FastSTI Documentation

Release 0.2.2

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Contents

CHAPTER 1

Introduction

FastSTI is a framework for implementing agent-based models of sexually transmitted infection epidemics.

It is designed to handle up to tens of millions of agents on a mid-range laptop, or to run many smaller simulations consisting of thousands of agents quickly in parallel. On a high performance computer it can run dozens of large simulations or hundreds of small ones in parallel.

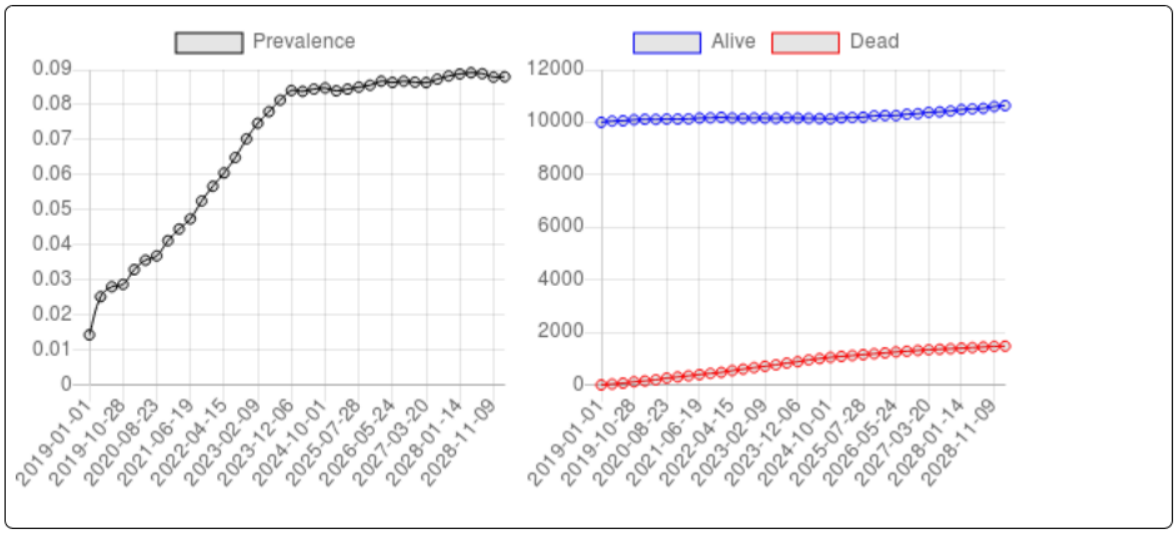
The output of the simulations is written to CSV files, which can be further processed in scripting languages like Python or R.

You can do sophisticated simulations without making any modifications to the code. But if you do wish to extend the framework, it is written in C. The framework has been designed with extensibility in mind.

FastSTI is developed and tested on GNU/Linux using the gcc compiler (and often the Clang compiler too). It uses two portable 3rd-party libraries: the GNU Scientific Library and GLib. The code adheres to the C11 standard and should compile on any standards-compliant modern C compiler.

FastSTI is free software (GPL licensed). If you are a C programmer, you can clone the source code on Github and modify it.

There's a web interface to a toy version of FastSTI on Simhub that you can play around with to get a feel for how it works. Here's a screenshot from Simhub:



Warning: FastSTI is in active development. It is usable (we think) but this documentation is changing almost daily. At this point no backwards compatibility is being implemented, and no warnings of incompatible changes are being documented. FastSTI is not yet at an alpha release stage. When it is more stable, we will remove this warning.

CHAPTER 2

Installation

FastSTI is easiest to run in a Posix environment (GNU Linux, FreeBSD, Unix etc), because we develop on Linux. Nevertheless, it isn't difficult to get it running on a Mac or Windows machine.

2.1 Linux etc.

1. FastSTI requires a standard C development environment, the GNU Scientific Library and Gnome's Glib utility library.

On Ubuntu, Debian, Mint etc. this should do the trick:

```
sudo apt install build-essential libgsl-dev libglib2.0-dev meson
```

2. Download FastSTI from https://www.simhub.online/media/dist/faststi/faststi-0.2.2.tar.gz and decompress it.

E.g.

wget https://www.simhub.online/media/dist/faststi/faststi-0.2.2.tar.gz; tar xzf faststi-0.2.2.tar.gz

This should create a directory called faststi-0.2.2 which contains the FastSTI files.

Now go to step 3.

2.2 Mac

1. Download and decompress this file: https://www.simhub.online/media/dist/faststi/latest.tar.gz
2. Using Homebrew install the dependencies:

```
brew install gcc pkg-config glib gsl meson
```

This should create a directory called faststi-0.2.2 which contains the FastSTI files.

Now go to step 3.

2.3 Windows

Under Windows you either need to install the Cygwin or MinGW environment, or if you are using Windows 10, you can install the Windows Subsystem for Linux. But to date we have only tested installation with Cygwin.

2.3.1 Cygwin

1. Use the Cygwin setup tool to install these packages:

- gcc-core
- make
- meson
- libgsl-dev
- libglib2.0-devel
- wget

2. After installation open the Cygwin terminal and run these steps:

```
wget https://www.simhub.online/media/dist/faststi/latest.tar.gz
tar xzvf latest.tar.gz
```

This should create a directory called faststi-0.2.2 which contains the FastSTI files.

Now go to step 3.

2.4 On all machines

3. Change into the directory that you've decompressed the distribution into: faststi-0.2.2

4. Now use the meson build system:

```
meson --buildtype release release
cd release
ninja
```

5. Then depending on your system either one of these should install the files:

```
sudo ninja install
```

Or:

```
ninja install
```

6. Now test that it works:

```
FSTI_DATA=../data faststi -t
```

This will run the test suite. If everything is properly installed then no failures should be reported.

Note: You may be wondering why we prefix the executable with *FSTI_DATA=../data*. The *FSTI_DATA* environment variable simply tells FastSTI where the data files are stored. As you work on FastSTI you may use a different directory for your data files. It's simply that the default data files are in the *data* directory.

To uninstall FastSTI simply go into the release directory and run:

```
sudo ninja uninstall
```

CHAPTER 3

Getting started

FastSTI takes as input a configuration file which tells it how many simulations to run, and how to run each simulation. It also takes data as input in files that we call datasets. And optionally, it takes a file of agents, though the agents can be generated by FastSTI itself, via instructions in the configuration file.

The outputs are a report of simulation results, and the agents.

3.1 Simulations

A simulation continuously iterates over sets of agents, executing events on the agents on each iteration (which we call a time step). The structure of a FastSTI simulation is:

```
Execute events before simulation runs
for each time-step
  for each event E
      for each agent A
          if E should be applied to A
              apply E to A
Execute events after simulation runs
```

The number of agents and the specific events to execute are specified in a configuration file. FastSTI's configuration file uses the *.ini* format, which are the standard simple configuration format used on MS Windows and the GTK framework popular on Linux systems.

You can configure the number of agents, the events and the order of events that execute upon them, the size of the time step (default 1 day), the number of time steps (default 10 years) and much else (see *Configuration file parameters*).

FastSTI has a number of useful built-in events useful for modelling STI epidemics (see *Events*). These include agent ageing, death, matching agents in sexual relationships, infection with the STI, disease advance, co-infection, and breakups.

There are also useful supporting events that read in agent files or generate the agents, write the agents to a CSV file, and write basic statistics to a CSV file.

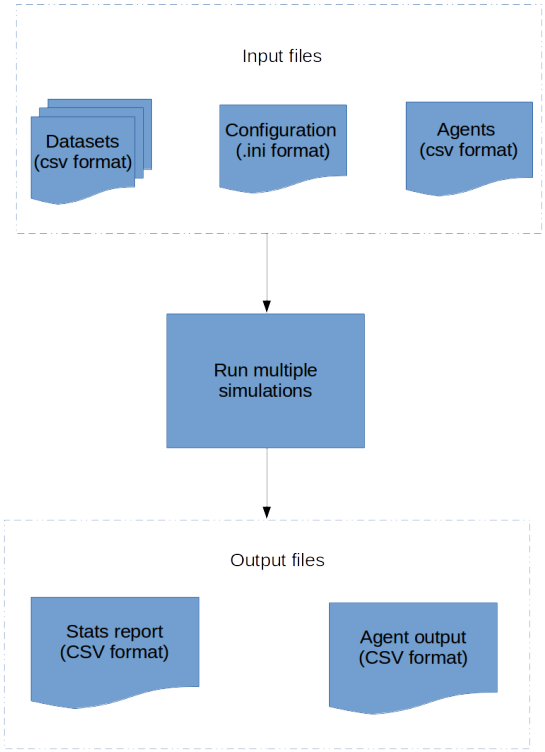


Fig. 1: FastSTI inputs include a configuration file, datasets and agent files. The outputs are an agent file and simulation results.

If you need more events, the framework has been designed with extensibility in mind. You can define new events in C, identify them to FastSTI, quickly recompile the code and use them.

3.2 Example

Let's start off with the simplest simulation. Change into the simulations/examples directory. Take a look at eg1.ini.

```
# Faststi "Hello world" equivalent simulation
[Simulation_0]
after_events=_report
```

The first line is a comment.

The second line is the name of the simulation group: *First simulation*. A simulation group can have one or more simulations. This particular group has only one simulation.

The third line is one of the dozens of parameters used to configure simulations. The *after_events* parameter tells FastSTI what events to execute when the simulation is finished. *_report* is a built-in event that prints out basic information about the state of a simulation. All built-in events are prefixed with an underscore, to differentiate them from ones you might code yourself.

To run the simulation:

```
FSTI_DATA=../../data faststi -f eg1.ini
```

The output may look something like this:

```
First simulation;0;0;2028-01-01;MIN_AGE_ALIVE;nan
First simulation;0;0;2028-01-01;MAX_AGE_ALIVE;nan
First simulation;0;0;2028-01-01;MEAN_AGE_ALIVE;nan
First simulation;0;0;2028-01-01;MEDIAN_AGE_ALIVE;nan
First simulation;0;0;2028-01-01;INFECT_RATE_ALIVE;-nan
First simulation;0;0;2028-01-01;POP_ALIVE;0
First simulation;0;0;2028-01-01;NUM_PARTNERS;0
First simulation;0;0;2028-01-01;MIN_AGE_DEAD;nan
First simulation;0;0;2028-01-01;MAX_AGE_DEAD;nan
First simulation;0;0;2028-01-01;MEAN_AGE_DEAD;nan
First simulation;0;0;2028-01-01;INFECT_RATE_DEAD;-nan
First simulation;0;0;2028-01-01;POP_DEAD;0
First simulation;0;0;2028-01-01;INITIAL_INFECTIONS;0
First simulation;0;0;2028-01-01;SIMULATION_INFECTIONS;0
First simulation;0;0;2028-01-01;INITIAL_MATCHES;0
First simulation;0;0;2028-01-01;SIMULATION_MATCHES;0
First simulation;0;0;2028-01-01;BREAKUPS;0
First simulation;0;0;2028-01-01;TIME_TAKEN;0
```

Note that it's in csv format, so you easily import it into Python or R and process it. You can also redirect the output to a file instead of standard output with the *results_file* parameter.

The fields of the csv file are: the name of the simulation, the number of the current simulation, the number of the simulation within the current simulation group, the date within the simulation for which the output applies, a description field, and the value of the description field. E.g. the last two columns of the last line are TIME_TAKEN and 0. This tells you that it took zero seconds for the simulation to run. Likewise the POP_ALIVE and POP_DEAD entries tell us that the population alive and dead in this simulation on 1 January 2028 is 0.

Prefixing every run with setting the FSTI_DATA directory is tedious. Let's fix that. In a POSIX environment (Linux, FreeBSD etc) that's easy. Change into the faststi-0.2.2 directory. Now set and export the FSTI_DATA environment

variable like this:

```
export FSTI_DATA=`pwd`/data
```

Test that it's working:

```
faststi -t
```

If no errors are reported, then it's working. But at present you'll have to execute the export command every time you open a terminal. To make it permanently part of your environment, place it in your .profile or .bashrc scripts, depending on the flavour of POSIX you're using.

3.2.1 A full simulation

The output of the eg1.ini simulation is rather uninteresting. To get more interesting output we need a more interesting simulation. Take a look at eg2.ini.

```
# First interesting simulation

[Full simulation]

num_simulations=4
num_agents=10000
time_step=1 DAY
simulation_period=10 YEARS

before_events=_write_agents_csv_header;_generate_and_pair;_report;_write_agents_csv
during_events=_age;_breakup_and_pair;_infect;_stage;_birth;_death
after_events=_write_agents_csv;_report

dataset_gen_sex=dataset_gen_sex.csv
dataset_gen_sex_preferred=dataset_gen_sex_preferred.csv
dataset_gen_infect=dataset_gen_infect.csv
dataset_gen_treated=dataset_gen_treated.csv
dataset_gen_resistant=dataset_gen_resistant.csv
dataset_gen_mating=dataset_gen_mating.csv

dataset_birth_infect=dataset_gen_infect.csv
dataset_birth_treated=dataset_birth_treated.csv
dataset_birth_resistant=dataset_birth_resistant.csv

dataset_rel_period=dataset_rel.csv
dataset_single_period=dataset_single.csv
dataset_infect=dataset_infect.csv
dataset_infect_stage=dataset_infect_stage.csv
dataset_mortality=dataset_mortality_simple.csv


agents_output_file=agents_out.csv
results_file=results.csv

threads=1

[Change time period]

threads=0 # As many threads as there are cores will execute
simulation_period=5 YEARS
```

Assuming you are in the simulations/examples directory you can run this simulation as follows:

```
faststi -f eg2.ini
```

This will take about 10 seconds to run, depending on your PC.

This is what the configuration does:

- Line 1 is a comment. Comments start with a #.
- Line 3 specifies the name of the first group of simulations: *Full simulation*
- Line 5 specifies the number of simulations to run in this group. Note that parameter names, like *num_simulations*, are case-sensitive.
- Line 6 specifies the number of agents in the simulation.
- Line 7 specifies the time period represented by each simulation iteration, 1 day in this case. The format for this parameter and others like it that specify a time period is a positive integer followed by either MINUTE, HOUR, DAY, WEEK, MONTH or YEAR. You can also use the plural of any of these time periods or any combination of lower and upper case (i.e. minute, minutes, hour, hours, day, days, week, weeks, month, months or year, years). You can also put a hyphen instead of a space between the integer and the time period. If you leave out the time period, it's assumed to be minutes. In FastSTI, the predefined time period have the following number of minutes:
  - hour: 60
  - day: 1,440
  - week: 10,080
  - month: 43,830
  - year: 525,949
- Line 8 specifies the simulation period: 10 years in this case. The number of time steps (or iterations) of the simulation is calculated by dividing the simulation_period by the time_step. In this simulation there are therefore 3,652 iterations: $10 \times 525949/1440$.
- Line 10 lists the events that are to be run before each simulation starts.
  - The _write_agents_csv_header event simply writes the first line of the csv file to which agents will be written.
  - The _generate_and_pair event generates agents (equal to the *num_agents* parameter) and pairs a subset of them in sexual relationships.
  - The _report event prints out some simple statistics about the agent population.
  - The _write_agents_csv event prints out the agents in csv format.
- Line 11 lists the events that are run on every iteration of the simulation.
  - The _age event increases the age of each agent by the *time_step* of the simulation (one day in this example).
  - The _breakup_and_pair event pairs a subset of agents into sexual partnerships and breaks up another subset of agents who are already in sexual partnerships.
  - The _infect event infects a subset of agents in sexual partnerships with other infected agents with the pathogen being studied, e.g. HIV.
  - The _stage event manages the infection progression of infected agents. For example, agents with HIV will first be in an acute sero-conversion phase, than a chronic infection stage, and then one or more stages that are analogous to progression to AIDS.
  - The _birth and _death events create new agents and kill agents respectively.

Many of these events depend on pre-specified parameters to calculate probabilities of the events occurring and, perhaps, other outcomes. These data are described in dataset files which are described in the *Datasets* section.

- Lines 14 to 29 list the names of the datasets associated with the various events. For example the *dataset_mortality* parameter tells the simulation the probability of an agent with a given set of characteristics dying.
- Line 32 tells the simulation to write agents out to a csv file called *agents_out.csv*.
- Line 33 tells the simulation to write simple population level statistical information produced by the *_report* event to a file called *results.csv*.
- Line 35 tells the simulation to run as a single thread. In other words each of the four simulations (specified on line 5) will run consecutively.
- Line 37 specifies a new simulation group called *Change time period*.
- Line 39 tells FastSTI to run the simulations in parallel, using up to as many threads as there are CPU cores in the machine. On a quad-core CPU, all four simulations could run at the same time.
- Line 40 specifies a different simulation period (5 years) to the *Full simulation* set of simulations. All other parameters set in the *Full simulation* set carry through to this simulation set.

There are more configuration examples in the simulation directory.

CHAPTER 4

Tutorial: Creating simulations

When you create an agent-based model, there are generally three things to consider: creating an initial population, agent behaviour during the simulation and reporting.

4.1 Initial population

FastSTI allows you to generate the initial population or to read agents in from a file.

The *before_events* parameter tells FastSTI how to initialize the agents.

4.1.1 Generating the population

The easiest way to generate a population is to use the *_generate_and_pair* event. E.g. in the simulation configuration file there would be a line like this:

```
before_events = _generate_and_pair; <other events to run before the simulation>
```

The _generate_and_pair event is a composite event which calls five other events: *_generate_agents*, *_initial_mating*, *_shuffle_mating*, *_rkpm* and *_initial_rel* events.

Together these events create the initial agents in the simulation, and place some of them into relationships. Click on each of these events to see how they work and how you can specify the number of agents, the ages of the agents, their sexes, sexual preferences and the distribution of the relationships in the set of initial agents.

4.1.2 Reading an agent file

Reading in an agent file perhaps gives greater flexibility than the built-in agent generating functionality of FastSTI.

The file would typically be created in a scripting language like R or Python or even be hand-crafted.

The *_read_agents* event is used to read in the agents. In the simulation configuration file there would be a line like this:

```
before_events = _read_agents; <other events to run before the simulation>
```

Read the *section on agent input formats* to find out how to set up the agent input CSV file.

4.2 Agent behaviour

In FastSTI agent behaviour takes place in events. There are predefined events that provide for agents to *age*, *form sexual relationships with other agents and break-up with them*, *become infected*, *start treatment <stage_ref>*, *change their infection status <stage_ref>* (e.g. become sicker or become better), be *born*, and *die*.

Most of these events are usually executed using the *during_events* parameter. Although it's conceivable you may also need to execute agent behaviour before and after a simulation using the *before_events* and *after_events* parameters respectively.

If these events don't meet your needs the FastSTI framework allows you to *code your own events* in C.

4.3 Reporting

Usually, you need statistics about the simulation before, during and after the simulation has run. FastSTI has a reporting facility to do write out demographic and statistical information at any stage of a simulation.

Reports are written to a single output file in CSV format. If you're running multiple simulations, the report lines from each simulation will be interleaved with each other throughout the file. But each report line has enough information for you to know which simulation produced it.

You'll usually need to use a spreadsheet program or a scripting language like R or Python to process the output CSV file. See the scripts directory for examples of report processing code that you make using FastSTI much easier for you.

Reporting is just another event in FastSTI. There are a few provided: *_report* - which outputs statistics, *_write_agents_csv* - which outputs every agent in the simulation, *_write_living_agents_csv* - which outputs every living agent in the simulation, and *_write_dead_agents_csv* - which outputs every dead agent in the simulation. There are also events to write the headers for the output CSV files.

The *report_frequency* parameter specifies how frequently to run these events during a simulation.

Use the events that output agents carefully. If you're executing *_write_agents_csv* during the simulation, having a report_frequency of 1 will slow your simulation down and use huge amounts of hard drive space.

A typical report setup for a simulation looks something like this:

```
results_file = results.csv
agents_output_file = agents_out.csv
report_frequency = 365
before_events =  _write_agents_csv_header; _write_results_csv_header; <other
events>; _report
during_events = <other events>; _report;  _write_living_agents_csv
after_events = <other events>; _report; write_agents_csv
```

If you don't need to know details about individual agents, then it's best not to execute the events that output agents. Your simulation will be faster and use much less disk space. Then you can also have much more frequent report writing. E.g.

```
results_file = results.csv
report_frequency = 10
```

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```
before_events =   _write_results_csv_header; <other
events>; _report
during_events = <other events>; _report
after_events = <other events>; _report
```

CHAPTER 5

Interesting example

Here is an experiment that we hope demonstrates the versatility of FastSTI.

It shows some interesting and counter-intuitive results, as well as how to use FastSTI in conjunction with a scripting language like R.

Here is the input configuration, which you can also find in simulations/examples/experiment.ini:

```
[Simulation Group 0]

threads=0
match_k = 1
num_simulations=30
num_agents=10000
time_step=1 DAY
simulation_period=10 YEARS
report_frequency=100

before_events=_write_results_csv_header;_generate_and_pair;_report
during_events=_age;_breakup_and_pair;_infect;_stage;_birth;_death;_report
after_events=_report

dataset_gen_sex=dataset_gen_sex.csv
dataset_gen_sex_preferred=dataset_gen_sex_preferred.csv
dataset_gen_infect=dataset_gen_infect.csv
dataset_gen_treated=dataset_gen_treated.csv
dataset_gen_resistant=dataset_gen_resistant.csv
dataset_gen_mating=dataset_gen_mating.csv

dataset_birth_infect=dataset_gen_infect.csv
dataset_birth_treated=dataset_birth_treated.csv
dataset_birth_resistant=dataset_birth_resistant.csv

dataset_rel_period=dataset_rel.csv
dataset_single_period=dataset_single.csv
dataset_infect=dataset_infect.csv
```

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```
dataset_infect_stage=dataset_infect_stage.csv
dataset_mortality=dataset_mortality_simple.csv

results_file=results.csv

[Simulation Group 1]
match_k = 100

[Simulation Group 2]
match_k = 1
num_agents=100000

[Simulation Group 3]
match_k = 100
```

It tells FastSTI to run four groups of simulations. Each group runs 30 simulations.

All groups run daily for ten years starting on 1 January 2018. For each simulation statistics are printed every 100 days, and then at the end, 1 January 2028. (The dates don't matter, by the way.)

- The first group (group 0) is 10,000 agents with random matching.
- The second group is 10,000 agents with k-nearest neighbour matching (using FastSTI's _rkpm event) xwith k=100.
- The third group is 100,000 agents with random matching.
- The fourth group is 100,000 agents with k-nearest neighbour matching with k=100.

The results are written to a file called results.csv. The file is large so we've compressed it. On a mid-range laptop with an i5 with four cores and 12GB of RAM it took just over 16 minutes to run the 120 simulations.

We then ran results.csv through this R script, which you can find in scripts/processResultsFile.R. (The equivalent Python script is in scripts/processResultsFile.py.)

```
# Takes a results CSV file produced by FastSTI and runs a function
# (default mean) over a statistic (description) grouping the result
# either by the maximum date or all the dates.

processFastSTIResults <- function(filename="results.csv",
                                  sep=";",
                                  description="INFECT_RATE_ALIVE",
                                  fun=mean,
                                  header=TRUE,
                                  filter_max_date=TRUE) {
    inp = read.csv(filename, sep=sep, header=header)
    values = inp[inp$description==description,]
    if (filter_max_date) {
        analysisDate = max(as.Date(values$date))
        values = values[as.Date(values$date)==analysisDate,]
    }
    mean_values = aggregate(values$value,
                            by=list(values$name,
                                    values$date),
                            FUN=fun)
}

print(processFastSTIResults())
```

This is the output:

```
   Simulation Group 0        2028-01-01      0.4280027667
   Simulation Group 1        2028-01-01      0.3647885667
   Simulation Group 2        2028-01-01      0.4283530667
   Simulation Group 3        2028-01-01      0.2342883667
```

What do the results tell us?

1. Random matching results in much higher infection rates than "intelligent" matching algorithms that try to pair agents using realistic criteria. This is expected. With random matching, one would expect an infection to spread quite rapidly through a population. With more realistic matching, we expect more sexual networks to form and the infection only occasionally moves from one network to another.
2. Random matching gives the same results irrespective of the number of agents (42.8%). This too is expected.
3. With "intelligent" matching prevalence decreases as the population increases (a mean of 36.5% for the 10,000 agent simulations after ten years vs 23.4% for the 100,000 agent simulations). This is not intuitive, at least not to us, though we have hypotheses for why it happens. We leave it to you to speculate further.

CHAPTER 6

Running FastSTI from Python

Warning: The Python interface to FastSTI is highly experimental. We hope to make Python the main way to use FastSTI because Python is so easy to use and popular among science researchers. But at this point we've only got the bare basics working. The entire Python interface to FastSTI is likely to change. Also currently if FastSTI exits because of an error, the Python interpreter also exits instead of throwing an exception, which is annoying. We will fix this in due course.

A basic Python 3 interface is supported (we don't support Python 2 and don't intend to). You'll need to install pandas.

In the scripts directory of the FastSTI folder is faststi.py.

To see the command line options it supports run (for example):

```
python faststi -h
```

To execute a set of simulations:

```
python faststi -c my_simulations.ini
```

Example of how to use faststi in a Python environment:

```
import faststi
import pandas

simset1 = faststi.SimulationSet(config_filename="my_simulations.ini")

# Runs all the simulations and save the results into a dataframe
dataframe = simset1.run()

# Slightly more sophisticated example
simset2 = faststi.SimulationSet(config_filename="my_simulations.ini")
print("There are", len(simset2.simulations), "simulations.")
# Change the match_k parameter in the third simulation (0-based indexing)
simset2.simulations[2].set_parm("match_k", 300)
```

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```
# Run the first four simulations: 0,1,2,3
dataframe2 = simset2.run(0, 4)
# Run the remaining simulations
dataframe3 = simset2.run(4)
```

In time, we hope to make this much more comprehensive, robust and useful.

CHAPTER 7

Input file formats

7.1 Configuration

The configuration file, which specifies the simulations, is in Windows ini format. Here is an example:

```
# Faststi test configuration file

[Simulation 0]

num_simulations=1
num_agents=10000
simulation_period=10 YEARS

agents_output_file=agents_out.csv
results_file=results.csv

dataset_gen_sex=dataset_gen_sex.csv
dataset_gen_sex_preferred=dataset_gen_sex_preferred.csv
dataset_gen_infect=dataset_gen_infect.csv
dataset_gen_treated=dataset_gen_treated.csv
dataset_gen_resistant=dataset_gen_resistant.csv
dataset_gen_mating=dataset_gen_mating.csv

dataset_birth_infect=dataset_gen_infect.csv
dataset_birth_treated=dataset_birth_treated.csv
dataset_birth_resistant=dataset_birth_resistant.csv

dataset_rel_period=dataset_rel.csv
dataset_single_period=dataset_single.csv
dataset_infect=dataset_infect.csv
dataset_infect_stage=dataset_infect_stage.csv
dataset_mortality=dataset_mortality_simple.csv

before_events=_write_agents_csv_header;_generate_and_pair;_report;_write_agents_csv
```

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```
during_events=_age;_breakup_and_pair;_infect;_stage;_birth;_death
after_events=_write_agents_csv;_report

match_k=100
threads=1

[Simulation 1]

dataset_mortality=dataset_mortality_complicated.csv
match_k=300
```

- Comment lines begin with a #.
- A # in the middle of a line also denotes a comment until the end of the line.
- A simulation group name is enclosed in square brackets *[]*.
- Within a simulation group, parameters are specified as key-value pairs. A key is separated from its value by an equals sign. White space before and after the = sign is ignored.
- Some parameters (e.g. *during_events* take multiple values. Each value must be separated by a semi-colon *;*. White space before or after the semi-colon is ignored.
- Blank lines are ignored.
- Each key must be a predefined parameter. If you use a key that isn't a predefined parameter, the FastSTI will give an error message and terminate. To see all the parameters, run:

```
faststi -p
```

- Key-values set in a simulation group are carried through to subsequent groups, unless they are specified again in the new group. E,g, in the example above, *dataset_mortality* and *match_k* are specified again for the simulation group called *Simulation 1*. All the other parameters are identical to *Simulation 0*.

Besides setting parameters in the input configuration file, you can modify them on the command line using this format:

```
faststi -c=<value>[;<value>]* -f <filename>
```

7.2 Datasets

Many events depend on datasets. The format of the dataset file is a little cumbersome but it is designed for a combination of speed and safety.

Datasets can either be placed in the *data* directory, or in the directory in which the simulation is being run. Alternately, the *FSTI_DATA* environment variable can be set to the location where the datasets are located.

Datasets are csv files. The default delimiter is a semi-colon, not a comma. You can change this by setting the csv_delimiter

A standard dataset consists of 0 or more columns representing the values of agent properties, followed by 1 or more columns representing probabilities or other derived values. Events typically match the properties of the current agent being operated upon to the corresponding row in the dataset in order to obtain the appropriate probability of the event occurring. Sometimes there

Let's start with the very simplest of the supplied datasets. It is *dataset_gen_sex.csv* and it is located in the *data* directory. It is used by the *_generate_agents* event to initialize the sex of agents at the beginning of simulations. Here it is:

```
1  Probability
2  0.5
```

Line 1 is simply the CSV header. It is called *Probability* here but we could have named it anything. Line 2 is 0.5, the odds of being male. The event uses this to set approximately half the agents to male and half to female when it generates agents.

Here's a more typical dataset, *dataset_gen_infect.csv*, also used by the *_generate_agents* event to determine the infection stage, if any, of agents when they are initialized.

```
1  sex;sex_preferred;age|10-YEAR;1;2;3;4|4
2  0;0;0;0;0;0;0
3  0;0;1;0;0;0;0
4  0;0;2;0.1;0.2;0.3;0.4
5  0;0;3;0.1;0.2;0.3;0.4
6  0;0;4;0.05;0.1;0.15;0.2
7  0;0;5;0.025;0.05;0.075;0.1
8  0;1;0;0;0;0;0
9  0;1;1;0;0;0;0
10 0;1;2;0.05;0.1;0.15;0.2
11 0;1;3;0.05;0.1;0.15;0.2
12 0;1;4;0.025;0.05;0.075;0.1
13 0;1;5;0.0125;0.025;0.0375;0.05
14 1;0;0;0;0;0;0
15 1;0;1;0;0;0;0
16 1;0;2;0.05;0.1;0.15;0.2
17 1;0;3;0.05;0.1;0.15;0.2
18 1;0;4;0.025;0.05;0.075;0.1
19 1;0;5;0.0125;0.025;0.0375;0.05
20 1;1;0;0;0;0;0
21 1;1;1;0;0;0;0
22 1;1;2;0.05;0.1;0.15;0.2
23 1;1;3;0.05;0.1;0.15;0.2
24 1;1;4;0.025;0.05;0.075;0.1
25 1;1;5;0.0125;0.025;0.0375;0.05
```

In the example HIV model provided, there are five possible values for *infection*:

- 0 = uninfected
- 1 = virally suppressed (usually on treatment)
- 2 = primary infection (highly infectious)
- 3 = chronic infection (usually lasts several years)
- 4 = Final stage (AIDS)

Let's start with the header (line 1). The last column is *4|4*. The first "4" is simply the name of the column (representing stage 4 infection), and could have been called anything. But the "4" after the pipe (|) tells FastSTI that the last four columns all represent probabilities. If a dataset contains more than one probability column then this must be specified. FastSTI then knows that the first three fields, *sex*, *sex_preferred* and *age* are not probability columns, and correspond precisely to the names of fields in the fsti_agent data structure. If they didn't, FastSTI would terminate with an error.

The dataset needs an entry (or row) for each combination of sex, sex_preferred and age. Also the first row of every dataset after the header must start with every property set to 0, and then cycle incrementally through all combinations of possible values for the properties. This may sound tiresome, but it ensures that probabilities can be looked up using a random access search, rather than having to sequentially search the table.

There is one important short-cut. Notice the column headed "age|10-YEAR". The pipe followed by either an integer

or a time period, tells FastSTI to divide the agent's age by this number, in this case 10 years, in order to get the value to search for in the dataset. So an agent with age 45 will have its age divided by 10 which gives it a lookup value for its age of 4 (the .5 is dropped - this is integer division).

What about an agent whose age is 60 or more (because the ages run from 0 to 5)? The dataset lookup algorithm assumes any agent property greater than the largest value is equal to the largest value.

Consider an agent who is male, prefers to have sex with females and is 31 years old. What is the probability they are HIV-positive (in this dataset)? And if HIV-positive, what infection stage is he likely to be in?

The agent matches line 11, which corresponds to male agents (first column with a value of 0) whose preferred sexual partner is female (second column with a value of 1) and agents aged 30 to 39 (third column with a value of 3, i.e. 31 / 3).

To determine if the agent is infected with HIV, the *_generate_agents* event samples a uniform random number, *r*.

- If *r* is less than 0.05 (the value in column 4 of line 11), the agent is in stage 1.
- If *r* is less than 0.1 (the value in column 5 of line 11), the agent is in stage 2.
- If *r* is less than 0.15 (the value in column 6 of line 11) the agent is in stage 3.
- If *r* is less than 0.2 (the value in column 7 of line 11) the agent is in stage 4.
- Else if *r* is greater than or equal to 0.2, the agent is uninfected.

With most events, the agent characteristics you use are up to you. You could create a dataset for generating the initial infection status of agents that doesn't take into account *sex_preferred* or *age*. Alternately, you could add a *coinfection* column (because there is a field called coinfection in the FastSTI agent structure), and make the infection probabilities dependent on that.

There is somewhat less flexibility with the probability fields. These are event-specific. As it happens the code that sets the infection stage expects one or more user-defined stages, so you can specify fewer or more than the four stages in the above example.

7.2.1 Two-agent datasets

Some events need to make a decision based on two agents. In modelling sexually transmitted infections, the most obvious example is an event that determines if an agent becomes infected. FastSTI's supplied *_infect* event does just this. It iterates over all pairs of agents in sero-discordant sexual relationships, and determines whether the negative partners becomes infected.

Consider two agents, *a* and *b*. One, *a*, is uninfected, and the other *b* is infected. If we want the risk of infection to be determined by *a*'s sex and whether it is in a same-sex or opposite-sex relationship with *b* then we need some way of specifying this in a dataset. Also, we are interested in what infection stage *b* is in. If *b* is on treatment, for example, the risk of infecting *a* may be very low.

The dataset_infect.csv dataset shows how this is handled in FastSTI.

```
1  sex;sex|1|~;infected;probability
2  0;0;0;0
3  0;0;1;0
4  0;0;2;0.02
5  0;0;3;0.008
6  0;0;4;0.008
7  0;1;0;0
8  0;1;1;0
9  0;1;2;0.01
10 0;1;3;0.004
11 0;1;4;0.004
```

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```
12  1;0;0;0
13  1;0;1;0
14  1;0;2;0.012
15  1;0;3;0.005
16  1;0;4;0.005
17  1;1;0;0
18  1;1;1;0
19  1;1;2;0.0001
20  1;1;3;0.0001
21  1;1;4;0.0001
```

The header (line 1) contains two columns named *sex*. The first one corresponds to the uninfected agent, *a*. The second and third columns are the sex and infection stage of *b*. How does FastSTI know this? Look at the second column heading: *sex|1|~*. The first pipe (|) is used to separate sex from the amount the property must be divided by. Well, unlike age, we don't want the sex to be more granular, so we specify it as 1. The second pipe is followed by a tilde (~). The tilde in the column header tells FastSTI that this is a two-agent lookup table and the second agent's properties start in this column. So the second and third columns belong to agent *b*. The final column, with name *probability*, is simply the probability of becoming infected. (By default events are executed daily, so the probability must correspond to this time-step.)

So if agent *a* is a female, and agent *b* is male in stage 2 (primary infection), what is the risk of *a* becoming infected on this iteration of the *_infect* event? The answer is given by line 14: 0.012.

7.3 Agents

Instead of generating agents, you can provide an agent file as input to the simulation. In fact, since the agent generation features of FastSTI are currently quite limited, you'll probably prefer to supply an agent file.

The agents must be specified in a CSV file. The column names in the header row must correspond to one or more field names in FastSTI's agent structure, which is declared as *struct fsti_agent* in the source file *src/fsti-agent.h*. The fields are:

- id: unsigned 32 bit integer, unique for each agent (If you do not include this field, FastSTI automatically provides this value for each agent, starting from 0.)
- sex: unsigned 8 bit integer (0 is male, 1 is female. Higher values are user-defined.)
- Either sex_preferred or orientation, an unsigned 8 bit integer (Do not use both fields. We recommend using sex_preferred rather than orientation. For sex_preferred 0 is male, 1 is female. For orientation either use 0 and 1 for heterosexual and homosexual respectively, or 0, 1, 2 and 3 for MSM, MSW, WSM and WSW respectively. Higher values are user-defined.)
- age: a positive year age of an agent between 0 and 120.
- birthday: a signed 32 bit integer (Unless you understand the internal workings of FastSTI very well, we recommend you rather use age)
- infected: unsigned 8 bit integer (0 is uninfected. 1 and up can correspond to stages of infection.)
- treated: unsigned 8 bit integer (0 is untreated. 1 and up can correspond to treatment regimens.)
- resistant: unsigned 8 bit integer (0 is no resistance. You can either use a simple approach to resistance, whereby 1 means resistant to treatment regimen 1, 2 to treatment regimen 2 etc, or you can use a more complex binary bitmask approach where 1 denotes resistance to regimen 1 only, 10, denotes resistance to regimen 2, 11 denotes resistance to regimen 1 and 2 etc.)

- coinfected (0 means not coinfected. 1 and up denotes different types of coinfection as chosen by the user. Once again, as with the resistant field, either a simple or bitmask approach can be used.)
- partners_0, partners_1, and partners_2: unsigned 32 bit integers denoting the id of a sexual partner of this agent (-1 implies agent is single. The agents are typically numbered from 0. Note: None of the default FastSTI events currently caters for concurrency. Only use partners_1 and partners_2 if you are implementing events that rely on partner concurrency. If you need more partners, change the value of FSTI_MAX_PARTNERS in fsti_userdefs.h.)
- relchange_0, relchange_1, and relchange_2: unsigned 32 bit integers corresponding to the iteration (i.e. time step) in the simulation when the agent's relationship status for partner_0, partner_1 and partner_2 respectively should change, either to single for agents with partners or to be placed in the mating pool if the agent is single

Here is an example CSV file. The default delimiter is a semi-colon, not a comma. You can change this by setting the csv_delimiter.

```
id;age;infected;sex;sex_preferred;partners_0
0;45.21;0;1;0;-1
1;47.35;1;0;1;0
2;36.62;0;1;0;-1
3;35.40;0;1;0;-1
4;24.25;0;0;1;-1
5;24.12;0;0;1;4
6;23.26;0;0;1;-1
7;45.17;0;0;1;-1
8;34.81;0;0;1;-1
9;35.80;0;0;1;8
```

CHAPTER 8

Output file formats

8.1 Results reports

Whenever the *_report* is executed, it writes output in CSV format either to the standard output device (default) or an output file as specified by the *results_file* key in the configuration. This output is meant to be post-processed by you either in a spreadsheet, or using a scripting language like R or Python.

Note: The *_report* event prints out quite basic information. If you feel comfortable writing C code, you can enhance it in the fsti_userdefs.h file by defining the *FSTI_HOOK_REPORT* macro. See the *FSTI_REPORT* macro in fsti-defaults.h.

Here is an example output from a set of simulations:

```
name;sim;num;date;description;value
Simulation_0;0;0;2018-01-01;MIN_AGE_ALIVE;15.000000
Simulation_0;0;0;2018-01-01;MAX_AGE_ALIVE;49.000000
Simulation_0;0;0;2018-01-01;MEAN_AGE_ALIVE;23.000000
Simulation_0;0;0;2018-01-01;MEDIAN_AGE_ALIVE;18.000000
Simulation_0;0;0;2018-01-01;INFECT_RATE_ALIVE;0.077900
Simulation_0;0;0;2018-01-01;POP_ALIVE;20000
Simulation_0;0;0;2018-01-01;NUM_PARTNERS;3573
Simulation_0;0;0;2018-01-01;MIN_AGE_DEAD;nan
Simulation_0;0;0;2018-01-01;MAX_AGE_DEAD;nan
Simulation_0;0;0;2018-01-01;MEAN_AGE_DEAD;nan
Simulation_0;0;0;2018-01-01;INFECT_RATE_DEAD;-nan
Simulation_0;0;0;2018-01-01;POP_DEAD;0
Simulation_0;0;0;2018-01-01;INITIAL_INFECTIONS;1558
Simulation_0;0;0;2018-01-01;SIMULATION_INFECTIONS;0
Simulation_0;0;0;2018-01-01;INITIAL_MATCHES;3573
Simulation_0;0;0;2018-01-01;SIMULATION_MATCHES;0
Simulation_0;0;0;2018-01-01;BREAKUPS;0
Simulation_0;0;0;2018-01-01;TIME_TAKEN;1
```

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```
Simulation_0;0;0;2028-01-01;MIN_AGE_ALIVE;15.000000
Simulation_0;0;0;2028-01-01;MAX_AGE_ALIVE;59.000000
Simulation_0;0;0;2028-01-01;MEAN_AGE_ALIVE;30.000000
Simulation_0;0;0;2028-01-01;MEDIAN_AGE_ALIVE;26.000000
Simulation_0;0;0;2028-01-01;INFECT_RATE_ALIVE;0.142421
Simulation_0;0;0;2028-01-01;POP_ALIVE;23592
Simulation_0;0;0;2028-01-01;NUM_PARTNERS;8442
Simulation_0;0;0;2028-01-01;MIN_AGE_DEAD;15.000000
Simulation_0;0;0;2028-01-01;MAX_AGE_DEAD;58.000000
Simulation_0;0;0;2028-01-01;MEAN_AGE_DEAD;31.000000
Simulation_0;0;0;2028-01-01;INFECT_RATE_DEAD;0.738192
Simulation_0;0;0;2028-01-01;POP_DEAD;741
Simulation_0;0;0;2028-01-01;INITIAL_INFECTIONS;1558
Simulation_0;0;0;2028-01-01;SIMULATION_INFECTIONS;2349
Simulation_0;0;0;2028-01-01;INITIAL_MATCHES;3573
Simulation_0;0;0;2028-01-01;SIMULATION_MATCHES;145574
Simulation_0;0;0;2028-01-01;BREAKUPS;140193
Simulation_0;0;0;2028-01-01;TIME_TAKEN;6
Simulation_0;1;1;2018-01-01;MIN_AGE_ALIVE;15.000000
Simulation_0;1;1;2018-01-01;MAX_AGE_ALIVE;49.000000
Simulation_0;1;1;2018-01-01;MEAN_AGE_ALIVE;23.000000
Simulation_0;1;1;2018-01-01;MEDIAN_AGE_ALIVE;18.000000
Simulation_0;1;1;2018-01-01;INFECT_RATE_ALIVE;0.080300
Simulation_0;1;1;2018-01-01;POP_ALIVE;20000
Simulation_0;1;1;2018-01-01;NUM_PARTNERS;3601
Simulation_0;1;1;2018-01-01;MIN_AGE_DEAD;nan
Simulation_0;1;1;2018-01-01;MAX_AGE_DEAD;nan
Simulation_0;1;1;2018-01-01;MEAN_AGE_DEAD;nan
Simulation_0;1;1;2018-01-01;INFECT_RATE_DEAD;-nan
Simulation_0;1;1;2018-01-01;POP_DEAD;0
Simulation_0;1;1;2018-01-01;INITIAL_INFECTIONS;1606
Simulation_0;1;1;2018-01-01;SIMULATION_INFECTIONS;0
Simulation_0;1;1;2018-01-01;INITIAL_MATCHES;3601
Simulation_0;1;1;2018-01-01;SIMULATION_MATCHES;0
Simulation_0;1;1;2018-01-01;BREAKUPS;0
Simulation_0;1;1;2018-01-01;TIME_TAKEN;6
Simulation_0;1;1;2028-01-01;MIN_AGE_ALIVE;15.000000
Simulation_0;1;1;2028-01-01;MAX_AGE_ALIVE;59.000000
Simulation_0;1;1;2028-01-01;MEAN_AGE_ALIVE;30.000000
Simulation_0;1;1;2028-01-01;MEDIAN_AGE_ALIVE;26.000000
Simulation_0;1;1;2028-01-01;INFECT_RATE_ALIVE;0.142754
Simulation_0;1;1;2028-01-01;POP_ALIVE;23516
Simulation_0;1;1;2028-01-01;NUM_PARTNERS;8432
Simulation_0;1;1;2028-01-01;MIN_AGE_DEAD;15.000000
Simulation_0;1;1;2028-01-01;MAX_AGE_DEAD;55.000000
Simulation_0;1;1;2028-01-01;MEAN_AGE_DEAD;31.000000
Simulation_0;1;1;2028-01-01;INFECT_RATE_DEAD;0.768553
Simulation_0;1;1;2028-01-01;POP_DEAD;795
Simulation_0;1;1;2028-01-01;INITIAL_INFECTIONS;1606
Simulation_0;1;1;2028-01-01;SIMULATION_INFECTIONS;2362
Simulation_0;1;1;2028-01-01;INITIAL_MATCHES;3601
Simulation_0;1;1;2028-01-01;SIMULATION_MATCHES;146416
Simulation_0;1;1;2028-01-01;BREAKUPS;141010
Simulation_0;1;1;2028-01-01;TIME_TAKEN;11
Simulation_1;2;0;2018-01-01;MIN_AGE_ALIVE;15.000000
Simulation_1;2;0;2018-01-01;MAX_AGE_ALIVE;49.000000
Simulation_1;2;0;2018-01-01;MEAN_AGE_ALIVE;23.000000
```

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```
Simulation_1;2;0;2018-01-01;MEDIAN_AGE_ALIVE;18.000000
Simulation_1;2;0;2018-01-01;INFECT_RATE_ALIVE;0.080600
Simulation_1;2;0;2018-01-01;POP_ALIVE;20000
Simulation_1;2;0;2018-01-01;NUM_PARTNERS;3569
Simulation_1;2;0;2018-01-01;MIN_AGE_DEAD;nan
Simulation_1;2;0;2018-01-01;MAX_AGE_DEAD;nan
Simulation_1;2;0;2018-01-01;MEAN_AGE_DEAD;nan
Simulation_1;2;0;2018-01-01;INFECT_RATE_DEAD;-nan
Simulation_1;2;0;2018-01-01;POP_DEAD;0
Simulation_1;2;0;2018-01-01;INITIAL_INFECTIONS;1612
Simulation_1;2;0;2018-01-01;SIMULATION_INFECTIONS;0
Simulation_1;2;0;2018-01-01;INITIAL_MATCHES;3569
Simulation_1;2;0;2018-01-01;SIMULATION_MATCHES;0
Simulation_1;2;0;2018-01-01;BREAKUPS;0
Simulation_1;2;0;2018-01-01;TIME_TAKEN;5
Simulation_1;2;0;2028-01-01;MIN_AGE_ALIVE;15.000000
Simulation_1;2;0;2028-01-01;MAX_AGE_ALIVE;59.000000
Simulation_1;2;0;2028-01-01;MEAN_AGE_ALIVE;30.000000
Simulation_1;2;0;2028-01-01;MEDIAN_AGE_ALIVE;26.000000
Simulation_1;2;0;2028-01-01;INFECT_RATE_ALIVE;0.136983
Simulation_1;2;0;2028-01-01;POP_ALIVE;23638
Simulation_1;2;0;2028-01-01;NUM_PARTNERS;8423
Simulation_1;2;0;2028-01-01;MIN_AGE_DEAD;15.000000
Simulation_1;2;0;2028-01-01;MAX_AGE_DEAD;59.000000
Simulation_1;2;0;2028-01-01;MEAN_AGE_DEAD;32.000000
Simulation_1;2;0;2028-01-01;INFECT_RATE_DEAD;0.717507
Simulation_1;2;0;2028-01-01;POP_DEAD;754
Simulation_1;2;0;2028-01-01;INITIAL_INFECTIONS;1612
Simulation_1;2;0;2028-01-01;SIMULATION_INFECTIONS;2167
Simulation_1;2;0;2028-01-01;INITIAL_MATCHES;3569
Simulation_1;2;0;2028-01-01;SIMULATION_MATCHES;145976
Simulation_1;2;0;2028-01-01;BREAKUPS;140568
Simulation_1;2;0;2028-01-01;TIME_TAKEN;10
Simulation_1;3;1;2018-01-01;MIN_AGE_ALIVE;15.000000
Simulation_1;3;1;2018-01-01;MAX_AGE_ALIVE;49.000000
Simulation_1;3;1;2018-01-01;MEAN_AGE_ALIVE;23.000000
Simulation_1;3;1;2018-01-01;MEDIAN_AGE_ALIVE;18.000000
Simulation_1;3;1;2018-01-01;INFECT_RATE_ALIVE;0.083850
Simulation_1;3;1;2018-01-01;POP_ALIVE;20000
Simulation_1;3;1;2018-01-01;NUM_PARTNERS;3550
Simulation_1;3;1;2018-01-01;MIN_AGE_DEAD;nan
Simulation_1;3;1;2018-01-01;MAX_AGE_DEAD;nan
Simulation_1;3;1;2018-01-01;MEAN_AGE_DEAD;nan
Simulation_1;3;1;2018-01-01;INFECT_RATE_DEAD;-nan
Simulation_1;3;1;2018-01-01;POP_DEAD;0
Simulation_1;3;1;2018-01-01;INITIAL_INFECTIONS;1677
Simulation_1;3;1;2018-01-01;SIMULATION_INFECTIONS;0
Simulation_1;3;1;2018-01-01;INITIAL_MATCHES;3550
Simulation_1;3;1;2018-01-01;SIMULATION_MATCHES;0
Simulation_1;3;1;2018-01-01;BREAKUPS;0
Simulation_1;3;1;2018-01-01;TIME_TAKEN;5
Simulation_1;3;1;2028-01-01;MIN_AGE_ALIVE;15.000000
Simulation_1;3;1;2028-01-01;MAX_AGE_ALIVE;59.000000
Simulation_1;3;1;2028-01-01;MEAN_AGE_ALIVE;30.000000
Simulation_1;3;1;2028-01-01;MEDIAN_AGE_ALIVE;26.000000
Simulation_1;3;1;2028-01-01;INFECT_RATE_ALIVE;0.139352
Simulation_1;3;1;2028-01-01;POP_ALIVE;23595
```

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```
Simulation_1;3;1;2028-01-01;NUM_PARTNERS;8456
Simulation_1;3;1;2028-01-01;MIN_AGE_DEAD;15.000000
Simulation_1;3;1;2028-01-01;MAX_AGE_DEAD;58.000000
Simulation_1;3;1;2028-01-01;MEAN_AGE_DEAD;31.000000
Simulation_1;3;1;2028-01-01;INFECT_RATE_DEAD;0.728205
Simulation_1;3;1;2028-01-01;POP_DEAD;780
Simulation_1;3;1;2028-01-01;INITIAL_INFECTIONS;1677
Simulation_1;3;1;2028-01-01;SIMULATION_INFECTIONS;2179
Simulation_1;3;1;2028-01-01;INITIAL_MATCHES;3550
Simulation_1;3;1;2028-01-01;SIMULATION_MATCHES;146061
Simulation_1;3;1;2028-01-01;BREAKUPS;140609
Simulation_1;3;1;2028-01-01;TIME_TAKEN;10
```

- The first column (name) is the simulation group name as specified in the configuration file.
- The second column (sim) is the unique simulation number. In every execution of FastSTI, each simulation will have its own unique id, starting from 0.
- The third column (num) is the number of the simulation within the simulation group. Here each of the two simulation groups (Simulation_0 and Simulation_1) executed two simulations each, numbered 0 and 1.
- The fourth column is the date within the simulation that this snapshot report is for. In these simulations, the start date was 1 January 2018, and the end date was 1 January 2028. The *_report* event ran before and after the simulation (it can run as often as you like during the simulation as well).
- The fifth column is the description of what's being reported. These are described below.
- The sixth column is the value of what's being reported. E.g. 10 for TIME_TAKEN means the simulation ran in 10 seconds up to that point.

Warning: The output in the example above is all in chronological order. This is because it was a single-threaded sequential execution. Normally you will do a multithreaded execution and the report lines will likely **not** come out in order. When analysing them in a spreadsheet, R or Python, remember to sort the output by the first four columns.

8.1.1 What the descriptions mean

MIN_AGE_ALIVE is the youngest age, in years, of a currently living agent

MAX_AGE_ALIVE is the oldest age, in years of a currently living agent

MEAN_AGE_ALIVE is the mean age, in years, of the living population

MEDIAN_AGE_ALIVE is the median age, in years, of the living population

INFECT_RATE_ALIVE is the infection rate of the living population

POP_ALIVE is the number of living agents

NUM_PARTNERS is the number of agents in relationships

MIN_AGE_DEAD is the age of the youngest agent who has died

MAX_AGE_DEAD is the age of the oldest agent who has died

INFECT_RATE_DEAD is the infection rate in the dead population

POP_DEAD is the number of dead agents

INITIAL_INFECTIONS is the number of infected agents at the start of the simulation

SIMULATION_INFECTIONS is the number of agents who became infected during the simulation

INITIAL_MATCHES is the number of pairs of agents in relationships at the start of the simulation

SIMULATION_MATCHES is the number of pairs of agents made during the simulation

BREAKUPS is the number of pairs that broke up during the simulation

TIME_TAKEN is the time taken by the simulation in seconds

8.2 Agent output

The *_write_agents_csv_header* prints out the header line in an output agent csv file. The *_write_agents_csv* event actually writes out all the agents (living and dead), and the *_write_living_agents_csv* and *_write_dead_agents_csv* write the living and dead agents respectively.

Here is an extract from sample output of the *_write_agents_csv_header* and *_write_agents_csv* events.

```
   sim;date;id;age;sex;sex_preferred;infected;treated;resistant;date_death;partner;
↪change_date
   1;2028-01-01;1547;25;0;1;0;0;0;0000-00-00;515;2035-10-24
   1;2028-01-01;1548;41;0;1;4;0;0;2023-10-11;-1;2025-10-30
   1;2028-01-01;1549;28;0;1;0;0;0;0000-00-00;6620;2028-04-22
   1;2028-01-01;1550;25;1;0;0;0;0;0000-00-00;3910;2029-09-04
   1;2028-01-01;1551;31;1;0;1;1;0;0000-00-00;22910;2028-01-13
   1;2028-01-01;1552;30;1;0;0;0;0;0000-00-00;18055;2028-01-03
   1;2028-01-01;1553;36;1;0;0;0;0;0000-00-00;7448;2028-10-14
   1;2028-01-01;1554;33;1;0;0;0;0;0000-00-00;694;2028-04-25
   1;2028-01-01;1555;28;0;0;0;0;0;0000-00-00;984;2028-03-23
   1;2028-01-01;1556;28;0;1;0;0;0;0000-00-00;4467;2030-03-27
   1;2028-01-01;1557;45;0;1;0;0;0;0000-00-00;15614;2035-01-22
   1;2028-01-01;1558;27;1;0;0;0;0;0000-00-00;3367;2030-02-17
   1;2028-01-01;1559;29;0;1;0;0;0;0000-00-00;10884;2030-01-10
   1;2028-01-01;1560;52;1;0;0;0;0;0000-00-00;19043;2028-05-24
   1;2028-01-01;1561;58;1;0;0;0;0;0000-00-00;13638;2028-07-01
   1;2028-01-01;1562;30;1;0;0;0;0;0000-00-00;14842;2030-02-19
   1;2028-01-01;1563;57;0;1;0;0;0;0000-00-00;17535;2029-03-13
   1;2028-01-01;1564;37;1;0;1;1;1;0000-00-00;15586;2031-10-26
   1;2028-01-01;1565;29;1;0;0;4;0;2026-11-30;-1;2027-08-30
   1;2028-01-01;1566;46;1;0;0;0;0;0000-00-00;-1;2030-03-21
   1;2028-01-01;1567;26;1;0;0;0;0;0000-00-00;16097;2029-03-04
```

The first column is the simulation number. The second column is the current simulation date. The third column is the unique agent id. The fourth to ninth columns are the agent's sex, preferred sex, infection stage, treatment regimen, and resistance status respectively. The tenth column is 0000-00-00 if the agent is alive, else the date the agent died. The eleventh column is the unique id of the agent's partner (-1 if the agent is single). The last column is the date the agent's relationship status will change, either to single if it's in a relationship, or to a relationship if it's single.

Note: FastSTI's agent output event assumes an agent has at most one partner. You can extend it if you're implementing concurrency.

Note: If you feel comfortable writing C code, you can modify or extend the output of the *_write_agents_csv*, *_write_living_agents_csv* and *_write_dead_agents_csv* events by redefining the

FSTI_AGENT_PRINT_CSV_HEADER and FSTI_AGENT_PRINT_CSV macros. Put your redefinition in *src/fsti-userdefs.h*. The default implementation is in *src/fsti-defaults.h*.

CHAPTER 9

Configuration file parameters

To see the list of configuration file parameters, along with a description and the value for each, run:

```
faststi -p
```

This prints out the parameters in a logical order. Here is an alphabetically arranged reference guide to the parameters:

9.1 after_events

These are the events executed after a simulation starts.

Default value: _no_op

Events used in: None

Examples::

```
after_events = _write_agents_csv;_report

after_events = _no_op # No events are executed after the simulation (default)
```

9.2 age_alpha

If instead of reading in an agent file, the agents are generated with the *_generate_agents* event, then the initial age of each agent is drawn a random alpha-beta distribution. This is the alpha parameter.

Default value: 0.3

Events used in: _generate_agents, _generate_and_pair

Example:

```
age_alpha = 0.5
```

9.3 age_beta

If instead of reading in an agent file, the agents are generated with the *_generate_agents* event, then the initial age of each agent is drawn a random alpha-beta distribution. This is the beta parameter.

Default: 1.0

Events used in: _generate_agents, _generate_and_pair

9.4 age_input_time_step

Denomination of agent ages used in input files. This is typically either a year or 5-year age groups.

Default: 1 year (525949 minutes)

Events used in: _read_agents

Examples:

```
age_input_time_step = 525949

age_input_time_step = YEAR

age_input_time_step = 5 YEARS
```

9.5 age_max

Oldest age that a generated agent at the beginning of a simulation can be initialized to.

Default: 50 years (26297450 minutes)

Events used in: _generate_agents, _generate_and_pair

Examples:

```
age_max = 26297450

age_max = 50 YEARS
```

9.6 age_min

Youngest age that a generated agent at the beginning of a simulation can be initialized to.

Default: 15 years (7889235 minutes)

Events used in: _generate_agents, _generate_and_pair

Examples:

```
age_max = 26297450

age_max = 50 YEARS
```

9.7 agents_input_file

Name of the csv file to read agents from. Use empty string for standard input.

Default: agents_in.csv

Events used in: _read_agents

Examples:

```
agents_input_file = agents_in.csv

agents_input_file = stdin # Reads agents from standard input
```

9.8 agents_output_file

Name of the csv file to write agents to. Use empty string for standard output.

Events used in: _write_agents_csv_header, _write_agents_csv, _write_living_agents_csv, _write_dead_agents_csv

Examples:

```
agents_output_file = agents_out.csv

agents_output_file = stdout # Writes agents to standard output
```

9.9 before_events

These are the events executed before a simulation starts.

Default: _no_op

Events used in: None

Examples:

```
before_events = _write_agents_csv_header;_write_results_csv_header;_generate_and_pair

before_events = _no_op # No events are executed after the simulation (default)
```

9.10 birth_event_every_n

Indicates how frequently (i.e. every nth iteration) the birth (_birth) event is executed.

The birth event creates new agents during the simulation. Each new agent is set to the minimum age. Because the number of agents might be too small for their to be births on every iteration, this parameter allows you to execute the births at specified iterations.

Also, births are discrete. There can only be a whole number of births executed by the _birth event. Even if births can take place daily, rounding the expected number of births to a whole number may create a severely inaccurate birth rate. Therefore it may be better to execute the _birth event infrequently but with more births taking place each time it executes, in order to reduce the difference between the births generated by the model and the births in the real-world population being studied.

Default: 73 (i.e. every 73rd iteration - by default this would be every 73rd day of the simulation)

Of course if your simulation doesn't use the _birth event, this parameter is irrelevant.

Events used in: _birth

Examples:

```
birth_event_every_n = 73
```

9.11 birth_rate

Birth rate for the period of birth_event_every_n

Events used in: _birth

Default: 0.003968

Example:

```
birth_rate = 0.002
```

9.12 csv_delimiter

Character that separates CSV fields

Events used in: any event that reads or writes a CSV file.

Default value: ;

Examples:

```
csv_delimiter = ,
```

Note: It's not currently possible to set the csv_delimiter in the configuration file to a semi-colon (;) because this is the delimiter for the configuration file itself. But the default value for csv_delimiter is the semi-colon, so it should be unnecessary to have to set it to anything other than a comma.

9.13 dataset_birth_infect

Specifies the location of a dataset used to set the infection stage of agents, if any, when they enter the simulation (when agents are born, so to speak, although since they are born at the minimum age of the simulation, e.g. 15 years old, they may already be sexually active).

See the data/dataset_birth_infect.csv file for an example of this dataset.

In this example file, the the agent characteristics of sex, sex_preferred and age (in 10-year groupings) are used to determine probability of an agent being uninfected (i.e. agent->infected is set to 0), or stage 1, 2, 3 or 4. Note the probabilities are ascending from stage 1 through 4. The _birth event first checks if a uniform random number, r, is < than the stage 1 probability. If it is, agent->infected is set to 1. Then it checks if r is < than the stage 2 probability and >= the stage 1 probability. If it is, agent->infected is set to 2. Etc. If r is >= the stage 4 probability, the agent is uninfected and agent->infected is set to 0. Your simulation can have many stages (up to 254, but this would almost certainly be unmanageable), so long as they are consistently treated across datasets.

Events used in: _birth

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_birth_infect = dataset_birth_infect.csv
```

9.14 dataset_birth_resistant

Specifies the location of a dataset used to set the resistance of infected agents, if any, when they enter the simulation (when agents are born, so to speak, although since they are born at the minimum age of the simulation, e.g. 15 years old, they may already be sexually active). The file can have any number of columns specifying agent characteristics (independent variables). It must have exactly one dependent variable column specifying the risk of resistance for agents with a given set of characteristics.

See the data/dataset_birth_resistant.csv file for an example of this dataset.

Events used in: _birth

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_birth_resistant = dataset_birth_resistant.csv
```

Note: This mechanism for modelling resistance at birth is a bit too simple and needs to be improved.

9.15 dataset_birth_treated

Specifies the location of a dataset used to set the probability of an infected agent being on treatment when they enter the simulation (when agents are born, so to speak, although since they are born at the minimum age of the simulation, e.g. 15 years old, they may already be sexually active). The file can have any number of columns specifying agent characteristics (independent variables). It must have exactly one dependent variable column specifying the probability of treatment for agents with a given set of characteristics

See the data/dataset_birth_treated.csv file for an example of this dataset.

Events used in: _birth

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_birth_treated = dataset_birth_treated.csv
```

9.16 dataset_coinfect

Specifies the location of a dataset used to set the coinfection status of an agent. You can have as many columns specifying agent characteristics (i.e. the independent variables) as you wish but the _coinfect event expects exactly one dependent variable, the probability of the agent being coinfected per time step.

See the data/dataset_coinfect.csv file for an example of this dataset.

Events used in: _coinfect

Examples:

```
dataset_coinfect = dataset_coinfect.csv
```

9.17 dataset_gen_infect

Specifies the location of a dataset used to set the infection stage of agents, if any, at the beginning of a simulation.

See the data/dataset_gen_infect.csv file for an example of this dataset.

In this example file, the agent characteristics of sex, sex_preferred and age (in 10-year groupings) are used to determine probability of an agent being uninfected (i.e. agent->infected is set to 0), or stage 1, 2, 3 or 4. Note the probabilities are ascending from stage 1 through 4. The _birth event first checks if a uniform random number, r, is < than the stage 1 probability. If it is, agent->infected is set to 1. Then it checks if r is < than the stage 2 probability and >= the stage 1 probability. If it is, agent->infected is set to 2. Etc. If r is >= the stage 4 probability, the agent is uninfected and agent->infected is set to 0. Your simulation can have many stages (up to 254, but this would almost certainly be unmanageable), so long as they are consistently treated across datasets.

Events used in: _generate_agents, _generate_and_pair

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_gen_infect = dataset_gen_infect.csv
```

9.18 dataset_gen_mating

Specifies the location of a dataset used to set the probability of an agent being in the mating pool at the beginning of a simulation. You can have as many columns specifying agent characteristics (i.e. the independent variables) as you wish but the events that use this dataset expect exactly one dependent variable, the probability of the agent being in the initial mating pool.

See the data/dataset_gen_mating.csv file for an example of this dataset.

Events used in: _generate_agents, _generate_and_pair

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_gen_mating = dataset_gen_mating.csv
```

9.19 dataset_gen_resistant

Specifies the location of a dataset used to set the resistance of infected agents, if any, at the beginning of a simulation. The file can have any number of columns specifying agent characteristics (independent variables). It must have exactly one dependent variable column specifying the risk of resistance for agents with a given set of characteristics.

See the data/dataset_gen_resistant.csv file for an example of this dataset.

Events used in: _generate_agents, _generate_and_pair

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_gen_resistant = dataset_gen_resistant.csv
```

Note: This mechanism for modelling resistance is a bit too simple and needs to be improved.

9.20 dataset_gen_sex

Specifies the location of a dataset used to set the sex of an agent at the beginning of a simulation. The file can have zero or more columns specifying agent characteristics (independent variables). It must have exactly one dependent variable column specifying the probability of the agent being male. Typically this is a one-column dataset with a header and one data row set to 0.5. But if you want need more sophisticated initiation of agent sex (e.g. by age), then this is the dataset in which you specify it.

See the data/dataset_gen_sex.csv file for an example of this dataset.

Events used in: _generate_agents, _generate_and_pair

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_gen_sex = dataset_gen_sex.csv
```

9.21 dataset_gen_sex_preferred

Specifies the location of a dataset used to set the sexual preference of an agent at the beginning of a simulation. The file can have zero or more columns specifying agent characteristics (independent variables). It must have exactly one dependent variable column specifying the probability of the agent preferring a male sexual partner.

See the data/dataset_gen_sex_preferred.csv file for an example of this dataset.

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_gen_sex_preferred = dataset_gen_sex_preferred.csv
```

9.22 dataset_gen_treated

Specifies the location of a dataset used to set the treatment status of an infected agent at the beginning of a simulation. The file can have zero or more columns specifying agent characteristics (independent variables). The number of dependent variable columns must correspond to the number of possible treatment statuses, incrementing from 1. Events that use this dataset generate a uniform random number, r, and then compare r from the first dependent column onwards. If r is less than the probability in a dependent column, the agent's treatment status is set to the dependent column number.

Here's a mixture of C and pseudocode showing how FastSTI does this:

```
num_stages = simulation->dataset_gen_treated->num_dependents;
rnd = uniform random number;
agent->treated = 0;
row = fsti_dataset_lookup_row(dataset_gen_treated, agent);
for (col = 1; col <= num_stages; col++) {
    prob = dataset_get(dataset_gen_treated, row, col);
    if (rnd < prob) {
        agent->treated = col;
        break;
    }
}
```

See the data/dataset_gen_treated.csv file for an example of this dataset.

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_gen_treated = dataset_gen_sex_treated.csv
```

9.23 dataset_infect

Specifies the location of a dataset used to determine whether an agent becomes infected by its sexual partner. This is a two-agent dataset, since the probability of infection is a function of the characteristics of both agents. See *Two-agent datasets* for details on how this works.

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_gen_infect = dataset_gen_infect.csv
```

9.24 dataset_infect_stage

Specifies the location of a dataset used to determine if an infected agent should change the infection stage it is in.

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_gen_infect = dataset_gen_infect.csv
```

This is quite a complicated dataset and is best understood by looking at the commented example in the data directory called dataset_infect_stage.csv. For convenience here it is:

```
    # Dataset used by _stage event (defined in fsti-events.c as fsti_event_stage)
    #
    # The first three columns are used for matching and correspond to agent fields
    # or properties.
    #
    # The next six columns are instructions on how and when to change the stage.
    #
    # Columns:
    #
    #  1. infected - the infection stage of the agent (0 is uninfected)
    #  2. treated - the treatment regimen of the agent. This particular file
    #               allows for 3 treatment regimens.
    #  3. resistant - 0 if the agent is drug-susceptible to this treatment regimen
    #                 1 if the agent is drug-resistant to this treatment regimen
    #  4. prob_stage_change - probability that the infection stage changes for
    #                         this time step (1 day)
    #  5. stage_incr - if a uniformly generated random number < prob_stage_change
    #                  then change the infect property by this increment
    #  6. prob_treatment_change - probability treatment changes
    #  7. treatment_incr - if a uniformly rand number < prob_treatment_change
    #                      then change the treatment property by this increment
    #  8. prob_resistant - probability resistance status changes
    #  9. resistant_incr - if a uniformly random number < prob_resistant_change
    #                      change the resistant value by this amount
    #
    # Note the |6 after resistant_incr means that there are six columns at the end
    # of each line that are not agent properties.
    #
    # Infection stages:;;;;;;;;
    #  0 = uninfected;;;;;;;;
    #  1 = virally suppressed (usually on treatment);;;;;;;;
    #  2 = primary infection (highly infectious);;;;;;;;
    #  3 = chronic infection;;;;;;;;
    #  4 = Final stage;;;;;;;;
    #
    # HEADER ROW FOLLOWS
    infected;treated;resistant;prob_stage_change;stage_incr;prob_treatment_change;
↪treatment_incr;prob_resistant;resistant_incr|6
    0;0;0;0;0;0;0;0;0
    0;0;1;0;0;0;0;0;0
    0;1;0;0;0;0;0;0;0
    0;1;1;0;0;0;0;0;0
    0;2;0;0;0;0;0;0;0
    0;2;1;0;0;0;0;0;0
    0;3;0;0;0;0;0;0;0
    0;3;1;0;0;0;0;0;0
    1;0;0;0.1;1;0.0001;1;0;0
    1;0;1;0.1;1;0.0001;1;0;0
    1;1;0;0.00001;1;0.00001;1;0.00001;1
    1;1;1;0.1;1;0.0001;1;0;0
    1;2;0;0.00001;1;0.00001;1;0.00001;1
    1;2;1;0.1;1;0.0001;1;0;0
    1;3;0;0.00001;1;0;0;0.0001;1
    1;3;1;0.1;1;0;0;0;0
    2;0;0;0.1;1;0.001;1;0;0
    2;0;1;0.1;1;0.001;1;0;0
    2;1;0;0.1;-1;0;0;0.0001;1
```

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```
    2;1;1;0.1;1;0.001;1;0;0
    2;2;0;0.1;-1;0;0;0.0001;1
    2;2;1;0.1;1;0.001;1;0;0
    2;3;0;0.1;-1;0;0;0.0001;1
    2;3;1;0.1;1;0;0;0;0
    3;0;0;0.004;1;0.0001;1;0;0
    3;0;1;0.001;1;0.0001;1;0;0
    3;1;0;0.1;-1;0;0;0.0001;1
    3;1;1;0.002;1;0.005;1;0;0
    3;2;0;0.1;-1;0;0;0.0001;1
    3;2;1;0.002;1;0.001;1;0;0
    3;3;0;0.1;-1;0;0;0.0001;1
    3;3;1;0.002;1;0;0;0;0
    4;0;0;0;0;0.005;1;0;0
    4;0;1;0;0;0.005;1;0;0
    4;1;0;0.1;-1;0;0;0.0001;1
    4;1;1;0;0;0.01;1;0;0
    4;2;0;0.1;-1;0;0;0.0001;1
    4;2;1;0;0;0.01;1;0;0
    4;3;0;0.1;-1;0;0;0.0001;1
    4;3;1;0;0;0;0;0;0
```

9.25 dataset_mortality

Specifies the location of a dataset used to determine if an agent should die on the current time step.

See the data/dataset_mortality.csv file for an example of this dataset.

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_mortality = dataset_mortality.csv
```

9.26 dataset_rel_period

Specifies the location of a dataset used to determine the length of time an agent relationship should be.

This dataset requires two dependent variable columns: scale and shape, which are used to draw a random number from a Weibull distribution for each agent in the relationship. The values returned are the number of time steps (iterations). The duration of the relationship is the mean of the two random numbers drawn.

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_rel_period = dataset_rel_period.csv
```

9.27 dataset_single_period

Specifies the location of a dataset used to determine the length of time an agent should remain single.

This dataset requires two dependent variable columns: scale and shape, which are used to draw a random number from a Weibull distribution for the agent. The value drawn is the number of time steps the agent should remain single.

Default: _no_op # i.e. there is no dataset file specified.

Examples:

```
dataset_single_period = dataset_single_period.csv
```

9.28 during_events

These are the events executed on every time step of a simulation.

Default: _no_op

Events used in: None

Examples:

```
during_events=_age;_breakup_and_pair;_infect;_stage;_birth;_death

during_events = _no_op # No events are executed during the simulation (default)
```

9.29 report_frequency

Indicates the frequency that the reporting events specified by the during_events parameter should be specified.

Default: 1, i.e. on every iteration or time step of the simulation. Make sure this is what you really want. If you're executing *_write_agents_csv* during the simulation, having a report_frequency of 1 will slow your simulation down and use huge amounts of hard drive space.

Events used in: _write_agents_csv, _write_live_agents_csv, _write_dead_agents_csv, _report

Examples:

```
report_frequency = 365 # Report every 365 time steps.
```

9.30 initial_infect_stage

When an agent is infected, this parameter determines the initial infection stage.

Default: 2. In the default simulation provided by FastSTI, the agent infected property of 1 implies it is on treatment. No one is on treatment when infected, so 2 represents the primary infection stage, and this is therefore the default value that initial_infect_stage is set to.

Events used in: _infect

Example:

```
initial_infect_stage = 2
```

9.31 match_k

The value of k when using nearest-neighbour type agent matching algorithms. The agent matching algorithm supplied with GroundUp (implemented by the *_rkpm* event) chooses the best match for the current agent being considered for matching in the mating pool from the k unmatched agents adjacent to it.

If k is set to 1, this is random matching matching. If k is set larger than the possible number of agents in the mating pool, then this is a kind of brute force matching.

Default: 100 This is usually a good compromise value. The algorithm will execute quickly and the agent selected will on average be a better match than 99% of the remaining agents in the mating pool.

Default: 100

Events used in: _rpkm

Example:

```
match_k = 300
```

9.32 mutual_csv_partners

Sometimes a CSV file of agents that is used to initialize a simulation only records one of the partners in a relationship. If this is the case then set this parameter to 1. FastSTI will then iterate through all the agents after they've been read in, but before the simulation loop begins, and properly initialise all relationships.

Leaving this at 0 if the CSV file does not mutually record agent relationships will give unpredictable results. But setting to 1 is always harmless, albeit resulting in very slightly slower execution.

This parameter has no effect if agents are generated (i.e. not read in via a CSV file).

Default: 1

Events used in: _read_agents

Example:

```
mutual_csv_partners = 1
```

9.33 num_agents

Determines the number of agents to generate for a simulation.

This parameter has no effect if agents are read in from a CSV file.

Default: 20000

Events used in: _generate_agents, _generate_and_pair

Example:

```
num_agents = 10000
```

9.34 num_simulations

Indicates the number of times to repeat a simulation in a simulation group.

Default: 1

Events used in: None

Example:

```
num_simulations = 1
```

9.35 partnerships_file

The csv file name to output partnerships. Set to empty string for stdout. This file will be empty unless one or more of record_breakups, record_infections or record_matches are set.

Default: Empty string (i.e. stdout)

Events used in: _rkpm, _infect, _breakup, _breakup_and_pair, _generate, _generate_and_pair

Example:

```
partnerships_file = "my_partnerships.csv"
```

TO DO

prob_birth_infected_msm; Probability a new msm agent is infected; 0.001000

prob_birth_infected_msw; Probability a new msw agent is infected; 0.000100

prob_birth_infected_wsm; Probability a new wsm agent is infected; 0.000500

prob_birth_infected_wsw; Probability a new wsw agent is infected; 0.000100

prob_birth_male; Probability a new agent is male; 0.500000

prob_birth_msw; Probability a new male agent is msw; 0.950000

prob_birth_wsm; Probability a new female agent is wsm; 0.950000

prob_gen_male; Probability a generated agent is male; 0.500000

prob_gen_msw; Probability a generated male agent is msw; 0.950000

prob_gen_wsm; Probability a generated female agent is wsm; 0.950000

record_breakups; Whether to output breakups to the partnership file; 0

record_infections; Whether to output infections to the partnership file; 0

record_matches; Whether to output matches to the partnership file; 0

results_file; File name to output results to (empty string for stdout);

simulation_period; Time period of the simulation (10 years); 5259490

stabilization_events; Events used to stabilize the agent characteristics before the actual simulation; _no_op

stabilization_steps; Number of time steps to run before executing various events; 0

start_date; Start date of simulation (yyyy;mm;dd); 2018; 1; 1

threads; Number of threads (0=system determined); 0

time_step; Time step for each iteration of simulation in minutes(default 1440 minutes == 1 day); 1440

treatment_infect_stage; When treated this is the integer to set infected to; 1

CHAPTER 10

Events

The events to run for a simulation are specified in these parameters: - before_events, - during_events, and - after_events.

These, respectively, are the events run once at the start of each simulation (before_events), on every iteration of the simulation (during_events), and once at the end of the simulation (after_events).

Here is a way to specify a comprehensive simulation:

```
before_events = _write_agents_csv_header; _write_results_csv_header; _generate_and_
↪pair; _write_agents_csv; _report

during_events = _age; _breakup_and_pair; _infect; _stage; _birth; _death; _report

after_events = _write_agents_csv
```

This tells FastSTI that before each simulation is run, it must:

- Write the header line for the output agents csv file (_write_agents_csv_header)
- Write the header line for the output results file (_write_results_csv_header)
- Generate and initialize properly a new set of agents and put some of them into relationships (_generate_and_pair)
- Write the set of initialised agents to a CSV file.
- Write some stats (e.g. prevalence, agents alive, agents dead etc) to the results file (_report).

On every time step of a simulation, it tells FastSTI to:

- Increment each living agent's by the time step (_age).
- Iterate through the living agents and put some of the single ones into relationships and break up some of those that are in relationships (_breakup_and_pair).
- Iterate through the agents with partners and infect some of those in sero-discordant relationships (_infect).
- Iterate through the infected agents and move some of them to a new disease stage (e.g. treated, resistant, ill - whatever you specify actually).

- Add some new agents to the simulation at the minimum age (_birth).
- Kill some of the agents (_death).
- Write some stats (e.g. prevalence, agents alive, agents dead etc) to the results file (_report).

At the end of each simulation it tells FastSTI to:

- Write the final state of the agents to a CSV file (_write_agents_csv).

The events provided by FastSTI (which include those in the example above) are prefixed with an underscore (_), to differentiate them from other 3rd-party events or ones that you choose to implement. Please don't name your events with a leading underscore.

If the events provided by FastSTI are not all you need, then you are encouraged to code your own events in C in the source code files fsti-userdefs.h and fsti-userdefs.c.

10.1 _read_agents

Reads in a csv file of agents at the beginning of a simulation. The file name is given by the *agents_input_file* parameter. The csv file delimiter is given by the csv_delimiter parameter, which defaults to a semi-colon (;).

The first time this event is executed, it saves the agents in memory so that on subsequent simulations, it doesn't have to process the file again.

If you don't have a file of agents to read in, consider using the _generate_agents event.

Parameters: agents_input_file, csv_delimiter, mutual_csv_partners

Datasets: None

10.2 _generate_agents

Generates agents for a simulation instead of reading them from a file.

It uses the *num_agents* parameter to determine the number of agents to generate.

The default implementation sets the following agent properties: age, sex, sex_preferred, infected, treated and resistant.

- age is set via a random beta distribution determined by the parameters *age_alpha* and *age_beta*.
- sex is set via the dataset dataset_gen_sex. (See data/dataset_gen_sex.csv for an example.)
- sex_preferred is set via the dataset dataset_gen_sex_preferred. (See data/dataset_gen_sex_preferred.csv for an example, which sets the agents to prefer the opposite sex with a probability of 95%, but you can change this according to the needs of your model.)
- infected (i.e. the infection stage of the agent with 0 by convention meaning the agent isn't infected) is set via the dataset dataset_gen_infect. (See data/dataset_gen_infect.csv for an example.)
- treated (i.e. which treatment line, if any, the agent is on) is set via the dataset dataset_gen_treated. (See data/dataset_gen_treated.csv for an example.)
- resistant (i.e. which treatment regimens the agent is resistant to, if any. (See data/dataset_gen_resistant.csv for an example.)

If you wish to set additional agent properties, you must provide hook in by defining a macro called FSTI_HOOK_GENERATE_AGENT in fsti-userdefs.h. The macro takes two parameters: simulation (a pointer to the current simulation) and agent (a pointer to the current agent whose property you wish to set).

Tip: Instead of using this event, it will usually make more sense to use the _generate_and_pair event which generates the initial set of agents, places them in a mating pool, shuffles the mating pool, mates the agents in the mating pool and then sets the number of time steps each agent will stay in its current relationship or stay single. This event is in fact called by _generate_and_pair.

See also: *_generate_and_pair*

Parameters: num_agents, age_alpha, age_beta,

Datasets: dataset_gen_sex, dataset_gen_sex_preferred, dataset_gen_treated, dataset_gen_resistant

10.3 _age

Iterates through all the living agents, and adds the time increment of the simulation to their age.

This is one of the simplest events provided by FastSTI, and so it makes a nice example of how events are implemented. Here is the source code:

```
1  void
2  fsti_event_age(struct fsti_simulation *simulation)
3  {
4      struct fsti_agent *agent;
5      FSTI_FOR_LIVING(*simulation, agent, {
6          agent->age += simulation->time_step;
7      });
8  }
```

All events are declared like this, i.e. a void function that takes one parameter: a pointer to the simulation itself.

On line 4 we declare a pointer to an agent on line three. When we iterate through the living agents, this will be a pointer to the current agent the code acts upon.

The FSTI_FOR_LIVING macro implements a for loop over the living agents. The code inside the macro's curly brackets simply adds the time step to each agent's age.

parameters: time_step

Datasets: None

10.4 _death

Iterates through the living agents and kills some of them.

Datasets: dataset_mortality

Here is a simple example of this dataset:

```
1      infected;0
2      0;0.00000296
3      1;0.00000315
4      2;0.00000315
5      3;0.00000630
6      4;0.001
```

The first column tells the event to determine the infection stage of the agent. The second column is the probability of the agent dying on this time step. Here the probabilities are specified per day. If you change the time step to, say, a week you have to update the probabilities in this file accordingly.

10.5 _initial_mating

Before a simulation starts but after agents have been generated or read in from a file, it is possible that none of the agents are in sexual relationships.

This event is responsible for creating the initial mating pool of agent sexual relationships. It is typically only run once per simulation, and only if the agent input file doesn't specify relationships. It is set as an event to run in the before_events parameter.

Note that it doesn't actually put the agents into relationships, only into a mating pool. An agent pairing event, such as _rkpm must then be executed in order to actually place agents in relationships with each other.

Tip: Instead of using this event, it will usually make more sense to use the _generate_and_pair event which generates the initial set of agents, places them in a mating pool, shuffles the mating pool, mates the agents in the mating pool and then sets the number of time steps each agent will stay in its current relationship or stay single. This event is in fact called by _generate_and_pair.

Datasets: dataset_gen_mating

Here is an example of this dataset. The first column is age in five-year periods. So for example line 5 corresponds to the probability of a person aged 15 to just shy of 20 being in a relationship (which in this example is 0.3 or 30%).

```
age|5-YEAR;0
0;0.0
1;0.0
2;0.0
3;0.3
4;0.35
5;0.4
6;0.45
7;0.5
8;0.5
9;0.5
10;0.5
11;0.5
12;0.4
13;0.4
14;0.35
15;0.3
16;0.25
17;0.2
18;0.15
19;0.1
20;0.5
21;0
```

See also: *_generate_and_pair*

10.6 _initial_rel

For each living agent make a correction to the duration (number of time steps) its current relationship, or if the agent is single, set the period it will stay single.

This event assumes the relchange (the date/time in the future at which it's current relationship or single status changes) property of agents in relationships has been set. It multiplies it by a uniform random number between 0 and 1. If the agent is single it sets the single period and also multiples it by a uniform random number between 0 and 1.

Why use this event? Because the simulation starts at an arbitrary time point in which people are already in the middle of relationships or a period of being being single. This event will on average halve the value of relchange. Whether that's a valid assumption at the beginning of a simulation is unclear to us.

Tip: Instead of using this event, it will usually make more sense to use the _generate_and_pair event which generates the initial set of agents, places them in a mating pool, shuffles the mating pool, mates the agents in the mating pool and then sets the number of time steps each agent will stay in its current relationship or stay single. This event is in fact called by _generate_and_pair.

Datasets: None

See also: *_generate_and_pair*, *_breakup* and *_rkpm*. The latter two also set the relchange property.

10.7 _mating_pool

Iterates through the living agents and places the single ones into the mating pool if they are due for a relationship status change. The relchange property of each single agent determines whether it is to be placed in the mating pool.

Note that placing agents in the mating pool is necessary but not sufficient to pair them into relationships. This event is typically followed by shuffling the mating pool (_shuffle_mating) and then placing them in sexual relationships with other agents in the mating pool using the pairing algorithm (_rkpm).

All of these events are included in the composite event _breakup_and_pair.

The C code for this event is simple and instructive:

```
1  void
2  fsti_event_mating_pool(struct fsti_simulation *simulation)
3  {
4      struct fsti_agent *agent;
5      fsti_agent_ind_clear(&simulation->mating_pool);
6      FSTI_FOR_LIVING(*simulation, agent, {
7          if (agent->num_partners == 0) {
8              if (agent->relchange[0] < simulation->iteration)
9                  fsti_agent_ind_push(&simulation->mating_pool, agent->id);
10         }
11     });
12 }
```

All events are declared like this, i.e. a void function that takes one parameter: a pointer to the simulation itself.

On line 4 we declare a pointer to an agent on line three. When we iterate through the living agents, this will be a pointer to the current agent the code acts upon.

The FSTI_FOR_LIVING macro implements a for loop over the living agents.

The code inside the macro's curly brackets first checks that the agent is single (i.e. it has zero partners). If it is it checks if the relchange property is less than the current iteration. If it is, it places the agent in the mating pool.

You may have noticed that agent->relchange on line 8 is subscripted with a 0 index. This is because FastSTI's data structures support agents having multiple concurrent partners. relchange[0] refers to the status of the first partner. By default, up to three partners are supported and this is determined by FSTI_MAX_PARTNERS set in fsti-defaults.h. To override this value, either with a bigger or smaller maximum number of partners, simply define an alternative value for FSTI_MAX_PARTNERS in fsti-userdefs.h. For example:

```
#define FSTI_MAX_PARTNERS 1
```

But although the FastSTI data structures support concurrent partnerships, all of the default events, including this one, do not support agents having more than one partner. This may and probably should change in the future. Of course you are also welcome to implement your own events that do account for concurrent partnerships.

Parameters: None

Datasets: None

See also: *_breakup_and_pair*.

10.8 _breakup

Iterates through the living agents, and breaks up some of those who are in relationships.

The event looks at the relchange properties of each agent in a relationship. If relchange is less than the current iteration, it's time for the relationship to end.

The period that each agent remains single is determined by the *dataset_single* dataset.

If you wish to record all the breakups, set the record_breakups parameter to 1 and the partnerships_file parameter to the name of the file to output to. But note that the number of breakups in a large simulation can be huge.

Parameters: record_breakups, partnerships_file

Datasets: dataset_single

See also: *_breakup_and_pair*.

10.9 _shuffle_living

Shuffles the living agents array. This is useful if an event is biased by the order in which it processes the agents. If the agents are shuffled before the event is run, over the long run this may remove the bias.

Parameters: None

Datasets: None

10.10 _shuffle_mating

Shuffles the mating pool. This is important to run before many pair-matching algorithms including the _rkpm event provided by FastSTI. Stochastic pair-matching events tend to assign better matches to agents at the beginning of an array. By shuffling the mating pool, this bias may be mitigated against over the long run.

Parameters: None

Datasets: None

See also: *_breakup_and_pair*.

10.11 _rkpm

This event runs the pair matching algorithm provided by FastSTI. For most purposes it's good and flexible.

RKPM stands for Random-k Pair-Matching. It may also have been called a k-Nearest Neighbour algorithm. It looks at the k agents adjacent (to the right if you think of an array as a set of objects arranged left to right) of the current agent in the mating pool, and selects the best match based on a distance measure.

The value of k is determined by the *match_k* parameter. Its default value is 100.

If k is set to 1 in the configuration input file, then in effect agents in the mating pool are randomly matched with each other. This is a very fast way to match agents but will not generate realistic matches.

If k is set to a large number greater than or equal to the possible number of agents that will enter the mating pool (e.g. set it to 1,000,000,000 to ensure it's bigger than any practically conceivable mating pool) , then in effect agents in the mating pool are matched using a brute force algorithm, i.e. the entire remainder of the mating pool is searched for a mate for the current agent. This usually obtains a set of matches that resemble the population being studied (assuming the distance measure is well implemented) but it can be very slow.

The distance measure is written in C. It can be easily modified be redefining the FSTI_AGENT_DISTANCE macro in fsti-userdefs.h and recompiling FastSTI.

This is how the default FSTI_AGENT_DISTANCE macro is defined:

```
#ifndef FSTI_AGENT_DISTANCE
#define FSTI_AGENT_DISTANCE(agent_a, agent_b)    \
     fsti_agent_default_distance(agent_a, agent_b)
#endif
```

The fsti_agent_default_distance function is defined in fsti-agent.c file and is very simple.

```
float fsti_agent_default_distance(const struct fsti_agent *a,
                                  const struct fsti_agent *b)
{
   float result = 0.0;
    if (a->sex_preferred != b->sex)
       result += 25.0;
    if (b->sex_preferred != a->sex)
       result += 25.0;
    result += abs(a->age - b->age);
    return result;
}
```

It minimises the distance between ages of compatible sexual orientation and similar age.

To define your own distance function, write a function to replace this in fsti-userdefs.c and redefine FSTI_AGENT_DISTANCE to call it.

If you wish to record all the matches in a file, set the record_matches parameter to 1 and the partnerships_file parameter to the name of the file to output to. But note that the number of partnerships in a large simulation can be huge.

The duration of the relationship is determined by the *dataset_rel* dataset.

Parameters: record_matches, partnerships_file

Datasets: dataset_rel

10.12 _breakup_and_pair

This is a composite event that executes the following events in this order:

- _breakup
- _mating
- _shuffle_mating
- _rkpm

10.13 _generate_and_pair

This is a composite event that executes the following events in this order:

- _generate_agents
- _initial_mating
- _shuffle_mating
- _rkpm
- _initial_rel

10.14 _infect

Iterates the living agent and infects some of those in sero-discordant relationships.

Whether an agent becomes infected depends on both its own characteristics and those of its partner. See *Two-agent datasets* for details.

If an agent becomes infected, the initial value of its infect property is set to the initial_infect_stage parameter. The default is 2. Although the infection stages are entirely user-defined, in the default settings of FastSTI, the following default setup is assumed for the infect property:

- 0: The agent is uninfected (this should be the case for any simulation)
- 1: The agent is infected but on treatment
- 2: The agent is in a primary infection stage
- 3: The agent is in a chronic infection stage
- 4: The agent is sick or in an end-stage of infection

This can be specified differently. But you must make sure that your stages are consistent across the simulation, else nonsensical things will happen. If you want a different infection stage setup, make sure your datasets and initial_infect_stage parameter are consistent with each other.

If you wish to record all the infections, set the record_infections parameter to 1 and the partnerships_file parameter to the name of the file to output to.

Parameters: record_infections, partnerships_file

Dataset: dataset_infect

10.15 _stage

Iterates over the living agents and changes the infection stage of some of the infected agents. It can also change the agent's treatment and resistant properties.

How many stages there are for the infection is entirely user-defined, but you have to make sure that the stages are consistent across events. Also, the possible values for the treatment and and resistant agent properties are also user-defined, but we think the default values FastSTI has been set up with are sensible for many models.

Although the infection stages are entirely user-defined, in the default settings of FastSTI, the following default setup is assumed for the infect property:

- 0: The agent is uninfected (this should be the case for any simulation)
- 1: The agent is infected but on treatment
- 2: The agent is in a primary infection stage
- 3: The agent is in a chronic infection stage
- 4: The agent is sick or in an end-stage of infection

This can be specified differently. But you must make sure that your stages are consistent across the simulation, else nonsensical things will happen. If you want a different infection stage setup, make sure your datasets and initial_infect_stage parameter are consistent with each other.

Dataset: dataset_infect_stage

This is quite a complicated dataset and is best understood by looking at the commented example in the data directory called dataset_infect_stage.csv. It's also included for convenience in the parameter description of *dataset_infect_stage*.

10.16 _coinfect

This is a very simple event that iterates over the living agents and sets the agent coinfected property to 1 for some agents. Users who want to model more sophisticated coinfection (e.g. TB for HIV) will likely have to write their own coinfection event.

Dataset: dataset_coinfect

10.17 _birth

Creates new agents with their ages set to the age_min property. (So if the minimum age of the simulation is, say, 15, then agents are not born as infants but as instant adolescents.)

Unless the simulation population is huge, creating agents daily (assuming the time_step is set to a day) makes no sense. For example consider a population of 10,000 agents with a daily time step over 20 years. On any given day, a sensible continuous random distribution of births will generate a fraction of births. But FastSTI is a discrete simulation framework and there is no such thing as a fractional agent. So instead the *birth_event_every_n* parameter must be set to how frequently the _birth event should be executed.

The event only creates agents every n_{th} time step. The *birth_rate* parameter is set to the birth rate and the GNU Scientific Library's gsl_ran_poisson function is used to determine the number of births.

Besides age, the default implementation sets the following agent properties: sex, sex_preferred, infected, treated and resistant.

- sex is set, with the proportion of males determined by the prob_birth_male parameter.

- sex_preferred is set using the prob_birth_msw (where msw stands for men who sex with women), prob_birth_wsm (where wsm stands for women who have sex with men) parameters. If the agent's sex is male, the prob_birth_msw value is used to determine the probability that the agent's preferred sexual partner is a female. Likewise if the agent's sex is female the prob_birth_wsm value is used to determine the probability that the agent's preferred sexual partner is a male.
- infected (i.e. the infection stage of the agent with 0 by convention meaning the agent isn't infected) is set via the dataset dataset_birth_infect. (See data/dataset_birth_infect.csv for an example.)
- treated (i.e. which treatment line, if any, the agent is on) is set via the dataset dataset_birth_treated. (See data/dataset_birth_treated.csv for an example.)
- resistant (i.e. which treatment regimens the agent is resistant to, if any) is set via the dataset dataset_birth_resistant (See data/dataset_birth_resistant.csv for an example.)

If you wish to set additional agent properties, you must provide hook in by defining a macro called FSTI_HOOK_BIRTH_AGENT in fsti-userdefs.h. The macro takes two parameters: simulation (a pointer to the current simulation) and agent (a pointer to the current agent whose property you wish to set).

Parameters: birth_event_every_n, prob_birth_male, prob_birth_msw, prob_birth_wsm,

Datasets: dataset_birth_infect, dataset_birth_treated and dataset_birth_resistant

10.18 _report

Reports statistics on the current state of the simulation.

This event can, and typically is, executed before, during and after a simulation. If it is executed during the simulation, the report_frequency parameter is used to determine how often. E.g. if set to 365, it will execute approximately once a year.

In addition to the statistics the event executes (defined in FSTI_REPORT in fsti-defaults.h which can be redefined in fsti-userdefs.h) you can define additional statistics using the FSTI_HOOK_REPORT macro.

The results_file parameter determines the name of the output file. By default this is left blank which means results are written to standard output.

Note that if multiple simulations are run in parallel, the output will be interleaved. At the end of the simulation you can simply sort these into the right order using the first three fields which are the simulation name, id and date of the report. You can use nearly any data manipulation tool to do this including R, Python, a spreadsheet program, or standard Posix utilities such as sort and awk.

Parameters: report_frequency

Datasets: None

10.19 _write_results_csv_header

Simply writes a header for the results csv file. You would only place this in the before_events parameter. It's clever enough to figure out that it should only write itself once to a results file.

Parameters: None

Datasets: None

10.20 _write_agents_csv

Writes the current state of every agent to an agent output csv file.

This event can be executed before, during and after a simulation. If it is executed during the simulation, the report_frequency parameter is used to determine how often. E.g. if set to 365, it will execute approximately once a year.

How an agent is written is determined by the FSTI_AGENT_PRINT_CSV macro. To write out agents differently redefine this macro in fsti-userdefs.h.

The agents_output_file parameter determines the name of the output file. By default this is left blank which means agents are written to standard output.

Note that if multiple simulations are run in parallel, the output will be interleaved. At the end of the simulation you can simply sort these into the right order using the first four fields which are the simulation name, id of the simulation, current date of the simulation and agent id. You can use nearly any data manipulation tool to do this including R, Python, a spreadsheet program, or standard Posix utilities such as sort and awk.

Also note that this file can get very large. If you have a million agents and you are running 100 simulations, it will write 100 million lines every time it is executed before, during and after each simulation. You could quickly run out of disk space. All this output also slows down simulations, so use this event sparingly.

Parameters: report_frequency

Datasets: None

10.21 _write_agents_csv_header

Simply writes a header for the agents csv file. You would only place this in the before_events parameter. It's clever enough to figure out that it should only write itself once to an agent output file.

Parameters: None

Datasets: None

10.22 _write_living_agents_csv

Exactly like _write_agents but only writes the living agents.

Parameters: report_frequency

Datasets: None

10.23 _write_dead_agents_csv

Exactly like _write_agents but only writes the dead agents.

Parameters: report_frequency

Datasets: None

10.24 _write_partnerships_csv_header

If the record_matches, record_breakups or record_infections parameters are set to 1, then it may be useful to write a header for the output csv file.

Parameters: record_matches, record_breakups, record_infections, partnerships_file

Datasets: None

CHAPTER 11

Extending FastSTI

FastSTI provides for a wide variety of models without any code being modified by the user. But some modellers are likely to encounter limitations. For example, they may want to model TB coinfection with HIV, or implement a cure event, or more sophisticated agent generation, or provide additional statistics.

To do this, you need to program in C. This guide assumes knowledge of C programming as well as the source code control system Git. FastSTI is developed under GNU/Linux. You need a POSIX compatible system to extend it. If you're using Windows, Cygwin should do the trick.

We recommend the following approach to developing FastSTI.

- Clone the latest version of FastSTI from the Github repository.
- Use either the gcc or Clang C compiler. We also strongly recommend installing Valgrind.
- Make sure the GNU autotools are installed. Then run the following to make sure FastSTI compiles and runs properly:

```
autoreconf;automake --add-missing; ./configure; make -j check
```

- Spend time looking at the source code in the src directory to understand it better. In particular we recommend examining the following files:
  - fsti-events.c which contains the events provided by FastSTI.
  - fsti-defaults.c where all the parameters are defined.
  - fsti-defaults.h where many of the macros that can be extended or redefined are defined. Note the Hooks section. These are macros that you can define in fsti-userdefs.h (or a file included by fsti-userdefs.h) to extend existing events and other functionality.
  - fsti-defs.h where some system wide constants and structs are defined.
  - fsti-agent.h where the fsti_agent struct is defined.
  - fsti-simulation.h where the fsti_simulation struct is defined.

Let's say you want to write an event to coinfect agents with TB. This is what you would need to do:

- In fsti-userdefs.c write a function to do the coinfection. For example:

```
void tb_coinfect(struct fsti_simulation *simulation)
{
    struct fsti_agent *agent;
    // Iterate through the living agents
    FSTI_FOR_LIVING(*simulation, agent, {
        // Put the event logic here
    });
}
```

- Put the prototype declaration for your event in fsti-userdefs.h. E.g.

```
void tb_coinfect(struct fsti_simulation *simulation)
```

- In the fsti-userdefs.h file you need to define the FSTI_HOOK_EVENTS_REGISTER macro. This is so that your event can be invoked via the before_events, during_events or after_events parameters in the input configuration file.

```
#define FSTI_HOOK_EVENTS_REGISTER fsti_register_add("tb_coinfect", tb_coinfect);
```

- Your event may need new parameters and datasets. It may also need new fields in the fsti_simulation struct and new fields in the fsti_agent struct.
  - To add new agent fields define them in the FSTI_AGENT_FIELDS macro in fsti-userdefs.h (or a file included by fsti-userdefs.h).
  - To add new simulation fields define them in the FSTI_SIMULATION_FIELDS macro in fsti-userdefs.h.
  - To provide additional parameters (or datasets) for input configuration files redefine the FSTI_ADDITIONAL_CONFIG_VARS parameter in fsti-userdefs.h. An example of how to do this is already in the fsti-defaults.h file.

```
#define FSTI_ADDITIONAL_CONFIG_VARS(config)             \
      FSTI_CONFIG_ADD(config, example_1,                \
      "Example configuration field", 0);                \
      FSTI_CONFIG_ADD_STR(config, dataset_example_2,    \
                  "Example dataset", FSTI_NO_OP)
```

    Note that the name of a dataset parameter must start *dataset_*.

  - If you want to save parameters or datasets into the current simulation redefine the FSTI_HOOK_CONFIG_TO_VARS macro in fsti-userdefs.h. E.g.

```
#define FSTI_HOOK_CONFIG_TO_VARS(simulation)                \
        simulation->example_1 = fsti_connfig_at0_long(      \
                                    &simulation->config,    \
                                    "example_1")
```

CHAPTER 12

Help improve FastSTI

We appreciate help with FastSTI, both with coding and documentation. Here are some things that need to be done:

- Built-in calibration: At present if you want to calibrate a FastSTI model, you'd best use R or Python to process agent output files from FastSTI, and generate .ini configuration files as input back into FastSTI with new parameters. We think it would probably be better if FastSTI's configuration could be enhanced to calibrate the model.
- Concurrent relationships: Although the fsti_agent data structure supports concurrent relationships, none of the events are currently designed to handle meaningfully concurrent relationships.
- More events: Code variations on the current events and new events.
- Build Python and R interfaces to FastSTI.
- Improve this documentation.

Feel free to clone the Github repository and submit patches. But before doing so, it may be best to email nathangeffen@gmail.com to inform us what you would like to do, so we can discuss the best way to proceed.

CHAPTER 13

Bugs and other issues

Please lodge bugs, requests for enhancements, etc at the FastSTI Github repository issues page.

CHAPTER 14

References

FastSTI citations in academic journals:

- Geffen, N, Scholz, SM. 2018. How various design decisions on matching individuals in relationships affect the outcomes of microsimulations of sexually transmitted infection epidemics. PLoS ONE 13(8): e0202516. https://doi.org/10.1371/journal.pone.0202516
- Geffen, N. and Scholz, S. 2017. Efficient and Effective Pair-Matching Algorithms for Agent-Based Models. Journal of Artificial Societies and Social Simulation 20(4) 8, 2017 Doi:10.18564/jasss.348. http://jasss.soc.surrey.ac.uk/20/4/8.html

CHAPTER 15

License

FastSTI is free software licensed under the GNU General Public License (GPL) version 3.

The license text is in the COPYING file of the distribution.

CHAPTER 16

Credits

- Nathan Geffen designed and implemented FastSTI.
- Stefan Scholz coded the syphilis model with Nathan.
- Eduard Grebe wrote the macOS installation instructions.
- Marcus Low helped get FastSTI running using Cygwin under Windows.