# Package 'RAC'

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Title R Package for Aqua Culture

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Depends R (>= 3.1.0), matrixStats, rstudioapi, plotrix

Suggests MASS, knitr, rmarkdown

Imports maps, maptools, ncdf4, rgdal, rgeos, sp, stats, utils, raster

**Description** Solves the individual bioenergetic balance for different aquaculture sea fish (Sea Bream and Sea Bass; Brigolin et al., 2014 <doi:10.3354/aei00093>) and shellfish (Mussel and Clam; Brigolin et al., 2009 <doi:10.1016/j.ecss.2009.01.029>; Solidoro et al., 2000 <doi:10.3354/meps199137>). Allows for spatialized model runs and population simulations.

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Bass\_ind\_dataloader

Function that loads forcings data for Seabass individual bioenergetic model and performs the interpolation

# Description

Function that loads forcings data for Seabass individual bioenergetic model and performs the interpolation

### Usage

```
Bass_ind_dataloader(userpath)
```

#### Arguments

userpath the path where folder containing model inputs and outputs is located

# Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

Bass\_ind\_equations Seabass bioenergetic individual model differential equations

### Description

Seabass bioenergetic individual model differential equations

# Usage

Bass\_ind\_equations(Param, Temp, G, Food, weight)

### Arguments

Param	vector containing all metabolic parameters
Temp	water temperature forcing at time t
G	food entering the cage at time t
Food	food characterization (Proteins, Lipids, Carbohydrates)
weight	individual weight at time t

# Value

model output at time t

Bass\_ind\_main

### Description

Solves the bioenergetic balance for Seabass

#### Usage

Bass\_ind\_main(userpath, forcings)

### Arguments

userpath	the path where forcing are located
forcings	a list containing the time series in the odd positions and realted forcings in the
	even positions. Forcings returned are: Water temperature [Celsius degrees] and
	feeding rate [g/individual x d]

### Value

A list containing model outputs: weight, excreted quantities and quantities to waste, actual and potential ingestion, temperature limitation functions and metabolic rates

Bass\_ind\_post Seabass bioenergetic individual model postprocessor

# Description

Seabass bioenergetic individual model postprocessor

# Usage

Bass\_ind\_post(userpath, output, times, Dates, CS)

# Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
CS	the commercial size of Seabass

# Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates Bass\_ind\_pre

### Description

Seabass bioenergetic individual model preprocessor

### Usage

```
Bass_ind_pre(userpath, forcings)
```

### Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing model forcings

# Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

Bass_ind_RKsolver	Solves the Seabass bioenergetic balance with a 4th order Runge Kutta
	method

#### Description

Solves the Seabass bioenergetic balance with a 4th order Runge Kutta method

# Usage

```
Bass_ind_RKsolver(Param, Temperature, G, Food, IC, times)
```

### Arguments

Param	vector containing all metabolic parameters
Temperature	water temperature forcing time series
G	food entering the cage time series
Food	food characterization (Proteins, Lipids, Carbohydrates)
IC	initial conditions
times	vector containing integration extremes and integration timestep

# Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates Bass\_ind\_skeleton Creates the folders structure for Seabass individual bioenergetic model

# Description

Creates the folders structure for Seabass individual bioenergetic model

#### Usage

Bass\_ind\_skeleton(userpath)

# Arguments

userpath the path where forcing are located

Bass_pop_dataloader	Function that loads forcings data for Seabass population model and
	performs the interpolation

# Description

Function that loads forcings data for Seabass population model and performs the interpolation

### Usage

```
Bass_pop_dataloader(userpath)
```

### Arguments

userpath the path where folder containing model inputs and outputs is located

#### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d] Bass\_pop\_equations Seabass bioenergetic population model differential equations

# Description

Seabass bioenergetic population model differential equations

# Usage

Bass\_pop\_equations(Param, N, Temp, G, Food, weight)

# Arguments

Param	vector containing all metabolic parameters
Ν	the number of individuals at time t
Temp	water temperature forcing at time t
G	food entering the cage at time t
Food	food characterization (Proteins, Lipids, Carbohydrates)
weight	individual weight at time t

## Value

model output at time t

Bass_pop_loop	Function that runs the Monte Carlo simulation for the Seabass popu-
	lation model

# Description

Function that runs the Monte Carlo simulation for the Seabass population model

# Usage

```
Bass_pop_loop(Param, Tint, Gint, Food, IC, times, N, userpath)
```

Param	a vector containing model parameters
Tint	the interpolated water temperature time series
Gint	the interpolated feeding rate time series
Food	the food characterization
IC	initial condition
times	integration extremes and integration timestep
Ν	time series with number of individuals
userpath	the path where the working folder is located

# Bass\_pop\_main

### Value

a list with RK solver outputs

Bass\_pop\_main Seabass bioenergetic population model

### Description

Seabass bioenergetic population model

#### Usage

Bass\_pop\_main(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

# Value

A list containing model outputs: weight, excreted quantities and quantities to waste, actual and potential ingestion, temperature limitation functions and metabolic rates

Bass_pop_post	Postprocess the Seabass population bioenergetic model results
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# Description

Postprocess the Seabass population bioenergetic model results

### Usage

```
Bass_pop_post(userpath, output, times, Dates, N, CS)
```

userpath	the path where the working folder is located
output	list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
Ν	the number of individuals time series
CS	the commercial size of Seabass

### Value

output: a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates

Bass\_pop\_pre Seabass bioenergetic population model preprocessor

# Description

Seabass bioenergetic population model preprocessor

### Usage

Bass\_pop\_pre(userpath, forcings)

# Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing model forcings

## Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

Bass_pop_RKsolver	Solves the Seabass population bioenergetic balance with a 4th order
	Runge Kutta method

# Description

Solves the Seabass population bioenergetic balance with a 4th order Runge Kutta method

# Usage

```
Bass_pop_RKsolver(Param, Temperature, G, Food, IC, times, N)
```

#### Arguments

Param	vector containing all metabolic parameters
Temperature	water temperature forcing time series
G	food entering the cage at time series
Food	food characterization (Proteins, Lipids, Carbohydrates)
IC	initial condition on weight
times	integration times
Ν	number of individuals time series

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### Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates

Bass\_pop\_skeleton Creates the folders structure for Seabass population model

### Description

Creates the folders structure for Seabass population model

### Usage

Bass\_pop\_skeleton(userpath)

#### Arguments

userpath the path where forcing are located

```
Bass_spatial_dataloader
```

Function that loads forcings data for Bass spatialized model and performs the interpolation

# Description

Function that loads forcings data for Bass spatialized model and performs the interpolation

#### Usage

Bass\_spatial\_dataloader(userpath)

#### Arguments

userpath the path where folder containing model inputs and outputs is located

#### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d] Bass\_spatial\_loop Bass bioenergetic spatialized model - spatialization loop

# Description

Solves the bioenergetic balance for Bass

# Usage

Bass\_spatial\_loop(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

### Value

a list containing the outputs that main script saves to .nc; .csv and .asc files

Bass\_spatial\_main Bass bioenergetic spatialized model - spatialization loop

# Description

Solves the bioenergetic balance for Bass

# Usage

Bass\_spatial\_main(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	list containing the time series in the odd positions and realted forcings in the even positions. Forcings imputted are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

# Value

saves .nc; .csv and .asc outputs in the 'Outputs' folder

Bass\_spatial\_post Postprocess the Mussel spatialized model results

# Description

Postprocess the Mussel spatialized model results

# Usage

Bass\_spatial\_post(userpath, output, times, Dates, CS)

# Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
CS	the commercial size of Bass

# Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates

Bass\_spatial\_pre Bass bioenergetic spatialized model preprocessor

# Description

Bass bioenergetic spatialized model preprocessor

### Usage

```
Bass_spatial_pre(userpath, forcings)
```

# Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing forcings used by the model

#### Value

a list containing the data used by the main script

Bass\_spatial\_pre\_int Bass bioenergetic spatialized model preprocessor - used inside spatialization loop

# Description

Bass bioenergetic spatialized model preprocessor - used inside spatialization loop

# Usage

```
Bass_spatial_pre_int(userpath, forcings)
```

### Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing forcings used by the model

#### Value

a list containing data used by the main script

Bass\_spatial\_RKsolver Solves the Seabass bioenergetic balance with a 4th order Runge Kutta method - used in spatialized model

# Description

Solves the Seabass bioenergetic balance with a 4th order Runge Kutta method - used in spatialized model

# Usage

```
Bass_spatial_RKsolver(Param, Temperature, G, Food, IC, times)
```

#### Arguments

Param	vector containing all metabolic parameters
Temperature	water temperature forcing time series
G	food entering the cage time series
Food	food characterization (Proteins, Lipids, Carbohydrates)
IC	initial conditions
times	vector containing integration extremes and integration timestep

### Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates Bass\_spatial\_skeleton Creates the folders structure for Bass spatialized model

# Description

Creates the folders structure for Bass spatialized model

#### Usage

```
Bass_spatial_skeleton(userpath)
```

# Arguments

userpath the path where forcing are located

Bream_ind_dataloader	Function that loads forcings data for Seabream individual bioener-
	getic model and performs the interpolation

# Description

Function that loads forcings data for Seabream individual bioenergetic model and performs the interpolation

### Usage

```
Bream_ind_dataloader(userpath)
```

# Arguments

userpath the path where folder containing model inputs and outputs is located

### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

Bream\_ind\_equations Seabream bioenergetic individual model differential equations

### Description

Seabream bioenergetic individual model differential equations

#### Usage

Bream\_ind\_equations(Param, Temp, G, Food, weight)

# Arguments

Param	vector containing all metabolic parameters
Temp	water temperature forcing at time t
G	food entering the cage at time t
Food	food characterization (Proteins, Lipids, Carbohydrates)
weight	individual weight at time t

# Value

model output at time t

Bream\_ind\_main Seabream bioenergetic individual model

# Description

Seabream bioenergetic individual model

# Usage

Bream\_ind\_main(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the
	even positions. Forcings returned are: Water temperature [Celsius degrees] and
	feeding rate [g/individual x d]

#### Value

A list containing model outputs: weight, excreted quantities and quantities to waste, actual and potential ingestion, temperature limitation functions and metabolic rates

Bream\_ind\_post

# Description

Postprocess the Seabream indivual bioenergetic model results

# Usage

Bream\_ind\_post(userpath, output, times, Dates, CS)

# Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
CS	the commercial size of Seabream

### Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates

Bream_ind_pre	Seabream bioenergetic individual model preprocessor	
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### Description

Preprocesses the data for the bioenergetic balance for Sea Bream

### Usage

Bream\_ind\_pre(userpath, forcings)

# Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing model forcings

# Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

Bream\_ind\_RKsolver

# Description

Solves the Seabream individual bioenergetic balance with a 4th order Runge Kutta method

### Usage

Bream\_ind\_RKsolver(Param, Temperature, G, Food, IC, times)

# Arguments

Param	vector containing all metabolic parameters
Temperature	water temperature forcing time series
G	food entering the cage time series
Food	food characterization (Proteins, Lipids, Carbohydrates)
IC	vector containing initial conditions on weight
times	vector containing integration extremes and timestep

### Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates

Bream\_ind\_skeleton Creates the folders structure for Seabream individual bioenergetic model

# Description

Creates the folders structure for Seabream individual bioenergetic model

#### Usage

```
Bream_ind_skeleton(userpath)
```

#### Arguments

userpath the path where forcing are located

Bream\_pop\_dataloader Function that loads forcings data for Seabream population model and performs the interpolation

# Description

Function that loads forcings data for Seabream population model and performs the interpolation

### Usage

```
Bream_pop_dataloader(userpath)
```

### Arguments

userpath the path where folder containing model inputs and outputs is located

### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

Bream\_pop\_equations Seabream bioenergetic population model differential equations

### Description

Seabream bioenergetic population model differential equations

### Usage

Bream\_pop\_equations(Param, N, Temp, G, Food, weight)

# Arguments

Param	vector containing all metabolic parameters
Ν	the number of individuals at time t
Temp	water temperature forcing at time t
G	food entering the cage at time t
Food	food characterization (Proteins, Lipids, Carbohydrates)
weight	individual weight at time t

#### Value

model output at time t

Bream\_pop\_loop

# Description

Function that runs the Monte Carlo simulation for the Seabream population model

# Usage

Bream\_pop\_loop(Param, Tint, Gint, Food, IC, times, N, userpath)

# Arguments

Param	a vector containing model parameters
Tint	the interpolated water temperature time series
Gint	the interpolated feeding rate time series
Food	the food characterization
IC	initial condition
times	integration extremes and integration timestep
Ν	time series with number of individuals
userpath	the path where the working folder is located

### Value

a list with RK solver outputs

Bream\_pop\_main Seabream bioenergetic population model

# Description

Seabream bioenergetic population model

# Usage

```
Bream_pop_main(userpath, forcings)
```

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate $[g/individual \ x \ d]$

#### Bream\_pop\_post

### Value

A list containing model outputs: weight, excreted quantities and quantities to waste, actual and potential ingestion, temperature limitation functions and metabolic rates

Bream\_pop\_post Postprocess the Bream population bioenergetic model results

### Description

Postprocess the Bream population bioenergetic model results

### Usage

```
Bream_pop_post(userpath, output, times, Dates, N, CS)
```

#### Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
Ν	the number of individuals
CS	the commercial size of Seabream

### Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates

Bream\_pop\_pre

Seabream bioenergetic population model preprocessor

### Description

Preprocesses the data for the bioenergetic balance for Sea Bream

### Usage

```
Bream_pop_pre(userpath, forcings)
```

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing model forcings

### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

Bream\_pop\_RKsolver Solves the Seabream population bioenergetic balance with a 4th order Runge Kutta method

#### Description

Solves the Seabream population bioenergetic balance with a 4th order Runge Kutta method

### Usage

Bream\_pop\_RKsolver(Param, Temperature, G, Food, IC, times, N)

### Arguments

Param	vector containing all metabolic parameters
Temperature	water temperature forcing time series
G	food entering the cage time series
Food	food characterization (Proteins, Lipids, Carbohydrates)
IC	initial condition on weight
times	integration times
Ν	number of individuals time series

# Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates

Bream\_pop\_skeleton Creates the folders structure for Seabream population model

#### Description

Creates the folders structure for Seabream population model

### Usage

```
Bream_pop_skeleton(userpath)
```

### Arguments

userpath the path where forcing are located

Bream\_spatial\_dataloader

Function that loads forcings data for Bream spatialized model and performs the interpolation

### Description

Function that loads forcings data for Bream spatialized model and performs the interpolation

### Usage

```
Bream_spatial_dataloader(userpath)
```

### Arguments

userpath the path where folder containing model inputs and outputs is located

### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

Bream\_spatial\_loop Bream bioenergetic spatialized model - spatialization loop

#### Description

Solves the bioenergetic balance for Bream

#### Usage

Bream\_spatial\_loop(userpath, forcings)

### Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees] and feeding rate [g/individual x d]

# Value

A list containing model outputs: weight, excreted quantities and quantities to waste, actual and potential ingestion, temperature limitation functions and metabolic rates

Bream\_spatial\_main Bream bioenergetic spatialized model - spatialization loop

# Description

Solves the bioenergetic balance for Bream

# Usage

Bream\_spatial\_main(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	list containing the time series in the odd positions and realted forcings in the
	even positions. Forcings imputted are: Water temperature [Celsius degrees] and
	feeding rate [g/individual x d]

# Value

saves .nc; .csv and .asc outputs in the 'Outputs' folder

Bream\_spatial\_post Postprocess the Bream spatialized model results

# Description

Postprocess the Bream spatialized model results

# Usage

Bream\_spatial\_post(userpath, output, times, Dates, CS)

# Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
CS	the commercial size of Bream

#### Value

a list containing the model outputs saved by the main script to .nc; .csv and .asc files

Bream\_spatial\_pre Bream bioenergetic spatialized model preprocessor

# Description

Bream bioenergetic spatialized model preprocessor

# Usage

```
Bream_spatial_pre(userpath, forcings)
```

# Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing forcings used by the model

#### Value

a list containing the data used in the main script

Bream\_spatial\_pre\_int Bream bioenergetic spatialized model preprocessor - used inside spatialization loop

# Description

Bream bioenergetic spatialized model preprocessor - used inside spatialization loop

### Usage

```
Bream_spatial_pre_int(userpath, forcings)
```

### Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing forcings used by the model

# Value

a list containing the data used by the main script

Bream\_spatial\_RKsolver

Solves the Seabream bioenergetic balance with a 4th order Runge Kutta method - used in spatialized model

### Description

Solves the Seabream bioenergetic balance with a 4th order Runge Kutta method - used in spatialized model

# Usage

```
Bream_spatial_RKsolver(Param, Temperature, G, Food, IC, times)
```

#### Arguments

Param	vector containing all metabolic parameters
Temperature	water temperature forcing time series
G	food entering the cage time series
Food	food characterization (Proteins, Lipids, Carbohydrates)
IC	initial conditions
times	vector containing integration extremes and integration timestep

#### Value

a list containing the fish weight, proteines, lipids and carbohydrates wasted or produced with excretions, potential and actual ingestion rates, temperature limitation functions and metabolic rates

Bream\_spatial\_skeleton

Creates the folders structure for Bream spatialized model

# Description

Creates the folders structure for Bream spatialized model

### Usage

```
Bream_spatial_skeleton(userpath)
```

### Arguments

userpath the path where forcing are located

ClamF\_ind\_dataloader Function that loads forcings data for Clam individual bioenergetic model (alternative version) and performs the interpolation

# Description

Function that loads forcings data for Clam individual bioenergetic model (alternative version) and performs the interpolation

### Usage

ClamF\_ind\_dataloader(userpath)

### Arguments

userpath the path where folder containing model inputs and outputs is located

### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3]

ClamF_ind_equations	Clam bioenergetic individual model differential equations (alternative
	version)

### Description

Clam bioenergetic individual model differential equations (alternative version)

# Usage

```
ClamF_ind_equations(Param, Tint, Chlint, Ww)
```

# Arguments

Param	a vector containing model parameters
Tint	the interpolated water temperature at time t
Chlint	the interpolated chlorophyll at time t
Ww	clam wet weight at time t

#### Value

a list containing the clam weights, temperature limitation functions and metabolic rates at time t

ClamF\_ind\_main

# Description

Clam bioenergetic individual model (alternative version)

#### Usage

ClamF\_ind\_main(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3]

# Value

A list containing model outputs: weights, temperature limitation functions and metabolic rates

ClamF_ind_post	Postprocess the Clam indivual bioenergetic model (alternative ver-
	sion) results

# Description

Postprocess the Clam indivual bioenergetic model (alternative version) results

# Usage

ClamF\_ind\_post(userpath, output, times, Dates, CS)

### Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
CS	the commercial size of Clam

# Value

a list containing the clam weights, temperature limitation functions and metabolic rates

ClamF\_ind\_pre Clam bioenergetic individual model preprocessor (alternativer version)

# Description

Clam bioenergetic individual model preprocessor (alternativer version)

### Usage

```
ClamF_ind_pre(userpath, forcings)
```

### Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing model forcings

# Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3]

ClamF_ind_RKsolver	Solves the Clam bioenergetic balance (alternative version) with a 4th
	order Runge Kutta method

# Description

Solves the Clam bioenergetic balance (alternative version) with a 4th order Runge Kutta method

### Usage

ClamF\_ind\_RKsolver(Param, times, IC, Tint, Chlint)

### Arguments

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition
Tint	the interpolated water temperature time series
Chlint	the interpolated chlorophyll a time series

### Value

a list containing the clam weights, temperature limitation functions and metabolic rates

ClamF\_ind\_skeleton Creates the folder (alternative versic

# Description

Creates the folders structure for Clam individual bioenergetic model (alternative version)

### Usage

ClamF\_ind\_skeleton(userpath)

# Arguments

userpath the path where forcing are located

ClamF_pop_dataloader	Function that loads forcings data for Clam population model (alter-
	native version) and performs the interpolation

# Description

Function that loads forcings data for Clam population model (alternative version) and performs the interpolation

### Usage

ClamF\_pop\_dataloader(userpath)

### Arguments

userpath the path where folder containing model inputs and outputs is located

### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3]

ClamF\_pop\_equations Clam bioenergetic population model differential equations (alternative version)

# Description

Clam bioenergetic population model differential equations (alternative version)

# Usage

```
ClamF_pop_equations(Param, Tint, Chlint, Ww)
```

# Arguments

Param	a vector containing model parameters
Tint	the interpolated water temperature at time t
Chlint	the interpolated chlorophyll at time t
Ww	clam wet weight at time t

## Value

a list containing the clam weights, temperature limitation functions and metabolic rates at time t

ClamF_pop_loop	Function that runs the Monte Carlo simulation for the Clam popula-
	tion model (alternative version)

# Description

Function that runs the Monte Carlo simulation for the Clam population model (alternative version)

### Usage

```
ClamF_pop_loop(Param, times, IC, Tint, Chlint, N, userpath)
```

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition
Tint	the interpolated water temperature time series
Chlint	the interpolated chlorophyll a time series
Ν	time series with number of individuals
userpath	the path where the working folder is located

### Value

a list with RK solver outputs

ClamF\_pop\_main Clam bioenergetic population model (alternative version)

### Description

Clam bioenergetic population model (alternative version)

# Usage

ClamF\_pop\_main(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3]

### Value

A list containing model outputs: weights, temperature limitation functions and metabolic rates

ClamF_pop_post	Postprocess the Clam population bioenergetic model results (alterna-
	tive model)

# Description

Postprocess the Clam population bioenergetic model results (alternative model)

#### Usage

```
ClamF_pop_post(userpath, output, times, Dates, N, CS)
```

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
Ν	the number of individuals
CS	the commercial size of Clam

# ClamF\_pop\_pre

### Value

a list containing the clam weights, temperature limitation functions and metabolic rates

ClamF_pop_pre	Clam bioenergetic population model (alternative version) preproces-
	sor

# Description

Clam bioenergetic population model (alternative version) preprocessor

# Usage

ClamF\_pop\_pre(userpath, forcings)

# Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing model forcings

## Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3]

ClamF_pop_RKsolver	Solves the Clam bioenergetic balance (alternative version) with a 4th
	order Runge Kutta method

### Description

Solves the Clam bioenergetic balance (alternative version) with a 4th order Runge Kutta method

### Usage

```
ClamF_pop_RKsolver(Param, times, IC, Tint, Chlint)
```

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition on weight
Tint	the interpolated water temperature time series
Chlint	the interpolated chlorophyll a time series

### Value

a list containing the clam weights, temperature limitation functions and metabolic rates

ClamF\_pop\_skeleton Creates the folders structure for Clam population model (alternative version)

# Description

Creates the folders structure for Clam population model (alternative version)

#### Usage

ClamF\_pop\_skeleton(userpath)

### Arguments

userpath the path where forcing are located

Clam\_ind\_dataloader Function that loads forcings data for Clam individual bioenergetic model and performs the interpolation

#### Description

Function that loads forcings data for Clam individual bioenergetic model and performs the interpolation

### Usage

```
Clam_ind_dataloader(userpath)
```

### Arguments

userpath the path where folder containing model inputs and outputs is located

#### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l], particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Clam\_ind\_equations Clam bioenergetic individual model differential equations

### Description

Clam bioenergetic individual model differential equations

### Usage

Clam\_ind\_equations(Param, Tint, Phy, DT, POCint, POMint, TSSint, Wd)

### Arguments

Param	a vector containing model parameters
Tint	the interpolated water temperature at time t
Phy	the interpolated phytoplankton at time t
DT	the interpolated detritus at time t
POCint	the interpolated POC at time t
POMint	the interpolated POM at time t
TSSint	the interpolated TSS at time t
Wd	the weight of the clam at time t

# Value

a list containing the clam weights, temperature limitation functions and metabolic rates at time t

Clam\_ind\_main Clam bioenergetic individual model

# Description

Clam bioenergetic individual model

# Usage

```
Clam_ind_main(userpath, forcings)
```

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees],
	Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l], particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

A list containing model outputs: weights, temperature limitation functions and metabolic rates

Clam\_ind\_post Postprocess the Clam individual bioenergetic model results

# Description

Postprocess the Clam individual bioenergetic model results

### Usage

Clam\_ind\_post(userpath, output, times, Dates, CS)

### Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
CS	the commercial size of Clam

# Value

a list containing the clam weights, temperature limitation functions and metabolic rates

Clam\_ind\_pre

Clam bioenergetic individual model preprocessor

# Description

Clam bioenergetic individual model preprocessor

# Usage

Clam\_ind\_pre(userpath, forcings)

### Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing model forcings

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a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l], particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

clam\_ind\_RKsolver Solves the Clam individual bioenergetic balance with a 4th order Runge Kutta method

# Description

Solves the Clam individual bioenergetic balance with a 4th order Runge Kutta method

# Usage

clam\_ind\_RKsolver(Param, times, IC, Tint, Phyint, DTint, POCint, POMint, TSSint)

# Arguments

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition
Tint	the interpolated water temperature time series
Phyint	the interpolated phytoplankton time series
DTint	the interpolated detritus time series
POCint	the interpolated POC time series
POMint	the interpolated POM time series
TSSint	the interpolated TSS time series

#### Value

a list containing the clam weights, temperature limitation functions and metabolic rates

Clam\_ind\_skeleton Creates the folders structure for Clam individual bioenergetic model

# Description

Creates the folders structure for Clam individual bioenergetic model

## Usage

```
Clam_ind_skeleton(userpath)
```

# Arguments

userpath the path where forcing are located

Clam_pop_dataloader	Function that loads forcings data for Clam population model and per-
	forms the interpolation

# Description

Function that loads forcings data for Clam population model and performs the interpolation

#### Usage

```
Clam_pop_dataloader(userpath)
```

# Arguments

userpath the path where folder containing model inputs and outputs is located

#### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l], particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Clam\_pop\_equations Clam bioenergetic population model differential equations

# Description

Clam bioenergetic population model differential equations

# Usage

Clam\_pop\_equations(Param, Tint, Phy, DT, POCint, POMint, TSSint, Wd)

# Arguments

Param	a vector containing model parameters
Tint	the interpolated water temperature at time t
Phy	the interpolated phytoplankton at time t
DT	the interpolated detritus at time t
POCint	the interpolated POC at time t
POMint	the interpolated POM at time t
TSSint	the interpolated TSS at time t
Wd	the weight of the clam at time t

## Value

a list containing the clam weights, temperature limitation functions and metabolic rates at time t

Clam_pop_loop	Function that runs the Monte Carlo simulation for the Clam popula-
	tion model

# Description

Function that runs the Monte Carlo simulation for the Clam population model

# Usage

Clam\_pop\_loop(Param, times, IC, Tint, Phyint, DTint, POCint, POMint, TSSint, N, userpath)

# Arguments

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition
Tint	the interpolated water temperature time series
Phyint	the interpolated phytoplankton time series
DTint	the interpolated detritus time series
POCint	the interpolated POC time series
POMint	the interpolated POM time series
TSSint	the interpolated TSS time series
Ν	time series with number of individuals
userpath	the path where the working folder is located

# Value

a list with RK solver outputs

Clam\_pop\_main Clam bioenergetic population model

# Description

Clam bioenergetic population model

# Usage

Clam\_pop\_main(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l], particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

# Value

A list containing model outputs: weights, temperature limitation functions and metabolic rates

Clam\_pop\_post

## Description

Postprocess the Clam population bioenergetic model results

# Usage

Clam\_pop\_post(userpath, output, times, Dates, N, CS)

#### Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
Ν	the number of individuals
CS	the commercial size of Clam

#### Value

a list containing the clam weights, temperature limitation functions and metabolic rates

Clam_pop_pre	Clam bioenergetic population model preprocessor
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# Description

Clam bioenergetic population model preprocessor

# Usage

Clam\_pop\_pre(userpath, forcings)

# Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing model forcings

# Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l], particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Clam\_pop\_RKsolver

# Description

Solves the Clam bioenergetic balance for population with a 4th order Runge Kutta method

# Usage

Clam\_pop\_RKsolver(Param, times, IC, Tint, Phyint, DTint, POCint, POMint, TSSint)

## Arguments

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition
Tint	the interpolated water temperature time series
Phyint	the interpolated phytoplankton time series
DTint	the interpolated detritus time series
POCint	the interpolated POC time series
POMint	the interpolated POM time series
TSSint	the interpolated TSS time series

## Value

a list containing the clam weights, temperature limitation functions and metabolic rates

Clam\_pop\_skeleton Creates the folders structure for Clam population model

# Description

Creates the folders structure for Clam population model

# Usage

Clam\_pop\_skeleton(userpath)

## Arguments

userpath the path where forcing are located

Mussel\_ind\_dataloader Function that loads forcings data for Mussel individual bioenergetic model and performs the interpolation

## Description

Function that loads forcings data for Mussel individual bioenergetic model and performs the interpolation

## Usage

Mussel\_ind\_dataloader(userpath)

## Arguments

userpath the path where folder containing model inputs and outputs is located

## Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Mussel\_ind\_equations Mussel bioenergetic individual model differential equations

## Description

Mussel bioenergetic individual model differential equations

## Usage

```
Mussel_ind_equations(Param, Tint, Phyint, DTint, POCint, Ccont, Ncont, Pcont,
POMint, TSSint, Wb, R, t, trip)
```

Param	a vector containing model parameters
Tint	the interpolated water temperature at time t
Phyint	the interpolated phytoplankton at time t
DTint	the interpolated detritus at time t
POCint	the interpolated POC at time t

Ccont	the C/C content of the POC at time t
Ncont	the N/C content of POC at time t
Pcont	the P/C content of POC at time t
POMint	the interpolated POM at time t
TSSint	the interpolated TSS at time t
Wb	the somatic tissue dry weight at time t
R	the gondadic tissue dry weight at time t
t	the time
trip	vector containing the flags with resting periods

the outputs at time t

Mussel_ind_main	Mussel bioenergetic individual model	
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# Description

Solves the bioenergetic balance for Mussel

# Usage

Mussel\_ind\_main(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

# Value

A list containing model outputs: weight, length mussel CNP, pseudofaeces CNP production, faeces CNP production, temperature limitation functions, metabolic rates and oxygen consumption

Mussel\_ind\_post Postprocess the Mussel indivual bioenergetic model results

#### Description

Postprocess the Mussel indivual bioenergetic model results

#### Usage

Mussel\_ind\_post(userpath, output, times, Dates, CS)

#### Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
CS	the commercial size of Mussel

## Value

a list containing the weights of the mussel, the excreted CNP, the mussel CNP, temperature limitation functions, metabolic rates, oxygen consumption

Mussel\_ind\_pre Mussel bioenergetic individual model preprocessor

# Description

Mussel bioenergetic individual model preprocessor

## Usage

Mussel\_ind\_pre(userpath, forcings)

## Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing model forcings

#### Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Mussel\_ind\_RKsolver Solves the Mussel individual bioenergetic balance with a 4th order Runge Kutta method

# Description

Solves the Mussel individual bioenergetic balance with a 4th order Runge Kutta method

# Usage

```
Mussel_ind_RKsolver(Param, times, IC, Tint, Phyint, DTint, POCint, Ccont, Ncont,
Pcont, POMint, TSSint)
```

# Arguments

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition
Tint	the interpolated water temperature time series
Phyint	the interpolated phytoplankton time series
DTint	the interpolated detritus time series
POCint	the interpolated POC time series
Ccont	the C/C content of the POC
Ncont	the N/C content of POC
Pcont	the P/C content of POC
POMint	the interpolated POM time series
TSSint	the interpolated TSS time series

## Value

a list containing the weights of the mussel, the excreted CNP, the mussel CNP, temperature limitation functions, metabolic rates, oxygen consumption Mussel\_ind\_skeleton Creates the folders structure for Mussel individual bioenergetic model

# Description

Creates the folders structure for Mussel individual bioenergetic model

#### Usage

```
Mussel_ind_skeleton(userpath)
```

## Arguments

userpath the path where forcing are located

Mussel\_pop\_dataloader Function that loads forcings data for Mussel population model and performs the interpolation

#### Description

Function that loads forcings data for Mussel population model and performs the interpolation

## Usage

Mussel\_pop\_dataloader(userpath)

#### Arguments

userpath the path where folder containing model inputs and outputs is located

## Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Mussel\_pop\_equations Mussel bioenergetic population model differential equations

# Description

Mussel bioenergetic population model differential equations

# Usage

```
Mussel_pop_equations(Param, N, Tint, Phyint, DTint, POCint, Ccont, Ncont, Pcont,
POMint, TSSint, Wb, R, t, trip)
```

# Arguments

Param	a vector containing model parameters
Ν	the number of individuals at time t
Tint	the interpolated water temperature at time t
Phyint	the interpolated phytoplankton at time t
DTint	the interpolated detritus at time t
POCint	the interpolated POC at time t
Ccont	the C/C content of the POC at time t
Ncont	the N/C content of POC at time t
Pcont	the P/C content of POC at time t
POMint	the interpolated POM at time t
TSSint	the interpolated TSS at time t
Wb	the somatic tissue dry weight at time t
R	the gondadic tissue dry weight at time t
t	the time
trip	vector containing the flags with resting periods

# Value

the outputs at time t

Mussel\_pop\_loop

# Description

Function that runs the Monte Carlo simulation for the Mussel population model

# Usage

```
Mussel_pop_loop(Param, times, IC, Tint, Phyint, DTint, POCint, Ccont, Ncont,
    Pcont, POMint, TSSint, N, userpath)
```

# Arguments

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition
Tint	the interpolated water temperature time series
Phyint	the interpolated phytoplankton time series
DTint	the interpolated detritus time series
POCint	the interpolated POC time series
Ccont	the C/C content of the POC
Ncont	the N/C content of POC
Pcont	the P/C content of POC
POMint	the interpolated POM time series
TSSint	the interpolated TSS time series
Ν	time series with number of individuals
userpath	the path where the working folder is located

#### Value

a list with RK solver outputs

Mussel\_pop\_main

## Description

Solves the bioenergetic balance for Mussel and simulates a population

# Usage

Mussel\_pop\_main(userpath, forcings)

# Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

# Value

A list containing model outputs: weight, length mussel CNP, pseudofecies CNP production, temperature limitation functions, metabolic rates and oxygen consumption

Mussel_pop_post	Postprocess the Musse	el population bioenergetic model results
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# Description

Postprocess the Mussel population bioenergetic model results

# Usage

```
Mussel_pop_post(userpath, output, times, Dates, N, CS)
```

userpath	the path where the working folder is located
output	output list containing the output of the RK solver
times	the vector containing informations on integration extremes
Dates	the vector containing the date
Ν	the number of individuals
CS	the commercial size of Seabass

## Mussel\_pop\_pre

#### Value

a list containing the weights of the mussel, the excreted CNP, the mussel CNP, temperature limitation functions, metabolic rates, oxygen consumption

Mussel\_pop\_pre Mussel bioenergetic population model preprocessor

## Description

Mussel bioenergetic population model preprocessor

## Usage

Mussel\_pop\_pre(userpath, forcings)

#### Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing forcings used by the model

## Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Mussel_pop_RKsolver	Solves the Mussel population bioenergetic balance with a 4th order
	Runge Kutta method

# Description

Solves the Mussel population bioenergetic balance with a 4th order Runge Kutta method

## Usage

Mussel\_pop\_RKsolver(Param, times, IC, Tint, Phyint, DTint, POCint, Ccont, Ncont, Pcont, POMint, TSSint, N)

# Arguments

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition
Tint	the interpolated water temperature time series
Phyint	the interpolated phytoplankton time series
DTint	the interpolated detritus time series
POCint	the interpolated POC time series
Ccont	the C/C content of the POC
Ncont	the N/C content of POC
Pcont	the P/C content of POC
POMint	the interpolated POM time series
TSSint	the interpolated TSS time series
Ν	the number of indivduals time series

## Value

a list containing the weights of the mussel, the excreted CNP, the mussel CNP, temperature limitation functions, metabolic rates, oxygen consumption

Mussel\_pop\_skeleton Creates the folders structure for Mussel population model

# Description

Creates the folders structure for Mussel population model

# Usage

```
Mussel_pop_skeleton(userpath)
```

# Arguments

userpath the path where forcing are located

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Mussel\_spatial\_dataloader

Function that loads forcings data for Mussel spatialized model and performs the interpolation

# Description

Function that loads forcings data for Mussel spatialized model and performs the interpolation

## Usage

Mussel\_spatial\_dataloader(userpath)

## Arguments

userpath the path where folder containing model inputs and outputs is located

## Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Mussel\_spatial\_loop Mussel bioenergetic spatialized model - spatialization loop

# Description

Solves the bioenergetic balance for Mussel

## Usage

```
Mussel_spatial_loop(userpath, forcings)
```

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

A list containing model outputs that main script saves to .nc; .csv and .asc files

Mussel\_spatial\_main Mussel bioenergetic spatialized model - spatialization loop

# Description

Solves the bioenergetic balance for Mussel

# Usage

```
Mussel_spatial_main(userpath, forcings)
```

# Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

#### Value

saves .nc; .csv and .asc outputs in the 'Outputs' folder

Mussel\_spatial\_post Postprocess the Mussel spatialized model results

## Description

Postprocess the Mussel spatialized model results

# Usage

```
Mussel_spatial_post(userpath, output, times, Dates, CS)
```

the path where the working folder is located
output list containing the output of the RK solver
the vector containing informations on integration extremes
the vector containing the date
the commercial size of Mussel

a list containing the weights of the mussel, the excreted CNP, the mussel CNP, temperature limitation functions, metabolic rates, oxygen consumption

Mussel\_spatial\_pre Mussel bioenergetic spatialized model preprocessor

# Description

Mussel bioenergetic spatialized model preprocessor

## Usage

Mussel\_spatial\_pre(userpath, forcings)

# Arguments

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing forcings used by the model

## Value

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Mussel\_spatial\_pre\_int

Mussel bioenergetic spatialized model preprocessor - used inside spatialization loop

# Description

Mussel bioenergetic spatialized model preprocessor - used inside spatialization loop

## Usage

Mussel\_spatial\_pre\_int(userpath, forcings)

userpath	the path where folder containing model inputs and outputs is located
forcings	a list containing forcings used by the model

a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l] and its characterization in terms of C/P and N/P molar ratios, particulated organic matter (POM) concentration [mgC/l], total suspended solids (TSS) concentration [mg/l]

Mussel\_spatial\_RKsolver

Solves the Mussel individual bioenergetic balance with a 4th order Runge Kutta method for spatialized model

# Description

Solves the Mussel individual bioenergetic balance with a 4th order Runge Kutta method for spatialized model

# Usage

```
Mussel_spatial_RKsolver(Param, times, IC, Tint, Phyint, DTint, POCint, Ccont,
Ncont, Pcont, POMint, TSSint)
```

## Arguments

Param	a vector containing model parameters
times	integration extremes and integration timestep
IC	initial condition
Tint	the interpolated water temperature time series
Phyint	the interpolated phytoplankton time series
DTint	the interpolated detritus time series
POCint	the interpolated POC time series
Ccont	the C/C content of the POC
Ncont	the N/C content of POC
Pcont	the P/C content of POC
POMint	the interpolated POM time series
TSSint	the interpolated TSS time series

## Value

a list containing the weights of the mussel, the excreted CNP, the mussel CNP, temperature limitation functions, metabolic rates, oxygen consumption

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Mussel\_spatial\_skeleton

Creates the folders structure for Mussel spatialized model

# Description

Creates the folders structure for Mussel spatialized model

# Usage

Mussel\_spatial\_skeleton(userpath)

# Arguments

userpath the path where forcing are located

Pop_fun	Function that solves the population dynamics equations including dis-
	continuities

# Description

Function that solves the population dynamics equations including discontinuities

## Usage

Pop\_fun(Nseed, mort, manag, times)

# Arguments

Nseed	number of seeded individuals
mort	mortality rate
manag	list of management actions (seeded/harvested individuals)
times	vector containing informations on integration times

## Value

a time series with the number of individuals

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