TB Vx model version 30 July 2020

Required packages

Install the following R packages first:

getopt
tools
assertthat
stringi
Matrix
xml2
lubridate
digest

dplyr

Running the model

There are two ways to run the model:

- a. from the command line
- b. from with R Studio

Run from the command line

Windows

- start a command prompt (type 'command' in the search box and run the suggested app)
- navigate to the folder where the model code is, for instance
 - C:\Users\roelb\GitLab\tb Ishtm\tbvax-current
- execute the following command
 - "C:\Program Files\R\R-4.0.2\bin\Rscript.exe" run_batch.R -s scenarios.txt -d .
 - Note that the path to Rscript.exe may be different on your computer
 - run_batch.R requires two command line arguments:
 - -s followed by the name of a tab delimited text file (e.g. scenarios.txt) with the following layout:

```
run model
runB.xml TBVxB.xml
runA.xml TBVxA.xml
```

where each line specifies a simulation run

-d. i.e. -d followed by a period to set the working directory to the current directory

- run_batch.R runs a batch of simulation scenarios and writes output to files in the ./output folder
- the output files are named as follows
 - [filename of model parameters file (without the xml extent)] followed by
 - _[filename of run parameters file (without the xml extent)]
 - _[small part of the md5 checksum of the in-memory R object with model parameters]
 - [small part of the md5 checksum of the in-memory R object with run parameters]
 - [small part of the time stamp]

- .txt
- for instance: TBVxA_noTBdeath_runA_07bc6_daf2e_24739.txt

Output will be generated depending on parameters in the XML run parameters file.

For now only start and stop year and age groupings are supported.

Example

YEAR	VXa	SES	RISK	HIV	TB	A0	A15	A50	A70
2020	never	poor	non-diabetic	HIV-	Un	8218.85	9772.3	3203.67	0
2020	never	poor	non-diabetic	HIV-	Uc	506.42	7009.12	7614.49	0
2020	never	poor	non-diabetic	HIV-	Lf	968.19	1616.43	566.57	0
2020	never	poor	non-diabetic	HIV-	Ls	3665.8	19645.44	7779.35	0
2020	never	poor	non-diabetic	HIV-	Ds	145.64	350.08	94.7	0

Mac OS X

Start a terminal session

Navigate to the directory of the TB Vx model, for instance by:

cd ./github/tbvax

Run the batch file with:

Rscript -s scenarios.txt -d .

Find the output in ./output

Run from within RStudio

Start RStudio and open the file run_manually.R

Execute the code line by line.

This file also contains an example for postprocessing the output.

The new 'run parameters' XML file

See runB.xml for an annotated example

The 'model parameters' XML file

Essentially the same as the previous version See **TBVxB.xml** for an example

HIV, ART and VXa incidence files

HIV

HIV incidence and ART 'incidence' should be provided in a tab delimited file with fractions per year per age group that move from one state to another (e.g. from HIV- to HIV1 for HIV incidence, from HIV1 to ART1 for

ART incidence, if required from HIV2 to ART2 for ART incidence). Separate files should be provided for each transition (for now anyway).

Format is as follows:

YEAR	country	dim	from	to	0	5	10	15	20	25 etc
1980	ZA	HIV	HIV-	HIV1	0	0	0	0	0	0
1981	ZA	HIV	HIV-	HIV1	0	0	0	0	0	0
1982	ZA	HIV	HIV-	HIV1	0	0	0	0	0	0
1983	ZA	HIV	HIV-	HIV1	4.9218e-05	0	0	0.000166218	0.000451423	0.000518
1984	ZA	HIV	HIV-	HIV1	8.2372e-05	0	0	0.00018899	0.000495274	0.000556
1985	ZA	HIV	HIV-	HIV1	9.4729e-05	0	0	0.000164355	0.000431587	0.000487

Vaccination

Vaccination is implemented using the same idea as it basically is not different from forcing a state transition from 'never' vaccinated to vaccinated and 'protected'.

Example:

YEAR	country	dim	from	to	0	5	10	15	20	25	30	35	40	etc
2019	ZA	VXa	never	vac	0	0	0	0	0	0	0	0	0	
2020	ZA	VXa	never	vac	0	0	0.1	0.1	0	0	0	0	0	
2021	ZA	VXa	never	vac	0	0	0.2	0.2	0	0	0	0	0	
2022	ZA	VXa	never	vac	0	0	0.3	0.3	0	0	0	0	0	
2023	ZA	VXa	never	vac	0	0	0	0	0	0	0	0	0	

In the two examples above, 5 year age groups were used. It is possible to use any age grouping, for instance 0,5,10,11,12,13,15,20