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**STREAMcom**

Version 2.0.19

**User Manual**

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Author(s)

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Content

[1 Introduction 3](#_Toc53491949)

[2 Run STREAMcom 3](#_Toc53491950)

[2.1 Input parameters 3](#_Toc53491951)

[2.2 Input files 4](#_Toc53491952)

[2.3 Output files 6](#_Toc53491953)

[2.3.1 Population development over time 6](#_Toc53491954)

[2.3.2 Spatial distribution 6](#_Toc53491955)

[3 Appendix 8](#_Toc53491956)

# Introduction

This manual describes version 2.0.17 of the computer program STREAMcom. The program 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

To start and run the program a simple python script can be used. The script is responsible for calling the STREAMcom.exe and hands over the necessary parameters. (A script example is attached at the end of this manual.)

## Input parameters

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

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

1. **Exposure.txt**

Txt File, which contains the exposure profile of the scenario, including the date and the substance concentration.

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 files 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 1: 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\_\*’). These 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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