On a stochastic epidemic SEIHR model and its diffusion approximation

Marco Ferrante[(1)], Elisabetta Ferraris[(1)] and Carles Rovira[(2)]

[(1)] Dipartimento di Matematica, Università di Padova (Italy) ,

[(2)] Facultat de Matemátiques, Universitat de Barcelona (Spain)

IMUB - Barcelona - 2014

Introduction

The analysis of the spread of a communicable disease dates back to the 18th century.
The mathematical models developed to describe this have been deterministic or stochastic and they may involve many factors such as

- mode of transmission,
- incubation periods,
- infectious periods,
- quarantine periods.

We will consider communicable disease models that describe a directly transmitted viral or bacterial agent in a closed population of fixed size **n**, consisting of susceptibles (S), infectives (I) and recovers (R).
Denoting by $S(t)$, $I(t)$ and $R(t)$ the numbers of individuals in each class at time t, the basic SIR models assume that

$$S \longrightarrow I \longrightarrow R$$

Basic assumptions:

- The population size **n** remains constant, i.e.

$$S(t) + I(t) + R(t) = n;$$

- At the beginning the population consists of **n-1** susceptibles and **1** infectious individual.
- Individuals that become infected are also infectious;

In this talk I will present the generalisation of a simple, discrete-time stochastic SIR type model defined by Tuckwell and Williams in Math. Biosci. **208** (2007) in order to include

1. incubation period (E);
2. quarantine procedures (H).

This allows us to model the evolution of diseases that presents large latency periods like **varicela**, which on the contrary are poorly described by standard SIR models.
Furthermore, we derive a diffusion approximation of these models which leads to stochastic differential equations with multiple delays in a natural way and that can represent a new class of models on his own.

The Greenwood - Reed and Frost model

Reed and Frost proposed the prototype of the SIR models in 1928.
Assume that the size of the population is fixed and equal to n and that the time is discrete $t = 0, 1, 2, \ldots$ The natural unit for the duration of an epoch is one day.
In this model, there are successive generations -indexed by t- of infective which are only able of infecting susceptible **for one generation**.

Let $X(t)$ denotes the number of individuals which are susceptible at time t, and $Y(t)$ the number of individuals which are new infective at time t. Then the initial condition is

$$X(0) + Y(0) = n$$

and

$$X(t+1) + Y(t+1) = X(t)$$

for $t = 0, 1, 2, \ldots$
Then, for any $t = 0, 1, 2, \ldots$

$$X(t) + \sum_{i=0}^{t} Y(i) = n \ .$$

Assuming that the number of infectives of generation $t+1$ is a binomial random variable with parameters $X(t)$ and $p(Y(t))$, which is the probability that an existing susceptible will become infected when the number of invectives is $Y(t)$, it is immediate that $\{X(t), Y(t)\}$ forms a Markov chain, with

$$P(Y(t+1) = k | X(t) = x, Y(t) = y) = \binom{x}{k} p(y)^k (1 - p(y))^{x-k}$$

In the Greenwood model, $p(y) = p$ is a constant not depending on y, while in the Reed-Frost model it is supposed that the probability any susceptible is infected escapes being infected when there are y invectives is

$$1 - p(y) = (1 - p)^y \ .$$

The SIR model by Tuckwell and Williams

Tuckwell and Williams in 2006 proposed a more sophisticated model, based on a discrete time Markovian approach. With respect to the Reed and Frost model they introduce the following new assumptions:

- *Definition af a sick individual*, given any individual i, with $i = 1, ...n$, we define a stochastic process $Y^i = \{Y^i(t), t = 0, 1, 2, ...\}$ such that $Y^i(t) = 1$ if the individual is infectious at time t, otherwise $Y^i(t) = 0$. The total number of infectious individuals at time $t \geq 0$ will be therefore equal to $Y(t) = \sum_{i=1}^{n} Y^i(t)$.
- *Daily encounters*, each individual i, over $(t, t+1]$, will encounter a number of other individuals equal to $N_i(t) = N_i + M_i(t)$ where N_i is a fixed number, while $M_i(t)$ is a random number of daily encounters.
- *Duration of the disease*, any individual remains infectious for r consecutive days, where r is a positive integer. After this period, the individual recovers and cannot be reinfected.

- If an individual who has never been diseased up to and including time t, encounters an individual in (t,t+1] who is infectious at time t, then independently of the results of other encounters, the encounter results in transmission of the disease with probability p.

Assuming that all the variables $N_i(t)$ are independent and identically distributed (i.i.d.) this model can be seen as a $(r+1)$-dimensional Markov chain. Indeed, let

- $Y_l(t)$ be the number of individuals who are infected at t and have been infected for exactly l time units, with l=0,1,2,...,r-1;
- $X(t)$ be the number of susceptible individual at time t;
- $Z(t)$ be the number of individual who were previously infected and are recovered at t;

Then it is clear that

$$V(t) = (X(t), Y_0(t), Y_1(t), \ldots, Y_{r-1}(t)), \qquad t = 0, 1, 2, ...$$

is a Markov chain with state space

$$S(n, r) = \Big\{(x, y_0, \ldots, y_{r-1}) : x, y_i \in \mathbb{Z}_+, \text{ for } i = 0, \ldots, r-1,$$

$$\text{and } x + \sum_{i=0}^{r-1} y_i \leq n\Big\}.$$

In addition to the process $Y^i = \{Y^i(t), t = 0, 1, 2, ...\}$, we can define the process $X^i = \{X^i(t), t = 0, 1, 2, ...\}$, for $i = 1, \ldots, n$, which indicates whether individual i is susceptible or not, and the variable

$$Z^i(t) = 1 - X^i(t) - Y^i(t)$$

which indicates if the individual i is recovered to the disease and no more infectious. We immediately get

$$X(t) = \sum_{i=0}^{n} X^i(t) \qquad Y(t) = \sum_{i=0}^{n} Y^i(t) \qquad Z(t) = \sum_{i=0}^{n} Z^i(t)$$

Furthermore we can consider the processes $Y_0^i, Y_1^i, ..., Y_{r-1}^i$, where $i = 1, 2, ..., n$, and $Y_k^i(t) = 1$ if the individual i at time t is infective for k days, zero otherwise.

With these definitions we can consider a new Markovian model

$$\mathbf{M}(t) = [X^i(t), Y_0^i(t), Y_1^i(t), ..., Y_{r-1}^i(t), i = 1, 2, ..., n] \qquad (1)$$

whose state space is now

$$S_1(n, r) = \begin{array}{l} \{(x^1, \ldots, y_{r-1}^1, \ldots, x^n, \ldots, y_{r-1}^n) \in \{0, 1\}^{n(r+1)} : \\ \quad \alpha_i = x^i + \sum_{k=0}^{r-1} y_k^i \leq 1 \text{ for } i = 1, \ldots, n, \text{ and } \sum_{j=0}^{n} \alpha_j \leq n\}. \end{array}$$

Let us fix the individual i and study the process

$$M_i(t) = [X^i(t), Y_0^i(t), Y_1^i(t), ..., Y_{r-1}^i(t)]$$

If one of the variables $Y_0^i(t), Y_1^i(t), ..., Y_{r-1}^i(t)$ is equal to 1, then the process at time $t+1$ is determined since the transitions in this case is sure.

The only interesting case is when $X^i(t) = 1$ and we have to calculate the probability that this susceptible individual becomes infected for the first time at $t + 1$.
First of all, assuming that n is much greater than N, we can approximate the probability of meeting exactly j infectives by the binomial law, obtaining

$$P_j^i(y, N; n) \approx \binom{N}{j} \left(\frac{y}{n-1}\right)^j \left(1 - \frac{y}{n-1}\right)^{N-j}, \tag{2}$$

where $y = Y(t)$ is the total number of diseased individuals and for simplicity we take $N_i(t) \equiv N$.

Assuming that the probability p_j of becoming infected if j infected are met is

$$p_j = 1 - (1 - p)^j, \tag{3}$$

then

$$P(Y_0^i(t+1) = 1 | X^i(t) = 1, Y(t) = y) = \sum_{j=1}^{N} p_j P_j^i(y, N; n)$$
$$\approx 1 - \left(1 - \frac{py}{n-1}\right)^N$$

As a particular case, Tuckwell and Williams consider the case where $N_i(t) \equiv N$ for any i and there is no recovery (that is, $r = \infty$). Under these assumptions, the process $Y(t)$ is a Markov chain whose transitions probabilities can be approximated in the following way

$$\begin{aligned} &P(Y(t+1) = y + w | Y(t) = y) \\ &\quad \approx \binom{n-y}{w} \left(1 - \left(1 - \frac{py}{n-1}\right)^N\right)^w \left(1 - \frac{py}{n-1}\right)^{N(n-y-w)} \end{aligned}$$

where $w = 0, 1, 2, \ldots$

The basic reproduction number

The basic reproduction number $\mathcal{R}_0$ of an infection is defined as the "*expected number of secondary cases per primary case in a virgin population*".
If $\mathcal{R}_0 > 1$, then an epidemic is expected to occur following the introduction of infection.
If $\mathcal{R}_0 < 1$ then the number infected in the population is expected to decrease following introduction and the infection will be eliminated over time.

In the present SIR model under the assumption that N is constant it is possible to calculate explicitly the basic reproduction number for small values of r.

Defining $\alpha(y) = 1 - \left(1 - \frac{py}{n-1}\right)^N$ and letting r the number of days any individual remains infectious and p the transmission probability, we get that:

$$R_0(1) = (n-1)\alpha(1) = (n-1)\left(1 - \left(1 - \frac{py}{n-1}\right)^N\right)$$

$$R_0(2) = (n-1)(2\alpha(1) - \alpha^2(1)) = (n-1)\left(1 - \left(1 - \frac{py}{n-1}\right)^{2N}\right)$$

$$R_0(3) \sim (n-1)(3\alpha(1) - 2\alpha^2(1))$$

Since we can assume that $\frac{py}{n-1}$ is small, we can approximate

$$\left(1-\frac{py}{n-1}\right)^N \sim 1-\frac{Npy}{n-1}$$

obtaining that

$$R_0(1) = (n-1)\alpha(1) \sim (n-1)(1-1+\frac{Np}{n-1}) = Np$$

$$R_0(2) \sim (n-1)(1-1+\frac{2Np}{n-1}) = 2Np$$

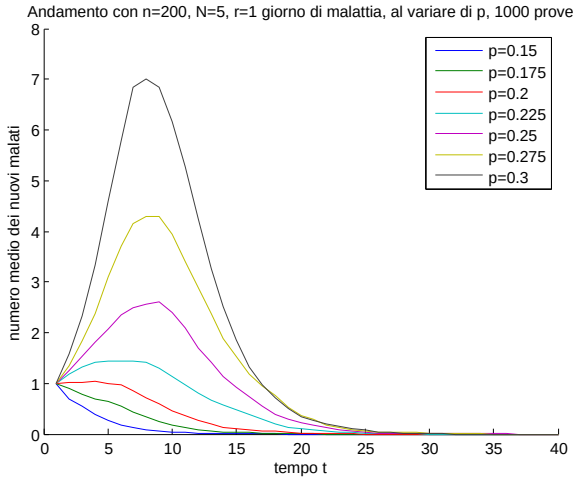
$$R_0(3) \sim (n-1)\left[3-3\left(1-\frac{py}{n-1}\right)^N-2\left[1+\left(1-\frac{py}{n-1}\right)^{2N}-2\left(1-\frac{py}{n-1}\right)^N\right]\right.$$

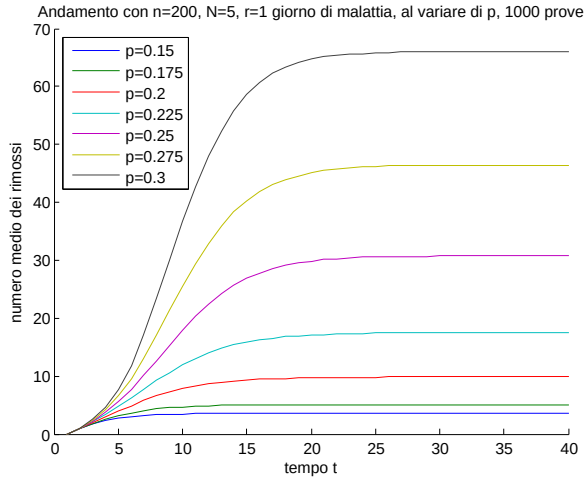
$$\sim (n-1)\left[1+\left[1-\frac{Np}{n-1}\right]-2\left[1-\frac{2Np}{n-1}\right]\right] = 3Np$$

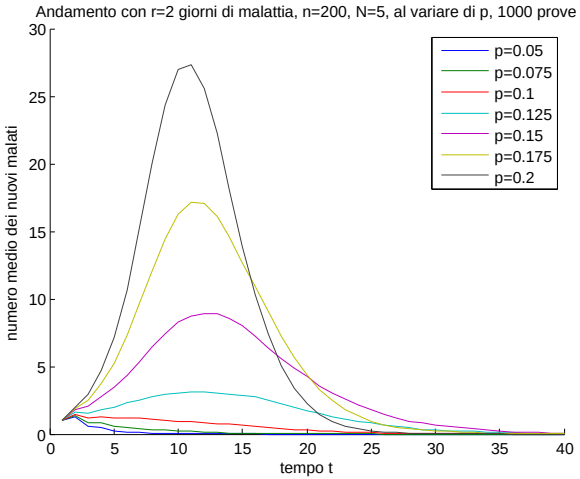
Our conjecture is that for every $k \in \mathbb{N}$, it holds that

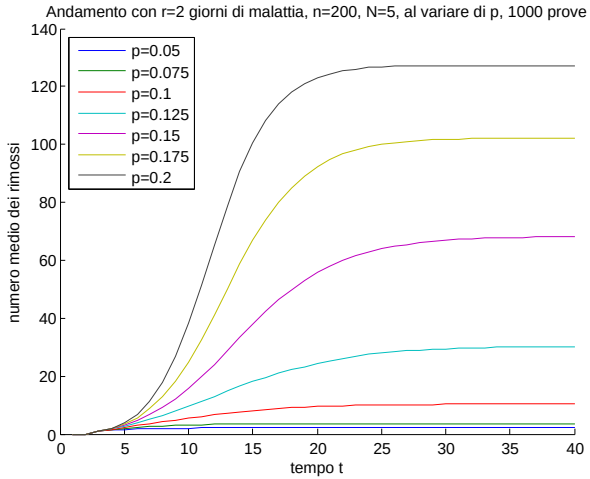
$$R_0(k) \sim kNp$$

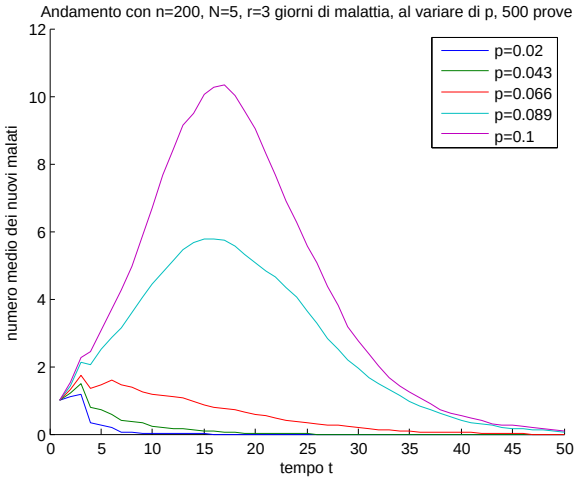
Let us see how the simulated behaviour of the epidemics in the cases N=5 and r=1,2,3 suggests that the role of the basic reproduction number is confirmed in this case too.

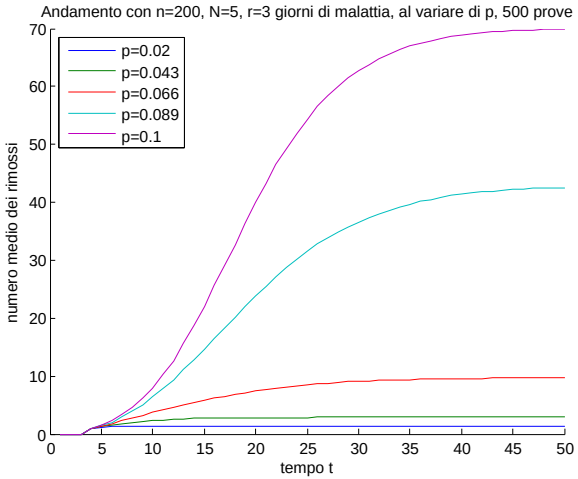

Andamento con n=200, N=5, r=1 giorno di malattia, al variare di p, 1000 prove
numero medio dei nuovi malati
tempo t
p=0.15
p=0.175
p=0.2
p=0.225
p=0.25
p=0.275
p=0.3
0
1
2
3
4
5
6
7
8
0
5
10
15
20
25
30
35
40


Andamento con n=200, N=5, r=1 giorno di malattia, al variare di p, 1000 prove
numero medio dei rimossi
tempo t
p=0.15
p=0.175
p=0.2
p=0.225
p=0.25
p=0.275
p=0.3
0
10
20
30
40
50
60
70
0
5
10
15
20
25
30
35
40


Andamento con r=2 giorni di malattia, n=200, N=5, al variare di p, 1000 prove
numero medio dei nuovi malati
tempo t
p=0.05
p=0.075
p=0.1
p=0.125
p=0.15
p=0.175
p=0.2
0
5
10
15
20
25
30
35
40


Andamento con r=2 giorni di malattia, n=200, N=5, al variare di p, 1000 prove
numero medio dei rimossi
tempo t
p=0.05
p=0.075
p=0.1
p=0.125
p=0.15
p=0.175
p=0.2
0
20
40
60
80
100
120
140
0
5
10
15
20
25
30
35
40


Andamento con n=200, N=5, r=3 giorni di malattia, al variare di p, 500 prove
numero medio dei nuovi malati
tempo t
p=0.02
p=0.043
p=0.066
p=0.089
p=0.1
0
2
4
6
8
10
12
0
5
10
15
20
25
30
35
40
45
50


Andamento con n=200, N=5, r=3 giorni di malattia, al variare di p, 500 prove
numero medio dei rimossi
tempo t
p=0.02
p=0.043
p=0.066
p=0.089
p=0.1
0
10
20
30
40
50
60
70
0
5
10
15
20
25
30
35
40
45
50

The SEHIR model

Starting from the previous model, we propose the following generalization, whose justification will be clear in the application to the varicella disease given in the last section.
We will add two new classes E and H in order to take into account the possibility of a latency period and when the individuals are infectious and sick, so often hospitalised.
As before we will assume that any individual will remain in each of these new class for a fixed, deterministic number of days.

To fix the ideas we will assume that:

- the class E includes the individuals in a latency period, when the individual has been infected but is still not infective or sick;
- the previous class I is now divided into two classes, I and H, where individuals are infective, but sick just in the second class. We will denote by $Y_I(t)$ and $Y_H(t)$ the number of individuals at time t in classes I and H, respectively;
- the probability of meeting with individuals in the classes I and H are different, since those in the class H are in hospital or in quarantine.

Any individual, once infected, in a deterministic fashion transits through the states E, I, H, where it remains, respectively, for r_E, r_I and r_H days, after that he becomes removed.
Since r_E, r_I and r_H are deterministic, the model will be similar to that defined in (1) and the state space of this new Markovian model will be again $S_1(n, r)$, where now $r = r_E + r_I + r_H$.
In this case, in order to calculate the probability of contagion at time t, we will **not** consider equal the probabilities to meet an individual in the classes S, E and R.

So, we will deal with three probabilities

- p_I which correspond to the probabilities of meeting an individual belonging to the class I;
- p_H which correspond to the probabilities of meeting an individual belonging to the class H;
- p_S which correspond to the probability of meeting an individual non infective, that is, belonging to the classes S, E and R.

In order to have p_H still proportional to the number of individual present in that class, but at a lower rate than for the I class, since the individuals in H are at some level isolated by the rest of the population, we will multiply this number by a constant $\lambda \in [0, 1]$.

$\lambda = 0$ will characterise the case of a perfect quarantine, adopted for a **severe, contagious disease**.

On the contrary, a value of λ close to 1 will characterise the case of a **mild disease**, like the flu.

With these ingredients, we will define the three values

$$\begin{aligned} p_H &= \frac{\lambda y_H}{n-1} \\ p_I &= \frac{y_I}{n-1-y_H}(1-\frac{\lambda y_H}{n-1}) \\ p_S &= (1-p_I-p_H) = (1-\frac{\lambda y_H}{n-1})(\frac{n-1-y_I-y_H}{n-1-y_H}) \end{aligned} \tag{4}$$

where y_I and y_H denotes the number of individuals in classes I and H, respectively, at time t. Note that when $\lambda \to 1$ we obtain the same probabilities of the model (1), while if $\lambda \to 0$, $p_H = 0$ and we have a perfect quarantine.

Denoting by j_{iI}, j_{iH} the number of meetings of the i-th individual at time t with individuals in the classes I and H, respectively, the probability to meet this proportion of individuals will be approximated by

$$P^{i}_{j_{iI},j_{iH}}(y_I, y_H, N; n) = \sum_{j_{iI},j_{iH}=1}^{N} \frac{N!}{j_{iI}!j_{iH}!j_{iS}!} p_I^{j_{iI}} p_H^{j_{iH}} p_S^{j_{iN}},$$

where $j_{iS} = N - j_{iI} - j_{iH}$ and N denotes the daily encounters of the individual i.

We can also derive the probability of contagion

$$p_{j_{il}+j_{iH}} = 1 - ((1 - q_I)^{j_{il}}(1 - q_H)^{j_{iH}})$$

where q_I and q_H denote the probability of transmission of the specific disease for individuals in the classes I and H, respectively.

Then the probability of contagion at time $t+1$ of a single individual is equal to

$$\begin{aligned}\beta &= P(Y_0^i(t+1)=1|X^i(t)=1, Y_I(t)=y_I, Y_H(t)=y_H)\\ &= \sum_{j_{iI},j_{iH}=1}^{N} p_{j_{iI}+j_{iH}} \frac{N!}{j_{iI}!j_{iH}!j_{iN}!} p_I^{j_{iI}} p_H^{j_{iH}} p_N^{j_{iN}}\\ &= 1 - \sum_{j_{iI},j_{iH}=1}^{N_i(t)} \frac{N_i(t)!}{j_{iI}!j_{iH}!j_{iN}!} (p_I(1-q_I))^{j_{iI}} (p_H(1-q_H))^{j_{iH}} p_N^{j_{iN}}.\end{aligned}$$

Substituing (4), we then get

$$\begin{aligned}\beta &= 1 - (p_I(1-q_I) + p_H(1-q_H) + (1-p_I-p_H))^N\\ &= 1 - \left(1 - \frac{1}{n-1}\left(\frac{y_I(n-1-\lambda y_H)}{n-1-y_H} q_I + \lambda y_H q_H\right)\right)^N\end{aligned}$$

Let V be number of individuals non susceptible, that is, the number of individuals in $E \cup I \cup H \cup R$. We get easily that

$$
\begin{aligned}
&P\Big(V(t+1) = y_E + y_I + y_H + y_R + y | V(t) - V(t - r_E) = y_E, \\
&\qquad V(t - r_E) - V(t - r_E - r_I) = y_I, \\
&\qquad V(t - r_E - r_I) - V(t - r_E - r_I - r_H) = y_H, \\
&\qquad V(t - r_E - r_I - r_H) = y_R\Big) \\
&= \binom{n - y_E - y_I - y_H - y_R}{y} \beta^y (1-\beta)^{n - y_E - y_I - y_H - y_R - y},
\end{aligned}
$$

where $y = 0, 1, 2, \ldots$.

So, the increment in the number of individuals infected has a mean and a variance given by

$$E\Big(V(t+1)-V(t)|V(t)-V(t-r_E)=y_E,\\ V(t-r_E)-V(t-r_E-r_I)=y_I,\\ V(t-r_E-r_I)-V(t-r_E-r_I-r_H)=y_H,\\ V(t-r_E-r_I-r_H)=y_R\Big)=(n-y_E-y_I-y_H-y_R)\beta,$$

and

$$\mathrm{Var}\Big(V(t+1)-V(t)|V(t)-V(t-r_E)=y_E,\\ V(t-r_E)-V(t-r_E-r_I)=y_I,\\ V(t-r_E-r_I)-V(t-r_E-r_I-r_H)=y_H,\\ V(t-r_E-r_I-r_H)=y_R\Big)=(n-y_E-y_I-y_H-y_R)\beta(1-\beta),$$

The basic reproduction number

For the SEIHR model too is possible to calculate the basic reproduction number $\mathcal{R}_0$, at least for small values of the incubation and infection durations.
For example, in the case when $r_I = r_H = 1$ and any r_E, denoting

$$\beta(y_I, y_H, \lambda) = 1 - \left(1 - \frac{1}{n-1}\left(\frac{y_I(n-1-\lambda y_H)}{n-1-y_H} q_I + \lambda y_H q_H\right)\right)^N$$

we get

$$R_0(r_E, 1, 1) = (n-1)\Big[\beta(1,0,\lambda) + \beta(0,1,\lambda) - \beta(1,0,\lambda)\beta(0,1,\lambda)\Big]$$

$$\sim N(q_I + \lambda q_H)$$

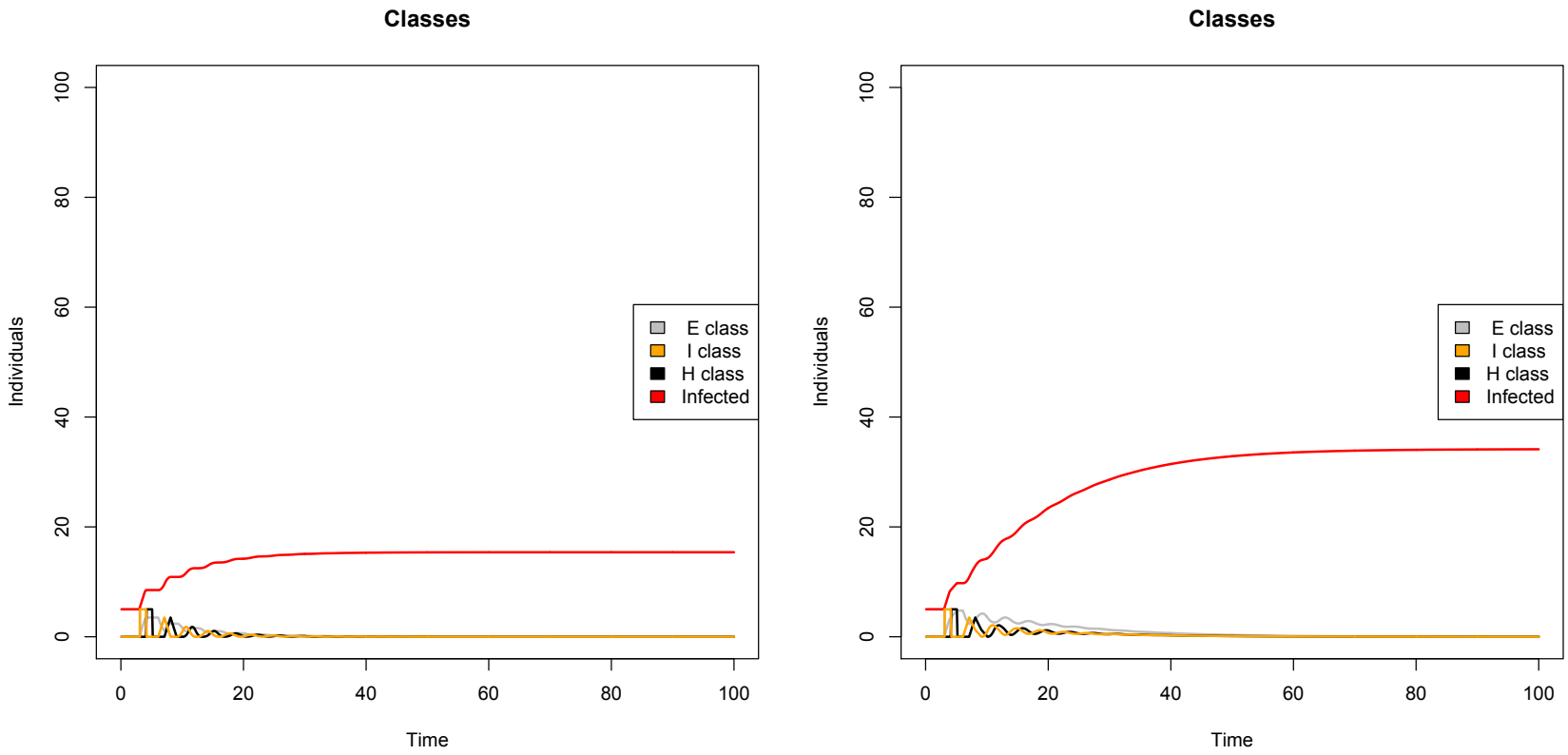


Figure : Spread of the epidemic for $\lambda = 0, 0.25$, $q_I = 0.15$, $q_H = 0.2$, $N = 5$, $n = 100$ and $r_E = 3$.

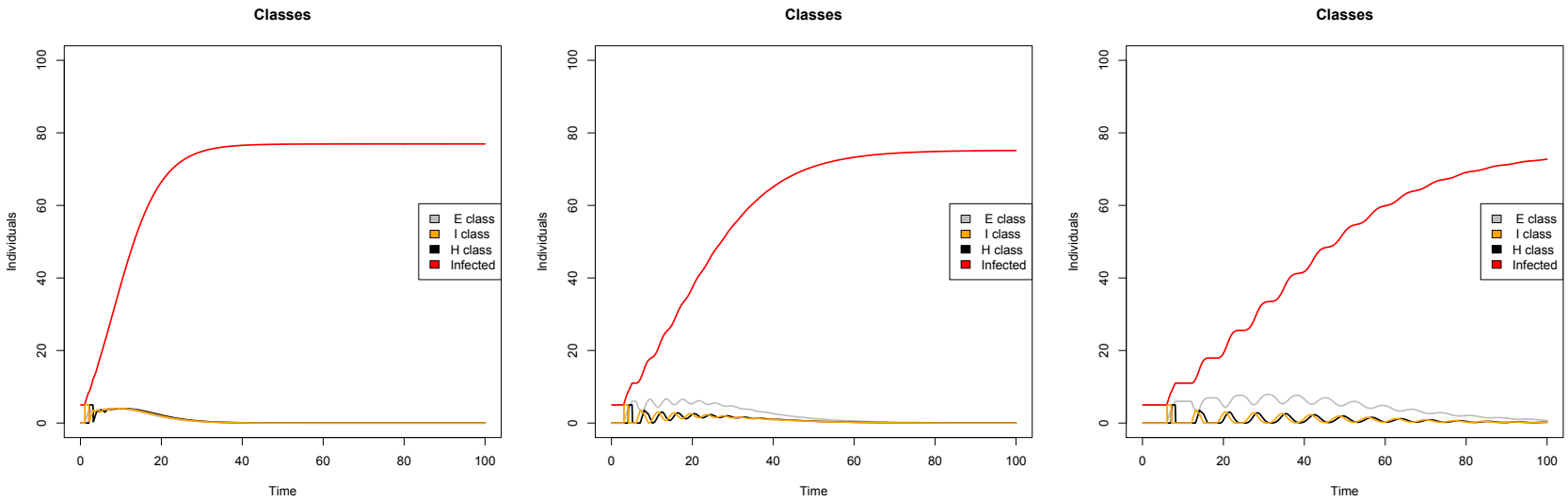


Figure : Spread of the epidemic for $\lambda = 0.5$, $q_I = 0.15$, $q_H = 0.2$,$N = 5$, $n = 100$ and $r_E = 1, 3, 6$.

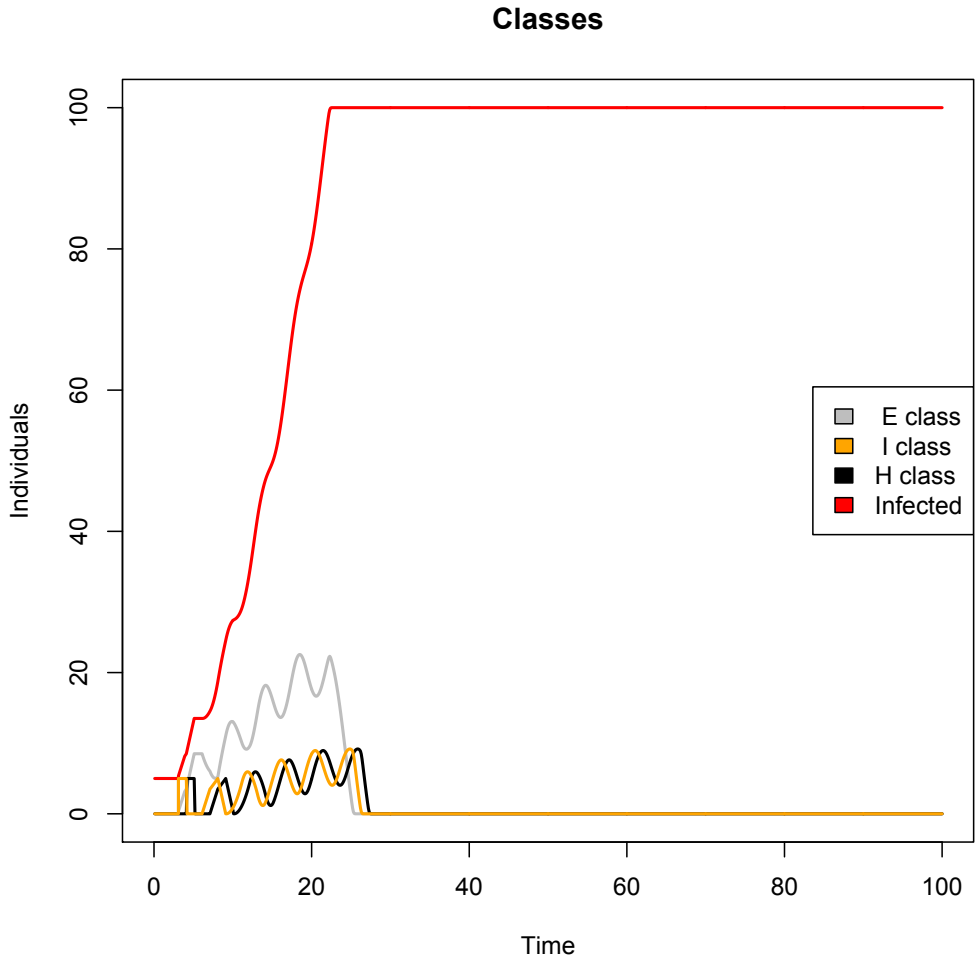


Figure : Spread of the epidemic for $\lambda = 1$, $q_I = 0.15$, $q_H = 0.2$,$N = 5$, $n = 100$ and $r_E = 3$.

Diffusion approximation

Following the ideas in Tuckwell and Williams, the study of the one-step increments of V indicates that for a large population size n and disease infectious probabilities q_I and q_H such that $nN(q_I + q_H)$ is of moderate size, we can approximate a rescaled version of V by a diffusion process. Indeed, if we speed up time and rescale the state to define

$$\hat{V}^n(t) = \frac{V([nt])}{n}, \qquad \text{for all } t > 0,$$

where $[\cdot]$ denotes the integer part, then $\hat{V}^n(t)$ is the fraction of the population that has been infected by the time $[nt]$ in the original time scale of V.

Then for large n and small q_I and q_M such that $\theta_I := nNq_I$ and $\theta_H := nNq_H$ are of moderate size, using again the approximation

$$1 - (1 - x)^N \sim Nx$$

for small x, we can compute the (conditional) mean and variance of

$$\hat{V}^n(t + \Delta t) - \hat{V}^n(t)$$

where $\Delta t = \frac{1}{n}$ and $t \in \{0, \frac{1}{n}, \frac{2}{n}, \ldots\}$.

$$
\begin{aligned}
&E\Big(\hat{V}^n(t+\Delta t)-\hat{V}^n(t)|\hat{V}^n(t)-\hat{V}^n(t-\frac{r_E}{n})=\hat{y}_E,\\
&\quad \hat{V}^n(t-\frac{r_E}{n})-\hat{V}^n(t-\frac{r_E}{n}-\frac{r_I}{n})=\hat{y}_I,\\
&\quad \hat{V}^n(t-\frac{r_E}{n}-\frac{r_I}{n})-\hat{V}^n(t-\frac{r_E}{n}-\frac{r_I}{n}-\frac{r_H}{n})=\hat{y}_H,\\
&\quad \hat{V}^n(t-\frac{r_E}{n}-\frac{r_I}{n}-\frac{r_H}{n})=\hat{y}_R\Big)\\
&\sim (1-\hat{y}_E-\hat{y}_I-\hat{y}_H-\hat{y}_R)N(\frac{1-\lambda\hat{y}_H}{1-\hat{y}_H}q_I\hat{y}_I+\lambda q_M\hat{y}_H)\\
&=(1-\hat{y}_E-\hat{y}_I-\hat{y}_H-\hat{y}_R)(\frac{1-\lambda\hat{y}_H}{1-\hat{y}_H}\theta_I\hat{y}_I+\theta_M\hat{y}_H)\Delta t,
\end{aligned}
$$

and

$$\mathrm{Var}(\hat{V}^n(t+\Delta t) - \hat{V}^n(t) | \hat{V}^n(t) - \hat{V}^n(t-r_E) = \hat{y}_E,$$
$$\hat{V}^n(t - \frac{r_E}{n}) - \hat{V}^n(t - \frac{r_E}{n} - \frac{r_I}{n}) = \hat{y}_I,$$
$$\hat{V}^n(t - \frac{r_E}{n} - \frac{r_I}{n}) - \hat{V}^n(t - \frac{r_E}{n} - \frac{r_I}{n} - \frac{r_H}{n}) = \hat{y}_H,$$
$$\hat{V}^n(t - \frac{r_E}{n} - \frac{r_I}{n} - \frac{r_H}{n}) = \hat{y}_R\Big)$$

$$\sim (1 - \hat{y}_E - \hat{y}_I - \hat{y}_H - \hat{y}_R)\frac{N}{n}(\frac{1 - \lambda\hat{y}_H}{1 - \hat{y}_H} q_I \hat{y}_I + \lambda q_M \hat{y}_H)$$

$$= (1 - \hat{y}_E - \hat{y}_I - \hat{y}_H - \hat{y}_R)\frac{1}{n}(\frac{1 - \lambda\hat{y}_H}{1 - \hat{y}_H} \theta_I \hat{y}_I + \theta_M \hat{y}_H)\Delta t,$$

To simplify the notation from now on we will denote by $\tau_E = \frac{r_E}{n}$, $\tau_{EI} = \tau_E + \frac{r_I}{n}$ and by $\tau_{EIH} = \tau_{EI} + \frac{r_H}{n}$. By the previous computation, we can approximate $\hat{V}^n$ by the diffusion process $\hat{V}$ that lives in $[0,1]$ and satisfies the stochastic delay differential equation

$$\begin{aligned} d\hat{V}_t &= (1-\hat{V}_t)\Big(\theta_I \frac{1-\lambda(\hat{V}_{t-\tau_{EI}} - \hat{V}_{t-\tau_{EIH}})}{1-(\hat{V}_{t-\tau_{EI}} - \hat{V}_{t-\tau_{EIH}})}(\hat{V}_{t-\tau_E} - \hat{V}_{t-\tau_{EI}}) \\ &\qquad + \theta_M(\hat{V}_{t-\tau_{EI}} - \hat{V}_{t-\tau_{EIH}})\Big)dt \\ &+ \Big[(1-\hat{V}_t)\frac{1}{n}\Big(\theta_I \frac{1-\lambda(\hat{V}_{t-\tau_{EI}} - \hat{V}_{t-\tau_{EIH}})}{1-(\hat{V}_{t-\tau_{EI}} - \hat{V}_{t-\tau_{EIH}})}(\hat{V}_{t-\tau_E} - \hat{V}_{t-\tau_{EI}}) \\ &\qquad + \theta_M(\hat{V}_{t-\tau_{EI}} - \hat{V}_{t-\tau_{EIH}})\Big)\Big]^{\frac{1}{2}} dW_t \end{aligned} \tag{5}$$

where W denotes a standard Brownian motion.

Since the periods that an individual remains in each class E, I and H are fixed and deterministic, we can obtain easily the proportion of the population in each class at time t from the process $\hat{V}$.
More precisely, rescaling in the original time scale of V, we have that $\hat{V}_t - \hat{V}_{t-\tau_E}$ gives the proportion of population at time t in the class E, $\hat{V}_{t-\tau_E} - \hat{V}_{t-\tau_{EI}}$ gives the proportion of population in the class I and $\hat{V}_{t-\tau_{EI}} - \hat{V}_{t-\tau_{EIH}}$ gives the proportion of population in the class H.

In order to compare the diffusion with the previous discrete-time model, we present a simulation, using the environment R, about the proportion of infected individuals of both processes for a given set of the parameters. To facilitate direct comparison of the two plots, in the diffusion plot the time has been rescaled by n. It appears clear that both process are very close and the same happens for any other choice of the parameters.

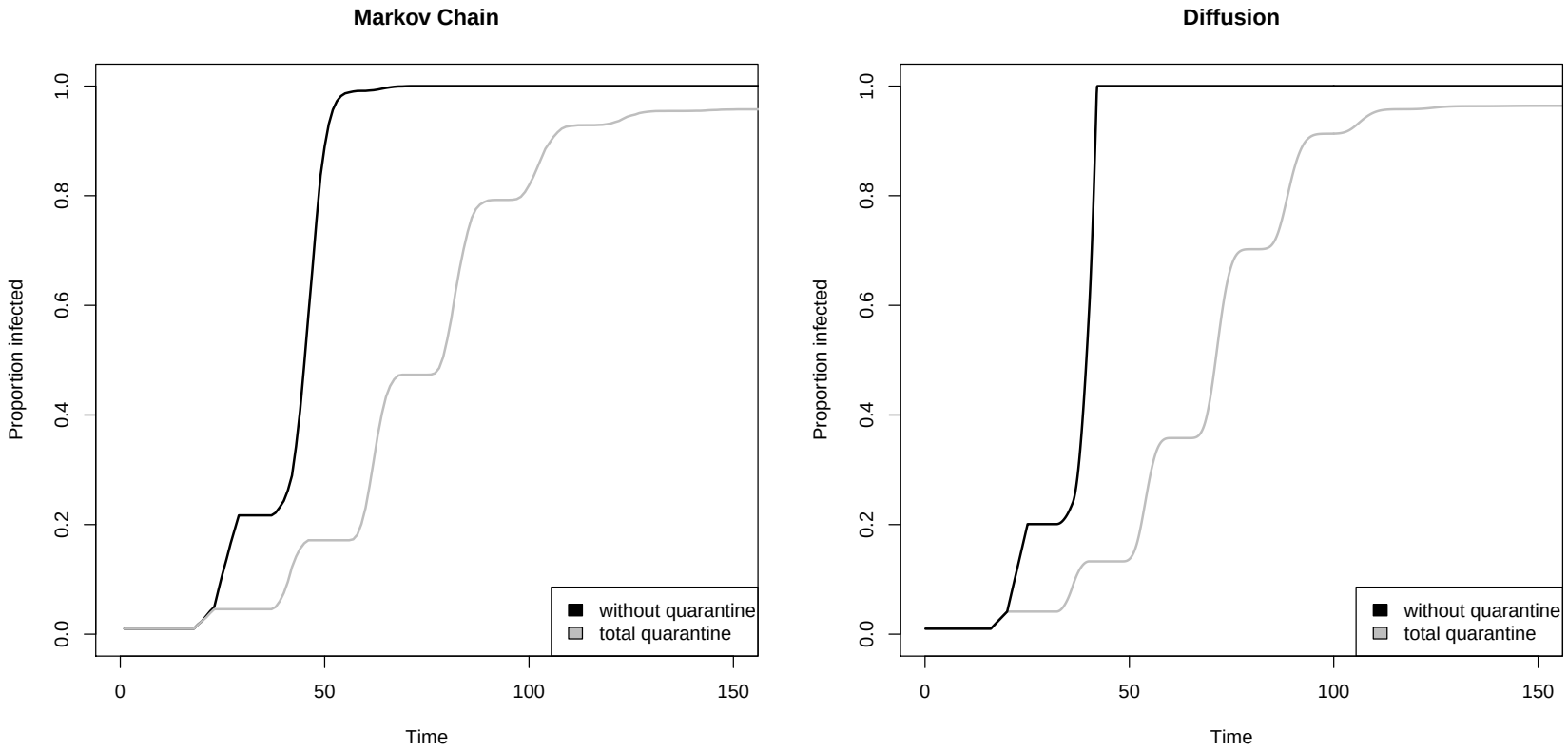


Figure : Comparison of the Markov and diffusion model for $q_I = 0.2, q_H = 0.8$, delays $r_E = 16, r_I = 4, r_H = 5, N = 5, n = 100$ and a unique starting infectious individual.

Varicela

The varicella, common known as chickenpox, is a highly contagious disease caused by primary infection with varicella zoster virus. Chickenpox is an airborne disease which spreads easily through coughing or sneezing of ill individuals or through direct contact with secretions from the rash. The virus is in a latent state for approximatively 15-20 days, and a person is infectious up to four days before the rash appears. They remain contagious until all lesions have crusted over (this takes approximately five days).

This disease can be very well described by a SEIHR model as that defined before. There are 15-20 days of permanency in the class E, then 4-5 days in the class I, when the probability of contagion is approximatively of 65-70%, and other 4-6 in the class H, when the probability of contagion reduces to 18-20%. Therefore to analyse the varicella disease we can use a SEIHR model with:

$$r_E = 16, r_I = 4, r_H = 5, q_I = 0.65 \text{ and } q_H = 0.18.$$

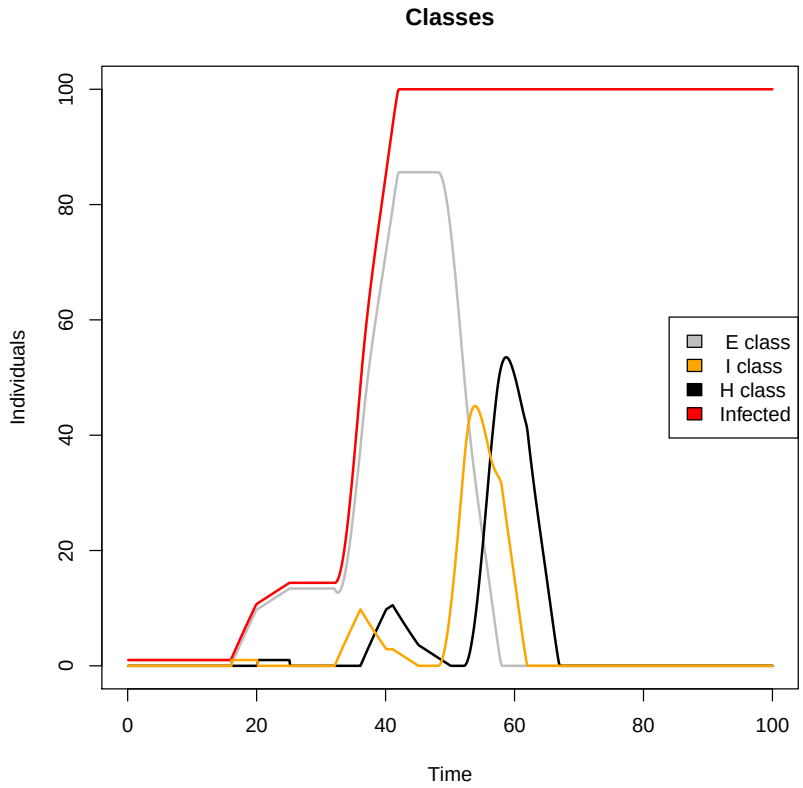


Figure : Multi-peaks evolution of the number of individuals in the various classes when $N = 4, n = 100$, a unique initial infected individual is present and there is no quarantine.

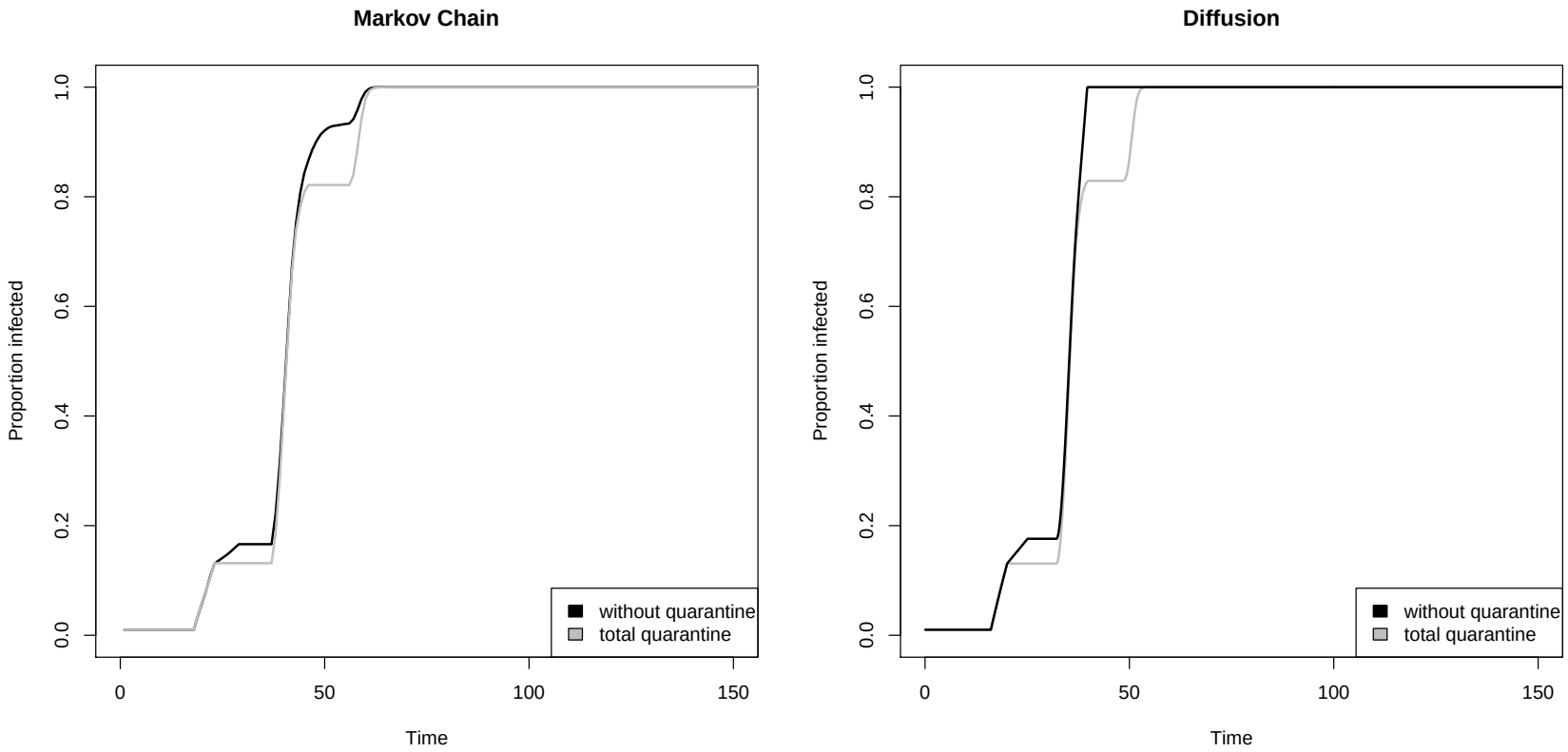


Figure : Comparison of the Markov and diffusive model of varicella disease for $N = 5, n = 100$ and a unique initial infectious individual.

References

[1] H.C.Tuckwell, R.J.Williams: *Some properties of a simple stochastic epidemic model of SIR type*. Math. Biosci. **208** (2007), 76–97.

[2] M.Ferrante, E.Ferraris and C.Rovira: *On a stochastic epidemic SEIHR model and its diffusion approximation*. submitted (2014).

[3] G.Huang, Y.Takeuchi, W.Ma and D.Wei: *Global stability for delay SIR and SEIR epidemic models with nonlinear incidence rate*. Bull. Math. Biol. **72**, 2010, 1192–1207.

[4] C.McCluskey: *Complete global stability for an SIR epidemic model with delay—distributed or discrete*. Nonlinear Anal. Real World Appl. **11**, (2010), 55–59.