

## SHIMMER ReadMe, 6<sup>th</sup> May 2016

### 1. Hardware and Software Requirement

SHIMMER is written and can be executed in the free open source computing environment and programming language R, which is available for download on the web (<http://www.r-project.org/>). SHIMMER uses the adaptive time-step solver “lsoda” from the deSolve package (Soetaert et al., 2010) **which must also be installed**. On a standard desktop computer running R, the model usually takes less than 1 min to simulate 10 years of succession.

### 2. Download SHIMMER

A package named “SHIMMER”, containing the source code of SHIMMER as well as example input and testing data is available at <http://jamesbradleyweb.weebly.com/research.html> under the sub-heading “SHIMMER” (click “Download SHIMMER .zip package”).

The package contains one folder named “demo”, containing 2 sub-folders:

- 1) demo\_MAC (if you are running RStudio on a Mac)
- 2) demo\_WIN (if you are running R on Windows)

The differences in the code are minor – mostly to do with plotting.

Within these two folders are further sub-folders:

- “SHIMMER”: containing the model source code for a single run of SHIMMER.
- “input\_data\_Svalbard”: containing the following time-series of forcings:
  - par.csv – solar radiation (already accounting for inhibition by snow)
  - temp.csv – soil temperature
  - snow.csv – snow depth
  - ICS1.csv – input (deposition) of C substrate (labile)
  - ICS2.csv – input (deposition) of (refractory)
  - IPON1.csv – input (deposition) of organic N (labile)
  - IPON2.csv – input (deposition) organic N (refractory)
  - IPOP1.csv – input (deposition) organic P (labile)
  - IPOP2.csv – input (deposition) organic P (refractory)
  - IDIN.csv – input (deposition) DIN
  - IDIP.csv – input (deposition) DIP
- “observations”: field data.
  - “C\_aut.dat”: total autotrophic microbial biomass
  - “C\_het.dat”: total heterotrophic microbial biomass
  - “CS.dat”: total organic carbon

The entire “demo” folder should be copied to a local computer such that the directory is: “C:/RFolder/model/demo/” (Windows) **or**

“/Users/jamesbradley/Documents/RFolder/model/demo/” (Macintosh) **or** the folder paths contained in SHIMMER.R script should be modified (*path*, *path\_root*, *pathdr* and *pathte*) according to where the “demo” folder is copied to.

### 3. Source Code Files Description

This section provides a brief description of all source code files present in the sub-folder “SHIMMER”. This should be read alongside the SHIMMER (1.0) *Geoscientific Model Development* publication (Bradley et al., 2015) for clarity on variables, parameters, balance equations etc.

#### *SHIMMER.R*

- Specify length of model run here (nyears) (note: must be a positive integer).
- Execute this code (copy and paste into R Console window) to run the model.

#### *Library > SHIMMER\_set\_parameter\_values.R*

- Specify parameter values here.
- The default settings of the model correspond to the Midtre Lovénbreen forefield, Svalbard (Bradley et al., 2016).
- See Bradley et al. (2015) for a description of parameters.

#### *Library > SHIMMER\_NEW\_load\_and\_make\_drivers.R*

- Load the forcing data and replicate for duration of model run (nyears).
- Note: forcing data must be specified as daily values (as per examples).

#### *Library > SHIMMER\_set\_start\_values.R*

- Specify initial conditions here (starting value for each state-variable).

#### *Library > SHIMMER\_NEW\_model\_definition.R*

- Contains the equations which formulate the model.

#### *Library > SHIMMER\_compute\_totals.R*

- Derive rates from time-series of output variables.

#### *Library > SHIMMER\_construct\_array.R*

- Construct 3-D array from output variables.

#### *Library > SHIMMER\_basic\_plots.R*

- Examples of basic plots of model output.

### 4. Model Operation

In R, specify working directory to: “C:/RFolder/model/demo/demo\_WIN/SHIMMER/” (if using Windows. For Mac, change path as appropriate).

Open SHIMMER.R script and execute in console (note: package “deSolve” (Soetaert et al., 2010) must be installed).

To run the model, copy and paste the *SHIMMER.R* script into the R Console window.

## 5. Output

Model output is created as variables within R (out, out2 and out\_array). By default, they are not saved locally, however this can be done by using a command such as:

```
write.table(out,file=paste("out","model_run.csv",sep="_"),sep="," ,row.names=FALSE)
```

The dataframe “out” is a 2-D time-series of output data comprised of columns for each output (variables, totals and rates), and rows for each day simulated. All units are in  $\mu\text{g g}^{-1}$  dry soil or equivalent.

Column Name	Description	Column Name	Description
<i>time</i>	Day of simulation	<i>cum_I_Sub</i>	Cumulative C substrate input
<i>A1</i>	A1 biomass	<i>cum_G_X</i>	Cumulative C substrate from losses (G) and exudates (X)
<i>A2</i>	A2 biomass	<i>years</i>	Year of simulation
<i>A3</i>	A3 biomass	<i>A_total</i>	Total autotrophic biomass
<i>H1</i>	H1 biomass	<i>H_total</i>	Total heterotrophic biomass
<i>H2</i>	H2 biomass	<i>S_total</i>	Total C substrate
<i>H3</i>	H3 biomass	<i>Cmic_total</i>	Total microbial biomass
<i>S1</i>	C substrate (labile)	<i>PON_total</i>	Total organic nitrogen
<i>S2</i>	C substrate (refractory)	<i>POP_total</i>	Total organic phosphorus
<i>DIN</i>	Dissolved Inorganic Nitrogen	<i>cum_A</i>	Cumulative growth (production) of autotrophs
<i>DIP</i>	Dissolved Inorganic Phosphorus	<i>cum_H</i>	Cumulative growth (production) of heterotrophs
<i>PON1</i>	Organic Nitrogen (labile)	<i>rate_A1</i>	Daily A1 growth rate
<i>PON2</i>	Organic Nitrogen (refractory)	<i>rate_A2</i>	Daily A2 growth rate
<i>POP1</i>	Organic Phosphorus (labile)	<i>rate_A3</i>	Daily A3 growth rate
<i>POP2</i>	Organic Phosphorus (refractory)	<i>rate_H1</i>	Daily H1 growth rate
<i>cum_A1</i>	Cumulative growth (production) of A1	<i>rate_H2</i>	Daily H2 growth rate
<i>cum_A2</i>	Cumulative growth (production) of A2	<i>rate_H3</i>	Daily H3 growth rate
<i>cum_A3</i>	Cumulative growth (production) of A3	<i>rate_DIC_A</i>	Daily DIC from autotrophs
<i>cum_H1</i>	Cumulative growth (production) of H1	<i>rate_DIC_H</i>	Daily DIC from heterotrophs
<i>cum_H2</i>	Cumulative growth (production) of H2	<i>rate_DIN</i>	Daily DIN assimilation
<i>cum_H3</i>	Cumulative growth (production) of H3	<i>rate_nf</i>	Daily nitrogen fixation
<i>cum_DIC_A</i>	Cumulative DIC from autotrophs	<i>rate_A</i>	Daily autotrophic growth (production)
<i>cum_DIC_H</i>	Cumulative DIC from heterotrophs	<i>rate_H</i>	Daily heterotrophic growth (production)
<i>cum_DIN</i>	Cumulative DIN assimilated into biomass	<i>rate_I_Sub</i>	Daily C substrate input

<i>cum_nf</i>	Cumulative nitrogen fixed	<i>rate_G_X</i>	Daily loss (G) and exudate (X) input
		<i>rate_G</i>	Daily loss (G) (necromass) input
		<i>rate_X</i>	Daily exudate (X) input

The dataframe “out2” is a 2-D time-series of annual totals (or rates), comprised of columns for each output, and rows for each year simulated. All units are in  $\mu\text{g g}^{-1}$  dry soil or equivalent.

Column Name	Description	Column Name	Description
<i>year</i>	Year of simulation	<i>annual_DIC_A</i>	Total annual DIC efflux from autotrophs
<i>annual_A1</i>	Total annual A1 production (biomass growth)	<i>annual_DIC_H</i>	Total annual DIC efflux from heterotrophs
<i>annual_A2</i>	Total annual A2 production	<i>annual_DIN</i>	Total annual DIN assimilated from soil
<i>annual_A3</i>	Total annual A3 production	<i>annual_nf</i>	Total annual nitrogen fixed from air
<i>annual_H1</i>	Total annual H1 production	<i>annual_A</i>	Total annual autotrophic production
<i>annual_H2</i>	Total annual H2 production	<i>annual_H</i>	Total annual heterotrophic production
<i>annual_H3</i>	Total annual H3 production		

The array “out\_array” is a 3-D array of data from “out”. The columns (x- axis) represent each output variable, total and rate, the rows (y-axis) represent each day of the year (1-365), and the depth (z-axis) represents each year. For example, out\_array[2,5,3] is the biomass of A1 (the 2<sup>nd</sup> column in out) for the 5<sup>th</sup> day of the 3<sup>rd</sup> year. All units are in  $\mu\text{g g}^{-1}$  dry soil or equivalent. The purpose of the array is that it is simpler to average and sum data across specific time-intervals.

## References

- BRADLEY, J. A., ANESIO, A. M., SINGARAYER, J. S., HEATH, M. R. & ARNDT, S. 2015. SHIMMER (1.0): a novel mathematical model for microbial and biogeochemical dynamics in glacier forefield ecosystems. *Geosci. Model Dev.*, 8, 3441-3470.
- BRADLEY, J. A., ARNDT, S., ŠABACKÁ, M., BENNING, L. G., BARKER, G. L., BLACKER, J. J., YALLOP, M. L., WRIGHT, K. E., BELLAS, C. M., TELLING, J., TRANTER, M. & ANESIO, A. 2016. Microbial dynamics in a High-Arctic glacier forefield: a combined field, laboratory, and modelling approach. *Biogeosciences Discuss.*, 2016, 1-34.
- SOETAERT, K., PETZOLDT, T. & SETZER, R. W. 2010. Solving Differential Equations in R: Package deSolve. *J Stat Softw*, 33, 1-25.