
SEIR Documentation

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Lukas Heumos

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CHAPTER 1

SEIR

SEIR modelling of covid19

- Free software: MIT
- Documentation: <https://SEIR.readthedocs.io>.

Compartmentalized SEIR

Python package for modeling epidemics using the SEIR model.

2.1 Installation

The package is available in the [Python Package Index](#), and can be installed using *pip*

```
pip install seir
```

An up-to-date version can be found in the *master* branch of the repository at [Github](#), and can be installed with pip like

```
pip install git+https://github.com/covid19-bh-biostats/seir
```

2.2 Command line simulation tool

2.2.1 Quickstart

Run the following command for an overview of all commands

```
SEIR --help
```

Run the following command from the root of this repository for a full demonstration of SEIR's features

```
SEIR -cf example_configs/finland_with_restrictions -cm contacts_matrices/finland --  
↪ visualize-compartments
```

2.2.2 Config-files

The SEIR package includes a command line interface for the simulation of a simple compartmentalized SEIR model. Basic use looks like the following

```
$ SEIR --config_file config
```

Here `config` is a configuration file containing information on the epidemic and the population. Examples of configuration files can be found in the `example_configs/` directory of the Github repository.

The configuration file should contain three sections, `[simulation]`, `[model]`, and `[initial state]`. Example files are provided in the `example_configs/` directory at the root of the repository.

`[simulation]`

The `[simulation]` section defines parameters relating to the numerical simulation of the SEIR ordinary differential equation. Supported parameters are

```
[simulation]
max_simulation_time = 300
method = DOP853
max_step = 0.5
```

Here the only required parameter is `max_simulation_time`, i.e., the number of simulated days.

The parameter `method` can be used to change the numerical integration routine. For supported values, please check the documentation of `scipy.integrate.solve_ivp`.

`max_step` defines the maximum time-step used in the integration.

`[model] (no compartmentalization)`

The `[model]` section defines the parameters of the disease model. In its simplest form, where you wish to model the entire population and do not wish to compartmentalize it, the `[model]` section looks like

```
[model]
population = 5e6
incubation_period = 3
infectious_period = 7
initial_R0 = 2.5
hospitalization_probability = 0.1
hospitalization_duration = 20
hospitalization_lag_from_onset = 7
icu_probability = 0.01
icu_duration = 10
icu_lag_from_onset = 11
death_probability = 0.1
death_lag_from_onset = 25
```

Here the parameters are

incubation_period Incubation period of the disease in days.

infectious_period How long a patient can infect others (in days) after the incubation period.

initial_R0 Basic reproductive number of the disease

hospitalization_probability Probability that an infected person needs hospitalization

hospitalization_duration Average duration of a hospitalization in days.

hospitalization_lag_from_onset Average time (in days) from the onset of symptoms to admission to hospital

icu_probability Probability that an infected person needs hospitalization.

icu_duration Average duration of the need for intensive care in days.

icu_lag_from_onset Average time (in days) from the onset of symptoms to admission to ICU.

death_probability Probability that an infected person dies from the disease.

death_lag_from_onset Average time from the onset of symptoms to death (in days).

population The total population.

[model] (compartmentalization)

The [model] section defines the parameters of the disease model. When you wish to separate your population into various compartments (e.g., age groups), your [model] section becomes more involved.

As an example, consider the population of Finland, divided to three compartments by ages: 0...15, 16...65, and 65+

```
[model]
compartments =
    0-15,
    16-65,
    65+

population =
    871036,
    3422996,
    1231274

incubation_period = 3
infectious_period = 7
initial_R0 = 2.5

hospitalization_probability =
    0.11,
    0.17,
    0.29

hospitalization_duration = 20
hospitalization_lag_from_onset = 7
icu_probability = 0.01
icu_duration = 10
icu_lag_from_onset = 11
death_probability = 0.1
death_lag_from_onset = 25
```

Here the parameters are

compartments A comma-separated list of the compartment names

population A comma-separated list of population of each compartment

incubation_period Incubation period of the disease in days. If a single number, the same number is used for all compartments. You can define a different incubation period for each compartment by supplying a comma-separated list.

infectious_period How long a patient can infect others (in days) after the incubation period. If a single number, the same number is used for all compartments. You can use a different value for each compartment by supplying a comma-separated list.

initial_R0 Basic reproductive number of the disease. A single number.

hospitalization_probability Probability that an infected person needs hospitalization. If a single number, the same number is used for all compartments. You can use a different value for each compartment by supplying a comma-separated list.

hospitalization_duration Average duration of a hospitalization in days.

hospitalization_lag_from_onset Average time (in days) from the onset of symptoms to admission to hospital.

icu_probability Probability that an infected person needs hospitalization. If a single number, the same number is used for all compartments. You can use a different value for each compartment by supplying a comma-separated list.

icu_duration Average duration of the need for intensive care in days.

icu_lag_from_onset Average time (in days) from the onset of symptoms to admission to ICU.

death_probability Probability that an infected person dies from the disease. If a single number, the same number is used for all compartments. You can use a different value for each compartment by supplying a comma-separated list.

death_lag_from_onset Average time from the onset of symptoms to death (in days).

[initial state] (no compartmentalization)

When there are no compartments in the model, the [initial state] section of the configuration file should look something like

```
[initial state]
probabilities = True
population_susceptible = 0.8
population_exposed = 0.15
population_infected = 0.05
```

Here the parameters are

probabilities If `true`, the rest of the parameters in this section are considered as probabilities, and the total number of exposed/infected people is computed by multiplying the total population by the provided value.

population_exposed The total number (or probability) of exposed people

population_infected The total number (or probability) of infected people

[initial state] (compartmentalized)

When there are compartments in the model, the [initial state] section of the configuration file should look something like

```
[initial state]
probabilities = True
population_exposed =
    0.001,
    0.01,
```

(continues on next page)

(continued from previous page)

```

0.005
population_infected =
0.001,
0.01,
0.005

```

Here the parameters are

probabilities If `true`, the rest of the parameters in this section are considered as probabilities, and the total number of exposed/infected people is computed by multiplying the total population by the provided value.

population_exposed The total number (or probability) of exposed people

population_infected The total number (or probability) of infected people

[restrictions]

We can model restrictions such as social distancing and closing of schools by introducing time-dependence in the infectivity rate (matrix, if compartmentalized model).

Restrictions can be defined in the *config* file within sections named `[restriction TITLE]`. You can define multiple restrictions in the same file.

The restrictions are implemented as prefactors of the infectivity rate as

Restrictions on all interactions

Define the day the restriction begins, the day the restriction is lifted, and the prefactor for the infectivity rate matrix between (and including) these days.

```

[restriction social-distancing]
day-begins = 20
day-ends = 180
infectivity modifier = 0.7

```

Restrictions on all some interactions

Define the day the restriction begins, the day the restriction is lifted, and the matrix-elements of the prefactor matrix *R* of the infectivity rate matrix.

You can define multiple elements of the prefactor-matrix on separate lines. For example, to decrease the contacts between the compartments 0-4, 5-9, 15-19 with the compartments 35-39, 40-44 (and vice versa) by 20%, and contacts between all compartments and the compartments 60-64 and 65+ by 80%, you specify the following

```

[restriction social-distancing experiment 2]
day-begins = 20
day-ends = 180
infectivity modifier =
  [ 0-4, 5-9, 15-19 ] : [ 35-39, 40-44 ] : 0.8
  all : [ 60-64, 65+ ] : 0.2

```

Restrictions from a file

Define the day the restriction begins, the day the restriction is lifted, and the file where the prefactor matrix is stored in CSV format,

```
[restriction social-distancing experiment 2]
day-begins = 20
day-ends = 180
infectivity modifier = file://my_data/restrictions_prefactor.csv
```

2.2.3 Contact patterns (compartmentalized models)

Sometimes we have the knowledge of how many different daily contacts a person in compartment i has with persons from compartment j . This is called the contacts matrix, $C[i, j]$.

The contacts matrix can be supplied to the SEIR command line tool with the flag `-c`

```
$ SEIR -cm my_contacts_matrix.csv configfile
```

The contacts matrix should be a space or comma separated file with the same number of columns and rows as there are compartments defined in the configuration file. For an example, please try:

```
$ SEIR -cm contacts_matrices/finland -cf example_configs/finland --visualize-
→compartments
```

Example contact pattern matrix can be found in the `contacts_matrices/` directory of the repository in Github.

2.2.4 Output file

The SEIR tool outputs the computed model in a file called `outfile.csv` (can be changed with the `-o` option). The outfile is a comma separated table containing the following simulation results:

time Array of days from the beginning of the simulation

('susceptible', <compartment name>) Number of susceptible people of compartment <compartment name> corresponding to each day in the 'time' array.

susceptible Number of susceptible people in all compartments.

('exposed', <compartment name>) Number of exposed people of compartment <compartment name> corresponding to each day in the 'time' array.

exposed Number of exposed people in all compartments.

('infected (active)', <compartment name>) Number of people with an active infection of compartment <compartment name> corresponding to each day in the 'time' array.

infected (active) Number of people with an active infection in all compartments.

('infected (total)', <compartment name>) Number of people who have an active infection (or have had one in the history) from compartment <compartment name> corresponding to each day in the 'time' array.

infected (total) Number of people who have an active infection (or have had one in the history) in all compartments.

('removed', <compartment name>) Number of removed of compartment <compartment name> corresponding to each day in the 'time' array.

removed Number of removed people in all compartments.

('hospitalized (active)', <compartment name>) Number of people who need hospitalization from compartment <compartment name> corresponding to each day in the 'time' array.

hospitalized (active) Total number of people who need hospitalization.

('in ICU', <compartment name>) Number of people who (currently) need intensive care from compartment <compartment name> corresponding to each day in the 'time' array.

in ICU (active) Total number of people who currently need intensive care.

('deaths', <compartment name>) Number of people from compartment <compartment name> who have died (cumulative sum).

deaths Total number of people who have died.

3.1 Stable release

To install SEIR, run this command in your terminal:

```
$ pip install SEIR
```

This is the preferred method to install SEIR, as it will always install the most recent stable release.

If you don't have `pip` installed, this [Python installation guide](#) can guide you through the process.

3.2 From sources

The sources for SEIR can be downloaded from the [Github repo](#).

You can either clone the public repository:

```
$ git clone git://github.com/covid19-bh-biostats/SEIR
```

Or download the [tarball](#):

```
$ curl -OJL https://github.com/covid19-bh-biostats/SEIR/tarball/master
```

Once you have a copy of the source, you can install it with:

```
$ python setup.py install
```


CHAPTER 4

Usage

To use SEIR in a project:

```
import SEIR
```


5.1 Biohackathon Biostats Team

- Janne Solanpää <janne@solanpaa.fi>
- Lukas Heumos <lukas.heumos@posteo.net>

This document records all notable changes to `seir`. This project adheres to [Semantic Versioning](#).

6.1 0.2.2 (2020-04-11)

Added

- Tests for `config_file_parser` and `restriction_section_parser`

Fixed

- Added `make`, `automake`, `gcc`, `g++`, `git` to `Dockerfile` to be able to compile `numpy`

Dependencies

Deprecated

- Travis build (less complete than Github workflows)

6.2 0.2.0 (2020-04-08)

Added

- Visualizations of restrictive measures
- Improved documentation
- `visualize_compartments` is now a flag
- short alternatives for parameters
- Added support for json file output

Fixed

Dependencies

Deprecated

6.3 0.1.1 (2020-04-07)

Added

Fixed * pep8 compatibility * bug when specifying compartment-specific initial populations not as probabilities

Dependencies

Deprecated

6.4 0.1.0 (2020-04-07)

Added * Created the project using COOKIETEMPLATE

Fixed

Dependencies

Deprecated

Contributor Covenant Code of Conduct

7.1 Our Pledge

In the interest of fostering an open and welcoming environment, we as contributors and maintainers pledge to making participation in our project and our community a harassment-free experience for everyone, regardless of age, body size, disability, ethnicity, gender identity and expression, level of experience, nationality, personal appearance, race, religion, or sexual identity and orientation.

7.2 Our Standards

Examples of behavior that contributes to creating a positive environment include:

- Using welcoming and inclusive language
- Being respectful of differing viewpoints and experiences
- Gracefully accepting constructive criticism
- Focusing on what is best for the community
- Showing empathy towards other community members

Examples of unacceptable behavior by participants include:

- The use of sexualized language or imagery and unwelcome sexual attention or advances
- Trolling, insulting/derogatory comments, and personal or political attacks
- Public or private harassment
- Publishing others' private information, such as a physical or electronic address, without explicit permission
- Other conduct which could reasonably be considered inappropriate in a professional setting

7.3 Our Responsibilities

Project maintainers are responsible for clarifying the standards of acceptable behavior and are expected to take appropriate and fair corrective action in response to any instances of unacceptable behavior.

Project maintainers have the right and responsibility to remove, edit, or reject comments, commits, code, wiki edits, issues, and other contributions that are not aligned to this Code of Conduct, or to ban temporarily or permanently any contributor for other behaviors that they deem inappropriate, threatening, offensive, or harmful.

7.4 Scope

This Code of Conduct applies both within project spaces and in public spaces when an individual is representing the project or its community. Examples of representing a project or community include using an official project e-mail address, posting via an official social media account, or acting as an appointed representative at an online or offline event. Representation of a project may be further defined and clarified by project maintainers.

7.5 Enforcement

Instances of abusive, harassing, or otherwise unacceptable behavior may be reported by opening an issue. The project team will review and investigate all complaints, and will respond in a way that it deems appropriate to the circumstances. The project team is obligated to maintain confidentiality with regard to the reporter of an incident. Further details of specific enforcement policies may be posted separately.

Project maintainers who do not follow or enforce the Code of Conduct in good faith may face temporary or permanent repercussions as determined by other members of the project's leadership.

7.6 Attribution

CHAPTER 8

Indices and tables

- `genindex`
- `modindex`
- `search`