Package 'RAC'

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Title R Package for Aqua Culture

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Imports matrixStats, rstudioapi, plotrix, raster, sp

Encoding UTF-8

Suggests MASS, knitr, rmarkdown

Description Solves the individual bioenergetic balance for different aquacul-

ture sea fish (Sea Bream and Sea Bass; Brigolin et al., 2014 <doi:10.3354/aei00093>) and shell-fish (Mussel and Clam; Brigolin et al., 2009 <doi:10.1016/j.ecss.2009.01.029>; Solidoro et al., 2000 <doi:10.3354/meps199137>). Allows for spatialized model runs and population simulations.

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Bass_ind_dataloader

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

Description

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

Usage

```
Bass_ind_dataloader(userpath)
```

Arguments

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

Value

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

Bass_ind_equations Seabass bioenergetic individual model differential equations

Description

Seabass bioenergetic individual model differential equations

Usage

Bass_ind_equations(Param, Temp, G, Food, weight)

Arguments

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

Value

model output at time t

Bass_ind_main

Description

Solves the bioenergetic balance for Seabass

Usage

Bass_ind_main(userpath, forcings)

Arguments

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

Value

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

Bass_ind_post Seabass bioenergetic individual model postprocessor

Description

Seabass bioenergetic individual model postprocessor

Usage

Bass_ind_post(userpath, output, times, Dates, CS)

Arguments

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

Value

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

Description

Seabass bioenergetic individual model preprocessor

Usage

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

Arguments

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

Value

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

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

Description

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

Usage

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

Arguments

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

Value

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

Description

Creates the folders structure for Seabass individual bioenergetic model

Usage

Bass_ind_skeleton(userpath)

Arguments

userpath the path where forcing are located

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

Description

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

Usage

```
Bass_pop_dataloader(userpath)
```

Arguments

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

Value

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

Description

Seabass bioenergetic population model differential equations

Usage

Bass_pop_equations(Param, N, Temp, G, Food, weight)

Arguments

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

Value

model output at time t

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

Description

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

Usage

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

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

Bass_pop_main

Value

a list with RK solver outputs

Bass_pop_main Seabass bioenergetic population model

Description

Seabass bioenergetic population model

Usage

Bass_pop_main(userpath, forcings)

Arguments

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

Value

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

Bass_pop_post	Postprocess the Seabass population bioenergetic model results
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Description

Postprocess the Seabass population bioenergetic model results

Usage

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

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

Value

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

Bass_pop_pre Seabass bioenergetic population model preprocessor

Description

Seabass bioenergetic population model preprocessor

Usage

Bass_pop_pre(userpath, forcings)

Arguments

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

Value

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

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

Description

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

Usage

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

Arguments

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

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Value

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

Bass_pop_skeleton Creates the folders structure for Seabass population model

Description

Creates the folders structure for Seabass population model

Usage

Bass_pop_skeleton(userpath)

Arguments

userpath the path where forcing are located

```
Bass_spatial_dataloader
```

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

Description

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

Usage

Bass_spatial_dataloader(userpath)

Arguments

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

Value

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

Description

Solves the bioenergetic balance for Bass

Usage

Bass_spatial_loop(userpath, forcings)

Arguments

userpath	the path where the working folder is located
forcings	a list containing the time series in the odd positions and realted forcings in the even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophylles, concentration [maChl.a/mA2], particulated ergenic earther (POC)
	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 bioener-
	getic model and performs the interpolation

Description

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

Usage

```
Bream_ind_dataloader(userpath)
```

Arguments

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

Value

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

Bream_ind_equations Seabream bioenergetic individual model differential equations

Description

Seabream bioenergetic individual model differential equations

Usage

Bream_ind_equations(Param, Temp, G, Food, weight)

Arguments

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

Value

model output at time t

Bream_ind_main Seabream bioenergetic individual model

Description

Seabream bioenergetic individual model

Usage

Bream_ind_main(userpath, forcings)

Arguments

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

Value

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

Bream_ind_post

Description

Postprocess the Seabream indivual bioenergetic model results

Usage

Bream_ind_post(userpath, output, times, Dates, CS)

Arguments

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

Value

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

Bream_ind_pre	Seabream bioenergetic individual model preprocessor	
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Description

Preprocesses the data for the bioenergetic balance for Sea Bream

Usage

Bream_ind_pre(userpath, forcings)

Arguments

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

Value

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

Bream_ind_RKsolver

Description

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

Usage

Bream_ind_RKsolver(Param, Temperature, G, Food, IC, times)

Arguments

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

Value

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

Bream_ind_skeleton Creates the folders structure for Seabream individual bioenergetic model

Description

Creates the folders structure for Seabream individual bioenergetic model

Usage

```
Bream_ind_skeleton(userpath)
```

Arguments

userpath the path where forcing are located

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

Description

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

Usage

```
Bream_pop_dataloader(userpath)
```

Arguments

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

Value

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

Bream_pop_equations Seabream bioenergetic population model differential equations

Description

Seabream bioenergetic population model differential equations

Usage

Bream_pop_equations(Param, N, Temp, G, Food, weight)

Arguments

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

Value

model output at time t

Bream_pop_loop

Description

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

Usage

Bream_pop_loop(Param, Tint, Gint, Food, IC, times, N, userpath)

Arguments

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

Value

a list with RK solver outputs

Bream_pop_main Seabream bioenergetic population model

Description

Seabream bioenergetic population model

Usage

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

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

Bream_pop_post

Value

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

Bream_pop_post Postprocess the Bream population bioenergetic model results

Description

Postprocess the Bream population bioenergetic model results

Usage

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

Arguments

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

Value

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

Bream_pop_pre

Seabream bioenergetic population model preprocessor

Description

Preprocesses the data for the bioenergetic balance for Sea Bream

Usage

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

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

Value

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

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

Description

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

Usage

Bream_pop_RKsolver(Param, Temperature, G, Food, IC, times, N)

Arguments

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

Value

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

Bream_pop_skeleton Creates the folders structure for Seabream population model

Description

Creates the folders structure for Seabream population model

Usage

```
Bream_pop_skeleton(userpath)
```

Arguments

userpath the path where forcing are located

Bream_spatial_dataloader

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

Description

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

Usage

Bream_spatial_dataloader(userpath)

Arguments

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

Value

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

Bream_spatial_loop Bream bioenergetic spatialized model - spatialization loop

Description

Solves the bioenergetic balance for Bream

Usage

Bream_spatial_loop(userpath, forcings)

Arguments

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

Description

Clam bioenergetic individual model (alternative version)

Usage

ClamF_ind_main(userpath, forcings)

Arguments

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

Value

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

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

Description

Postprocess the Clam indivual bioenergetic model (alternative version) results

Usage

ClamF_ind_post(userpath, output, times, Dates, CS)

Arguments

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

Value

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

ClamF_ind_pre Clam bioenergetic individual model preprocessor (alternativer version)

Description

Clam bioenergetic individual model preprocessor (alternativer version)

Usage

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

Arguments

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

Value

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

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

Description

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

Usage

ClamF_ind_RKsolver(Param, times, IC, Tint, Chlint)

Arguments

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

Value

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

ClamF_ind_skeleton Creates the folder (alternative versic

Description

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

Usage

ClamF_ind_skeleton(userpath)

Arguments

userpath the path where forcing are located

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

Description

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

Usage

ClamF_pop_dataloader(userpath)

Arguments

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

Value

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

ClamF_pop_equations Clam bioenergetic population model differential equations (alternative version)

Description

Clam bioenergetic population model differential equations (alternative version)

Usage

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

Arguments

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

Value

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

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

Description

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

Usage

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

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

Value

a list with RK solver outputs

ClamF_pop_main Clam bioenergetic population model (alternative version)

Description

Clam bioenergetic population model (alternative version)

Usage

ClamF_pop_main(userpath, forcings)

Arguments

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

Value

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

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

Description

Postprocess the Clam population bioenergetic model results (alternative model)

Usage

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

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

ClamF_pop_pre

Value

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

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

Description

Clam bioenergetic population model (alternative version) preprocessor

Usage

ClamF_pop_pre(userpath, forcings)

Arguments

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

Value

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

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

Description

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

Usage

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

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

Value

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

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

Description

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

Usage

ClamF_pop_skeleton(userpath)

Arguments

userpath the path where forcing are located

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

Description

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

Usage

```
Clam_ind_dataloader(userpath)
```

Arguments

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

Value

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

Clam_ind_equations Clam bioenergetic individual model differential equations

Description

Clam bioenergetic individual model differential equations

Usage

Clam_ind_equations(Param, Tint, Phy, DT, POCint, POMint, TSSint, Wd)

Arguments

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

Value

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

Clam_ind_main Clam bioenergetic individual model

Description

Clam bioenergetic individual model

Usage

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

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

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

Clam_ind_post Postprocess the Clam individual bioenergetic model results

Description

Postprocess the Clam individual bioenergetic model results

Usage

Clam_ind_post(userpath, output, times, Dates, CS)

Arguments

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

Value

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

Clam_ind_pre

Clam bioenergetic individual model preprocessor

Description

Clam bioenergetic individual model preprocessor

Usage

Clam_ind_pre(userpath, forcings)

Arguments

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

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

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

Description

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

Usage

```
clam_ind_RKsolver(
  Param,
  times,
  IC,
  Tint,
  Phyint,
  DTint,
  POCint,
  POMint,
  TSSint
```

)

Arguments

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

Value

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

Clam_ind_skeleton Creates the folders structure for Clam individual bioenergetic model

Description

Creates the folders structure for Clam individual bioenergetic model

Usage

```
Clam_ind_skeleton(userpath)
```

Arguments

userpath the path where forcing are located

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

Description

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

Usage

```
Clam_pop_dataloader(userpath)
```

Arguments

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

Value

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

Clam_pop_equations Clam bioenergetic population model differential equations

Description

Clam bioenergetic population model differential equations

Usage

Clam_pop_equations(Param, Tint, Phy, DT, POCint, POMint, TSSint, Wd)

Arguments

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

Value

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

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

Description

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

Usage

```
Clam_pop_loop(
Param,
times,
IC,
Tint,
Phyint,
DTint,
POCint,
```

```
POMint,
TSSint,
N,
userpath
)
```

Arguments

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

Value

a list with RK solver outputs

Clam_pop_main Clam bioenergetic population model

Description

Clam bioenergetic population model

Usage

Clam_pop_main(userpath, forcings)

Arguments

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

Value

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

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Clam_pop_post

Description

Postprocess the Clam population bioenergetic model results

Usage

Clam_pop_post(userpath, output, times, Dates, N, CS)

Arguments

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

Value

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

Clam_pop_pre	Clam bioenergetic population model preprocessor
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Description

Clam bioenergetic population model preprocessor

Usage

Clam_pop_pre(userpath, forcings)

Arguments

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

Value

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

Clam_pop_RKsolver

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
)
```

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

Mussel_ind_main

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 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, 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)
```

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

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

Mussel_ind_pre Mussel bioenergetic individual model preprocessor

Description

Mussel bioenergetic individual model preprocessor

Usage

Mussel_ind_pre(userpath, forcings)

Arguments

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

Value

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

Mussel_ind_RKsolver

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

Description

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

Mussel_ind_skeleton

Usage

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

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Mussel_pop_equations

Usage

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

)

Arguments

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

Value

the outputs at time t

Mussel_pop_loop

Description

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

Usage

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

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

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
Ν	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 mo	del preprocessor
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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
)
```

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

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]

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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)
```

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]

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)

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

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

Mussel_spatial_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

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Pop_fun

Usage

Mussel_spatial_skeleton(userpath)

Arguments

userpath	the path where forcing are located
----------	------------------------------------

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

Description

Function that solves the population dynamics equations including discontinuities

Usage

Pop_fun(Nseed, mort, manag, times)

Arguments

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

Value

a time series with the number of individuals

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