SIGMUND user manual

This is the user manual of mutualistic model[1] simulator SIGMUND.

Github repository: https://github.com/jgalgarra/sigmund

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1 Installation

1.1 Requirements

SIGMUND requires *python* 3.2 or higher to run. Packages `numpy`, `scipy`, `matplotlib` and `PyQt` must be installed. A good option is downloading the `Anaconda` distribution[2] that includes all the required software. In addition, `git` must be enabled. The simulator has been succesfully tested under *Windows* and *Ubuntu*.

Go to the directory where you want to install SIGMUND. From the UNIX shell or git bash in Windows, invoque:

```
git clone https://github.com/jgalgarra/sigmund
```

SIGMUND is ready to run. Navigate to the directory `sigmund/src/pak_tfm` that has been created under the directory from where you invoked the `git clone` command. Under Windows double click on the sigmund_tool.py icon to launch the program. Under Linux write the command:

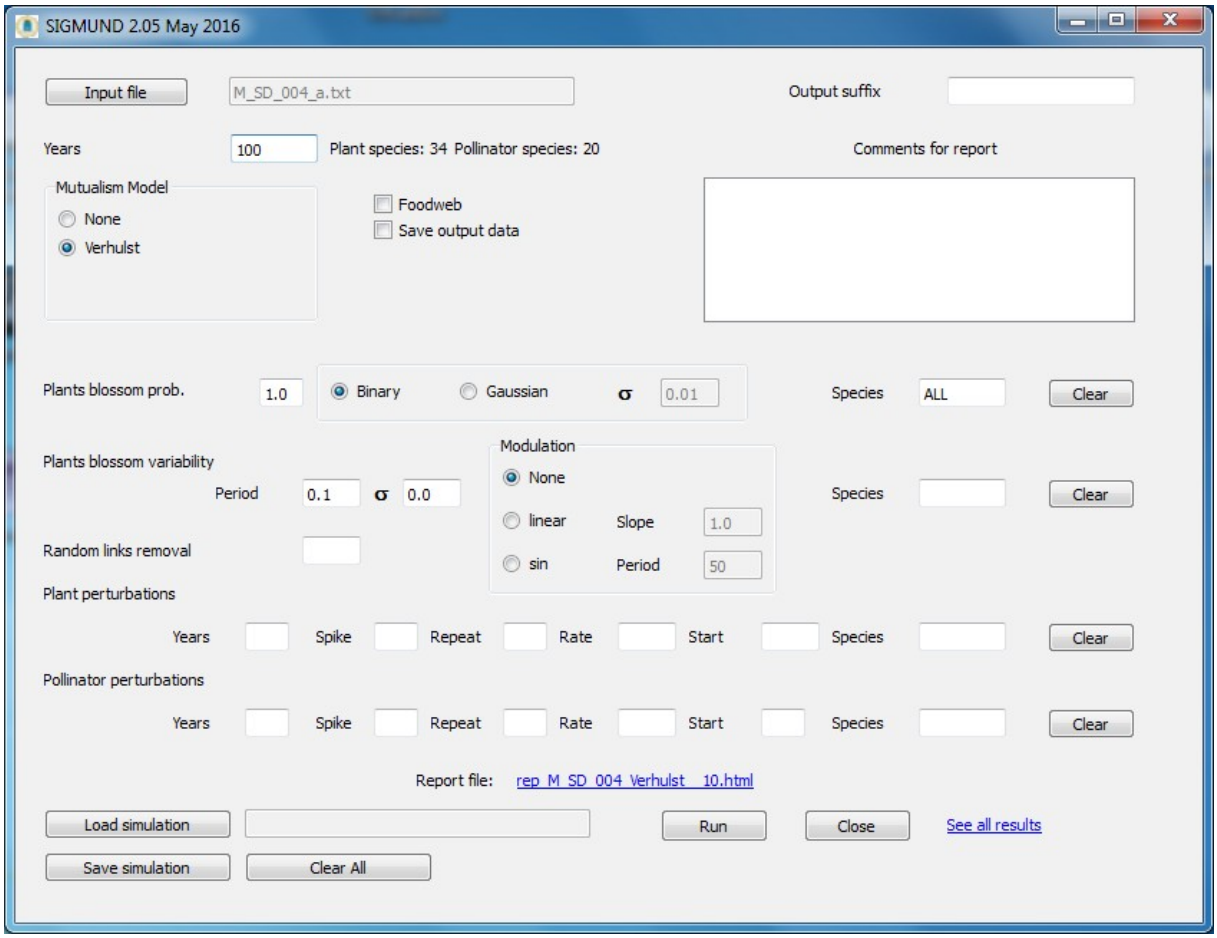
```
./sigmund_tool.py
```

1 The model is described in Javier García-Algarra et al. (2014) "Rethinking the logistic approach for population dynamics of mutualistic interactions", *Journal of Theoretical Biology,* 363, 332-343.

2 https://store.continuum.io/cshop/anaconda/

1.2 User interface

SIGMUND user interface is built with the `Qt` framework, so details may look slightly different depending on your machine and Operating System.



SIGMUND User interface

This is the meaning of the different fields:

- **Input File**. Name of simulation configuration files stored in /input . You must choose it or it may be automatically picked if you load an stored simulation. The UI will show the number of species of each guild.
- **Years.** Span of simulation, mandatory.
- **Output suffix.** Optional suffix that will be appended to the results files that are written in /output.
- **Comments for report**. Optional field to include a free text describing the experiment that will be included in the report file.

- **Mutualism Model.** Allows choosing between no mutalism and logistic like (Verhulst) mode of simulation.
- **Food web**. Check if there is a superimposed food web.
- **Save output data**. Check if you want to save numeric simualtion data in text files.

The system may be attacked with four classes of perturbations (optional).

- **Random links removal.** Percentage of mutualistic links that are randomly removed (No effect if the field is left blank or set to zero).
- **Plants blossom probability**. Simulation of random strength of plants blossom.
    - **Probability**. Blossom probability, (range 0 to 1.0, default 1.0).
    - **Type of distribution**. Binary or Gaussian. Binary performs a Bernouilli trial with the set probability for each year. Intensity is 100% is result is successful or zero otherwise. Gaussian modulates intensity with a normal distribution, with mean equal to the probability parameter and the set standard deviation.
    - **Species**. List of affected plant species (from `1` to `n`, or `ALL`).
- **Plants blossom variability**. Simulation of random blossom period.
    - **Period**. Fraction of year.
    - **Deviation**. Variability of blossom period.
    - **Type**. None, linear (define by slope) or sinusoidal (defined by period).
    - **Species**. List of affected plant species (from `1` to `n`, or `ALL`).
- **Forced external perturbations**. Exogen attacks (epidemics, droughts, migrations, etc) that may lead to step death rate increases.
    - **Years**. Perturbation span.
    - **Spike**. Fraction of the perturbation span where the perturbation is active (useful for repetitions).
    - **Repeat**. Number of times the perturbation is repeated.
    - **Rate**. Yearly death rate increase.
    - **Start**. Year when the perturbation starts.
    - **Species**. List of affected species.
- **Load simulation**. Load stored simulation parameters.
- **Save simulation**. Store simulation parameters.

1.3 Experiment results

Each experiment produces a set of results. The system console shows real time information on the experiment behavior. These data are written to the HTML report file in the directory /output.. Figures and data of population and growth rates are also stored in that directory.

```
Binomial simulated mutualistic interaction. Input file: exp18
============================================================
User Comment: Example of simulation for the user manual
Span: 100 years
ALGORITHM: Verhulst
Release 2.03
Plants matrix: exp18_a.txt
Pollinators matrix: exp18_b.txt
Plant species: 4
Plant initial populations [800, 900, 700, 270]
Pollinator species: 4
Pollinator initial populations [1100, 700, 400, 350]
Blossom probability 1.0, type Binary. Plant affected species:['ALL']
Blossom variability active. Period: 0.10 (% of year), Initial moment standard
dev.: 0.0100 (% of year), Type: sin, Period 20.00 . Affected species:[1, 2]
Elapsed time 6.51 s

Created 2014-10-03 23:52:18.363000
```

1.4 Offline scripts

SIGMUND may be launched from the command line in batch mode to perform multiple experiments. The script is called `sigmund_standalone.py` . The simulation will take the parameters stored in the simfile unless they are changed using the optional command arguments:

1.4.1 sigmund_standalone.py

```
usage: sigmund_standalone.py [-h] [-simfile SIMFILE_NAME] [-g] [-v]
                             [-years SIM_YEARS] [-fw] [-outsf OUTSF] [-ds]
                             [-dsdir DSDIR] [-stop] [-rlink RLINK]
                             [-Blprob BLPROB] [-Blsd BLSD] [-Bltype BLTYPE]
                             [-Blspecies BLSPECIES] [-Bssvarper BSSVARPER]
                             [-Bssvarsd BSSVARSD] [-Bssvartype BSSVARTYPE]
                             [-Bssvartype_param BSSVARTYPE_PARAM]
                             [-Bssvarspecies BSSVARSPECIES]
                             [-pl_ext_period PL_EXT_PERIOD]
                             [-pl_ext_spike PL_EXT_SPIKE]
                             [-pl_ext_numperiod PL_EXT_NUMPERIOD]
                             [-pl_ext_rate PL_EXT_RATE]
                             [-pl_ext_start PL_EXT_START]
                             [-pl_ext_species PL_EXT_SPECIES]
                             [-pol_ext_period POL_EXT_PERIOD]
                             [-pol_ext_spike POL_EXT_SPIKE]
                             [-pol_ext_numperiod POL_EXT_NUMPERIOD]
                             [-pol_ext_rate POL_EXT_RATE]
                             [-pol_ext_start POL_EXT_START]
                             [-pol_ext_species POL_EXT_SPECIES]

optional arguments:
  -h, --help              show this help message and exit
  -simfile SIMFILE_NAME   Simulation parameters file
  -g                      Generate and store graphs
  -v                      Verbose output
  -years SIM_YEARS        Simulation span in years
  -fw                     Superimposed food web
  -outsf OUTSF            Append suffix to output file names
  -ds                     Results data save
  -dsdir DSDIR            Data save directory
  -stop                   On extinction stop simulation
  -rlink RLINK            Randomlinks removal
  -Blprob BLPROB         Blossom probability
  -Blsd BLSD             Blossom deviation
  -Bltype BLTYPE         Blossom type: Binary, Gaussian
  -Blspecies BLSPECIES   Blossom species
  -Bssvarper BSSVARPER   Blossom variability period
  -Bssvarsd BSSVARSD     Blossom variability deviation
  -Bssvartype BSSVARTYPE Blossom variability modulation type: None, linear, sin
  -Bssvartype_param BSSVARTYPE_PARAM Blossom variability modulation parameter
  -Bssvarspecies BSSVARSPECIES Blossom variability affected species
  -pl_ext_period PL_EXT_PERIOD Plants external perturbation, period in years
  -pl_ext_spike PL_EXT_SPIKE Plants external perturbation, spike (fraction of
period)
  -pl_ext_numperiod PL_EXT_NUMPERIOD Plants external perturbation, repeat
perturbation
  -pl_ext_rate PL_EXT_RATE Plants external perturbation, rate
  -pl_ext_start PL_EXT_START Plants external perturbation, initial year
```

```
  -pl_ext_species PL_EXT_SPECIES Plants external perturbation, affected species
  -pol_ext_period POL_EXT_PERIOD Pollinators external perturbation, period in years
  -pol_ext_spike POL_EXT_SPIKE Pollinators external perturbation, spike (fraction
of period)
  -pol_ext_numperiod POL_EXT_NUMPERIOD Pollinators external perturbation, repeat
perturbation
  -pol_ext_rate POL_EXT_RATE Pollinators external perturbation, rate
  -pol_ext_start POL_EXT_START Pollinators external perturbation, initial year
  -pol_ext_species POL_EXT_SPECIES Pollinators external perturbation, affected
species
```

Usage example:

```
./sigmund_standalone.py -simfile exp18_Verhulst_oso_20.sim -y 50 -g -rlink 0.1 -v
```

This example loads the simulation conditions stored in `exp18_Verhulst_oso_20.sim` sets a sapn of 50 years, generates and stores the pictures, removes a 10% of links and runs in verbose mode (the same console output as if it was launched from the User Interface).

If flag -v is not activated, the program is run in quiet mode. If the `-stop` flag is set it returns either `SURVIVAL` or `EXTINCTION`. This feature may be used to run multiple simulations to check survavility of the whole system under certain parameters, because simulation stops if the system goes below the vital minimum

1.4.2 survival.py

This is an example of a python script to compute the rate of survival when a 70% of links are removed at random. The simulation span is set to 50 years and the scripts ends in the moment extinction is detected:

```
import subprocess
survival_success  =  0
no_experiments  =  50
com_base =  "python3 sigmund_standalone.py -simfile exp18_10.sim -
y 50 -stop -rlink 0.7"
for i in range(0,no_experiments):
      b = subprocess.check_output(com_base+str(rrate), shell=True)
      if str(b).find("EXTINCTION") == -1:
          print("remove links "+str(rrate)+" survival")
          survival_success += 1
      else:
          print("remove links "+str(rrate)+" extinction")
print("Experiments "+str(no_experiments)+"/ Network survived " +
str(survival_success)+" times")
```

Please, note that we are invoking the `sigmund_standalone.py` as an external process. You can get the same results writing your own script in your preferred programming language or scripting.

1.4.3 sigmund_createinput_atmax.py

This scripts takes the last population values of an stored simulation, and creates two new input files with the _MAX suffix.

```
./sigmund_createinput_atmax.py -fichout
output/output_data_M1_A1_all_Verhulst_a_populations__100.txt
```