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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

Seabass bioenergetic individual model differential equations

Description

Seabass bioenergetic individual model differential equations

Usage

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

Arguments

Param vector containing all metabolic parameters

Temp water temperature forcing at time t

G food entering the cage at time t

Food food characterization (Proteins, Lipids, Carbohydrates)

weight individual weight at time t

Value

model output at time t

Bass_ind_main 5

Description

Solves the bioenergetic balance for Seabass

Usage

```
Bass_ind_main(userpath, forcings)
```

Arguments

userpath the path where forcing are located

forcings a list containing the time series in the odd positions and realted forcings in the

even positions. Forcings returned are: Water temperature [Celsius degrees] and

feeding rate [g/individual x d]

Value

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

Bass_ind_post	Seabass bioenergetic individual model postprocessor
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Description

Seabass bioenergetic individual model postprocessor

Usage

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

Arguments

userpath the path where the working folder is located output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date
CS the commercial size of Seabass

Value

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

Bass_ind_RKsolver

Bass	ind	nra

Seabass bioenergetic individual model preprocessor

Description

Seabass bioenergetic individual model preprocessor

Usage

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

Arguments

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

forcings a list containing model forcings

Value

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

Bass_ind_RKsolver

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

method

Description

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

Usage

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

Arguments

Param vector containing all metabolic parameters

Temperature water temperature forcing time series

G food entering the cage time series

Food food characterization (Proteins, Lipids, Carbohydrates)

IC initial conditions

times vector containing integration extremes and integration timestep

Value

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

Bass_ind_skeleton 7

Bass_ind_skeleton	Creates t	he folders	structure	for	Seabass	individual	bioenergetic
	model						

Description

Creates the folders structure for Seabass individual bioenergetic model

Usage

```
Bass_ind_skeleton(userpath)
```

Arguments

userpath the path where forcing are located

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

Description

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

Usage

```
Bass_pop_dataloader(userpath)
```

Arguments

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

Value

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

8 Bass_pop_loop

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Seabass bioenergetic population model differential equations

Description

Seabass bioenergetic population model differential equations

Usage

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

Arguments

Param vector containing all metabolic parameters

N the number of individuals at time t
Temp water temperature forcing at time t
G food entering the cage at time t

Food food characterization (Proteins, Lipids, Carbohydrates)

weight individual weight at time t

Value

model output at time t

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

lation model

Description

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

Usage

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

Arguments

Param	a vector containing	model parameters
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Tint the interpolated water temperature time series

Gint the interpolated feeding rate time series

Food the food characterization

IC initial condition

times integration extremes and integration timestep

N time series with number of individuals

userpath the path where the working folder is located

Bass_pop_main 9

Value

a list with RK solver outputs

Bass_pop_main Seabass bioenergetic population model

Description

Seabass bioenergetic population model

Usage

Bass_pop_main(userpath, forcings)

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

even positions. Forcings returned are: Water temperature [Celsius degrees] and

feeding rate [g/individual x d]

Value

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

Bass_pop_post

Postprocess the Seabass population bioenergetic model results

Description

Postprocess the Seabass population bioenergetic model results

Usage

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

Arguments

userpath the path where the working folder is located output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date

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

10 Bass_pop_RKsolver

Value

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

Bass_pop_pre

Seabass bioenergetic population model preprocessor

Description

Seabass bioenergetic population model preprocessor

Usage

```
Bass_pop_pre(userpath, forcings)
```

Arguments

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

forcings a list containing model forcings

Value

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

Bass_pop_RKsolver

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

Description

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

Usage

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

Arguments

Param vector containing all metabolic parameters

Temperature water temperature forcing time series

G food entering the cage at time series

Food food characterization (Proteins, Lipids, Carbohydrates)

IC initial condition on weight

times integration times

N number of individuals time series

Bass_pop_skeleton 11

Value

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

Bass_pop_skeleton

Creates the folders structure for Seabass population model

Description

Creates the folders structure for Seabass population model

Usage

Bass_pop_skeleton(userpath)

Arguments

userpath

the path where forcing are located

Bass_spatial_dataloader

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

Description

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

Usage

Bass_spatial_dataloader(userpath)

Arguments

userpath

the path where folder containing model inputs and outputs is located

Value

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

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Bass_spatial_loop

Bass bioenergetic spatialized model - spatialization loop

Description

Solves the bioenergetic balance for Bass

Usage

Bass_spatial_loop(userpath, forcings)

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

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

solids (TSS) concentration [mg/l]

Value

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

Bass_spatial_main

Bass bioenergetic spatialized model - spatialization loop

Description

Solves the bioenergetic balance for Bass

Usage

Bass_spatial_main(userpath, forcings)

Arguments

userpath the path where the working folder is located

forcings list containing the time series in the odd positions and realted forcings in the

even positions. Forcings imputted are: Water temperature [Celsius degrees] and

feeding rate [g/individual x d]

Value

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

Bass_spatial_post 13

Description

Postprocess the Mussel spatialized model results

Usage

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

Arguments

userpath the path where the working folder is located output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date
CS the commercial size of Bass

Value

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

Bass_spatial_pre Bass bioenergetic spatialized model preprocessor

Description

Bass bioenergetic spatialized model preprocessor

Usage

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

Arguments

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

forcings a list containing forcings used by the model

Value

a list containing the data used by the main script

Bass_spatial_pre_int Bass bioenergetic spatialized model preprocessor - used inside spatialization loop

Description

Bass bioenergetic spatialized model preprocessor - used inside spatialization loop

Usage

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

Arguments

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

forcings a list containing forcings used by the model

Value

a list containing data used by the main script

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

Description

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

Usage

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

Arguments

Param vector containing all metabolic parameters
Temperature water temperature forcing time series
G food entering the cage time series

Food food characterization (Proteins, Lipids, Carbohydrates)

IC initial conditions

times vector containing integration extremes and integration timestep

Value

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

Bass_spatial_skeleton 15

Bass_spatial_skeleton Creates the folders structure for Bass spatialized model

Description

Creates the folders structure for Bass spatialized model

Usage

```
Bass_spatial_skeleton(userpath)
```

Arguments

userpath the path where forcing are located

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

Description

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

Usage

```
Bream_ind_dataloader(userpath)
```

Arguments

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

Value

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

Bream_ind_main

Bream_ind_equations

Seabream bioenergetic individual model differential equations

Description

Seabream bioenergetic individual model differential equations

Usage

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

Arguments

Param vector containing all metabolic parameters

Temp water temperature forcing at time t
G food entering the cage at time t

Food food characterization (Proteins, Lipids, Carbohydrates)

weight individual weight at time t

Value

model output at time t

Bream_ind_main

Seabream bioenergetic individual model

Description

Seabream bioenergetic individual model

Usage

```
Bream_ind_main(userpath, forcings)
```

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

even positions. Forcings returned are: Water temperature [Celsius degrees] and

feeding rate [g/individual x d]

Value

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

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Bream_ind_post Postprocess the Seabream indivual bioenergetic model results

Description

Postprocess the Seabream indivual bioenergetic model results

Usage

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

Arguments

userpath the path where the working folder is located output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date
CS the commercial size of Seabream

Value

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

Bream_ind_pre	Seabream bioenergetic individual model preprocessor

Description

Preprocesses the data for the bioenergetic balance for Sea Bream

Usage

```
Bream_ind_pre(userpath, forcings)
```

Arguments

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

forcings a list containing model forcings

Value

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

18 Bream_ind_skeleton

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

Description

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

Usage

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

Arguments

Param vector containing all metabolic parameters

Temperature water temperature forcing time series

G food entering the cage time series

Food food characterization (Proteins, Lipids, Carbohydrates)

IC vector containing initial conditions on weight

times vector containing integration extremes and timestep

Value

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

Description

Creates the folders structure for Seabream individual bioenergetic model

Usage

```
Bream_ind_skeleton(userpath)
```

Arguments

userpath the path where forcing are located

Bream_pop_dataloader

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

Description

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

Usage

Bream_pop_dataloader(userpath)

Arguments

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

Value

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

Bream_pop_equations

Seabream bioenergetic population model differential equations

Description

Seabream bioenergetic population model differential equations

Usage

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

Arguments

Param vector containing all metabolic parameters

N the number of individuals at time t
Temp water temperature forcing at time t
G food entering the cage at time t

Food food characterization (Proteins, Lipids, Carbohydrates)

weight individual weight at time t

Value

model output at time t

20 Bream_pop_main

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

Description

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

Usage

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

the path where the working folder is located

Arguments

Param	a vector containing model parameters
Tint	the interpolated water temperature time series
Gint	the interpolated feeding rate time series
Food	the food characterization
IC	initial condition
times	integration extremes and integration timestep
N	time series with number of individuals

Value

userpath

a list with RK solver outputs

Bream_pop_main	Seabream bioenergetic population model	
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Description

Seabream bioenergetic population model

Usage

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

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

even positions. Forcings returned are: Water temperature [Celsius degrees] and

feeding rate [g/individual x d]

Bream_pop_post 21

Value

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

Bream_pop_post

Postprocess the Bream population bioenergetic model results

Description

Postprocess the Bream population bioenergetic model results

Usage

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

Arguments

userpath the path where the working folder is located output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date N the number of individuals

CS the commercial size of Seabream

Value

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

Bream_pop_pre

Seabream bioenergetic population model preprocessor

Description

Preprocesses the data for the bioenergetic balance for Sea Bream

Usage

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

Arguments

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

forcings a list containing model forcings

22 Bream_pop_skeleton

Value

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

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

Runge Kutta method

Description

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

Usage

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

Arguments

Param vector containing all metabolic parameters

Temperature water temperature forcing time series

G food entering the cage time series

Food food characterization (Proteins, Lipids, Carbohydrates)

IC initial condition on weight

times integration times

N number of individuals time series

Value

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

Bream_pop_skeleton Creates the folders structure for Seabream population model

Description

Creates the folders structure for Seabream population model

Usage

```
Bream_pop_skeleton(userpath)
```

Arguments

userpath the path where forcing are located

Bream_spatial_dataloader

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

Description

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

Usage

Bream_spatial_dataloader(userpath)

Arguments

userpath

the path where folder containing model inputs and outputs is located

Value

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

Bream_spatial_loop

Bream bioenergetic spatialized model - spatialization loop

Description

Solves the bioenergetic balance for Bream

Usage

Bream_spatial_loop(userpath, forcings)

Arguments

userpath

the path where the working folder is located

forcings

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

solids (TSS) concentration [mg/l]

Value

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

24 Bream_spatial_post

Bream_spatial_main Bream bioenergetic spatialized model - spatialization loop

Description

Solves the bioenergetic balance for Bream

Usage

```
Bream_spatial_main(userpath, forcings)
```

Arguments

userpath the path where the working folder is located

forcings list containing the time series in the odd positions and realted forcings in the

even positions. Forcings imputted are: Water temperature [Celsius degrees] and

feeding rate [g/individual x d]

Value

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

Description

Postprocess the Bream spatialized model results

Usage

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

Arguments

userpath the path where the working folder is located output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date
CS the commercial size of Bream

Value

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

Bream_spatial_pre 25

Bream_spatial_pre

Bream bioenergetic spatialized model preprocessor

Description

Bream bioenergetic spatialized model preprocessor

Usage

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

Arguments

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

forcings a list containing forcings used by the model

Value

a list containing the data used in the main script

Bream_spatial_pre_int Bream bioenergetic spatialized model preprocessor - used inside spatialization loop

Description

Bream bioenergetic spatialized model preprocessor - used inside spatialization loop

Usage

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

Arguments

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

forcings a list containing forcings used by the model

Value

a list containing the data used by the main script

Bream_spatial_RKsolver

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

Description

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

Usage

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

Arguments

Param vector containing all metabolic parameters

Temperature water temperature forcing time series

G food entering the cage time series

Food food characterization (Proteins, Lipids, Carbohydrates)

IC initial conditions

times vector containing integration extremes and integration timestep

Value

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

Bream_spatial_skeleton

Creates the folders structure for Bream spatialized model

Description

Creates the folders structure for Bream spatialized model

Usage

```
Bream_spatial_skeleton(userpath)
```

Arguments

userpath the path where forcing are located

ClamF_ind_dataloader

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

Description

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

Usage

```
ClamF_ind_dataloader(userpath)
```

Arguments

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

Value

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

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

Description

Clam bioenergetic individual model differential equations (alternative version)

Usage

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

Arguments

Param a vector containing model parameters

Tint the interpolated water temperature at time t

Chlint the interpolated chlorophyll at time t

Ww clam wet weight at time t

Value

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

28 ClamF_ind_post

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

Description

Clam bioenergetic individual model (alternative version)

Usage

```
ClamF_ind_main(userpath, forcings)
```

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

even positions. Forcings returned are: Water temperature [Celsius degrees],

Chlorophyll a concentration [mgChl-a/m^3]

Value

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

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

Description

Postprocess the Clam indivual bioenergetic model (alternative version) results

Usage

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

Arguments

userpath	the path where the working folder is located
output	output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date CS the commercial size of Clam

Value

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

ClamF_ind_pre 29

ClamF_ind_pre	Clam bioenergetic individual model preprocessor (alternativer version)
---------------	--

Description

Clam bioenergetic individual model preprocessor (alternativer version)

Usage

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

Arguments

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

forcings a list containing model forcings

Value

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

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

Description

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

Usage

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

Arguments

Param a vector containing model parameters

times integration extremes and integration timestep

IC initial condition

Tint the interpolated water temperature time series
Chlint the interpolated chlorophyll a time series

Value

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

ClamF_ind_skeleton

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

Description

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

Usage

```
ClamF_ind_skeleton(userpath)
```

Arguments

userpath

the path where forcing are located

ClamF_pop_dataloader

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

Description

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

Usage

```
ClamF_pop_dataloader(userpath)
```

Arguments

userpath

the path where folder containing model inputs and outputs is located

Value

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

ClamF_pop_equations 31

ClamF_pop_equations	Clam bioenergetic population model differential equations (alterna-
	tive version)

Description

Clam bioenergetic population model differential equations (alternative version)

Usage

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

Arguments

Param a vector containing model parameters

Tint the interpolated water temperature at time t

Chlint the interpolated chlorophyll at time t

Ww clam wet weight at time t

Value

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

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

Description

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

Usage

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

Arguments

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

32 ClamF_pop_post

Value

a list with RK solver outputs

ClamF_pop_main

Clam bioenergetic population model (alternative version)

Description

Clam bioenergetic population model (alternative version)

Usage

```
ClamF_pop_main(userpath, forcings)
```

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

even positions. Forcings returned are: Water temperature [Celsius degrees],

Chlorophyll a concentration [mgChl-a/m^3]

Value

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

ClamF_pop_post

Postprocess the Clam population bioenergetic model results (alternative model)

Description

Postprocess the Clam population bioenergetic model results (alternative model)

Usage

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

Arguments

userpath the path where the working folder is located output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date

N the number of individuals

CS the commercial size of Clam

ClamF_pop_pre 33

Value

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

ClamF_pop_pre Clam bioenergetic population model (alternative version) preprocessor

Description

Clam bioenergetic population model (alternative version) preprocessor

Usage

```
ClamF_pop_pre(userpath, forcings)
```

Arguments

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

forcings a list containing model forcings

Value

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

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

Description

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

Usage

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

Arguments

Chlint

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

the interpolated chlorophyll a time series

34 Clam_ind_dataloader

Value

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

ClamF_pop_skeleton

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

Description

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

Usage

ClamF_pop_skeleton(userpath)

Arguments

userpath

the path where forcing are located

Clam_ind_dataloader

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

Description

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

Usage

Clam_ind_dataloader(userpath)

Arguments

userpath

the path where folder containing model inputs and outputs is located

Value

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

Clam_ind_equations 35

~ 7		
Clam	ınd	equations

Clam bioenergetic individual model differential equations

Description

Clam bioenergetic individual model differential equations

Usage

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

Arguments

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

Value

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

Clam	ind	main	
CTaill_	_IIIU_	_IIIIa I I I	

Clam bioenergetic individual model

Description

Clam bioenergetic individual model

Usage

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

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l], particulated organic matter (POM) concentration [mgC/l],

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

36 Clam_ind_pre

Value

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

Clam_ind_post

Postprocess the Clam individual bioenergetic model results

Description

Postprocess the Clam individual bioenergetic model results

Usage

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

Arguments

userpath the path where the working folder is located output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date CS the commercial size of Clam

Value

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

Clam_ind_pre

Clam bioenergetic individual model preprocessor

Description

Clam bioenergetic individual model preprocessor

Usage

```
Clam_ind_pre(userpath, forcings)
```

Arguments

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

forcings a list containing model forcings

clam_ind_RKsolver 37

Value

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

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

Description

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

Usage

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

Arguments

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

Value

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

Clam_ind_skeleton

Creates the folders structure for Clam individual bioenergetic model

Description

Creates the folders structure for Clam individual bioenergetic model

Usage

Clam_ind_skeleton(userpath)

Arguments

userpath

the path where forcing are located

Clam_pop_dataloader

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

Description

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

Usage

Clam_pop_dataloader(userpath)

Arguments

userpath

the path where folder containing model inputs and outputs is located

Value

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

Clam_pop_equations 39

Clam	non	equations
CTalli	טטט	_equations

Clam bioenergetic population model differential equations

Description

Clam bioenergetic population model differential equations

Usage

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

Arguments

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

Value

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

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

Description

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

Usage

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

40 Clam_pop_main

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

Arguments

Param a vector containing model parameters

times integration extremes and integration timestep

IC initial condition

Tint the interpolated water temperature time series

Phyint the interpolated phytoplankton time series

DTint the interpolated detritus time series

POCint the interpolated POC time series

POMint the interpolated POM time series

TSSint the interpolated TSS time series

N time series with number of individuals

userpath the path where the working folder is located

Value

a list with RK solver outputs

Clam_pop_main

Clam bioenergetic population model

Description

Clam bioenergetic population model

Usage

```
Clam_pop_main(userpath, forcings)
```

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

even positions. Forcings returned are: Water temperature [Celsius degrees], Chlorophyll a concentration [mgChl-a/m^3], particulated organic carbon (POC) concentration [mgC/l], particulated organic matter (POM) concentration [mgC/l],

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

Value

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

Clam_pop_post 41

Clam_pop_post	Postprocess the Clam population bioenergetic model results

Description

Postprocess the Clam population bioenergetic model results

Usage

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

Arguments

userpath the path where the working folder is located output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date

N the number of individuals

CS the commercial size of Clam

Value

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

Clam_pop_pre	Clam bioenergetic population model preprocessor

Description

Clam bioenergetic population model preprocessor

Usage

```
Clam_pop_pre(userpath, forcings)
```

Arguments

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

forcings a list containing model forcings

Value

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

42 Clam_pop_RKsolver

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

Description

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

Usage

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

Arguments

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

Value

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

Clam_pop_skeleton 43

Clam_pop_skeleton

Creates the folders structure for Clam population model

Description

Creates the folders structure for Clam population model

Usage

Clam_pop_skeleton(userpath)

Arguments

userpath

the path where forcing are located

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

Description

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

Usage

Mussel_ind_dataloader(userpath)

Arguments

userpath

the path where folder containing model inputs and outputs is located

Value

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

Description

Mussel bioenergetic individual model differential equations

Usage

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

Arguments

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

Mussel_ind_main 45

Value

the outputs at time t

Mussel_ind_main Mussel bioenergetic individual model

Description

Solves the bioenergetic balance for Mussel

Usage

Mussel_ind_main(userpath, forcings)

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

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

solids (TSS) concentration [mg/l]

Value

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

Description

Postprocess the Mussel indivual bioenergetic model results

Usage

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

Arguments

userpath the path where the working folder is located output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date CS the commercial size of Mussel

Value

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

Mussel_ind_pre

Mussel bioenergetic individual model preprocessor

Description

Mussel bioenergetic individual model preprocessor

Usage

Mussel_ind_pre(userpath, forcings)

Arguments

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

forcings a list containing model forcings

Value

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

Mussel_ind_RKsolver

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

Description

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

Mussel_ind_skeleton 47

Usage

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

Arguments

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

Value

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

Mussel_ind_skeleton Creates the folders structure for Mussel individual bioenergetic model

Description

Creates the folders structure for Mussel individual bioenergetic model

Usage

```
Mussel_ind_skeleton(userpath)
```

Arguments

userpath

the path where forcing are located

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

Description

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

Usage

Mussel_pop_dataloader(userpath)

Arguments

userpath

the path where folder containing model inputs and outputs is located

Value

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

Mussel_pop_equations Mussel bioenergetic population model differential equations

Description

Mussel bioenergetic population model differential equations

Usage

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

Arguments

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

Value

the outputs at time t

50 Mussel_pop_loop

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

Description

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

Usage

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

Arguments

Param

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

a vector containing model parameters

Mussel_pop_main 51

Value

a list with RK solver outputs

Mussel_pop_main

Mussel bioenergetic population model

Description

Solves the bioenergetic balance for Mussel and simulates a population

Usage

Mussel_pop_main(userpath, forcings)

Arguments

userpath

the path where the working folder is located

forcings

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

solids (TSS) concentration [mg/l]

Value

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

Mussel_pop_post

Postprocess the Mussel population bioenergetic model results

Description

Postprocess the Mussel population bioenergetic model results

Usage

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

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Arguments

userpath the path where the working folder is located

output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date

N the number of individuals

CS the commercial size of Seabass

Value

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

Mussel_pop_pre

Mussel bioenergetic population model preprocessor

Description

Mussel bioenergetic population model preprocessor

Usage

Mussel_pop_pre(userpath, forcings)

Arguments

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

forcings a list containing forcings used by the model

Value

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

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

Description

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

Usage

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

Arguments

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

Value

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

Mussel_pop_skeleton

Creates the folders structure for Mussel population model

Description

Creates the folders structure for Mussel population model

Usage

```
Mussel_pop_skeleton(userpath)
```

Arguments

userpath

the path where forcing are located

Mussel_spatial_dataloader

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

Description

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

Usage

```
Mussel_spatial_dataloader(userpath)
```

Arguments

userpath

the path where folder containing model inputs and outputs is located

Value

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

Mussel_spatial_loop 55

Mussel_spatial_loop

Mussel bioenergetic spatialized model - spatialization loop

Description

Solves the bioenergetic balance for Mussel

Usage

Mussel_spatial_loop(userpath, forcings)

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

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

solids (TSS) concentration [mg/l]

Value

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

Mussel_spatial_main

Mussel bioenergetic spatialized model - spatialization loop

Description

Solves the bioenergetic balance for Mussel

Usage

Mussel_spatial_main(userpath, forcings)

Arguments

userpath the path where the working folder is located

forcings a list containing the time series in the odd positions and realted forcings in the

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

solids (TSS) concentration [mg/l]

56 Mussel_spatial_pre

Value

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

Mussel_spatial_post

Postprocess the Mussel spatialized model results

Description

Postprocess the Mussel spatialized model results

Usage

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

Arguments

userpath the path where the working folder is located

output output list containing the output of the RK solver

times the vector containing informations on integration extremes

Dates the vector containing the date
CS the commercial size of Mussel

Value

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

Mussel_spatial_pre

Mussel bioenergetic spatialized model preprocessor

Description

Mussel bioenergetic spatialized model preprocessor

Usage

```
Mussel_spatial_pre(userpath, forcings)
```

Arguments

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

forcings a list containing forcings used by the model

Value

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

Mussel_spatial_pre_int

Mussel bioenergetic spatialized model preprocessor - used inside spatialization loop

Description

Mussel bioenergetic spatialized model preprocessor - used inside spatialization loop

Usage

```
Mussel_spatial_pre_int(userpath, forcings)
```

Arguments

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

forcings a list containing forcings used by the model

Value

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

Mussel_spatial_RKsolver

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

Description

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

Usage

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

Arguments

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

the interpolated TSS time series

Value

TSSint

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

```
Mussel_spatial_skeleton
```

Creates the folders structure for Mussel spatialized model

Description

Creates the folders structure for Mussel spatialized model

Pop_fun 59

Usage

```
Mussel_spatial_skeleton(userpath)
```

Arguments

userpath the path where forcing are located

Pop_fun Function that solves the population dynamics equations including dis-

continuities

Description

Function that solves the population dynamics equations including discontinuities

Usage

```
Pop_fun(Nseed, mort, manag, times)
```

Arguments

Nseed number of seeded individuals

mort mortality rate

manag list of management actions (seeded/harvested individuals)

times vector containing informations on integration times

Value

a time series with the number of individuals

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