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Communication

On the Redundancy of Birth and Death Rates in Homogeneous Epidemic SIR Models

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Abstract: The dynamics of fractional population sizes $y_i = Y_i/N$ in homogeneous compartment models with time-dependent total population N is analyzed. Assuming constant per capita birth and death rates, the vector field $\dot{Y}_i = V_i(Y)$ naturally projects to a vector field $F_i(Y)$ tangent to the leaves of constant population N. A universal formula for the projected field F_i is given. In this way, in many SIR-type models with standard incidence, all demographic parameters become redundant for the dynamical system $\dot{y}_i = F_i(y)$. They may be put to zero by shifting the remaining parameters appropriately. Normalizing eight examples from the literature this way, they unexpectedly become isomorphic for corresponding parameter ranges. Thus, some recently published results turn out to have been covered already by papers 20 years ago.

Keywords: SIRS model; demographic parameters; birth and death rates; parameter reduction; normalization

MSC: 34C23; 34C26; 37C25; 92D30

1. Introduction

The classic SIR model was introduced by Kermack and McKendrick in 1927 [1] as one of the first models in mathematical epidemiology. The model divides a population into three compartments with fractional sizes S (Susceptibles), I (Infectious) and R (Recovered), such that $S + I + R = 1$. The flow diagram between compartments, as given in Figure 1, leads to the dynamical system

$$\dot{S} = -\beta SI, \qquad \dot{I} = \beta SI - \gamma I, \qquad \dot{R} = \gamma I. \tag{1}$$

Figure 1. Flow diagram of the SIR model.

Here, γ denotes the recovery rate and β the effective contact rate (i.e., the number of contacts/time leading to infection of a Susceptible, given the contacted was infectious). Members of R are supposed to be immune forever. Due to (1), S decreases monotonically, eventually causing $\beta S < \gamma$ and $\dot{I} < 0$. At the end, the disease dies out, $I(\infty) = 0$, and one stays with a nonzero final size $S(\infty) > 0$, thus providing a model for *Herd immunity*.

To construct models also featuring *endemic* scenarios one needs enough supply of susceptibles to keep the incidence βSI ongoing above a positive threshold. The literature discusses three basic methods to achieve this, see Figure 2.

- Heathcote's *classic endemic model* adds balanced birth and death rates μ to the SIR model and assumes all newborns are susceptible. This leads to a bifurcation from a stable disease-free equilibrium point to a stable endemic scenario when raising the basic reproduction number $r_0 = \beta/\gamma$ above one [2–4].

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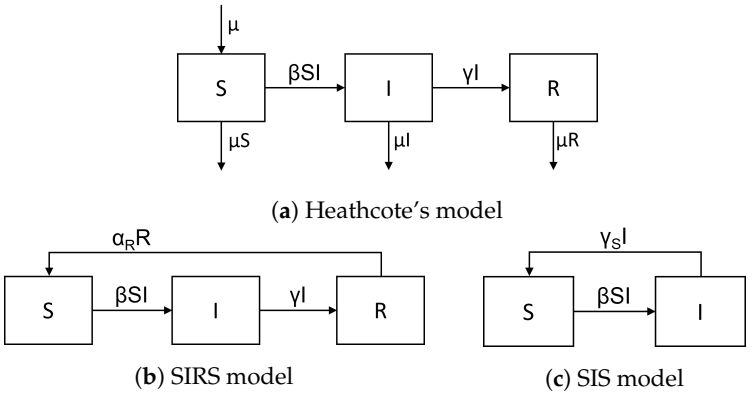
- The *SIRS model* adds an immunity waning flow, $\alpha_R R$ from R to S, to the SIR model, leading to the same result.
- The *SIS model* considers recovery without immunity, i.e., a recovery flow $\gamma_S I$ from I to S, while putting $R = 0$. Again, this leads to the same result.



(**a**) Heathcote's model

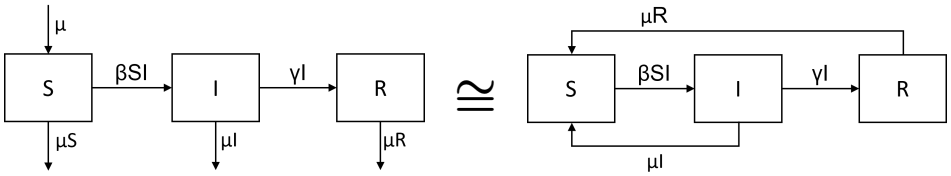
(**b**) SIRS model

(**c**) SIS model

Figure 2. Standard models featuring endemic equilibria.

In what follows the reader is assumed to be familiar with the basic notions in these models. For a comprehensive and self-contained overview of the history, methods and results in mathematical epidemiology see the textbook by M. Martcheva [5], wherein an extensive list of references to original papers is also given.

As a starting point for this paper, observe, from Figure 3, that Heathcote's model could equivalently be reformulated by disregarding birth and death rates and instead introducing a combined SI(R)S ≡ SIRS/SIS model with flow rates $\gamma_S = \alpha_R = \mu$. More generally, adding Heathcote's balanced birth and death rates μ to a SI(R)S model with independent parameters (γ_S, α_R) apparently becomes equivalent to considering the SI(R)S model without birth and death rates and with shifted parameters $\tilde{\gamma}_S = \gamma_S + \mu$ and $\tilde{\alpha}_R = \alpha_R + \mu$ [6].



(**a**) Heathcote's model

(**b**) SI(R)S model

Figure 3. Equivalence of models using $\mu - \mu S = \mu I + \mu R$.

The aim of this paper is to generalize this observation to homogeneous three-compartment models with the following:

(A) positive susceptibility of the R-compartment describing incomplete immunity (in which case it makes sense to rename $S \equiv S_1$ and $R \equiv S_2$),

(B) a non-trivial birth matrix and a time varying population size N due to the compartment-dependent constant per capita birth and death rates.

As a result, we see that, for coinciding birth minus death rates in compartments $S_1 \equiv S$ and $S_2 \equiv R$, in the dynamics of fractional variables, all demographic parameters become redundant by shifting the remaining parameters appropriately. In particular, transmission coefficients β_i describing S_i-susceptibility are replaced by $\tilde{\beta}_i = \beta_i - \Delta\mu_I$, where $\Delta\mu_I$ denotes the excess mortality in compartment I. Hence, $\tilde{\beta}_i$ may possibly become negative.

This result leads to a unifying normalization prescription when always considering these models without vital dynamics and, instead, with two distinguished, and possibly also negative, incidence rates $\tilde{\beta}_i \in \mathbb{R}$. When normalized this way, seemingly different models in the literature become isomorphic at coinciding shifted parameters. As an example, the recent results in [7] follow from earlier results in [8] (for $\tilde{\beta}_2 > 0$) and [9] (for $\tilde{\beta}_2 < 0$).

2. Compartment Models

For simplicity, all maps are supposed to be $\mathcal{C}^\infty$. Let $\mathcal{V} = \mathbb{R}^n$ and $V : \mathcal{V} \to \mathcal{V}$ be a homogeneous vector field, $V(\lambda Y) = \lambda V(Y)$ for all $\lambda \in \mathbb{R}_+$ and $Y \in \mathcal{V}$. Denote $\mathcal{V}^*$ the dual of $\mathcal{V}$ and $\langle \cdot | \cdot \rangle : \mathcal{V}^* \otimes \mathcal{V} \to \mathbb{R}$ the dual pairing. Let $\phi_t : \mathcal{V} \to \mathcal{V}$ be the local flow of V. For functions $f : \mathcal{V} \to \mathbb{R}$ we denote their time derivative along ϕ_t by $\dot{f} := d/dt|_{t=0}(f \circ \phi_t) = \langle \nabla f | V \rangle$. Let $0 \notin \mathcal{P} \subset \mathcal{V}$ be a cone and $N : \mathcal{P} \to \mathbb{R}_+$ be a homogeneous function, $N(\lambda Y) = \lambda N(Y)$, satisfying $\nabla N \neq 0$ on $\mathcal{P}$. In this case, the local flow ϕ_t naturally projects to a local flow ψ_t, leaving the leaves $\{N = \text{const.}\}$ invariant.

$$\psi_t(Y) := N(Y) N(\phi_t(Y))^{-1} \phi_t(Y)$$

Using $\phi_t(\lambda Y) = \lambda \phi_t(Y)$ one immediately checks

$$\psi_0 = \mathrm{id}, \qquad \psi_{t+s} = \psi_t \circ \psi_s, \qquad N \circ \psi_t = N\,.$$

The vector field $F : \mathcal{P} \to \mathbb{R}^n$ generating ψ_t is given by

$$F(Y) := V(Y) - \frac{\dot{N}}{N} Y \quad \Longrightarrow \quad \dot{\psi}_t = F \circ \psi_t\,. \tag{2}$$

Clearly, F is also homogeneous and by putting $y := Y/N$ we have $\dot{y} = F(y)$.

Now, let us focus specifically on compartment models,= where Y_i gives the population in compartment i, $N(Y) := \sum_i Y_i$ the total population and $\mathcal{P} := \mathbb{R}^n_{\geq 0} \setminus \{\mathbf{0}\}$. To guarantee $\mathcal{P}$ being forward invariant one also needs $Y_i = 0 \Rightarrow V_i(Y) \geq 0$.

Definition 1. *The compartment model $\dot{Y} = V(Y)$ is said to have constant per capita demographic rates, if there exists $\nu = (\nu_1, \cdots, \nu_n) \in \mathcal{V}^*$, such that $\dot{N} = \nu$, i.e., $\sum_i V_i(Y) = \sum_i \nu_i Y_i$. We call ν_i the total birth minus death rate in compartment i.*

In such models, one usually decouples the time development of N and analyzes the dynamics of fractional variables $y = Y/N$, $\dot{y} = F(y)$. The main observation of this paper states that, in many standard models, the correction term $N^{-1}\dot{N}Y$ in Equation (2) can be absorbed by redefining the parameters determining V.

Lemma 1. *Assume $\dot{N} = \nu$ and denote $Q_{ijk} = [\delta_{ij}(\nu_k - \nu_j) + \delta_{ik}(\nu_j - \nu_k)]/2$. Putting $Q_i(Y) := \sum_{j,k} Q_{ijk} Y_j Y_k$ we have*

$$\frac{\dot{N}}{N} Y_i = \nu_i Y_i + \frac{1}{N} Q_i(Y) \tag{3}$$

Proof. Use $y_i = 1 - \sum_{j \neq i} y_j$ and, therefore, $\langle \nu | y \rangle = \nu_i + \sum_j (\nu_j - \nu_i) y_j$, for all $i = 1, \cdots, n$. □

Let us apply this to vector fields V of the form

$$V_i(Y) = \sum_j L_{ij} Y_j + \sum_j M_{ij} Y_j + \frac{1}{N} \sum_{j,k} \Lambda_{ijk} Y_j Y_k\,, \tag{4}$$

where $\Lambda_{ijk} = \Lambda_{ikj}$, $\sum_i M_{ij} = \sum_i \Lambda_{ijk} = 0$ and $L_{ij} = B_{ij} - \delta_{ij}\mu_j$. Here, $\mu_j \geq 0$ is the mortality rate in compartment j, $B_{ij} Y_j \geq 0$ denotes the number of newborns from compartment j landing in compartment i, and the parameters M_{ij} and Λ_{ijk} determine the population flow from compartment j to i, due to infection transmission, recovery, loss of immunity, vaccination, etc. Thus, $\delta_j := \sum_i B_{ij}$ is the total birth rate in compartment j and $\nu_j = \sum_i L_{ij} = \delta_j - \mu_j$. Forward invariance of the non-negative orthant $\mathcal{P}$ for zero birthrates requires (a) M to be essentially non-negative, i.e., $M_{ij} \geq 0$ for $i \neq j$, whence $M_{jj} = -\sum_{i \neq j} M_{ij} \leq 0$, and (b) $\sum_{k \neq i} \Lambda_{ijk} \geq -M_{ij}$ for $i \neq j$. Now put

$$\tilde{M}_{ij} := M_{ij} + L_{ij} - \delta_{ij}\nu_j \equiv M_{ij} + B_{ij} - \delta_{ij}\delta_j\,, \qquad \tilde{\Lambda}_{ijk} := \Lambda_{ijk} - Q_{ijk}\,. \tag{5}$$

Using $B_{ij} \geq 0$, $Q_{ijk} = Q_{ikj}$, $\sum_i Q_{ijk} = 0$ and $Q_{ijk} = 0$ for $j \neq i \neq k$, the new parameters $\tilde{M}$ and $\tilde{\Lambda}$ have the same properties as M and Λ and we obtain

$$F_i(Y) = \sum_j \tilde{M}_{ij}Y_j + \frac{1}{N}\sum_{j,k}\tilde{\Lambda}_{ijk}Y_jY_k\,. \tag{6}$$

Hence, in the dynamics for fractional variables $y = Y/N$, all birth and death rates may be absorbed by redefining M and Λ. Note that standard models typically satisfy $\Lambda_{ijj} = 0$, which is consistent with $Q_{ijj} = 0$. On the other hand, $\tilde{\Lambda}_{iik} = \tilde{\Lambda}_{iki}$ might change sign as compared to epidemiological requirements.

Remark 1. *If the vector field V is of the form (4), with μ_i replaced by $\Delta\mu_i + f(Y)$ for some function f, and constant excess mortality $\Delta\mu_i$, then V is no longer homogeneous but still $\dot{y} = N^{-1}F(Y)$. In this case, Equation (3) still holds with $\nu_i := \delta_i - \Delta\mu_i - f(Y)$. Hence, the function f does not appear in the definition of $\tilde{M}$ and $\tilde{\Lambda}$ in (5), implying that F in Equation (6) is independent of f and still homogeneous, whence $\dot{y} = F(y)$.*

3. The Three-Compartment Master Model

As a kind of master example, consider an abstract SI(R)S-type model consisting of three compartments, $\mathbb{S}_1$, $\mathbb{S}_2$ and $\mathbb{I}$, with total population $N = \mathbb{S}_1 + \mathbb{S}_2 + \mathbb{I}$. Members of $\mathbb{I}$ are infectious, members of $\mathbb{S}_1$ are highly susceptible (not immune) and members of $\mathbb{S}_2$ are less susceptible (partly immune). The flow diagram between compartments is completely symmetric with respect to permuting $1 \leftrightarrow 2$, and is depicted in Figure 4.

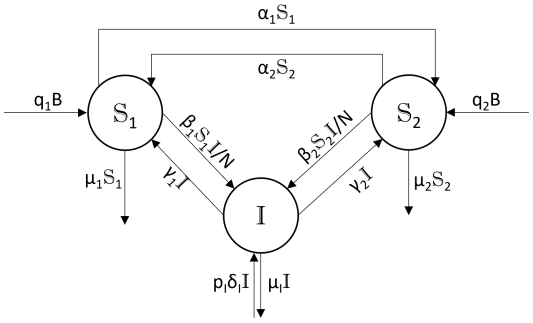


Figure 4. Flow diagram of the master model. $B = \delta_1\mathbb{S}_1 + \delta_2\mathbb{S}_2 + (1 - p_I)\delta_I\mathbb{I}$ denotes the number of newborns who are not infected per unit of time.

The parameters in this model are:

α_1: Vaccination rate.
α_2: Immunity waning rate.
β_i: Number of effective contacts per unit time of a susceptible from $\mathbb{S}_i$.
γ_i : Recovery rate from $\mathbb{I} \to \mathbb{S}_i$.
μ_i: Mortality rate in $\mathbb{S}_i$.
μ_I: Mortality rate in $\mathbb{I}$.
p_I: Probability of a newborn from $\mathbb{I}$ to be infected.
δ_I: Rate of newborns from $\mathbb{I}$.
δ_i: Rate of newborns from $\mathbb{S}_i$. These newborns are not supposed to be infected.
B: Sum of newborns who are not infected, $B = \delta_1\mathbb{S}_1 + \delta_2\mathbb{S}_2 + (1 - p_I)\delta_I\mathbb{I}$.
q_i: Portion of newborns who are not infected landing in $\mathbb{S}_i$, $q_1 + q_2 = 1$. So, q_2 is the portion of newborns who are not infected and who are vaccinated.

All parameters are assumed to be non-negative. Furthermore, $p_I \leq 1$, $q_1 + q_2 = 1$, $\beta_1 + \beta_2 > 0$ and $\gamma_1 + \gamma_2 > 0$. Putting $B := \delta_1 \mathbb{S}_1 + \delta_2 \mathbb{S}_2 + (1 - p_I)\delta_I \mathbb{I}$ the dynamics is given by

$$\dot{\mathbb{S}}_1 = q_1 B + \gamma_1 \mathbb{I} - [\mu_1 + \alpha_1 + \beta_1 \mathbb{I}/N]\mathbb{S}_1 + \alpha_2 \mathbb{S}_2 \tag{7}$$

$$\dot{\mathbb{S}}_2 = q_2 B + \gamma_2 \mathbb{I} - [\mu_2 + \alpha_2 + \beta_2 \mathbb{I}/N]\mathbb{S}_2 + \alpha_1 \mathbb{S}_1 \tag{8}$$

$$\dot{\mathbb{I}} = [\beta_1 \mathbb{S}_1/N + \beta_2 \mathbb{S}_2/N - \gamma_1 - \gamma_2 - \mu_I + p_I \delta_I]\, \mathbb{I} \tag{9}$$

So, in total, this model counts 14 independent parameters. A list of prominent examples is discussed below. Let us now cast this model into the formalism of Section 2. Putting $Y = (\mathbb{S}_1, \mathbb{S}_2, \mathbb{I})^T$ and $\Lambda_i(Y) = \sum_{j,k} \Lambda_{ijk} Y_j Y_k$ we have

$$M = \begin{pmatrix} -\alpha_1 & \alpha_2 & \gamma_1 \\ \alpha_1 & -\alpha_2 & \gamma_2 \\ 0 & 0 & -\gamma_1 - \gamma_2 \end{pmatrix} \qquad L = \begin{pmatrix} q_1\delta_1 - \mu_1 & q_1\delta_2 & q_1(1-p_I)\delta_I \\ q_2\delta_1 & q_2\delta_2 - \mu_2 & q_2(1-p_I)\delta_I \\ 0 & 0 & p_I\delta_I - \mu_I \end{pmatrix} \tag{10}$$

$$\Lambda(Y) = \begin{pmatrix} -\beta_1 \mathbb{S}_1 \mathbb{I} \\ -\beta_2 \mathbb{S}_2 \mathbb{I} \\ (\beta_1 \mathbb{S}_1 + \beta_2 \mathbb{S}_2)\mathbb{I} \end{pmatrix} \qquad Q(Y) = \begin{pmatrix} (\nu_I - \nu_1)\mathbb{S}_1 \mathbb{I} + (\nu_2 - \nu_1)\mathbb{S}_1 \mathbb{S}_2 \\ (\nu_I - \nu_2)\mathbb{S}_2 \mathbb{I} + (\nu_1 - \nu_2)\mathbb{S}_1 \mathbb{S}_2 \\ [(\nu_1 - \nu_I)\mathbb{S}_1 + (\nu_2 - \nu_I)\mathbb{S}_2]\mathbb{I} \end{pmatrix} \tag{11}$$

Here $\nu_i = \delta_i - \mu_i$, $\nu_I = \delta_I - \mu_I$ and we get $\dot{N} = \nu_1 \mathbb{S}_1 + \nu_2 \mathbb{S}_2 + \nu_I \mathbb{I}$. So now introduce

$$\begin{array}{lllllll} \tilde{\alpha}_1 & := & \alpha_1 + q_2\delta_1\,, & \tilde{\alpha}_2 & := & \alpha_2 + q_1\delta_2\,, \\ \tilde{\gamma}_1 & := & \gamma_1 + q_1(1-p_I)\delta_I\,, & \tilde{\gamma}_2 & := & \gamma_2 + q_2(1-p_I)\delta_I\,, \\ \tilde{\beta}_1 & := & \beta_1 + \nu_I - \nu_1\,, & \tilde{\beta}_2 & := & \beta_2 + \nu_I - \nu_2\,. \end{array} \tag{12}$$

to conclude from (5)

$$\tilde{M} = \begin{pmatrix} -\tilde{\alpha}_1 & \tilde{\alpha}_2 & \tilde{\gamma}_1 \\ \tilde{\alpha}_1 & -\tilde{\alpha}_2 & \tilde{\gamma}_2 \\ 0 & 0 & -\tilde{\gamma}_1 - \tilde{\gamma}_2 \end{pmatrix} \quad \tilde{\Lambda}(Y) = \begin{pmatrix} -\tilde{\beta}_1 \mathbb{S}_1 \mathbb{I} \\ -\tilde{\beta}_2 \mathbb{S}_2 \mathbb{I} \\ (\tilde{\beta}_1 \mathbb{S}_1 + \tilde{\beta}_2 \mathbb{S}_2)\mathbb{I} \end{pmatrix} + \mathbb{S}_1 \mathbb{S}_2 \begin{pmatrix} \nu_1 - \nu_2 \\ \nu_2 - \nu_1 \\ 0 \end{pmatrix} \tag{13}$$

In summary, denoting fractions of the total population by $S_i = \mathbb{S}_i/N$ and $I = \mathbb{I}/N$, and assuming the condition $\nu_1 = \nu_2 =: \nu$, the dynamics for fractional variables becomes

$$\begin{pmatrix} \dot{S}_1 \\ \dot{S}_2 \\ \dot{I} \end{pmatrix} = \begin{pmatrix} -\tilde{\alpha}_1 & \tilde{\alpha}_2 & \tilde{\gamma}_1 \\ \tilde{\alpha}_1 & -\tilde{\alpha}_2 & \tilde{\gamma}_2 \\ 0 & 0 & -\tilde{\gamma}_1 - \tilde{\gamma}_2 \end{pmatrix} \begin{pmatrix} S_1 \\ S_2 \\ I \end{pmatrix} + \begin{pmatrix} -\tilde{\beta}_1 S_1 I \\ -\tilde{\beta}_2 S_2 I \\ (\tilde{\beta}_1 S_1 + \tilde{\beta}_2 S_2) I \end{pmatrix} \tag{14}$$

So, for $\nu_1 = \nu_2 = \nu$, all birth and death rates become redundant and may be absorbed by redefining β_i, α_i and γ_i. The price to pay is that $\tilde{\beta}_i = \beta_i + \nu_I - \nu$ might become negative. Hence, the space of admissible parameters for the system (14) becomes (Due to the permutation symmetry $1 \leftrightarrow 2$, there is no loss, assuming $\tilde{\beta}_1 > \tilde{\beta}_2$. The case $\tilde{\beta}_1 = \tilde{\beta}_2$ is ignored, since, in this case, putting $S = S_1 + S_2$ one can easily check that (S, I) obeys the dynamics of a SIS model, which can immediately be solved by separation of variables.):

$$\mathcal{A} := \{(\tilde{\alpha}_i, \tilde{\beta}_i, \tilde{\gamma}_i) \in \mathbb{R}^6 \mid \tilde{\alpha}_i \geq 0,\ \tilde{\gamma}_i \geq 0,\ \tilde{\gamma}_1 + \tilde{\gamma}_2 > 0,\ \tilde{\beta}_1 > \tilde{\beta}_2\} \tag{15}$$

Concerning the dynamics of fractional variables, any two models mapping to the same set of shifted parameters $\mathbf{a} \in \mathcal{A}$ become isomorphic. In particular, the case of constant population, $\nu_i = \nu_I = 0$, yields $\tilde{\beta}_i = \beta_i$. In summary, we get

Proposition 1. *Referring to the parameter transformation* (12) *and the normalized dynamics of fractional variables* (14)*, assume* $\nu_1 = \nu_2 =: \nu$*, and put* $\Delta\nu_I := \nu - \nu_I$*.*

(i) If $\Delta\nu_I < \beta_2$ *the model with variable population is isomorphic to a model with constant population and transmission coefficients* $\beta_i' = \beta_i - \Delta\nu_I > 0$*.*

(ii) If $\Delta\nu_I > \beta_2$ *it is isomorphic to a variable population SI(R)S model with two recovery flows* $I \to S_1$ *and* $I \to S_2$ *and parameters* $\beta_2' = 0$*,* $\beta_1' = \beta_1 - \beta_2$ *and* $\Delta\nu_I' = \Delta\nu_I - \beta_2$*.*

(iii) If $\Delta\nu_I = \beta_2$ it is isomorphic to a SI(R)S model as in ii) with constant population.

4. Examples from the Literature

For simplicity, from now on let us assume the rate of newborns who are not infected to be compartment-independent, $\delta_1 = \delta_2 = (1 - p_I)\delta_I = \delta$, implying $B = \delta N$. In this case, one may without loss assume $p_I = 0$ by redefining μ_I. Hence, $\nu_1 = \nu_2 \Leftrightarrow \mu_1 = \mu_2 =: \mu$ and, in this case, $\Delta\nu_I = \Delta\mu_I := \mu_I - \mu$ gives the *excess mortality* in the infectious compartment.

Below there is a list of prominent examples from the literature. Table 1 maps these examples to the present set of parameters.

Heth Heathcote's classic endemic model [2–4] by putting $\delta = \mu_i = \mu_I > 0$, $q_1 = 1$, $\beta_1 > 0$, $\gamma_2 > 0$ all other parameters vanish.

BuDr The 7-parameter SIRS model with time varying population size in [10], adds to Heathcote's model an immunity waning rate α_2 and allows non-balancing mortality and birth rates $\delta \neq \mu_i \neq \mu_I$.

SIRI The 6-parameter SIRI model of [11], replaces the immunity waning rate α_2 in [10] with the transmission rate $\beta_2 > 0$ and also requires $\mu_1 = \mu_2$.

SIRS The 8-parameter constant population SI(R)S model with vaccination and two recovery flows $I \to S_1$ and $I \to S_1$. Hence $\delta = \mu_i = \mu_I$ and $\beta_2 = 0$.

HaCa The 6-parameter core system in [12], with transmission and recovery rates $\beta_i, \gamma_i > 0$, a vaccination term $\alpha_1 > 0$ and a constant population with balanced birth and death rates, $\delta = \mu_i = \mu_I > 0$ and $q_1 = 1$.

KZVH The 7-parameter vaccination model of [8] adds an immunity waning rate $\alpha_2 > 0$ to the model in [12].

LiMa The 8-parameter SIS-model with vaccination and varying population size of [9] keeps only $\gamma_2 = \beta_2 = 0$ and assumes $\mu_1 = \mu_2 = \mu$. (Actually the authors let $\mu_1 = \mu_2 = \mu = f(N)$ be a function of N and put $\mu_I = \mu + \Delta\mu_I$ with constant excess mortality $\Delta\mu_I$. Still, $\mu = f(N)$ disappears when passing to tilde parameters (12), see also Remark 1.)

AABH The 8-parameter SIRS-type model analyzed recently by [7], keeps only $\gamma_1 = q_2 = 0$ and all other parameters are positive. The authors allow a varying population size by first discussing the general case of all mortality rates being different and then concentrating on $\mu_1 = \mu_2 \neq \delta$ and $\Delta\mu_I > 0$.

Table 1. Mapping models in the literature [1] to the present choice of parameters. The column # counts the number of free parameters in the original models. Passing to fractional variables (S_1, S_2, I) and tilde parameters, Equation (12), $\#_{\text{eff}}$ counts the number of effectively independent parameters as determined in Equations (16)–(22).

	α_1	α_2	β_1	β_2	γ_1	γ_2	δ	μ_1	μ_2	μ_I	q_1	q_2	#	$\#_{\text{eff}}$
Heth	0	0	✓	0	0	✓	$\delta = \mu_1 = \mu_2 = \mu_I$				1	0	3	3
BuDr	0	✓	✓	0	0	✓	✓	✓	✓	✓	1	0	7	5 [2]
SIRI_1	0	0	✓	✓	0	✓	✓	$\mu_1 = \mu_2$		✓	1	0	6	4
SIRI_2	0	0	✓	✓	✓	0	✓	$\mu_1 = \mu_2$		✓	0	1	6	4
SIRS	✓	✓	✓	0	✓	✓	$\delta = \mu_1 = \mu_2 = \mu_I$				✓	✓	7	5
HaCa	✓	0	✓	✓	✓	✓	$\delta = \mu_1 = \mu_2 = \mu_I$				1	0	6	6
KZVH	✓	✓	✓	✓	✓	✓	$\delta = \mu_1 = \mu_2 = \mu_I$				1	0	7	6
LiMa	✓	✓	✓	0	✓	0	✓	$\mu_i = f(N)$		✓	✓	✓	8	6
AABH_1	✓	✓	✓	✓	0	✓	✓	$\mu_1 = \mu_2$ [3]		✓	1	0	8	6
AABH_2	✓	✓	✓	✓	✓	0	✓	$\mu_1 = \mu_2$ [3]		✓	0	1	8	6

[1] SIRI and AABH come in two versions, since the authors also allow $\beta_1 < \beta_2$. The subscript 1 refers to $\beta_1 > \beta_2$ and 2 to $\beta_1 < \beta_2$. [2] Referring to the sub-case $\mu_1 = \mu_2$ in BuDr. [3] The bulk of results in Sections 5 and 6 of AABH [7] assume $\mu_1 = \mu_2$.

Assuming $\mu_1 = \mu_2$, and applying the transformations (12), we acquire a classification in terms of the redundancy-free 6-parameter set $\mathcal{A}$.

$$\mathcal{A}_{\text{SIRS}} = \mathcal{A} \cap \{\tilde{\beta}_2 = 0\} \tag{16}$$
$$\mathcal{A}_{\text{Heth}} = \mathcal{A} \cap \{\tilde{\alpha}_1 = 0 \wedge \tilde{\gamma}_2 > 0 \wedge \tilde{\gamma}_1 = \tilde{\alpha}_2 \wedge \tilde{\beta}_2 = 0\} \tag{17}$$
$$\mathcal{A}_{\text{SIRI}_i} = \mathcal{A} \cap \{\tilde{\alpha}_i = 0 \wedge \tilde{\gamma}_j > 0 \wedge \tilde{\gamma}_i = \tilde{\alpha}_j,\ j \neq i\} \tag{18}$$
$$\mathcal{A}_{\text{BuDr}} = \mathcal{A} \cap \{\tilde{\alpha}_1 = 0 \wedge \tilde{\gamma}_2 > 0 \wedge \tilde{\beta}_2 < 0\}\dagger \tag{19}$$
$$\mathcal{A}_{\text{KZVH}} = \mathcal{A} \cap \{\tilde{\beta}_2 > 0\} = \mathcal{A}_{\text{HaCa}}\,\dagger\dagger \tag{20}$$
$$\mathcal{A}_{\text{LiMa}} = \mathcal{A} \cap \{\tilde{\beta}_2 < 0 \wedge \tilde{\gamma}_1 > 0\}\,\dagger\dagger\dagger \tag{21}$$
$$\mathcal{A}_{\text{AABH}_i} = \mathcal{A} \cap \{\tilde{\gamma}_j > 0,\ j \neq i\} \tag{22}$$

†: To be comparable, Equation (19) refers to the sub-case $\mu_1 = \mu_2$ in BuDr, so $\beta_2 = 0$ implies $\tilde{\beta}_2 = -\Delta\mu_I \leq 0$. Also, $\tilde{\gamma}_1 = \delta$ as in SIRI_1, but $\tilde{\alpha}_2 = \alpha_2 + \delta \neq \tilde{\gamma}_1$ becomes independent.
††: For $q_1 > 0$ one of the three parameters $(\gamma_1, \alpha_2, \delta)$ always is redundant. So $\mathcal{A}_{\text{KZVH}} = \mathcal{A}_{\text{HaCa}}$.
†††: For $q_2 = 1$ the mapping $(\alpha_1, \alpha_2, \gamma_1, \delta) \mapsto (\tilde{\alpha}_1, \tilde{\alpha}_2, \tilde{\gamma}_1, \tilde{\gamma}_2)$ is bijective.

The dimensions of these parameter spaces are listed in the last column of Table 1. In summary, we arrive at

Corollary 1. *Consider the dynamics of fractional variables in the models of Table 1, for BuDr and AABH under the restriction $\mu_1 = \mu_2$. Disregarding boundary configurations $\tilde{\gamma}_i = 0$ in parameter space $\mathcal{A}$, the following relations hold.*

(i) The model of AABH [7] is isomorphic to the master model (14) and covers all other models.
(ii) The SIS-type model of LiMa [9], with time-dependent population size, coincides with the subcase $\min\{\beta_1, \beta_2\} < \Delta\mu_I$ of AABH [7].
(iii) The constant population model of KZVH [8] coincides with the subcase $\min\{\beta_1, \beta_2\} > \Delta\mu_I$ of AABH [7].
(iv) The subcase $\min\{\beta_1, \beta_2\} = \Delta\mu_I$ of AABH [7] reduces to the SI(R)S model (16).
(v) The models of HaCa [12] and KZVH [8] are isomorphic.

5. Summary

We have seen in Lemma 1 that, in a large class of homogeneous compartment models with constant per capita demographic rates and time-dependent total population N, the dynamics of fractional variables $y = Y/N$ can be rewritten such that all demographic parameters become redundant. In this way, various prominent SI(R)S-type models with standard incidence, demographic parameters and possibly susceptible R-compartments may be normalized, such that the dynamics of fractional variables appear as a sub-case of a master model with zero birth and death rates, see Equations (16)–(22). Since, apparently, none of the original papers used the identity (3) of Lemma 1, these relations were not realized before. The price to pay is that, in the normalized master model, infection transmission rates $\tilde{\beta}_i$ may also be negative. As a particular example, recent results on backward bifurcation in models with time-varying total population $N(t)$, coinciding mortality rates $\mu_1 = \mu_2$ and an excess mortality $0 < \Delta\mu_I < \min\{\beta_1, \beta_2\}$ by AABH [7] were already covered by the isomorphic model with constant population of KZVH [8], published in 2000. The complementary case $\Delta\mu_I > \min\{\beta_1, \beta_2\}$ turns out to be isomorphic to the variable population SIS model with $\beta_2 = 0$, published by LiMa [9] in 2002.

The normalized master model (14) is also the starting point of an ongoing analysis of symmetry operations in these kinds of models, giving rise to further parameter reductions, see the work in progress in [13,14].

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