

R package rodeoFABM: Basic Use and Sample Applications

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1 Main features of rodeoFABM

The package `rodeoFABM` is a collection of small tools to help create water quality models that can be coupled to physical host models using the `FABM` interface (Bruggeman and Bolding (2014)). As the name suggests it is heavily influenced by the R package `rodeo` (Kneis, Petzoldt, and Berendonk (2017)). The principle idea is to have a system that:

- Helps users that don't have the technical know how
- make model adaptation, communication, and maintenance easy

Therefore the water quality model is written in the standard Peterson matrix notation and stored in text files or spread sheets. The package `rodeoFABM` automatically generates `FABM` specific FORTRAN code from these files and can automatically compile `GOTM` coupled with the newly created model, as well as `.yaml` control files for the water quality model.

2 Installation and requirements

In order to fully use `rodeoFABM` and run the examples some tools are needed:

- The GNU compilers
- GNU Make

- GNU CMake
- Rdevtools
- R packages: `readODs`, `gotmtools`

The package `rodeoFABM` can be installed from github using:

```
library("devtools")
install_github("JFeldbauer/rodeoFABM")
```

3 Basic use

A simple example that is extended along the way

3.1 First example (how it works)

To demonstrate the workflow we will use a very simple model that is provided in the package. The files are contained in the package and can be loaded using:

```
# copy example ods file
example_model <- system.file("extdata/simple_model.ods", package = "rodeoFABM")
file.copy(from = example_model, to = ".", recursive = TRUE)
```

Now we can read in the tables with the declaration of the state variables, model parameters, used functions and external dependencies, process rate descriptions, and the stoichiometry matrix.

```
library(readODS)

# read in example ods file
odf_file <- "simple_model.ods"
vars <- read_ods(odf_file, 1)
pars <- read_ods(odf_file, 2)
funs <- read_ods(odf_file, 3)
pros <- read_ods(odf_file, 4)
stoi <- read_ods(odf_file, 5)
```

From these we can now generate FORTRAN files

```
library(rodeoFABM)

# generate fabm code
gen_fabm_code(vars,pars,funs,pros,stoi,"simple_model.f90",diags = TRUE)
```

And compile GOTM-FABM with them. Therfore first we need to clone the lake branche of GOTM-FABM from github and prepare the build process using cmake. This needs only to be done once, using the function `clone_GOTM()`:

```
# clone github repo
clone_GOTM(build_dir = "build", src_dir = "gotm_src")
```

Now we can build GOTM-FABM with our own model using:

```
# build GOTM
build_GOTM(build_dir = "build",fabm_file = "simple_model.f90",
            src_dir = "gotm_src/extern/fabm/src/models/tuddhyb/rodeo")
```

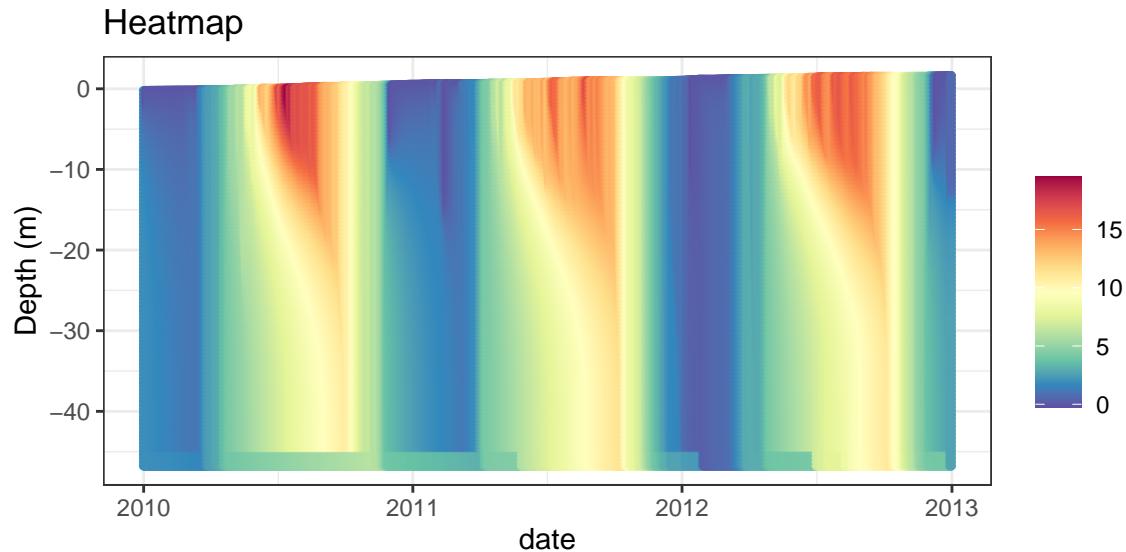
After copying the example `gotm.yaml` (the GOTM controll file), the exymple hypsograph, and the example forcing data, we finally can run GOTM-FABM with our own small model using:

```
# copy example gotm.yaml
yaml <- system.file("extdata/gotm.yaml", package = "rodeoFABM")
file.copy(from = yaml, to = ".", recursive = TRUE)
# write hypsograph
write.table(hypsograph, "hypsograph.dat", sep = "\t", row.names = FALSE,
            quote = FALSE)
# write meteo data
write.table(meteo_file, "meteo_file.dat", sep = "\t", row.names = FALSE,
            quote = FALSE)
# run gotm
system2("./gotm")
```

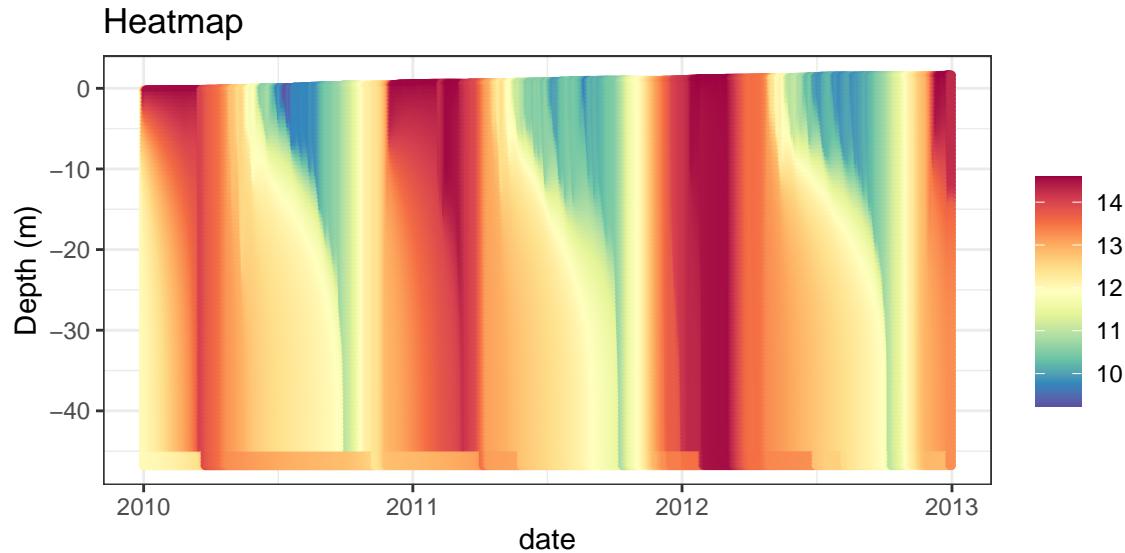
We can plot the results e.g. using the `gotmtools` library, which can be installed from the AEMON-J github using:

```
devtools:::install_github("aemon-j/gotmtools")

library(gotmtools)
# plot temperature
plot_vari("output.nc", "temp")
```



```
# plot oxygen
plot_vari("output.nc", "rodeo_C_02")
```



These are the essential steps used. In the next section we will go into the details of building a model using the `rodeoFABM` package step by step.

3.2 Create a model step by step

In order to demonstrate the necessary steps and functionality we will create a very simple phytoplankton-nutrients model and step by step add more processes.

The libre office spread sheets with the model information, GOTM controll file, and forcing data are contained in the `rodeoFABM` package. You can copy all necessary files to run GOTM using the same method as before. We will use the same meteorological forcing (`meteo_file.dat`) and hypsographic curve (`hypsograph.dat`) as in the first example. Additionally we now have one inflow and one outflow (files `inflow_m.dat`, `outflow.dat`, and `inflow_wq_m.dat` containing the nutrient concentrations of the inflow)

```
# GOTM controll file
yaml <- system.file("extdata/examples/gotm.yaml",
                     package = "rodeoFABM")
file.copy(from = yaml, to = ".", recursive = TRUE)
# inflow hydrological data
infl <- system.file("extdata/examples/inflow_m.dat",
                     package = "rodeoFABM")
file.copy(from = infl, to = ".", recursive = TRUE)
# inflow nutrient data
nut <- system.file("extdata/examples/inflow_wq_m.dat",
                     package = "rodeoFABM")
file.copy(from = nut, to = ".", recursive = TRUE)
# outflow data
out <- system.file("extdata/examples/outflow.dat",
                     package = "rodeoFABM")
file.copy(from = out, to = ".", recursive = TRUE)
```

The inflows and especially the inflow of state variables to a *FABM* model are defined in the `stream` section of the GOTM control file (`gotm.yaml`). The section looks like this:

```
streams:
  inflow:                                     # stream configuration
```

```

method: 4                                # inflow method, default=1
zu: 0.0                                    # upper limit m
z1: 0.0                                    # lower limit m
flow:
  method: 2                                # 0=constant, 2=from file, default = 0
  constant_value: 1.0                      # constant value( m^3/s)
  file: inflow_m.dat                      # path to file with time series
  column: 1                                 # index of column to read from
temp:
  method: 2                                # 0=constant, 2=from file; default=0
  constant_value: 10.0                     # constant value (°C)
  file: inflow_m.dat                      # path to file with time series
  column: 2                                 # index of column to read from
salt:
  method: 0                                # 0=constant, 2=from file; default=0
  constant_value: -1.0                     # constant value (PSU)
  file: inflow.dat                         # path to file with time series
  column: 3                                 # index of column to read from
rodeo_HPO4:
  method: 0                                # 0=constant, 2=from file; default=0
  constant_value: 0.5                       # constant value (gP/m^3)
  file: inflow_wq_m.dat                   # path to file with time series
  column: 4                                 # index of column to read from

```

Within the `streams` section several in- and outflows can be defined with any desired name (here `inflow`). The inflow/outflow depth is defined by `streams/method`, whereas 1 means surface, 2 means bottom, 3 mean a specified range of depths defined by `streams/zu` (upper) and `streams/z1` (l), and 4 means inflow to the depth with same temperature as the inflow temperature. Every in- or outflow needs the `streams/flow` section defining the flow rate in m^3/s and can have additional entries like `streams/temp` for temperature or inflowing state variables of the *FABM* model (like `streams/rodeo_HPO4`). The *FABM* state variables need to start with `rodeo_` followed by the defined state variable name. The values can either be constant (`streams/rodeo_HPO4/method = 0`) or a time series given by a tab separated file (`streams/rodeo_HPO4/method = 2`) with first column datetime (as `YYYY-mm-dd HH:MM:ss`). The name of the file is supplied by `streams/rodeo_HPO4/file` and the column the variable is in by `streams/rodeo_HPO4/column`, take care: the first column with datetime is not counted and if the columns have a header it needs to start with an exclamation mark “!”.

We can creat the firs phytoplankton nutrients model similar to how we created the first example:

```

# copy the spread sheet
ods <- system.file("extdata/examples/simple_alg.ods",
                    package = "rodeoFABM")
file.copy(from = ods, to = ".", recursive = TRUE)

# declare data frames for vars, pars, funs, pros, and stoi
vars <- read_ods("simple_alg.ods", sheet = "vars")
pars <- read_ods("simple_alg.ods", sheet = "pars")
funs <- NULL
pros <- read_ods("simple_alg.ods", sheet = "pros")
stoi <- read_ods("simple_alg.ods", sheet = "stoi")

```

This first model is a very simple model with two state variables, which are declared in the `vars` data frame. The table needs to have at least three columns *name* giving the identifier of the state variable, *unit* giving the used unit, and *description* giving a short description of the state variable. If additionally the column *default* is supplied the initial value will be included in the *FABM* control file (`fabm.yaml`), which is automatically generated by `gen_fabm_code()`.

Table 1: Data set `vars`: Declaration of state variables.

name	unit	description	default
C	gDM/m ³	algae concentration	0.0
$HPO4$	gP/m ³	phosphorus concentration	0.1

The models parameters are defined in the `pars` data frame in a similar fashion. They need the same three columns *name*, *unit*, and *description* and can have the additional column *default* as well. Take care that *FABM* requires all parameters with relation to time to be in units of second.

Table 2: Data set `pars`: Declaration of model parameters.

name	unit	description	default
μ_{max}	1/s	maximum growth rate	1e-05
K_P	W/m ²	half saturation concentration of HPO4 limitation	2e-02
k_{death}	1/s	death rate	2e-06
a_P	gP/gDM	phosphorus content of phytoplankton	5e-02

External functions, or forcing data that needs to be obtained from the physical host model (e.g. water temperature) are defined in `funs`. As the first simple model has no such things this is explained in the later steps. As in this example the data frame is not needed it has to be set to `NULL`.

The declaration of the processes and process rates is done in the `pros` data frame. It has four required columns: *name* giving the name of the process, *unit* giving the unit of the process rate (again in seconds!), *description* giving a short description of the process, and *expression* giving the mathematical expression of the process. There can be additional columns to define the spatial domain of the process, or to declare sinking processes, but they will be explained later.

Table 3: Data set `pros`: Declaration of processes.

name	unit	description	expression
growth	g/m ³ /d	growth of algae	$C \cdot \mu_{max} \cdot HPO4 / (HPO4 + K_P)$
death	g/m ³ /d	death of algae	$C \cdot k_{death}$

The phytoplankton have a simple linear growth term with a Monod like limitation for the limiting nutrient Phosphorus and a linear decay/death term.

The last data frame `stoi` gives the stoichiometry table (in long format) connecting the process rates with the state variables. It has three required columns: *variable* giving the variable affected by the *process*, and *expression* giving a factor to multiply the process rate by:

Table 4: Data set `stoi`: Declaration of stoichiometry matrix in long format.

variable	process	expression
C	growth	1
C	death	-1
$HPO4$	growth	$-1 \cdot a_P$

The growth of phytoplankton is increasing its concentration C and decreasing the nutrient $HPO4$ by the

fraction of a_P , which is the Phosphorus content of the phytoplankton. Decay/death is just decreasing phytoplankton concentration C .

Having declared all five data frames we can now generate the fortran code using `gen_fabm_code()`. This will also perform some automated checks e.g. if all used parameters and state variables are also declared, and will issue a warning if the used units are not using seconds for time. It will also create the *FABM* control file `fabm.yaml` and insert the default values for parameters and initial values (if declared). If the argument `diags` is set to `TRUE` the process rates are stored as diagnostic variables in the output netcdf file.

```
# create the fabm code
gen_fabm_code(vars, pars, funs, pros, stoi, "model_1.f90", diags = TRUE)
```

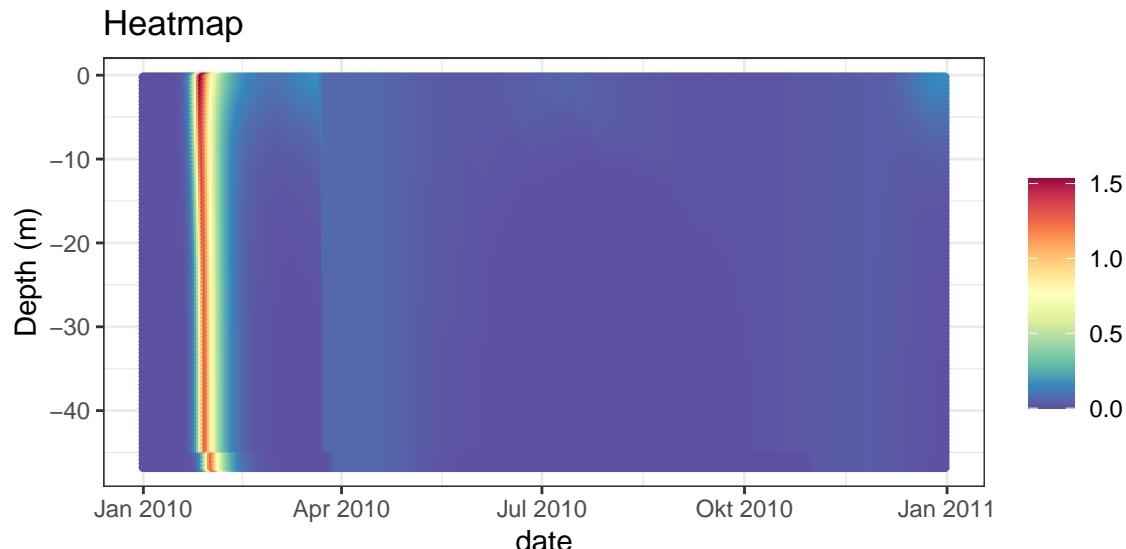
After creating the fortran source code, *GOTM-FABM* can be automatically compiled using the function `build_GOTM()` (assuming the source code was already fetched and prepared for compilation using `clone_GOTM()`), this will also copy the compiled executable to the current working directory, which then can be ran using e.g. `system2("./gotm")`.

```
# build GOTM with the model
build_GOTM(build_dir = "build", src_dir = "gotm_src/extern/fabm/src/models/tuddhyb/rodeo/",
            fabm_file = "model_1.f90")

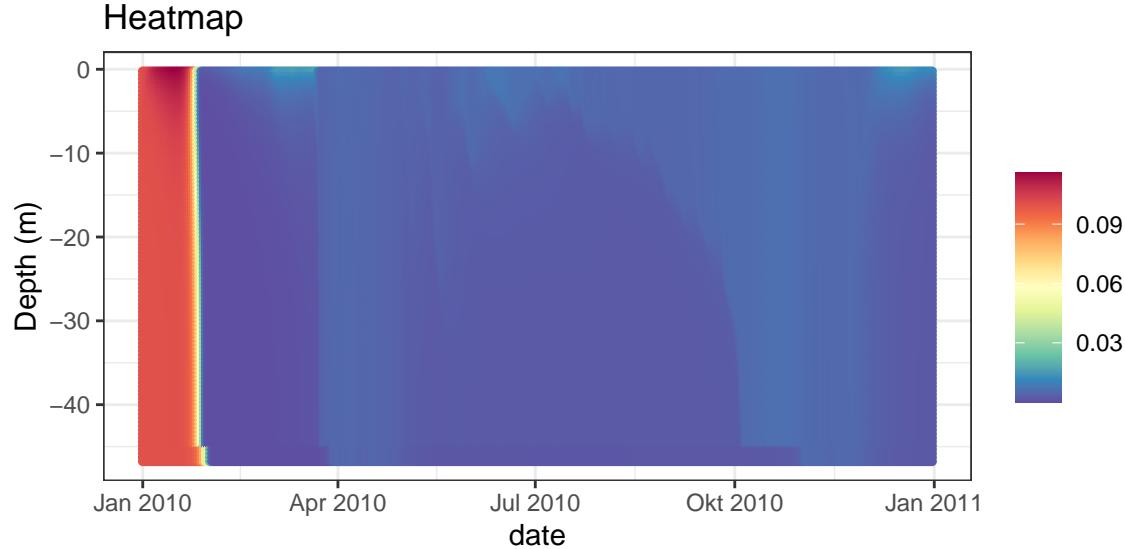
# run the model
system2("./gotm")
```

We can now plot the model results e.g. using `gotmtools::plot_vari()`.

```
# plot the variables
plot_vari("output.nc", "rodeo_C")
```



```
plot_vari("output.nc", "rodeo_HP04")
```



3.2.1 Getting dependencies from the host model

As many biogeochemical processes depend on external forcing, such as temperature or available irradiation, these values can be obtained from the physical host model. In the next step we want to add the dependency of phytoplankton growth on available irradiation. We first copy the prepared spread sheet and declare the data frames:

```
ods <- system.file("extdata/examples/simple_alg_par.ods",
                   package = "rodeoFABM")
file.copy(from = ods, to = ".", recursive = TRUE)

# declare data frames for vars, pars, funs, pros, and stoi
vars <- read_ods("simple_alg_par.ods", sheet = "vars")
pars <- read_ods("simple_alg_par.ods", sheet = "pars")
funs <- read_ods("simple_alg_par.ods", sheet = "funs")
pros <- read_ods("simple_alg_par.ods", sheet = "pros")
stoi <- read_ods("simple_alg_par.ods", sheet = "stoi")
```

Now we need to get values for the photosynthetic active radiation (PAR) from GOTM. *FABM* has so called “standard-variables” with defined names (stored in the `std_names_FABM` data). If you want to access these variables you need to define them as a function in the `funs` data frame and add the additional column *dependency* which contains the full standard-variable name. The data frame `funs` has three required columns that are the same as in `vars`, and `pars`: *name*, *unit*, and *description*, additionally the column *dependency*. If you declare several functions of whom some are not dependencies the corresponding entry in column *dependency* needs to be `NA` for these and the corresponding standard-name for the ones that are dependencies.

Table 5: Data set `funs`: Declaration of model functions and dependencies from the host model.

name	unit	description	dependency
<code>par</code>	<code>W/m^2</code>	Downwelling photosynthetic radiative flux	<code>downwelling_photosynthetic_radiative_flux</code>

The declared functions/dependencies can now be used in the process expression, same as parameters and state variables. We added a Monod Term for light limitation in the *growth* process:

Table 6: Data set `pros`: Declaration of processes.

name	unit	description	expression
growth	g/m ³ /d	growth of algae	$C \cdot \mu_{max} \cdot HPO_4 / (HPO_4 + K_P) \cdot par / (par + K_{par})$
death	g/m ³ /d	death of algae	$C \cdot k_{death}$

For this we need to declare the additional parameter for the half-saturation irradiation in the `pars` data frame:

Table 7: Data set `pars`: Declaration of model parameters.

name	unit	description	default
μ_{max}	1/s	maximum growth rate	1.0e-05
K_P	W/m ²	half saturation of photosyntetic flux	2.0e-02
k_{death}	1/s	death rate	2.0e-06
a_P	gP/gDM	phosphorus content of phytoplankton	5.0e-02
K_{par}	W/m ²	half saturation of photosyntetic flux	2.7e+01

Now we can generate the fortran code, compile *GOTM-FABM*, and run the adapted model.

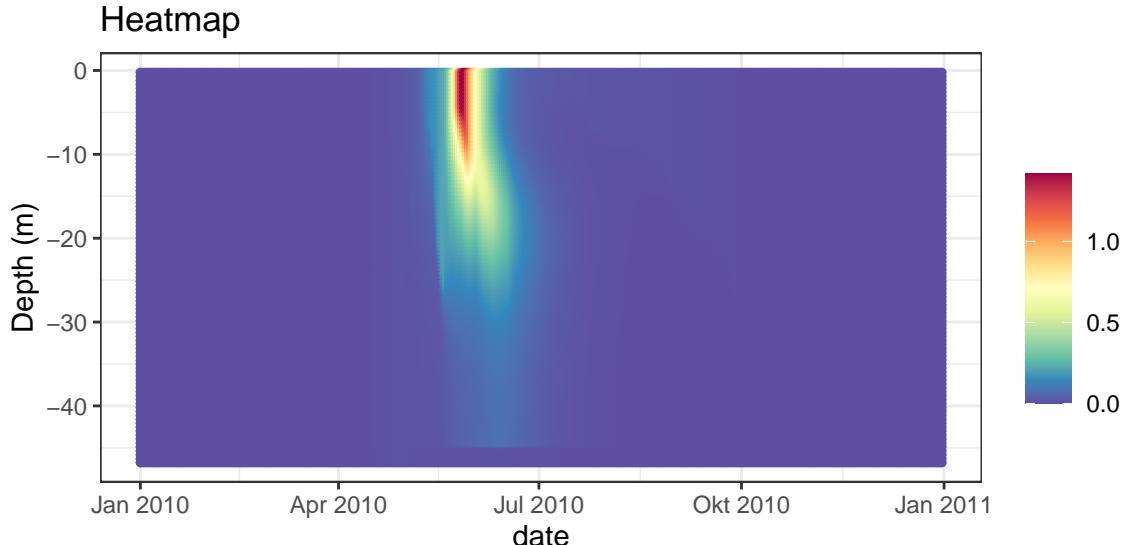
```
# create the fabm code
gen_fabm_code(vars, pars, funs, pros, stoi, "model_2.f90", diags = TRUE)

# build GOTM with the model
build_GOTM(build_dir = "build", src_dir = "gotm_src/extern/fabm/src/models/tuddhyb/rodeo/",
           fabm_file = "model_2.f90")

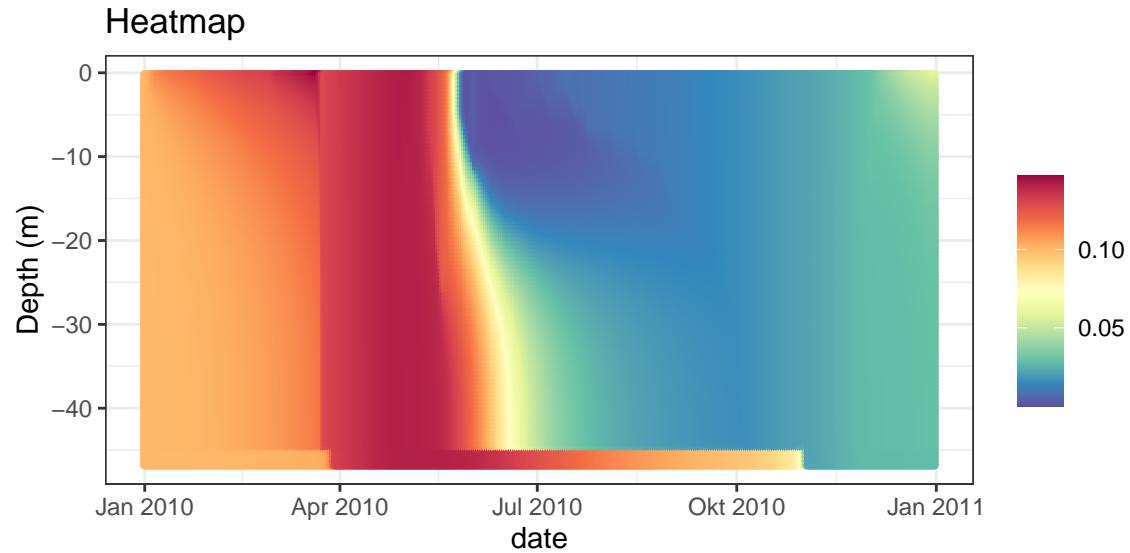
# run the model
system2("./gotm")
```

And plot some of the simulated state variables:

```
# plot the variables
plot_vari("output.nc", "rodeo_C")
```

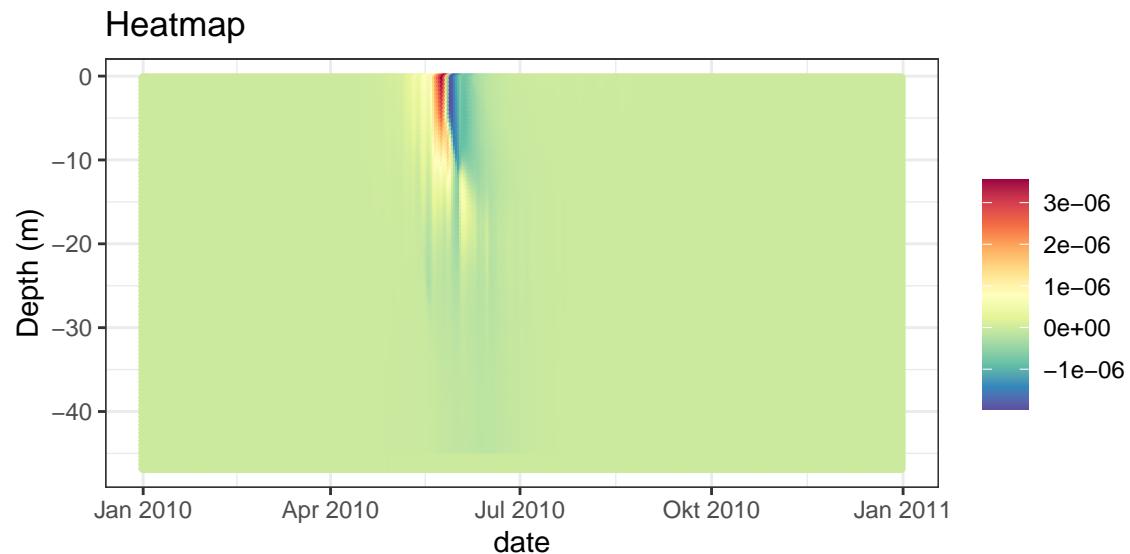


```
plot_vari("output.nc", "rodeo_HP04")
```



From the saved process rates (the diagnostic variables) we can plot e.g. the net. growth rate. We can acces the values stored in the netcdf file e.g. using the function `gotmtools::get_vari()` and plot them using `gotmtools::long_heatmap()`:

```
# also plot net. growth
growth <- get_vari("output.nc", "rodeo_growth")
death <- get_vari("output.nc", "rodeo_death")
net_growth <- cbind(growth$Datetime, growth[, -1] - death[, -1])
z <- get_vari("output.nc", var = "z", incl_time = TRUE)
long_heatmap(wide2long(net_growth, z))
```



3.3 Sedimentation

Often in biogeochemical models some state variables are sinking in the water body (e.g. phytoplankton or particular organic matter). In the next adaptation of the model we want to include a constant sinking velocity for the phytoplankton. Therefore, again we first copy the spread sheets from the package data and declare the data frames:

```
ods <- system.file("extdata/examples/simple_alg_par_sed.ods",
                    package = "rodeoFABM")
file.copy(from = ods, to = ".", recursive = TRUE)

# declare data frames for vars, pars, funs, pros, and stoi
vars <- read_ods("simple_alg_par_sed.ods", sheet = "vars")
pars <- read_ods("simple_alg_par_sed.ods", sheet = "pars")
funs <- read_ods("simple_alg_par_sed.ods", sheet = "funs")
pros <- read_ods("simple_alg_par_sed.ods", sheet = "pros")
stoi <- read_ods("simple_alg_par_sed.ods", sheet = "stoi")
```

FABM allows for time varying sinking of state variables. This is implemented in *rodeoFABM* as a process declared in the *pros* data frame that has a logical flag set in an additional column called *sedi*. The expression for this can also be a function of external dependencies (e.g. water density) or internal state variables (e.g. nutrient concentration), in this simple case we choose a constant sinking velocity:

Table 8: Data set *pros*: Declaration of processes.

name	unit	description	expression	sedi
growth	g/m ³ /d	growth of algae	$C \cdot mu_max \cdot HPO4 / (HPO4 + K_P) \cdot par / (par + K_par)$	NA
death	g/m ³ /d	death of algae	$C \cdot k_death$	NA
sed	g/m ³ /s	sinking	v_sed	TRUE

For this to work we need to declare the additional parameter for the sinking velocity:

Table 9: Data set *pars*: Declaration of model parameters.

name	unit	description	default
<i>mu_max</i>	1/s	maximum growth rate	1.0e-05
<i>K_P</i>	W/m ²	half saturation of photosynthetic flux	2.0e-02
<i>k_death</i>	1/s	death rate	2.0e-06
<i>a_P</i>	gP/gDM	phosphorus content of phytoplankton	5.0e-02
<i>K_par</i>	W/m ²	half saturation of photosynthetic flux	2.7e+01
<i>v_sed</i>	m/s	sedimentation velocity	1.0e-06

And add the process to the stoichiometry table:

Table 10: Data set *stoi*: Declaration of stoichiometry matrix in long format.

variable	process	expression
<i>C</i>	growth	1
<i>C</i>	death	-1
<i>C</i>	sed	-1

variable	process	expression
<i>HPO4</i>	growth	$-1 \cdot a_P$

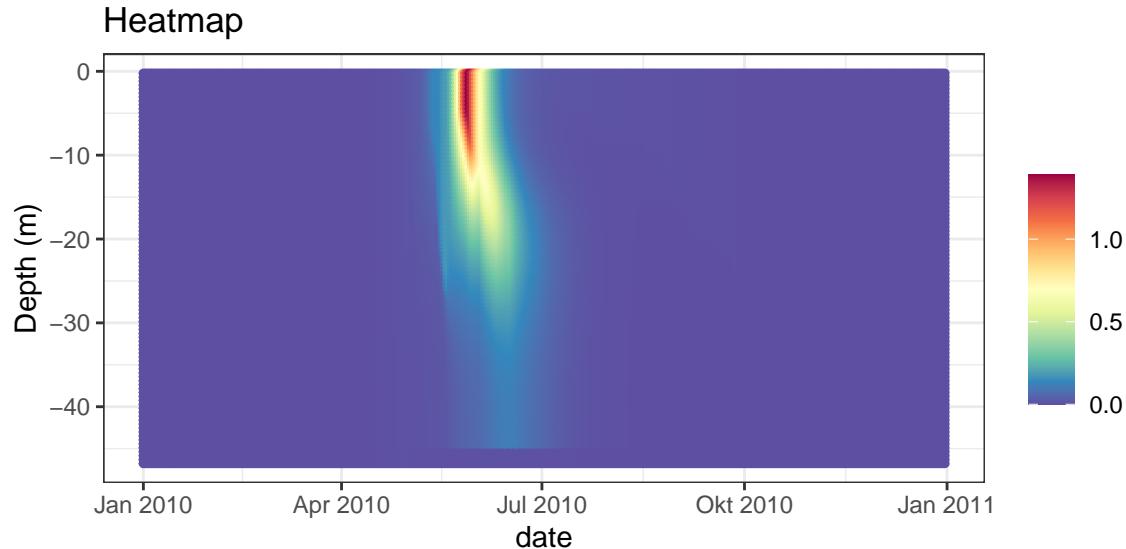
Now we can create the fortran source file, compile *GOTM-FABM*, run the model and plot some of the results:

```
# create the fabm code
gen_fabm_code(vars, pars, funs, pros, stoi, "model_3.f90")

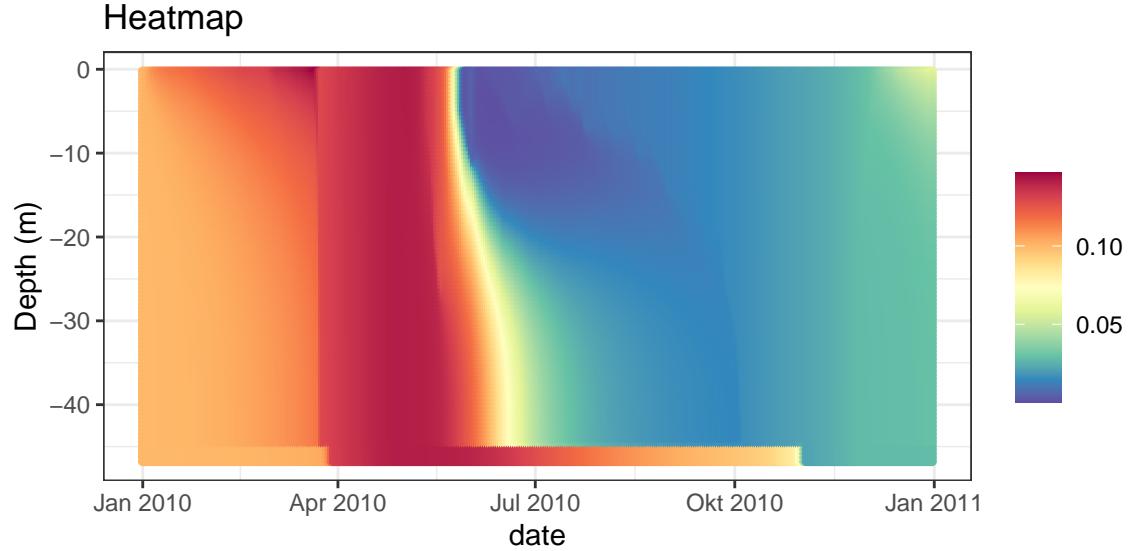
# build GOTM with the model
build_GOTM(build_dir = "build", src_dir = "gotm_src/extern/fabm/src/models/tuddhyb/rodeo/",
            fabm_file = "model_3.f90")

# run the model
system2("./gotm")

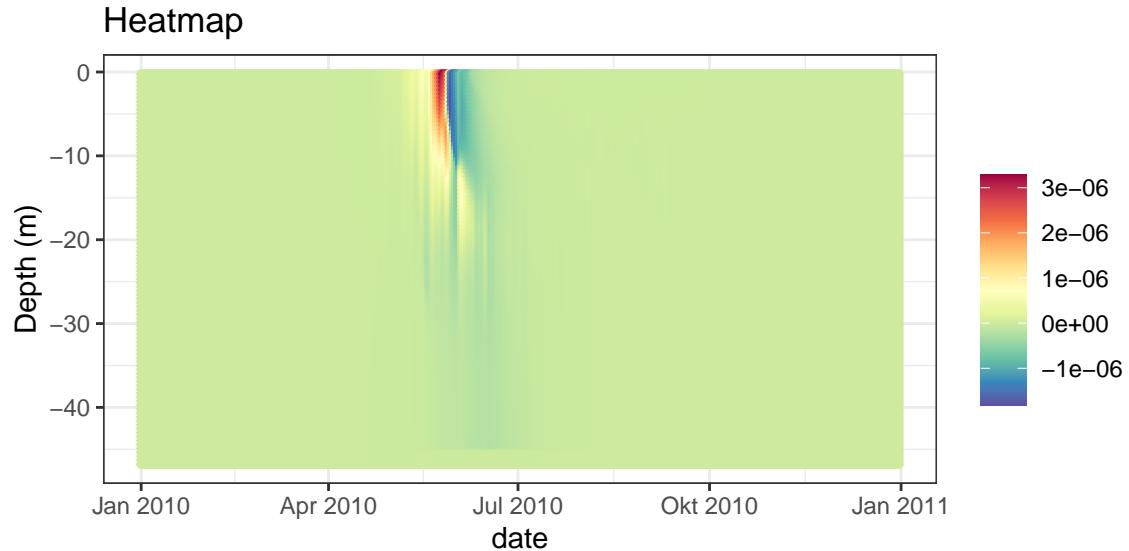
# plot the variables
plot_vari("output.nc", "rodeo_C")
```



```
plot_vari("output.nc", "rodeo_HPO4")
```



```
# also plot net. growth
growth <- get_vari("output.nc", "rodeo_growth")
death <- get_vari("output.nc", "rodeo_death")
net_growth <- cbind(growth$Datetime, growth[, -1] - death[, -1])
z <- get_vari("output.nc", var = "z", incl_time = TRUE)
long_heatmap(wide2long(net_growth, z))
```



3.3.1 Processes at the upper and lower boundaries (surface and sediment)

There are some processes that only take place at the surface or bottom (sediment) of lakes. *FABM* knows three spatial domains: open water (pelagial), surface, and bottom (sediment) and processes can be declared to only take place at one of these domains. To demonstrate this we add oxygen along with surface exchange and a constant oxygen consumption in the sediment to the model. We again start by copying the spread sheet from the package data:

```

ods <- system.file("extdata/examples/simple_alg_02.ods",
  package = "rodeoFABM")
file.copy(from = ods, to = ".", recursive = TRUE)
# read in first simple model
vars <- read_ods("simple_alg_02.ods", sheet = "vars")
pars <- read_ods("simple_alg_02.ods", sheet = "pars")
funs <- read_ods("simple_alg_02.ods", sheet = "funs")
pros <- read_ods("simple_alg_02.ods", sheet = "pros")
stoi <- read_ods("simple_alg_02.ods", sheet = "stoi")

```

Now we need to add the new state variable $O2$ to the `vars` data frame:

Table 11: Data set `vars`: Declaration of state variables.

name	unit	description	default
C	gDM/m^3	algae concentration	0.0
$HPO4$	gP/m^3	phosphorus concentration	0.1
$O2$	gO/m^3	oxygen concentration	10.0

If processes occur only at the surface or bottom interface we can declare this by setting a logical flag in additional columns in the `pros` data frame called `bot` and `surf`. We add two new processes $O2_exch$, and $O2_cons$ and set the flag in the corresponding columns to TRUE:

Table 12: Data set `pros`: Declaration of processes.

name	unit	description	expression
growth	$\text{g}/\text{m}^3/\text{d}$	growth of algae	$C \cdot mu_max \cdot HPO4 / (HPO4 + K_P) \cdot par / (par + K_pa)$
death	$\text{g}/\text{m}^3/\text{d}$	death of algae	$C \cdot k_death$
sed	$\text{g}/\text{m}^3/\text{s}$	sinking	v_sed
$O2_exch$	$\text{g}/\text{m}^3/\text{d}$	exchange of Oxygen at the surface	$v_O2 \cdot (exp(7.7117 - 1.31403 \cdot log(Temp + 45.93)) \cdot (p/101$
$O2_cons$	$\text{g}/\text{m}^3/\text{d}$	consumption of Oxygen in the pelagic	$O2 / (O2 + K_O2) \cdot k_O2_cons$

We need to declare the two additional parameter for the oxygen exchange velocity and the constant consumption in the sediment:

Table 13: Data set `pars`: Declaration of model parameters.

name	unit	description	default
mu_max	1/s	maximum growth rate	1.0e-05
K_P	W/m^2	half saturation of photosynthetic flux	2.0e-02
k_death	1/s	death rate	2.0e-06
a_P	gP/gDM	phosphorus content of phytoplankton	5.0e-02
K_par	W/m^2	half saturation of photosynthetic flux	2.7e+01
v_sed	m/s	sedimentation velocity	1.0e-06
v_O2	1/s	speed of oxygen transfer	1.0e-05
k_O2_cons	$1/\text{s}/\text{m}^2$	Oxygen consumption rate in sediment	5.0e-07
K_O2	gO/m^3	half saturation concentration of oxygen consumption	5.0e+00
a_O	gO/gDM	oxygen production per growth of algae	1.0e+00

And we need to declare the two functions used `log`, and `exp`, as well as the external dependencies `p` (the

barometric pressure at the surface), and *Temp* (water temperature) which are needed to calculate the oxygen saturation concentration:

Table 14: Data set **funs**: Declaration of model functions and dependencies from the host model.

name	unit	description	dependency
<i>par</i>	W/m ²	Downwelling photosynthetic radiative flux	downwelling_photosynthetic_radiative_flux
<i>p</i>	Pa	Atmospheric Pressure	surface_air_pressure
<i>Temp</i>	celsius	Water temperature	temperature
<i>exp</i>	-	exponential function	NA
<i>log</i>	-	logarithmic function	NA

After adding the new processes to the stoichiometry table:

Table 15: Data set **stoi**: Declaration of stoichiometry matrix in long format.

variable	process	expression
<i>C</i>	growth	1
<i>C</i>	death	-1
<i>C</i>	sed	-1
<i>HPO</i> ₄	growth	-1 · <i>a_P</i>
<i>O</i> ₂	<i>O</i> ₂ _exch	1
<i>O</i> ₂	<i>O</i> ₂ _cons	-1
<i>O</i> ₂	growth	<i>a_O</i>

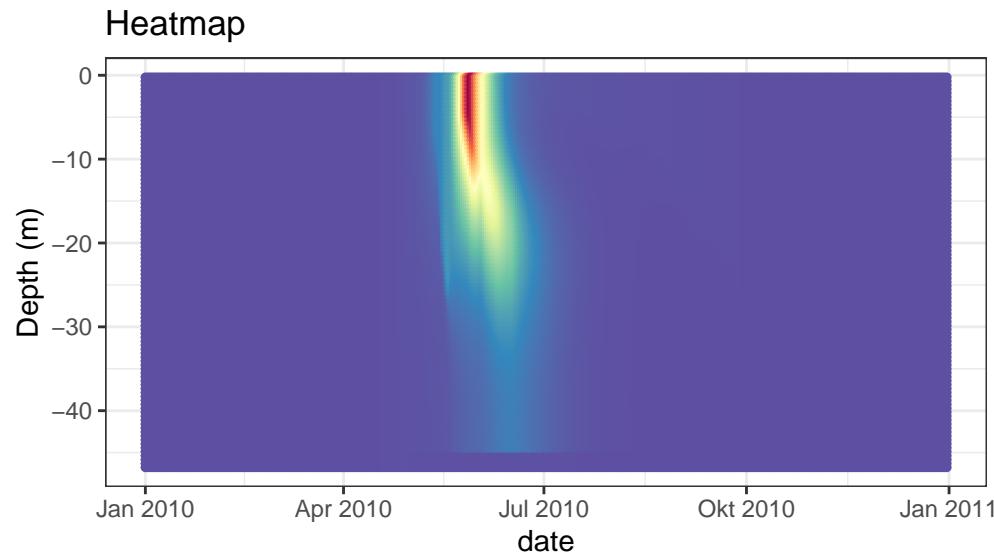
We can generate the source code, compile *GOTM-FABM*, run the model, and plot some of the results:

```
# create the fabm code
gen_fabm_code(vars, pars, funs, pros, stoi, "model_4.f90")

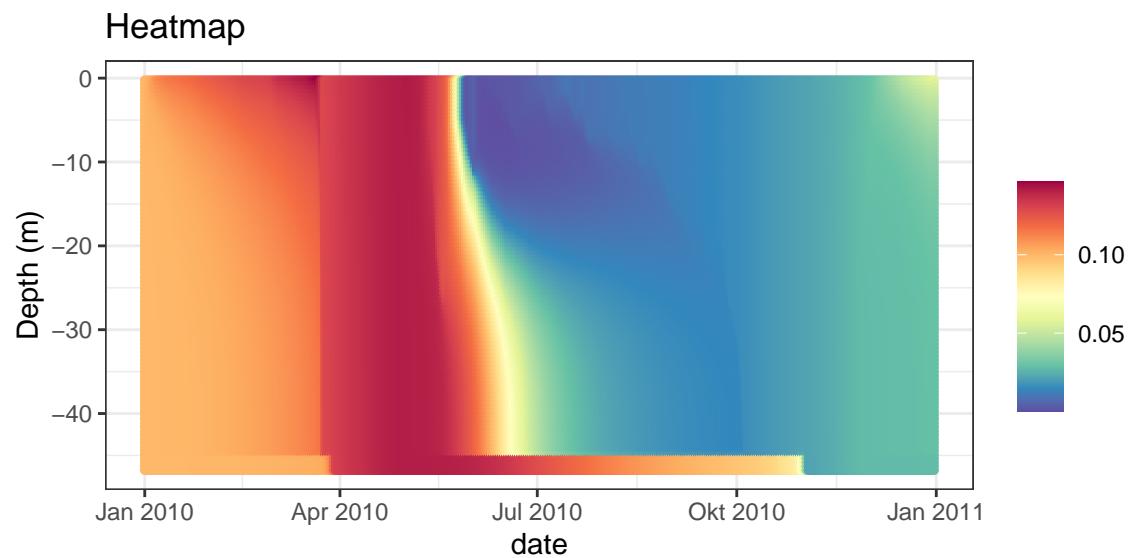
# build GOTM with the model
build_GOTM(build_dir = "build", src_dir = "gotm_src/extern/fabm/src/models/tuddhyb/rodeo/",
            fabm_file = "model_4.f90")

# run the model
system2("./gotm")

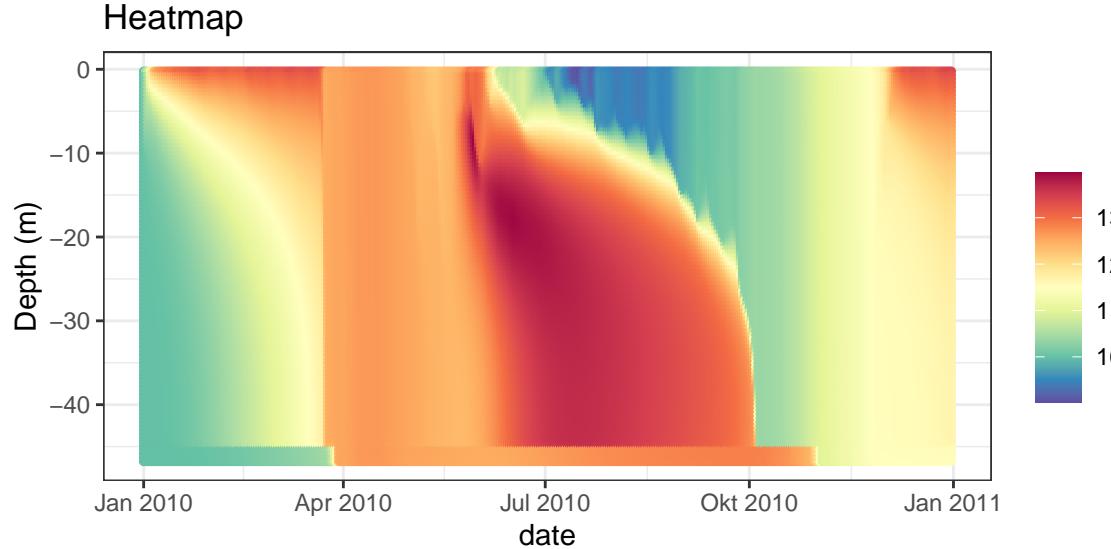
# plot the variables
plot_vari("output.nc", "rodeo_C")
```



```
plot_vari("output.nc", "rodeo_HP04")
```



```
plot_vari("output.nc", "rodeo_02")
```



3.3.2 Sediment or Surface attached state variables

death of algae generates POM which sediments faster and can become SPOM and be mineralized at the sediment faster

```
ods <- system.file("extdata/examples/simple_alg_02_POM.ods",
                   package = "rodeoFABM")
file.copy(from = ods, to = ".", recursive = TRUE)

# read in first simple model
vars <- read_ods("simple_alg_02_POM.ods", sheet = "vars")
pars <- read_ods("simple_alg_02_POM.ods", sheet = "pars")
funs <- read_ods("simple_alg_02_POM.ods", sheet = "fun")
pros <- read_ods("simple_alg_02_POM.ods", sheet = "pros")
stoi <- read_ods("simple_alg_02_POM.ods", sheet = "stoi")
```

Add two new state variables POM and SPOM, declare SPOM as bottom bound state variable:

Table 16: Data set `vars`: Declaration of state variables.

name	unit	description	default	bot
<i>C</i>	gDM/m ³	algae concentration	0.0	NA
<i>HPO4</i>	gP/m ³	phosphorus concentration	0.1	NA
<i>O2</i>	gO/m ³	oxygen concentration	10.0	NA
<i>POM</i>	gDM/m ³	particulated organic matter	0.0	NA
<i>SPOM</i>	gDM/m ²	sedimented particulated organic matter	0.0	TRUE

Add new process:

Table 17: Data set `pros`: Declaration of processes.

name	unit	description	expression
growth	gDW/m ³ /d	growth of algae	$C \cdot \mu_{max} \cdot HPO4 / (HPO4 + K_P) \cdot par / (par + K_K)$

name	unit	description	expression
death	gDW/m^3/d	death of algae	$C \cdot k_death$
sed_ALG	gDW/m^3/s	sinking of algae	v_sed_ALG
O2_exch	gO/m^3/d	exchange of Oxygen at the surface	$v_O2 \cdot (exp(7.7117 - 1.31403 \cdot log(Temp + 45.93))$
O2_cons	gO/m^3/d	consumption of Oxygen in the pelagic	$O2/(O2 + K_O2) \cdot k_O2_cons$
sed_POM	gDW/m^3/s	sinking of POM	v_sed_POM
miner_POM	gDW/m^3/s	mineralization of POM	$POM \cdot k_miner_POM \cdot O2/(O2 + K_miner_O2)$
miner_SPOM	gDW/m^3/s	mineralization of SPOM	$SPOM \cdot k_miner_SPOM \cdot O2/(O2 + K_miner_O2)$
set_POM	gDW/m^3/s	settling of POM	$v_sed_POM \cdot POM$

Change Stoicheometry:

Table 18: Data set `stoi`: Declaration of stoichiometry matrix in long format.

variable	process	expression
C	growth	1
C	death	-1
C	sed_ALG	-1
$HPO4$	growth	$-1 \cdot a_P$
$HPO4$	miner_POM	a_P
$HPO4$	miner_SPOM	a_P
$O2$	O2_exch	1
$O2$	O2_cons	-1
$O2$	growth	a_O
$O2$	miner_POM	$-1 \cdot a_miner$
$O2$	miner_SPOM	$-1 \cdot a_miner$
POM	sed_POM	-1
POM	set_POM	-1
POM	death	1
POM	miner_POM	-1
$SPOM$	set_POM	1
$SPOM$	miner_SPOM	-1

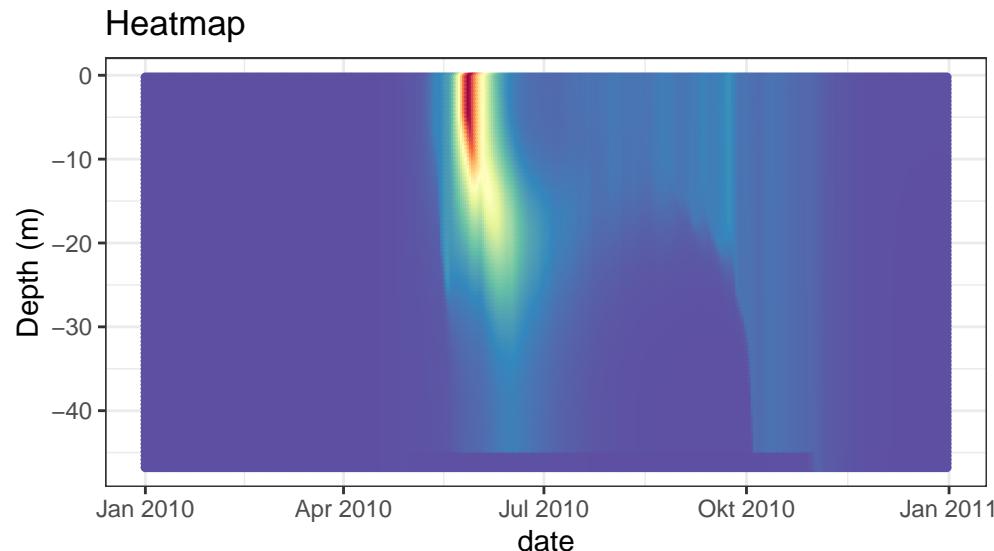
Create fortran source code, compile *GOTM-FABM*, run the model, and plot results:

```
# create the fabm code
gen_fabm_code(vars, pars, funs, pros, stoi, "model_5.f90")

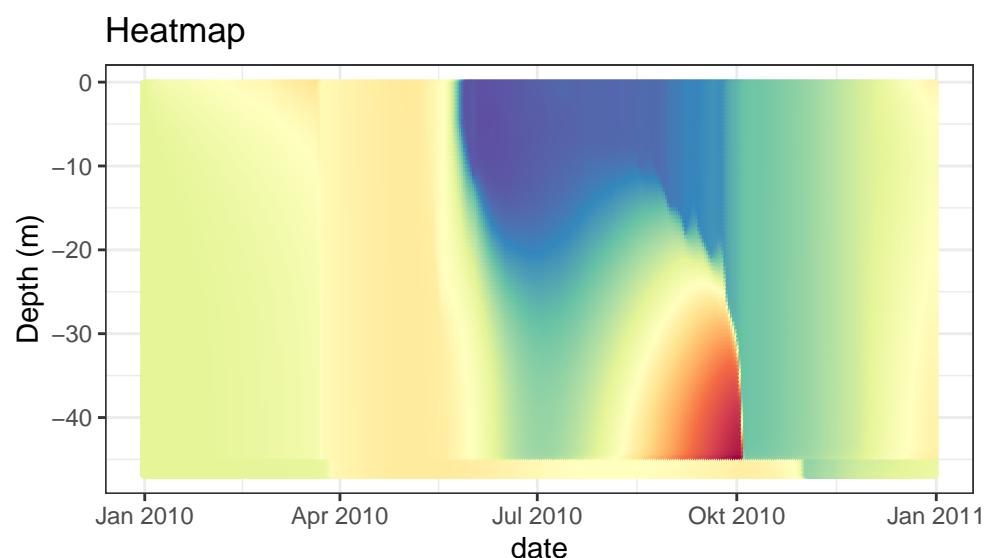
# build GOTM with the model
build_GOTM(build_dir = "build", src_dir = "gotm_src/extern/fabm/src/models/tuddhyb/rodeo/",
            fabm_file = "model_5.f90")

# run the model
system2("./gotm")

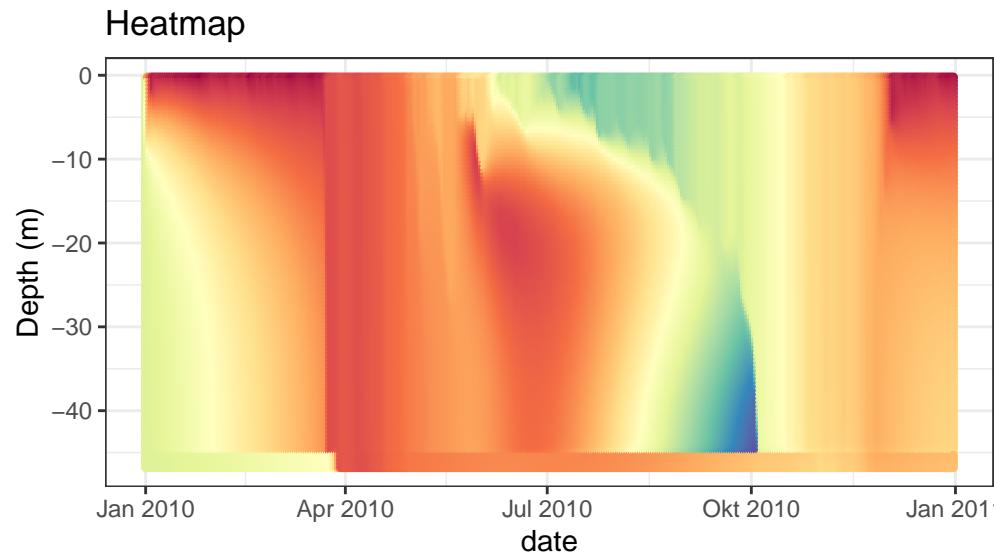
# plot the variables
plot_vari("output.nc", "rodeo_C")
```



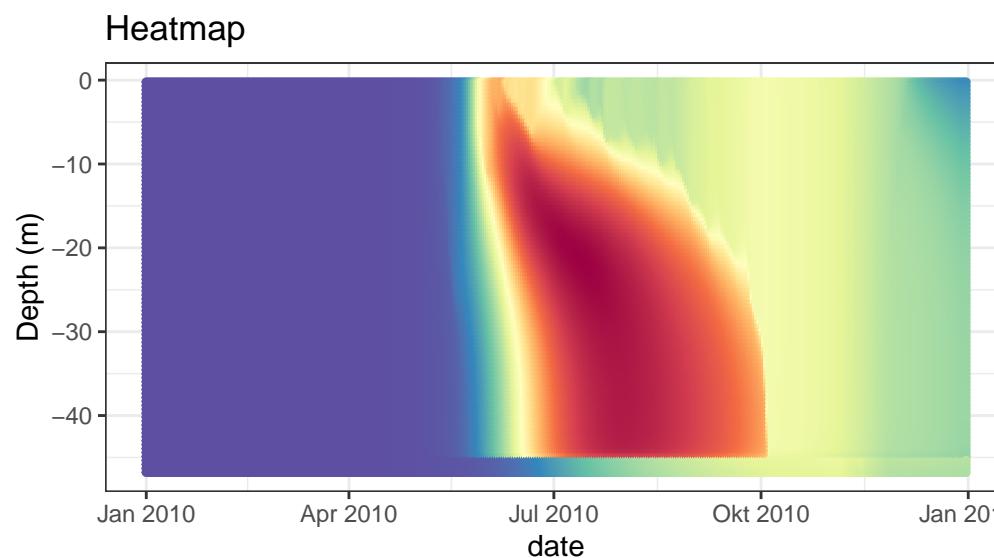
```
plot_vari("output.nc", "rodeo_HP04")
```



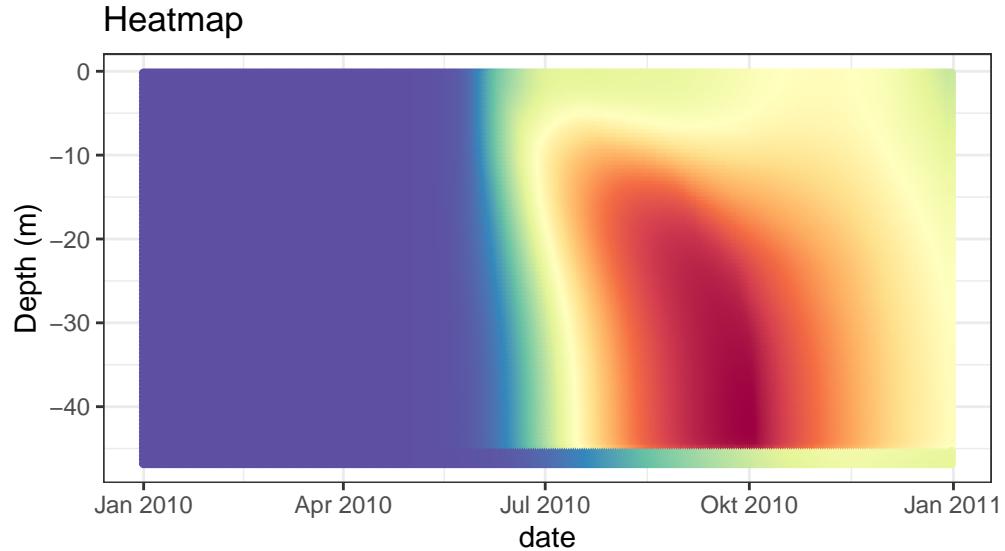
```
plot_vari("output.nc", "rodeo_02")
```



```
plot_vari("output.nc", "rodeo_POM")
```



```
plot_vari("output.nc", "rodeo_SPOM")
```



3.4 Additional features

3.4.1 Additional state variable arguments

There are a few additional arguments for state variables that can be defined in FABM. In order to use them a new column in the state variable data frame needs to be added with exactly the name.

- minimum: minimum allowed value for the state variable
- maximum: maximum allowed value for the state variable
- specific_light_extinction: specific light extinction coefficient of this variable
- no_precipitation_dilution: the variable is not diluted by precipitation
- no_river_dilution: the variable is not diluted by river inflows

3.4.2 Profile initial values for the state variables

By default the initial values for the *FABM* state variables are constant throughout the whole profile. With some tinkering we can provide profiles of initial values. Therefore, you need to have (a) text file(s) with (the) profiles that you want to initialise and install the R packages `ncdf4`, `data.table`, `gotmtools` from the AEMON-J github. The approach is to first run GOTM with 0 time steps (stop date = start date). After a run with GOTM, a `restart.nc` file is created, that can be used to restart a simulation with the same settings that ended the previous simulation. By running with 0 time steps, this file contains the “standard” initial values, including the ones in your biogeochemical model. Then you need to replace the homogeneous initial profiles by your specified profiles in the `restart.nc` file. Lastly, you need to set the `restart` option to “true”. If you run `gotm` now, it will run with the initial profiles for your biogeochemical model (note that you’ll have to rerun this approach every time before you want to run GOTM, because every new GOTM run overwrites the `restart.nc` file). Alternatively you can save the created `restart.nc` file e.g. as `restart_init_profiles.nc` and use this file to override the `restart.nc` before you run GOTM.

3.4.3 Automatic model documentation

If wanted `rodeoFABM` can automatically generate LaTeX documentation of the state variables, parameters, processes and stoichiometry. Still under development! For table generation use e.g. the package `xtable`.

References

- Bruggeman, Jorn, and Karsten Bolding. 2014. "A General Framework for Aquatic Biogeochemical Models." *Environmental Modelling & Software* 61 (November): 249–65. <https://doi.org/10.1016/j.envsoft.2014.04.002>.
- Kneis, David, Thomas Petzoldt, and Thomas U. Berendonk. 2017. "An R-Package to Boost Fitness and Life Expectancy of Environmental Models." *Environmental Modelling & Software* 96 (October): 123–27. <https://doi.org/10.1016/j.envsoft.2017.06.036>.