Multi-compartment SEIR model with age classes and vaccinated

Geir Evensen

April 7, 2021

Abstract

This document gives a complementary description of the EnKF_seir model. For additional information see Evensen et al. (2020).

Multi-compartment SEIR model with age classes and vaccinated

A ubiquitous but straightforward model for epidemic modeling is the SEIR (Susceptible, Exposed, Infectious, and Recovered) model Blackwood and Childs (2018). However, for a realistic description of the SARS-CoV-2 epidemic, we need to use an extended SEIR-model variant. A better formulation is the one conceptualized in Figure 1 and is described by the following system of equations,

$$\frac{\partial \mathbf{V}_i(n)}{\partial t} = \frac{v_i}{\tau_{\text{vac}}}\,\mathbf{S}_i(n) \tag{1}$$

$$\frac{\partial \mathbf{S}_i(n)}{\partial t} = -\sum_{m=1}^{n_c}\frac{N_m}{N_n}R^{\text{C}}_{nm}R_t(n)\left(\sum_{j=1}^{n_a}\frac{R^{\text{A}}_{ij}(n)\mathbf{I}_j(m)}{\tau_{\text{inf}}}\right)\mathbf{S}_i(n) - \frac{v_i}{\tau_{\text{vac}}}\,\mathbf{S}_i(n) \tag{2}$$

$$\frac{\partial \mathbf{E}_i(n)}{\partial t} = \sum_{m=1}^{n_c}\frac{N_m}{N_n}R^{\text{C}}_{nm}R_t(n)\left(\sum_{j=1}^{n_a}\frac{R^{\text{A}}_{ij}(n)\mathbf{I}_j(m)}{\tau_{\text{inf}}}\right)\mathbf{S}_i(n) - \frac{1}{\tau_{\text{inc}}}\,\mathbf{E}_i(n) \tag{3}$$

$$\frac{\partial \mathbf{I}_i(n)}{\partial t} = \frac{1}{\tau_{\text{inc}}}\,\mathbf{E}_i(n) - \frac{1}{\tau_{\text{inf}}}\,\mathbf{I}_i(n) \tag{4}$$

$$\frac{\partial \mathbf{Q}_{\text{m}}(n)}{\partial t} = \sum_{i=1}^{n_a}\frac{p^i_{\text{m}}(n)}{\tau_{\text{inf}}}\,\mathbf{I}_i(n) - \frac{1}{\tau_{\text{recm}}}\,\mathbf{Q}_{\text{m}}(n) \tag{5}$$

$$\frac{\partial \mathbf{Q}_{\text{s}}(n)}{\partial t} = \sum_{i=1}^{n_a}\frac{p^i_{\text{s}}(n)}{\tau_{\text{inf}}}\,\mathbf{I}_i(n) - \frac{1}{\tau_{\text{hosp}}}\,\mathbf{Q}_{\text{s}}(n) \tag{6}$$

$$\frac{\partial \mathbf{Q}_{\text{f}}(n)}{\partial t} = \sum_{i=1}^{n_a}\frac{p^i_{\text{f}}(n)}{\tau_{\text{inf}}}\,\mathbf{I}_i(n) - \frac{1}{\tau_{\text{hosp}}}\,\mathbf{Q}_{\text{f}}(n) \tag{7}$$

$$\frac{\partial \mathbf{H}_{\text{s}}(n)}{\partial t} = \frac{1}{\tau_{\text{hosp}}}\,\mathbf{Q}_{\text{s}}(n) - \frac{1}{\tau_{\text{recs}}}\,\mathbf{H}_{\text{s}} \tag{8}$$

$$\frac{\partial \mathbf{H}_{\text{f}}(n)}{\partial t} = \frac{p_{\text{h}}}{\tau_{\text{hosp}}}\,\mathbf{Q}_{\text{f}}(n) - \frac{1}{\tau_{\text{death}}}\,\mathbf{H}_{\text{f}}(n) \tag{9}$$

$$\frac{\partial \mathbf{C}_{\text{f}}(n)}{\partial t} = \frac{(1-p_{\text{h}})}{\tau_{\text{hosp}}}\,\mathbf{Q}_{\text{f}}(n) - \frac{1}{\tau_{\text{death}}}\,\mathbf{C}_{\text{f}}(n) \tag{10}$$

$$\frac{\partial \mathbf{R}_{\text{m}}(n)}{\partial t} = \frac{1}{\tau_{\text{recm}}}\,\mathbf{Q}_{\text{m}}(n) \tag{11}$$

$$\frac{\partial \mathbf{R}_{\text{s}}(n)}{\partial t} = \frac{1}{\tau_{\text{recs}}}\,\mathbf{H}_{\text{s}}(n) \tag{12}$$

$$\frac{\partial \mathbf{D}(n)}{\partial t} = \frac{1}{\tau_{\text{death}}}\,\mathbf{H}_{\text{f}} + \frac{1}{\tau_{\text{death}}}\mathbf{C}_{\text{f}}(n) \tag{13}$$

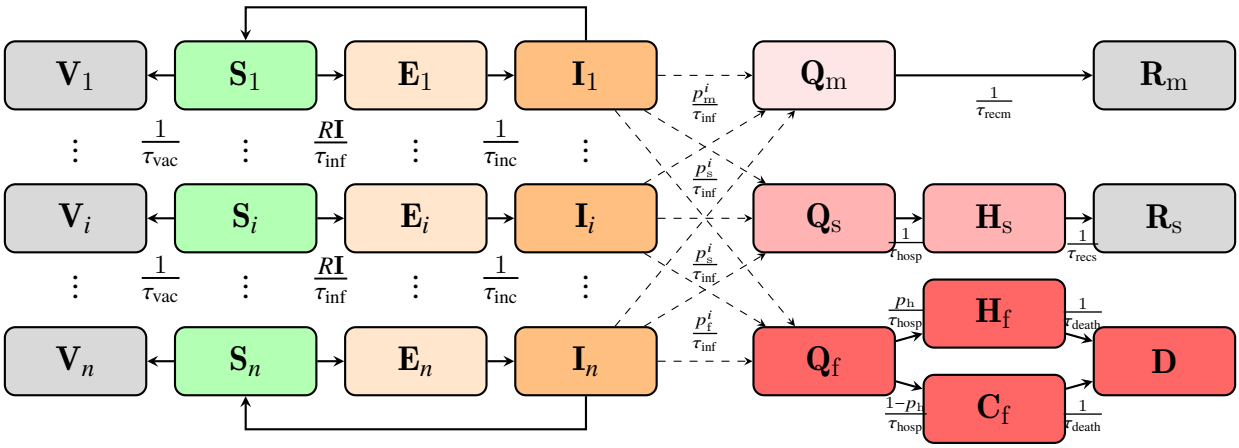

Figure 1: Flow diagram of the SEIR model.

Variable	Variable name	Description
$\mathbf{S}_i(n)$	Suceptible	Those that can be infected
$\mathbf{V}_i(n)$	Vaccinated	The number of vaccinated
$\mathbf{E}_i(n)$	Exposed	The number of infected but not yet infectious
$\mathbf{I}_i(n)$	Infected	The number of infectious
$\mathbf{Q}_\mathrm{m}(n)$	Quaranteened	The number of quaranteened with mild symptoms
$\mathbf{Q}_\mathrm{s}(n)$	Quaranteened	The number of quaranteened with severe symptoms
$\mathbf{Q}_\mathrm{f}(n)$	Quaranteened	The number of quaranteened with fatal symptoms
$\mathbf{H}_\mathrm{s}(n)$	Hospitalized	The number of hospitalized with severe symptoms
$\mathbf{H}_\mathrm{f}(n)$	Hospitalized	The number of hospitalized with fatal symptoms
$\mathbf{C}_\mathrm{f}(n)$	Carehomes	The number of fatally sick in carehomes
$\mathbf{R}_\mathrm{m}(n)$	Recovered	The number of recovered with mild symptoms
$\mathbf{R}_\mathrm{s}(n)$	Recovered	The number of recovered with severe symptoms
$\mathbf{D}(n)$	Deceased	The number of decesed

Table 1: Overview of model variables.

The model includes an arbitrary number of countries or groups that can interact with each other. We model each group with the variables listed in Tab. 1 We have stratified the populations of vaccinated, susceptible, exposed, and infectious into age groups $\mathbf{V}_i$, $\mathbf{S}_i$, $\mathbf{E}_i$, and $\mathbf{I}_i$, see, e.g., Cao and Zhou (2012). We have used the following notation: n is an index running over all the n_c countries or compartments. The index i is running over n_a different agegroups. The total population number per group normalizes these equations. Thus the sum of all model variables in a group, including the deceased $\mathbf{D}$, equals one and is time-invariant. For the whole population to stay constant in time, the equations' right-hand sides need to sum to zero.

As in the standard SEIR model, Eqs. (2) and (3) describe how the interaction between the infectious and the susceptible leads to the newly exposed. The effective reproductive numbers R between different age groups together with the infection time scale τ_inf determine the rate of new infections. We will discuss the formulation used for R in detail below. Note that the interaction between the susceptible and infectious constitutes the only source of nonlinearity in the model. Table 2 provides a set of default values of all the transition time scales in the model.

Eq. (1) describes the susceptible persons' transfer from $\mathbf{S}_i$ into the vaccinated groups $\mathbf{V}_i$ at a rate given by the vaccination time scale τ_vac for a period defined by $v_i = 1$ (the default is $v_i = 0$ zero, so no vaccinations).

Eq. (2) describes the susceptible persons' transfer from $\mathbf{S}_i$ into the exposed $\mathbf{E}_i$ and vaccinated groups $\mathbf{V}_i$ at a rate given by the incubation time scale τ_inc and the vaccination time scale τ_vac.

Eq. (3) describes the transfer of susceptible persons into exposed $\mathbf{E}_i$, and then Eq. (4) describes the exposed persons' transfer from $\mathbf{E}_i$ into the infectious group $\mathbf{I}_i$ at a rate given by the incubation time scale τ_inc.

The different age groups of infectious $\mathbf{I}_i$, transition into the various quarantined groups of sick, $\mathbf{Q}_\mathrm{m}$, $\mathbf{Q}_\mathrm{s}$, and

Parameter	First guess	Description
τ_{vac}	20.0	Vaccination time
τ_{inc}	5.5	Incubation period
τ_{inf}	3.8	Infection time
τ_{recm}	14.0	Recovery time mild cases
τ_{recs}	5.0	Recovery time severe cases
τ_{hosp}	6.0	Time until hospitalization
τ_{death}	16.0	Time until death
p_{f}	0.009	Case fatality rate
p_{s}	0.039	Hospitalization rate (severe cases)
p_{h}	0.4	Fraction of fatally ill going to hospital

Table 2: Timescales of the model.

$\mathbf{Q}_{\text{f}}$, based on the fractions p^i_{m}, p^i_{s}, p^i_{f}, and the infection time scale τ_{inf}, as modeled by Eqs. (5–7). The fractions refer to the portion of patients with mild symptoms, hospitalized patients with severe symptoms, and the fatally ill patients, and specify how the virus affects people of different age groups. The subscripts m, s, and f refer to mild, severe, and fatal symptoms. Thus, the model includes different probabilities for dying or being hospitalized dependent on the age group. The fractional coefficients sum to one for each age group. Table 3 provides an example set of fractions that illustrate how the SARS-CoV-2 virus affects older people more severely. We have assumed that a patient will not infect anyone while in a quarantined group.

Eq. (11) describes how the patients with mild symptoms in $\mathbf{Q}_{\text{m}}$ will recover and transition into the group of recovered with mild symptoms $\mathbf{R}_{\text{m}}$, on a time scale τ_{recm}, without going to the hospital. Severely sick patients in $\mathbf{Q}_{\text{s}}$ transfer to the hospital compartment $\mathbf{H}_{\text{s}}$, on a time scale τ_{hosp}, as described by Eq. (8). After that, Eq. (12) models their recovery, which occurs on a time scale τ_{recs}, into the compartment of patients recovered from severe disease $\mathbf{R}_{\text{s}}$.

Eq. (9) models the fraction p_{h} of fatally-ill patients in $\mathbf{Q}_{\text{f}}$ admitted to a hospital $\mathbf{H}_{\text{f}}$ on the time scale τ_{hosp}. In Norway, the fraction p_{h} is around 0.4 since many fatalities were older people living in care homes, and they were usually not admitted to hospitals when they got infected by SARS-CoV-2. Thus, in Eq. (10) we also allow for a fraction, $1 - p_{\text{h}}$, of fatally-ill patients that are not admitted to a hospital but rather transfer to $\mathbf{C}_{\text{f}}$. The purpose of the $\mathbf{C}_{\text{f}}$ variable is to include the fatally-ill patients not measured as hospitalized. Introducing $\mathbf{C}_{\text{f}}$ allows us to use realistic fractions p_{f} of fatally-ill patients and still condition on the measured hospitalization numbers $\mathbf{H}_{\text{s}} + \mathbf{H}_{\text{f}}$. Within a few weeks of the pandemic, we had access to accurate estimates of the fraction dying within and outside hospitals for several countries. This partition of the fatally-ill patients turned out to be important for most of the cases discussed in this paper.

The fatally ill patients in $\mathbf{H}_{\text{f}}$ and $\mathbf{C}_{\text{f}}$ end up in the group of dead $\mathbf{D}$, on a time scale τ_{death}, as described by Eq. (13).

We initialize the model with a country's total population divided among the age groups. We set an initial number of exposed and infectious reflecting the situation in a country, e.g., a sudden import of exposed or infectious split within some age groups. All other variables are set to zero initially. Tables 2 and 3 provide all the default model parameters.

Interaction term for infections

We model the interaction between countries using the elements of $\mathbf{R}^{\text{C}} \in \Re^{n_{\text{c}} \times n_{\text{c}}}$ (the diagonal must always be 1). The effective reproductive number per country is a scalar function of time, $R_t(n)$, and is a parameter function that we estimate. We model the relative differences in infections between age groups using the coefficients in $R^{\text{A}}_{i,j}(n)$ which can differ between countries (the model default is to set all elements $R^{\text{A}}_{i,j}(n) = 1$ assuming equal transmission rates among age groups). In the equations below, we assume the same $R^{\text{A}}_{i,j}(n)$ when interacting with other countries as within a country (the only sound alternative would be to set $R^{\text{A}}_{i,j}(n) = 1$ when $m \neq n$, given the number of coefficients we would otherwise need to specify). The total poulations of two countries, n and m, are N_n and N_m. We have normalized the variables per country by the total population number N_n (which is why we need the factor N_m/N_n in the interaction term).

Age group	1	2	3	4	5	6	7	8	9	10	11
Age range	0–5	6–12	13–19	20–29	30–39	40–49	50–59	60–69	70–79	80–89	90–105
Population	351159	451246	446344	711752	730547	723663	703830	582495	435834	185480	45230
p–mild	1.0000	1.0000	0.9998	0.9913	0.9759	0.9686	0.9369	0.9008	0.8465	0.8183	0.8183
p–severe	0.0000	0.0000	0.0002	0.0078	0.0232	0.0295	0.0570	0.0823	0.1160	0.1160	0.1160
p–fatal	0.0000	0.0000	0.0000	0.0009	0.0009	0.0019	0.0061	0.0169	0.0375	0.0656	0.0656

Table 3: The p numbers per age group indicate the fraction of sick people in an age group ending up with mild symptoms, severe symptoms (hospitalized), and fatal infection. The population-weighted averages (for the Norwegian population) of the case-fatality rate is $p_{\mathrm{f}} = 0.0090$, and the rate of severe (hospitalized) cases is $p_{\mathrm{s}} = 0.039$.

The fractions of fatally ill, severely ill, and mild desease, p_{f}, p_{s}, and p_{m}, can differ between countries. Currently, we have used the same hospitalization fraction of fatally ill p_{h} for all countries.

In the case with only one country $n = m = 1$, we have $N_m/N_n = 1$, and $R^{\mathrm{C}}(n, m) = 1$. Thus, the equations reduce to the standard SEIR model. The use of a multi-compartment model only changes the nonlinear interaction term. Besides the interaction term, each country evolve independently of each other.

References

Blackwood, J. C. and L. M. Childs. An introduction to compartmental modeling for the budding infectious disease modeler. *Letters in Biomathematics*, 5:195–221, 2018. doi:10.1080/23737867.2018.1509026.

Cao, H. and Y. Zhou. The discrete age-structured seit model with application to tuberculosis transmission in china. *Mathematical and Computer Modelling*, 55:385–395, 2012. doi:10.1016/j.mcm.2011.08.017.

Evensen, G., J. Amezcua, M. Bocquet, A. Carrassi, A. Farchi, A. Fowler, P. L. Houtekamer, C. K. Jones, R. J. de Moraes, M. Pulido, C. Sampson, and F. C. Vossepoel. An international initiative of predicting the sars-cov-2 pandemic using ensemble data assimilation. *Foundations of Data Science*, page 65, 2020. doi:10.3934/fods.2021001.

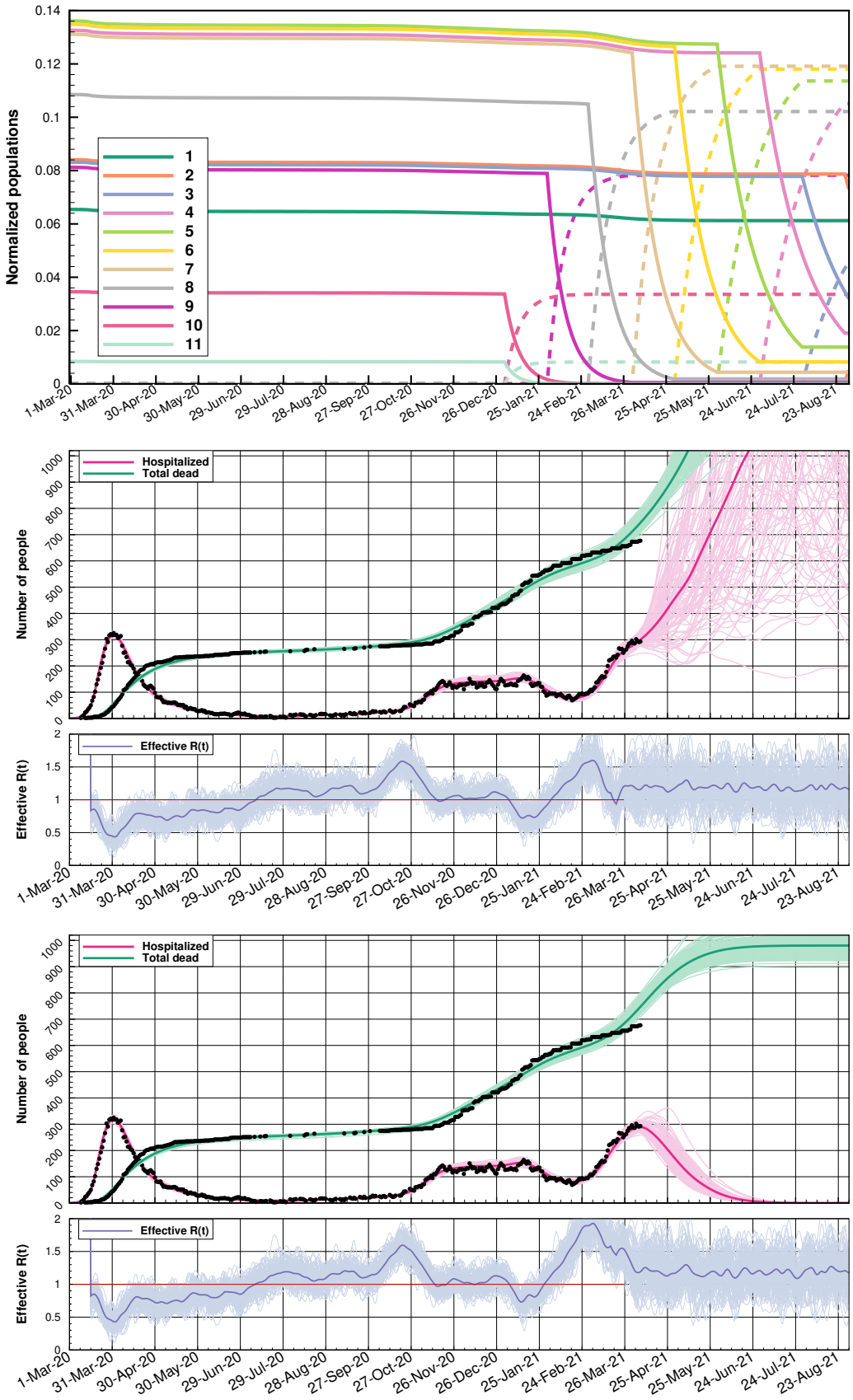

Figure 2: Example for Norway without and with vaccinations. The upper plot shows the time evolution of $\mathbf{S}_i$ and $\mathbf{V}_i$ (dashed lines) to illustrate the impact of a vaccination plan for the different age groups. The two lower plots show the time evolution of hospitalized and dead for the cases without and with vaccinations as resulting from the data assimliation runs.