# Package 'RAC'

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4 Bass\_ind\_equations

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

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 5

#### **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
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## **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\_RKsolver

Bass	ind	nra

Seabass bioenergetic individual model preprocessor

#### **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 7

Bass_ind_skeleton	Creates t	he 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]

8 Bass\_pop\_loop

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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

N 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)
```

#### Arguments

Param	a vector containing	model parameters
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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

N time series with number of individuals

userpath the path where the working folder is located

Bass\_pop\_main 9

#### 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

## **Description**

Postprocess the Seabass population bioenergetic model results

## Usage

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

## **Arguments**

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

N the number of individuals time series
CS the commercial size of Seabass

10 Bass\_pop\_RKsolver

#### 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

N number of individuals time series

Bass\_pop\_skeleton 11

## 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]

12 Bass\_spatial\_main

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], 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 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 13

## **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 15

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 bioenergetic 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\_main

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 17

Bream_ind_post Postprocess the Seabream indivual bioenergetic model results
---

## 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

# 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]

18 Bream\_ind\_skeleton

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

## **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

## 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

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

N 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

20 Bream\_pop\_main

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

## 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)
```

the path where the working folder is located

## **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
N	time series with number of individuals

#### Value

userpath

a list with RK solver outputs

Bream_pop_main	Seabream bioenergetic population model	
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## Description

Seabream bioenergetic population model

# Usage

```
Bream_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]

Bream\_pop\_post 21

#### 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 N 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)
```

## **Arguments**

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

forcings a list containing model forcings

22 Bream\_pop\_skeleton

#### 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

N 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], 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, excreted quantities and quantities to waste, actual and potential ingestion, temperature limitation functions and metabolic rates

24 Bream\_spatial\_post

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

## **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 25

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

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]

 ${\tt ClamF\_ind\_equations} \qquad {\tt Clam\ bioenergetic\ individual\ model\ differential\ equations\ (alternative\ version)}$ 

## **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

28 ClamF\_ind\_post

ClamF_ind_main Clam bioenergetic individual model (alternative version)	
---	--

#### **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 29

ClamF_ind_pre	Clam bioenergetic individual model preprocessor (alternativer version)
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## 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 folders structure for Clam individual bioenergetic model (alternative version)

## **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 (alternative 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 31

ClamF_pop_equations	Clam bioenergetic population model differential equations (alterna-
	tive 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

	t runs the Monte Carlo simulation for the Clam popula- lternative 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)
```

## 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
N	time series with number of individuals
userpath	the path where the working folder is located

32 ClamF\_pop\_post

#### 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 (alternative model)

# Description

Postprocess the Clam population bioenergetic model results (alternative model)

## Usage

```
ClamF_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

N the number of individuals

CS the commercial size of Clam

ClamF\_pop\_pre 33

## Value

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

ClamF\_pop\_pre Clam bioenergetic population model (alternative version) preprocessor

## **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)
```

#### **Arguments**

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

the interpolated chlorophyll a time series

34 Clam\_ind\_dataloader

#### 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 35

~ 7		
Clam	ınd	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	
CTaill_	_IIIU_	_IIIIa I I I	

Clam bioenergetic individual model

# Description

Clam bioenergetic individual model

#### Usage

```
Clam_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], particulated organic matter (POM) concentration [mgC/l],

total suspended solids (TSS) concentration [mg/l]

36 Clam\_ind\_pre

#### Value

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

clam\_ind\_RKsolver 37

# 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 [mgChla/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 performs 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 39

Clam	non	equations
CTalli	טטט	_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,
```

40 Clam\_pop\_main

```
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

N 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 41

Clam_pop_post	Postprocess the Clam population bioenergetic model results

# **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

N 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

# 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]

42 Clam\_pop\_RKsolver

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

# 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 43

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]

# 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
)
```

# Arguments

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

Mussel\_ind\_main 45

### Value

the outputs at time t

Mussel\_ind\_main Mussel bioenergetic individual model

# **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

### 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

Mussel\_ind\_skeleton 47

# 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
N	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

50 Mussel\_pop\_loop

Mussel\_pop\_loop Function that runs the Monte Carlo simulation for the Mussel population model

# 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,
  Ν,
  userpath
)
```

# Arguments

Param

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
N	time series with number of individuals
userpath	the path where the working folder is located

a vector containing model parameters

Mussel\_pop\_main 51

### Value

a list with RK solver outputs

Mussel\_pop\_main

Mussel bioenergetic population model

### **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 Mussel population bioenergetic model results

# Description

Postprocess the Mussel population bioenergetic model results

# Usage

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

52 Mussel\_pop\_pre

### **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

N the number of individuals

CS the commercial size of Seabass

### 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
N	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

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 55

Mussel\_spatial\_loop

Mussel bioenergetic spatialized model - spatialization loop

### **Description**

Solves the bioenergetic balance for Mussel

### Usage

Mussel\_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], 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 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]

56 Mussel\_spatial\_pre

### 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)
```

### **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\_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)
```

# **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\_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

the interpolated TSS time series

### Value

**TSSint** 

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

```
Mussel_spatial_skeleton
```

Creates the folders structure for Mussel spatialized model

# Description

Creates the folders structure for Mussel spatialized model

Pop\_fun 59

# 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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