

System requirements

- Operating System Linux/FreeBSD based
- Intel x86 Cpu
- clang version 11.0.0 (clang-1100.0.33.17)
- GSL - GNU Scientific Library

Versions the software has been tested on

- MacOS Catalina (version 10.15.5)
- GSL (version 2.6)

Compile code

Launch script

src/compile.sh

Demo

- Demo vaccination: launch script
src/run_demo_vax.sh
- Demo no vaccination: launch script
src/run_demo_novax.sh

Example of launch script:

```
./gen ../exp -w CHI -s 0 -selReff 1.3 -ni 40 -selVAXEFF 80 -selIMM 0 -is 1 -cov 70 -capacity 3000000 -interv 1 -omega_1 0.04761905-omega_2 0.07142857 -waning_rate 0 -tstartvax 15 -tstartinf 0 -pdetected 1 -vax_only_susc 1 -vax_prevent 0
```

Table 1: Command line arguments

Argument	Type	Description	Baseline values
argv[1]	string	Path to output directory	../exp
-w	string	Specifier of region/state	CHI
-s	int	Random seed	[0,Inf)
-selReff	double	Selector of transmissibility (used to read corresponding input vector of attenuated scale factors for transmission betas)	1.1;1.3;1.5; 2.5
-selVAXEFF	int	Selector for vaccine efficacy file, indicates vaccine efficacy achieved after the 2nd dose in people aged 20-59y (used to read corresponding matrix of vaccine efficacy by age in the different vaccination compartments)	0 (corresponds to scenario without vaccination); 80
-selIMM	Int	Identifier of scenario considered for initial immunity ("0" corresponds to 0% of immune in each age group).	0

-is	int	Susceptibility to infection	1 (age-specific)
-cov	Int	Vaccination coverage (used to select input file of number of doses administered over time)	70
-capacity	Int	System capacity - daily number of first doses the system is capable to administer (used to select input file of number of doses administered over time)	3mln
-interv	int	Identifier of population priority (used to select input file of number of doses administered over time)	1
-ni	double	Initial number of infections	40
-omega_1	double	Rate of transition between V0 and V1 (1/interval between 1st and 2nd dose).	0.04761905
-omega_2	double	Rate of transition between V1 and V2 (1/time needed by 2nd dose to become effective)	0.07142857
-waning_rate	double	Rate of transition between V2 and W	0
-tstartvax	int	Time at which vaccination starts (days)	15
-tstartinf	int	Time at which epidemic is seeded (days)	0
-pdetected	double	Percentage of symptomatic cases detected	1
-vax_only_susc	Int	Parameter identifying to who vaccination is administered	1 (vaccinate susceptible only, i.e. all symptomatic/asymptomatic infections are detected)
-vax_prevent	Int	Identifier of type of vaccine, either preventing SARS-CoV-2 infection or symptoms only	0 (vaccine prevents infection)

Table: Description of input and output files. Symbols in brackets (e.g. $\{-w\}$) in file name represent the value of the specified command line parameter.

File name	Path from common_input folder	Dimension (rows x columns) ^a	Type	Sep	Description
INPUT					
parameters	./	4x2	<i>gamma</i> : double <i>ZETA</i> : int <i>Nit</i> : int <i>Tmax</i> : int	Tab	Column 1: parameter name <i>gamma</i> : recovery rate γ <i>ZETA</i> : time steps per day <i>Nit</i> , <i>Tmax</i> : see note ^a Column 2: parameter value
age_structure_{-w}_u	./age_structure/	Ax3	Int	Tab	Column 1: lower age limit Column 2: upper age limit Column 3: population with underlying conditions in age group
age_structure_{-w}_nu	./age_structure/	Ax3	Int	Tab	Column 1: lower age limit Column 2: upper age limit Column 3: population without underlying conditions in age group
beta_{-w}_SUSC_{-is}_Reff_{-selReff}	./betas/{-w}/{-selIMM}	Nx1	double	-	Scaling factor shaping the transmissibility (<i>N</i> stochastic samples ^b)
relative_susceptibility_matrix_susc_{-is}	./	AxN	double	Tab	Age-specific relative susceptibility (<i>N</i> stochastic samples ^b)
<ul style="list-style-type: none"> - ac_h_ext_* - ac_s_ext_* - ac_w_ext_* - ac_r_ext_* <p>* runs from 1 to <i>Nit</i> ^a</p>	./contact_matrices/{-w}	AxA	double	Tab	<p>Average number of contacts of an individual of age group <i>a</i> (row) with individuals of age group <i>ã</i> (column).</p> <ul style="list-style-type: none"> - ac_h_ext_*: household contacts - ac_s_ext_*: school contacts - ac_w_ext_*: contacts at work - ac_r_ext_*: community contacts

initial_immunity_{-selIMM}	./initial_immunity/{-w}	AxN	double	Tab	Age-specific proportion of immune individuals at the beginning of simulations (assumed to be the same for individuals with/without underlying conditions)
psym	./	1xA	Double	Tab	Age-specific probability of developing symptoms
vaccine_efficacy_{-selVAXEFF}	./vaccination/vaccine_efficacy	Ax3 [*] [*] 3=number of vaccination compartments (fixed)	double	Tab	Age-specific vaccine efficacy in the different ramp-up stages (V_0, V_1, V_2)
u_ndoses_CHI_capacity_{-capacity}_cov_{-cov}	./vaccination/ndoses/{-w}/{-priority}	(TxZETA)xA	int	Tab	Age-specific number of doses to be administered in each time step to individuals with underlying conditions
nu_ndoses_CHI_capacity_{-capacity}_cov_{-cov}	./vaccination/ndoses/{-w}/{-priority}	(TxZETA)xA	int	Tab	Age-specific number of doses to be administered in each time step to individuals without underlying conditions

OUTPUT					
resA_{-w}_phi{-selReff}_vaxeff{-selVAXEFF}_susc{-is}_interv{-interv}_iscen{-selIMM}_capacity{-capacity}_cov{-cov}_sim_^s.tsv	{argv[1]}/{-w}/interv_{-interv}	Tx(Ax2)	int	Tab	Number of new infections in age group a at time t . The first A columns correspond to individuals with underlying conditions, the second A columns corresponds to the population without ^b
resB_{-w}_phi{-selReff}_vaxeff{-selVAXEFF}_susc{-is}_interv{-interv}_iscen{-selIMM}_capacity{-capacity}_cov{-cov}_sim_^s.tsv	{argv[1]}/{-w}/interv_{-interv}	Tx(Ax2)	int	Tab	Number of new infections in age among individuals in age group a in compartment V2 at time t . The first A columns correspond to individuals with underlying conditions, the second A columns corresponds to the population without ^b

^a: A: number of age groups (18); N: number of stochastic simulations (equal to Nit , set to 200); T: number of simulation days (equal to $Tmax$).

^b: Each execution of the code runs Nit model simulations and prints the corresponding output file (identified by $\$in\{1,2,3,...,Nit\}$)