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**STREAMcom**

Version 2.0.19

**User Manual**

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Author(s)

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# Introduction

This manual describes version 2.0.19 of the computer program STREAMcom integrated in the Landscape Model. The program STREAMcom is developed by gaiac® - Research Institute for Ecosystem Analysis and Assessment.

The STREAMcom IBM integrates information of the habitat scenarios, the functional traits and life history (DEB) parameters of individual species as well as chemical effects (TKTD) to simulate stream community dynamics in a temporal and spatial manner.

# Run STREAMcom

When calling STREAMcom by the Landscape Model there are three different levels in which parameter settings can be made.

The \*.xrun file defines the whole experiment and thus is responsible for the parameters which are relevant for all included modules. In this file the user can also switch the different modules on or off. To run the STREAMcom module within the landcape model the parameter “RunEffects” in the \*.xrun file must be set to true. In the \*.xrun file also the duration of the simulation, the application scenario and the simulated species are defined. This is the file where the enduser should make his settings.

In the Python file the needed parameters for the capped STREAMcom module are set. For example input- and output-paths, the name of the toxicant and the settings responsible for the effect calculation are set in this file. There is no need for the enduser to change any settings in this file.

The settings.txt within the defined STREAMcom input folder contains the default parameters for the environmental conditions. These parameters should also not be adjusted by the enduser. Further description of these parameters can be found in section 2.2.

## Input seetings

To run a specific simulation the program needs the following input parameters:

*Table 1: All required simulation settings of the STREAMcom model*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| parameter name | description | Level | User | type |
| sim\_duration | Duration of a single mc simulation in days | Xrun | enduser | Required |
| species | Name of species to include in simulation | Xrun | enduser | Required |
| Application scenario | Application rate and time window of application | Xrun | enduser | Required |
| num\_mc | Number of monte carlo simulations to run | Xrun/  Python file | enduser/ poweruser | Required |
| site\_name | Name of the site to simulate | Python file | poweruser | Required |
| input\_path | Path to input files | Python file | poweruser | Required |
| output\_path | Path to output folder | Python file | poweruser | Required |
| tox\_name | Name of toxicant to use in simulation | Python file | poweruser | Optional |
| tox\_lethal | Use lethal toxic effects in simulation | Python file | poweruser | Optional |
| tox\_sublethal | Use sublethal toxic effects in simulation | Python file | poweruser | Optional |
| biomass\_ind | Use individuals/m² as unit for start biomass | Python file | poweruser | Optional |

1. **valid site names:**

* site\_niers\_driesdonck.txt
* site\_niers\_peutenweg.txt
* site\_inde.txt
* site\_vichtbach.txt

1. **valid species names are:**

* Asellus aquaticus
* Baetis rhodani
* Dikerogammarus villosus
* Ecdyonurus dispar
* Epeorus assimilis
* Gammarus fossarum
* Gammarus pulex
* Gammarus roeselii
* Habrophlebia lauta
* Lymnaea stagnalis
* Planorbis planorbis
* Potamopyrgus antipodarum
* Rhithrogena semicolorata
* Sphaerium corneum
* Stagnicola palustris
* Gasterosteus aculeatus
* Perca fluviatilis
* Salmo trutta

(species names MUST NOT contain commas)

1. **valid tox names are:**

* tox\_Deltamethrin.txt

1. Input\_path and output\_path need to be passed as absolute paths

## Input files

To run without errors the STREAMcom model requires the following files in the previously declared input folder.

1. **Exposure.txt**

Txt File, which contains the exposure profile of the scenario, including the date and the substance concentration. The exposure file is created based on the application settings the user has defined in the \*.xrun file.

1. **Site\_\*.txt**

txt-file, which contains the raster map information about the selected site in list form. For every cell of the sites, it includes information about the x/y-coordinate, the organic and mineral substrate, the velocity, shadowing and water depth.

Additionally, the file contains the general properties that are constant for the entire site. This includes the site name, the stream name and a short location description, the latitude of the site. Moreover, it specifies the gauge station where the water temperature was measured, the stream type in categories of “LAWA-types” and the actual stream zone. It also includes the information about the site size in cell numbers (x-and y-cells) and the cell size.

1. **Species.xml**

The species list contains all relevant model parameters for the modelled species. Including DEB-parameters, habitat preferences, food preferences and life cycle parameters.

1. **Temperature.txt**

The temperature file has the same structure as the exposure file. It includes the measured temperature for the selected site at a specific date.

1. **Tox\_parameters.txt**

This file gives general information on the modelled chemical substance, the substance name and the concentration unit. Moreover in includes a list with all GUTS-SD parameters (kd, z, kk, c0, cT) for the different species. (make sure that the unit of the GUTS parameters and the unit of substance concentration match)

1. **Settings.txt**  
   Contains the default parameters for the environmental setup.

*Table 2: default parameter values and initial conditions for the environmental settings*

|  |  |  |
| --- | --- | --- |
| **Description** | **Value** | **Unit** |
| Threshold population size for super individuals | 10 | # |
| Number of siblings per super individual | 70 | # |
| Maximum periphyton growth rate | 3.05 | 1/d |
| Periphyton carrying capacity | 17 | g/m² |
| Periphyton energy density | 4623 | J/g |
| Periphyton Arrhenius temperature | 5500 | K |
| Initial leaf litter density | 9 | g/m² |
| Leaf litter energy density | 7227.5 | J/g |
| Day of year for leaf litter addition | 270 | D |
| C-POM settlement rate | 0.1 | 1/d |
| Maximum velocity class for C-POM addition | 4 | - |
| Initial F-POM density | 80000 | J/m² |
| F-POM settlement rate | 0.3 | 1/d |
| Initial S-POM density | 500 | J/m² |
| Fraction of S-POM available to filter feeders | 0.0001 | - |

1. **Species\_biomass.txt**  
   Contains the complete species list and the default initial biomasses per species in individuals/m² and g/m².

## Output files

STREAMcom provides two types of output files and two endpoints. The population output display the total number of individuals in the stream section. The output for the traits doesn’t contain the individuals per trait but the proportion of the presented trait in relation to the other habitat- or feeding traits. Using similar habitat or feeding preferences we devided the overall community in 6 feeding traits (active filterer, passive filterer, gatherer, grazer, shredder, predator) and 7 habitat traits (akal, argylal, lithal, pelal, phytal, pom, psammal).

### Population development over time

For every simulated species and trait group the program generates an own output file (‘population\_output\_\*’ or ‘\*\_trait\_output\_\*’). These files contain the development of the species or traits per day over the simulated time. If more than one Monte Carlo simulation was simulated, for each single simulation a new column in the file is created. Table 2 shows the population development of a species for the first 10 days and five Monte Carlo simulations.

Table 2: Population Result of a simulation over 10 days and 5 MC



### Spatial distribution

In the second type of output file the final distribution of a species population or trait is saved (‘xy\_output\_\*’ or ‘xy\_trait\_\*’). This output contains the spatial distribution at the end of the simulation. For every x/y-coordinate of the map, the number of individuals or trait fraction that is located on that cell are saved. Additionally the water depth for every map cell is reported. Table 3 shows an extract of an output distribution file for five Monte Carlos.

Table 3: Trait Distribution Result for 9 cells with 5 MC



# Appendix

**3.1 example python script for STREAMcom call**

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import os

import subprocess

exe\_path = "./ProjectStreamCom.exe"

site\_name = "site\_inde.txt"

num\_mc = 1

sim\_duration = 365

input\_path = "./input"

output\_path = "./output"

tox\_name = "tox\_Deltamethrin.txt"

tox\_lethal = True

tox\_sublethal = True

biomass\_ind = True

species = ['Gammarus fossarum']

assert(os.path.isdir(input\_path) and os.path.isdir(output\_path))

subprocess.call([

exe\_path,

"--site\_name", site\_name,

"--num\_mc", str(num\_mc),

"--sim\_duration", str(sim\_duration),

"--input\_path", os.path.abspath(input\_path),

"--output\_path", os.path.abspath(output\_path),

"--species", ','.join(species),

"--tox\_name", tox\_name,

"--tox\_lethal" if tox\_lethal else "",

"--tox\_sublethal" if tox\_sublethal else "",

"--biomass\_ind" if biomass\_ind else "",

])

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