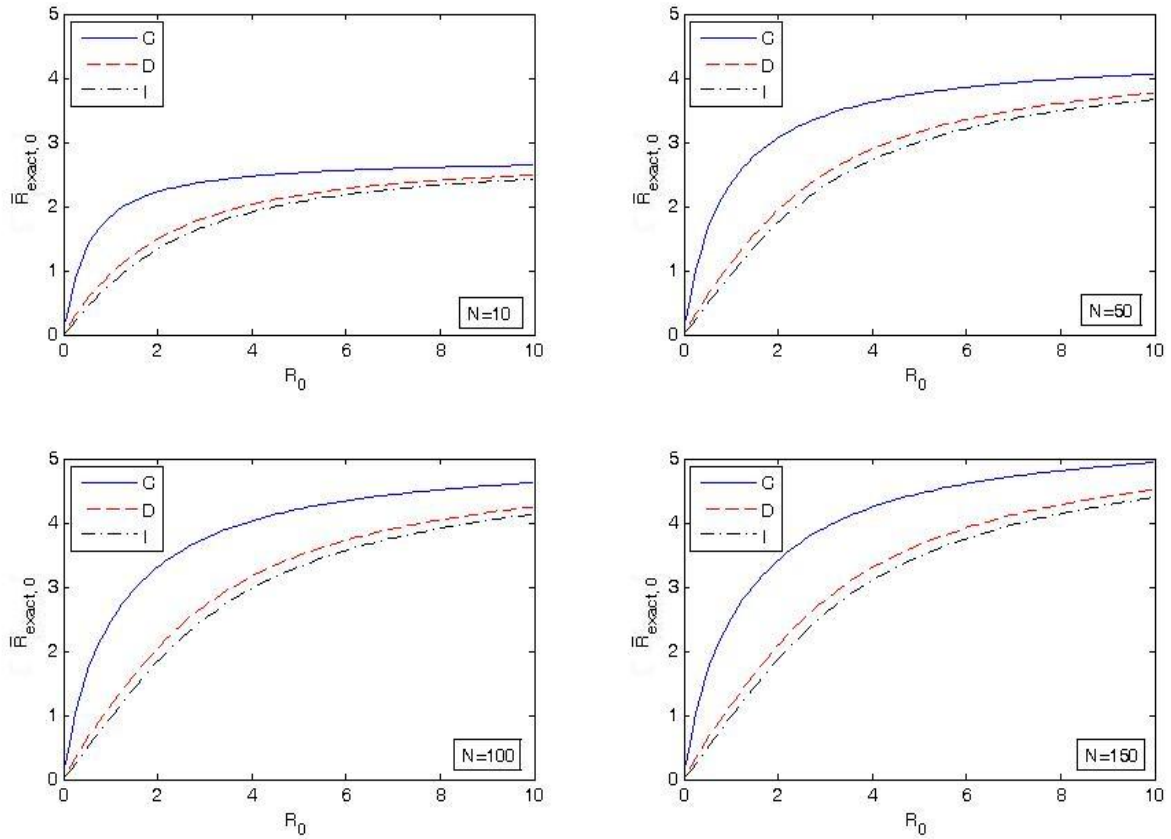

Figure: 3 The expected value $\overline{R}_{exact,0}$ versus the basic reproduction number $\mathcal{R}_0$ for scenarios C, D and I and sizes $N \in \{10, 50, 100, 150\}$

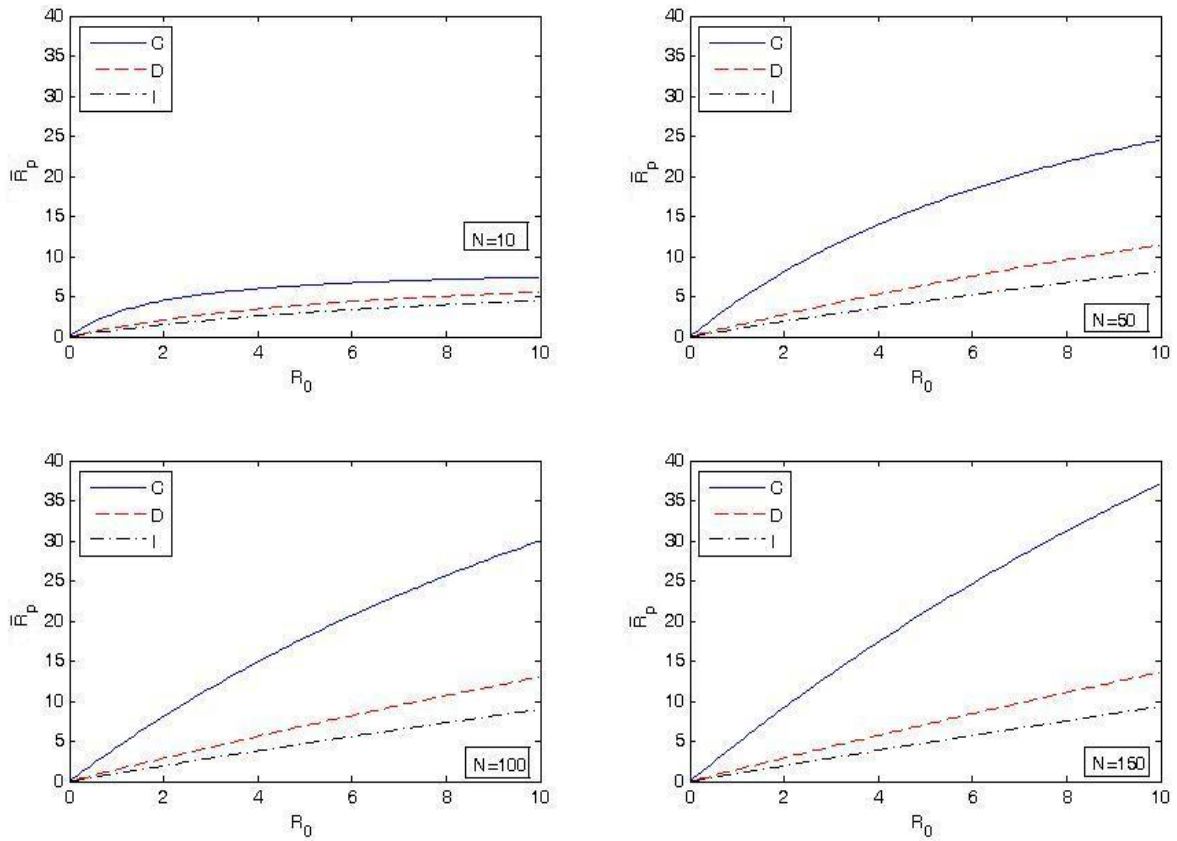

Figure: 6 The expected value $\overline{R}_p$ versus the basic reproduction number $\mathcal{R}_0$ for scenarios C, D and I and sizes $N \in \{10, 50, 100, 150\}$

Conclusions

- We develop a stochastic modeling framework that incorporates correlation between events into the dynamics of the SIR-model
- We construct Markov-modulated versions of the basic SIR-model $\mathcal{X}$ by allowing one to deal with non-exponential distributional assumptions on the contacts between I and S individual, and the random duration of infectiousness.

- We construct an augmented Markovian process $(\mathcal{X}, \mathcal{Y})$ describing the number of infectives and susceptibles in the basic SIR-model, and an auxiliary variable called phase.
- The augmented process $(\mathcal{X}, \mathcal{Y})$ is a regular, time-homogeneous CTMC exhibiting correlation between events, and the phase process $\mathcal{Y}$ amounts to a state-dependent version of a MMAP where the types of marked events correspond to either a new infection or the removal of an infective in the basic SIR-model.

- The process $\mathcal{X}$ and its augmented version $(\mathcal{X}, \mathcal{Y})$ possess identical structural properties regarding the infinitesimal rates $\lambda_{i,s}$ and μ_i, and the fundamental arrival rates $\bar{\lambda}_{(i,s)}(z_1, z_2)$ of type-(z_1, z_2) marked events.
- We study an alternative to the basic reproduction number $\mathcal{R}_0$ $\rightarrow \overline{R}_{exact,0}$ and $\overline{R}_p$.
- We compare $\mathcal{R}_0$ with the expected values $\overline{R}_{exact,0}$ and $\overline{R}_p$ at the invasion time, that is, by assuming that the invasion starts at time $t = 0$ with $(I(0), S(0)) = (1, N - 1)$ and $R(0) = 0$.

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Thank you for your attention.

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