Supplementary material: *A unified stochastic modelling framework for the spread of nosocomial infections*

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Abstract

In this Supplementary Material, we discuss about how systems of equations in Ref. [1] can be represented in matrix form and iteratively solved. Moreover, we report here parameter values considered in case studies 1-5 in Ref. [1], obtained from Refs. [2, 3, 4, 5, 6], and summarise in Table S6 the function rates $\lambda_j(i_1,\ldots,i_M)$, $\mu_j(i_1,\ldots,i_M)$ and $\delta(i_1,\ldots,i_M)$ for these case studies.

1 Matrix-oriented solutions

1.1 Number of infections caused by an individual at compartment j until he/she is removed or the outbreak is detected

The objective here is to compute probabilities

$$\nu^{(j)}_{(i_1,\ldots,i_M)}(n) \;=\; \mathbb{P}(R^{(j)}_{(i_1,\ldots,i_M)}=n), \quad n\geq 0,$$

by solving the systems of equations given by [1, Eq. (2.3)]. We can rewrite this system into a matrix equation of the form

$$\mathbf{D}^{(j)}\boldsymbol{\nu}^{(j)}(n) \;=\; \mathbf{e}^{(j)}(n), \tag{1}$$

where matrix $\mathbf{D}^{(j)}$ is independent of the value $n\geq 0$, while column vectors $\boldsymbol{\nu}^{(j)}(n)$ and $\mathbf{e}^{(j)}(n)$ depend on this value. In particular,

$$\begin{aligned}
(\mathbf{D}^{(j)})_{(i_1,\ldots,i_M),(i_1,\ldots,i_k-1,\ldots,i_M)} &= \frac{1}{\theta_{(i_1,\ldots,i_M)}}\mu_k\left(i_k 1_{k\neq j}\right.\\
&\quad \left.+(i_k-1)1_{k=j}\right), \quad 1\leq k\leq M,\\
(\mathbf{D}^{(j)})_{(i_1,\ldots,i_M),(i_1,\ldots,i_k+1,\ldots,i_M)} &= \frac{1}{\theta_{(i_1,\ldots,i_M)}}\Bigg(\lambda_k\\
&\quad + \sum_{l=1,\ l\neq j}^{M}\lambda_{lk}i_l+(i_j-1)\lambda_{jk}\Bigg)(N_k-i_k), \quad 1\leq k\leq M,\\
(\mathbf{e}^{(j)}(n))_{(i_1,\ldots,i_M)} &= \frac{1}{\theta_{(i_1,\ldots,i_M)}}\Bigg(1_{n>0}\sum_{k=1}^{M}(N_k-i_k)\lambda_{jk}\\
&\quad \times\nu^{(j)}_{(i_1,\ldots,i_k+1,\ldots,i_M)}(n-1)+1_{n=0}(\mu_j+\delta(i_1,\ldots,i_M))\Bigg).
\end{aligned}$$

Dimensionality of system in Eq. (1) is not $\#\mathcal{C} = \prod_{k=1}^{M}(N_k+1)$, but $N_j\prod_{k=1,\ k\neq j}^{M}(N_k+1)$, since probabilities $\nu^{(j)}_{(i_1,\ldots,i_M)}(n)$ are only defined for states $(i_1,\ldots,i_M)\in\mathcal{C}$ with $i_j>0$. Moreover, we are storing in Eq. (1) probabilities $\nu^{(j)}_{(i_1,\ldots,i_M)}(n)$ in the column vector

$$\boldsymbol{\nu}^{(j)}(n) \;=\; \begin{pmatrix}
\nu^{(j)}_{(0,0,\ldots,0,0)}(n)\\
\nu^{(j)}_{(0,0,\ldots,0,1)}(n)\\
\nu^{(j)}_{(0,0,\ldots,0,2)}(n)\\
\vdots\\
\nu^{(j)}_{(0,0,\ldots,0,N_M)}(n)\\
\nu^{(j)}_{(0,0,\ldots,1,0)}(n)\\
\nu^{(j)}_{(0,0,\ldots,1,1)}(n)\\
\nu^{(j)}_{(0,0,\ldots,1,2)}(n)\\
\vdots\\
\nu^{(j)}_{(N_1,N_2,\ldots,N_{M-1},N_M)}(n)
\end{pmatrix},$$

so that each row in this matrix system represents a state $(i_1,\ldots,i_M)\in\mathcal{C}$, with $i_j>0$. Due to the lexicographic order followed above when ordering these states by rows, each state $(i_1,\ldots,i_M)$ with $i_j>0$ corresponds to the $\sum_{k=1}^{M}(1_{k\neq j}i_k+1_{k=j}(i_j-1))\prod_{p=k+1}^{M}(1_{p\neq j}(N_p+1)+1_{p=j}N_p)^{th}$ row (*i.e.*, equation) in Eq. (1). Finally, since matrix $\mathbf{D}^{(j)}$ is significantly sparse, for numerical results in [1, Section 3] we solve this system of linear equations by using the *scipy.sparse.linalg* Python package. This involves solving Eq. (1) for $n=0$, and then iteratively solving it for values $n\geq 1$ using probabilities $\nu^{(j)}_{(i_1,\ldots,i_M)}(n-1)$, which are stored in column vector $\boldsymbol{\nu}^{(j)}(n-1)$ previously computed.

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1.2 Number of infections caused by an individual at compartment j, among individuals at compartment k, until he/she is removed or the outbreak is detected

The objective here is to compute probabilities

$$\nu^{(j)}_{(i_1,\dots,i_M)}(k;n) \quad = \quad \mathbb{P}(R^{(j)}_{(i_1,\dots,i_M)}(k)=n), \quad n\geq 0,$$

by solving the systems of equations given by [1, Eq. (2.2)]. Again, we can construct and iteratively solve matrix systems of the form

$$\mathbf{D}^{(j)}(k)\boldsymbol{\nu}^{(j)}(k;n) \quad = \quad \mathbf{e}^{(j)}(k;n),$$

where

$$(\mathbf{D}^{(j)}(k))_{(i_1,\dots,i_M),(i_1,\dots,i_l-1,\dots,i_M)} = \frac{1}{\theta_{(i_1,\dots,i_M)}}\mu_l\left(i_l 1_{l\neq j}\right. \\ \left.+(i_l-1)1_{l=j}\right), \quad 1\leq l\leq M,$$

$$(\mathbf{D}^{(j)}(k))_{(i_1,\dots,i_M),(i_1,\dots,i_l+1,\dots,i_M)} = \frac{1}{\theta_{(i_1,\dots,i_M)}}\Bigg(1_{l\neq k}\,(\lambda_l \\ +\sum_{p=1}^{M}\lambda_{pl}i_p)(N_l-i_l)+1_{l=k}(\lambda_l+\sum_{p=1,\ p\neq j}^{M}\lambda_{pl}i_p \\ +\lambda_{jl}(i_j-1))\,(N_l-i_l)\Bigg), \quad 1\leq l\leq M,$$

$$(\mathbf{e}^{(j)}(k;n))_{(i_1,\dots,i_M)} = \frac{1}{\theta_{(i_1,\dots,i_M)}}\Bigg(1_{n>0}(N_k-i_k)\lambda_{jk} \\ \times\,\nu^{(j)}_{(i_1,\dots,i_k+1,\dots,i_M)}(k;n-1)+1_{n=0}(\mu_j+\delta(i_1,\dots,i_M))\Bigg),$$

and where probabilities $\nu^{(j)}_{(i_1,\dots,i_M)}(k;n)$ are stored in the column vectors $\boldsymbol{\nu}^{(j)}(k;n)$, as in subsection 1.1 of this Supplementary Material.

2 Parameter values for case studies 1-5

In Tables S1-S5, we report parameter values considered in case studies 1-5 in Ref. [1], directly obtained from Refs. [2, 3, 4, 5, 6]. In Table S6, we summarise the functional forms of rates $\lambda_j(i_1,\dots,i_M)$, $\mu_j(i_1,\dots,i_M)$ and $\delta(i_1,\dots,i_M)$ for case studies 1-5, according to the corresponding model assumptions and model parameters described in Ref. [1].

	Meaning	Value
N_p	Number of patients	20
N_{HCW}	Number of HCWs	3
μ	Patient discharge rate	0.1
γ	Patient detection rate	0.1
μ'	HCW hand-washing rate	14
β	HCW-to-patient colonization rate	$\frac{1}{6}$
β'	Patient-to-HCW contamination rate	$\frac{1}{6}$
σ	Fraction of admitted patients colonized	0.01

Table S1: Parameter values from Artalejo (2014) [2], for the spread of MRSA in an hypothetical intensive care unit. Time units: *days*. Case study 1

	Meaning	RICU
N_P	Number of patients	7
N_{HCW}	Number of HCWs	14
N_V	Number of volunteers	2
φ	Fraction of admitted patients colonized	0.165
$\frac{1}{\delta_U}$	Length of stay, non-colonized patients	7
$\frac{1}{\delta_C}$	Length of stay, colonized patients	13
η	Hygienic level, HCW-patient	0.46
ξ	Hygienic level, volunteer-patient	0.23
β_{PH}	Patient-HCW contact rate	0.72
β_{PV}	Patient-volunteer contact rate	0.20
γ_H	HCW hand-washing rate	24
γ_V	Volunteer hand-washing rate	12

Table S2: Parameter values from Wang et al. (2011) [3], for the spread of MRSA in the Respiratory Intensive Care Unit (RICU) at Beijing Tongren Hospital. Time units: *days*. Case study 2

	Meaning	Value
N_p	Number of patients	20
N_s	Number of HCWs	5
N_e	Number of surfaces	100
ϕ	Fraction of admitted patients colonized	0.1
γ	Discharge rate, non-colonized patients	0.1
γ'	Discharge rate, colonized patients	0.05
μ	Staff decontamination rate	24
κ	Surfaces decontamination rate	1
β_{sp}	Staff-to-patient colonization rate	0.3
β_{se}	Staff-to-surface contamination rate	2
β_{ps}	Patient-to-staff contamination rate	2
β_{pe}	Patient-to-surface contamination rate	2
β_{es}	Surface-to-staff contamination rate	2
β_{ep}	Surface-to-patient colonization rate	0.3

Table S3: Parameter values from Wolkewitz et al. (2008) [4], for an VRE outbreak in the onco-haematological unit at the University Medical Center Freiburg in Germany. Time units: *days*. Case study 3

References

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		Rate function			
CS	M	$\mu_j(i_1,\ldots,i_M)=\mu_j i_j$	$\lambda_j(i_1,\ldots,i_M)=(N_j-i_j)\left(\lambda_j+\sum\limits_{k=1}^{M}\lambda_{kj}i_k\right)$		$\delta(i_1,\ldots,i_M)$
1	2	$\mu_1=(1-\sigma)\mu$, $\mu_2=\mu'$	$\lambda_1=\sigma\mu$, $\lambda_2=0$	$\lambda_{12}=\beta'$, $\lambda_{21}=\beta$	$\delta(i_1,i_2)=\gamma i_1$
2	3	$\mu_1=\delta_C(1-\varphi)$, $\mu_2=\gamma_H$ $\mu_3=\gamma_V$	$\lambda_1=\delta_U\varphi$, $\lambda_2=0$ $\lambda_3=0$	$\lambda_{12}=\frac{1-\eta}{N_P}\beta_{PH}$, $\lambda_{13}=\frac{1-\xi}{N_P}\beta_{PV}$ $\lambda_{21}=\frac{1-\eta}{N_P}\beta_{PH}$, $\lambda_{23}=0$ $\lambda_{31}=\frac{1-\xi}{N_P}\beta_{PV}$, $\lambda_{32}=0$	$\delta(i_1,i_2,i_3)=0$
3	3	$\mu_1=\gamma'(1-\phi)$, $\mu_2=\mu$ $\mu_3=\kappa$	$\lambda_1=\gamma\phi$, $\lambda_2=0$ $\lambda_3=0$	$\lambda_{12}=\frac{\beta_{ps}}{N_p}$, $\lambda_{13}=\frac{\beta_{pe}}{N_p}$ $\lambda_{21}=\frac{\beta_{sp}}{N_s}$, $\lambda_{23}=\frac{\beta_{se}}{N_s}$ $\lambda_{31}=\frac{\beta_{ep}}{N_e}$, $\lambda_{32}=\frac{\beta_{es}}{N_e}$	$\delta(i_1,i_2,i_3)=0$
4	4	$\mu_j=\nu(1-p_C)$, $1\le j\le 4$	$\lambda_j=\nu p_C+\lambda$, $1\le j\le 4$	$\lambda_{jk}=\beta_{DR}$, $1\le j\ne k\le 4$ $\lambda_{jj}=\beta_{SR}$, $1\le j\le 4$	$\delta(i_1,\ldots,i_4)=0$
5	11	$\mu_j=\gamma$, $1\le j\le 4$ $\mu_j=\mu$, $5\le j\le 11$	$\lambda_j=0$, $1\le j\le 11$	$\lambda_{51}=\lambda_{15}=\lambda_{62}=\lambda_{26}=\beta_{AP1}$ $\lambda_{73}=\lambda_{37}=\lambda_{84}=\lambda_{48}=\beta_{AP1}$ $\lambda_{91}=\lambda_{19}=\lambda_{92}=\lambda_{29}=\beta_{AP2}$ $\lambda_{10,3}=\lambda_{3,10}=\lambda_{10,4}=\lambda_{4,10}=\beta_{AP2}$ $\lambda_{11,1}=\lambda_{1,11}=\lambda_{11,2}=\lambda_{2,11}=\beta_{Peri}$ $\lambda_{11,3}=\lambda_{3,11}=\lambda_{11,4}=\lambda_{4,11}=\beta_{Peri}$ For others (j,k): $\lambda_{jk}=0$	$\delta(i_1,\ldots,i_{11})=0$

Table S6: Functional forms for case studies 1-5 (CS 1-5)

	Meaning	Value
N_p	Number of patients	9
ν	Discharge rate	0.1
p_C	Fraction of admitted patients colonized	0.01
β_{DR}	Cross-colonization rate, different rooms	0.0238
β_{SR}	Cross-colonization rate, same room	0.0366
λ	Spontaneous colonization rate	0.0037

Table S4: Parameter values from López-García (2016) [5], for an MRSA outbreak in an intensive care unit with four rooms. Parameter values ν and p_C from Artalejo et al. (2014) [2]. Time units: *days*. Case study 4

	Meaning	Value
β_{AP1}	Patient-AP1 transmission rate	0.35
β_{AP2}	Patient-AP2 transmission rate	0.12
β_{Peri}	Patient-peripatetic transmission rate	0.07
μ	Hand-washing rate for all HCWs	$1-24$
γ^{-1}	Length of stay for all patients	10

Table S5: Parameter values from Temime et al. (2009) [6], for a bacterial outbreak in an hypothetical intensive-care unit. Time units: *days*. Case study 5

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