Package 'RAC'

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Title R Package for Aqua Culture

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Encoding UTF-8

Suggests MASS, knitr, rmarkdown

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 *Seabass bioenergetic individual model*

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   *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`	*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
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 population 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
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

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

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

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],
                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 ra-
                tios, 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   *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 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_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   *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]

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

---

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
`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

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)
```

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
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)
```

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_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

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

---

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	*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 version) 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 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 (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 population 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)
```

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

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

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

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)
```

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_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

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_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   *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 population 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
`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   *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]

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   *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
)
```

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

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

---

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
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

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,
  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
N	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   *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 ra-
                tios, 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, tem-
perature 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)
```

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   *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]

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
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_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 discontinuities*

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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