Package ‘RAC’

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Title R Package for Aqua Culture

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Imports matrixStats, rstudioapi, plotrix, raster, sp

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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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Contents

`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 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` *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 (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` *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 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)
```

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

Index