# Package 'r4fish'

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Type Package

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Title r4fish analysis

Author Elmer O. Quispe Salazar
Maintainer The package maintainer <qselmer@gmail.com></qselmer@gmail.com>
<b>Description</b> Assessment for Marine Resources Toolkit.
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2 calculateJuv

```
{\it assigner Peruvian Grid} \quad \textit{Title} \quad
```

## Description

Title

## Usage

```
assignerPeruvianGrid(
  data,
  xlon = "lon",
  ylat = "lat",
  by = "onedegree",
  metadata = F,
  save = T,
  cout = "."
)
```

## Arguments

cout

calculateJuv

Title

## Description

Title

# Usage

```
calculateJuv(vec, marks, mjuv, abs = T)
```

## Arguments

abs

curve.sel 3

curve.sel

Title

## Description

Title

## Usage

```
curve.sel(
    sp = NA,
    stock = NA,
    marks = NA,
    par = c(NA, NA),
    method = "log3",
    add.plot = T,
    add.inv = T
)
```

# Arguments

add.inv

 ${\tt distCoast}$ 

Title

# Description

Title

# Usage

```
distCoast(lon, lat)
```

# Arguments

lat

4 g2plotSurvey

estimateMode

Estima moda de una frecuencia de tallas

#### **Description**

Estima moda de una frecuencia de tallas

#### Usage

```
estimateMode(len, freq, tol.n = 150, nmodes = 2, tol.freq = 10)
```

#### **Arguments**

len vector completo de tallas

freq vector completo de frecuencias

tol.n valor de tolerancia del numero de la muestra

nmodes numero de modas a estimar

tol.freq valor de tolerancia para ser considerada moda

g2plotSurvey

Title

#### **Description**

Title

#### Usage

```
g2plotSurvey(
  dat = dat,
  col.var = "biomasa",
  col.factor = 2,
  factor = NA,
  cols.factor = c("red", "blue"),
  box = "boxplot",
  model = "lm",
  lambda = 1e-04,
  IC.model = TRUE,
  info = TRUE,
  marf = c(0.5, 0.5, 0, 0.5),
  omaf = c(3, 4.5, 2, 2),
  hline = TRUE,
  cline = "white",
  bgf = "white",
  lwdf = 1,
  ltyf = 1,
  pchf = 16,
  cexf = 1.5,
```

getModeSpecies 5

```
unitf = 1,
saveplot = T,
outf = "./",
widthf = 1800,
heightf = 1200,
resf = 250,
labels.f = c("\nverano", "\ninvierno-\nprimavera"),
labels.y = "Biomasa ton",
...
)
```

## Arguments

labels.y

getModeSpecies

Title

## Description

Title

## Usage

```
getModeSpecies(
  Length = Length,
  sp = "anchoveta",
  src = "fsh",
  nmodes = 2,
  tol = 0,
  savePlot = TRUE,
  dirout = "Outputs/")
```

## Arguments

dirout

 ${\tt getStockInfo}$ 

Title

## Description

Title

# Usage

```
getStockInfo(sp, data = NULL, ...)
```

## Arguments

. . .

6 MapPeruGrid

getSurveyLmax

Title

## Description

Title

## Usage

```
getSurveyLmax(dat = dat, sp = "anchoveta", src = "pope", col.var = 4:78)
```

#### **Arguments**

col.var

MapPeruGrid

Title

## Description

Title

## Usage

```
MapPeruGrid(
  data,
  colcode = "code",
  colval = "freq",
  typeval = "#",
  xxlim = c(-86, -70),
  yylim = c(-21, -3),
  by = "onedegree",
  gradient = c("yellow", "red"),
  border = NA,
  all.grid = F,
  land.col = "gray90",
  land.border = "gray90",
  legend = T,
  txtleg = "(n)",
  xaxis = 1,
  yaxis = 4,
  portImport = 2,
  save = T,
  cout = "."
)
```

## **Arguments**

cout

plot2CompSizeTime 7

plot2CompSizeTime

Title

#### **Description**

Title

#### Usage

```
plot2CompSizeTime(
  dat = dat_marks,
  sp = "anchoveta",
  stock = "nc",
  type = "B",
  ab = NA,
  factor = NA,
  cexf = 3,
  col.in = "gray90",
  col.bd = "black",
  marp = c(3, 3, 2, 2),
  omap = c(1, 2, 1, 1),
  mgpp = c(1, 0.5, 0),
  widthFig = 2600,
  heightFig = 3200,
  resFig = 380,
  SavePlot = T,
  dirout = "Outputs/"
)
```

## Arguments

dirout

PlotSimpleFrec2

Title

## Description

Title

## Usage

```
PlotSimpleFrec2(
  data,
  sp = sp,
  stock = stock,
  col.sp = "red",
  colset = "navajowhite",
  cout = ".",
```

8 renderBiometric

```
save = T,
format = ".png",
ylim = c(0, 0.5),
width = 2625,
height = 1750
)
```

## **Arguments**

colset

plot\_envir

Title

## Description

Title

# Usage

```
plot_envir(
   what = NA,
   year.limit = c(1990, 2022),
   ylim = c(-2, 3.5),
   magnitude = F,
   axis.x = T
)
```

## Arguments

axis.x

 ${\tt renderBiometric}$ 

Crea, unifica archivo biometrico

## Description

Crea, unifica archivo biometrico

# Usage

```
renderBiometric(
  cin = "inputs",
  cout = ".",
  file = "data.xlsx",
  encoding = "latin",
  save = T,
  ...
)
```

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#### **Arguments**

cin	vector de caracteres que contienen la ruta de entrada
cout	vector de caracteres que contienen la ruta de salida
file	vector de caracteres que contienen el nombre del archivo
encoding	vector de caracteres para tipo de codificacion
save	logico; ¿Se deben guardar el archivo?

## Value

base de datos biométrico

## **Examples**

```
\code{renderBiometric(cin = "input",
cout = NA,
file = "Biometria por especies 03032023.xlsx",
save = T)}
```

SimpleFrecSp

Plot: Estructura de tallas para "anchoveta "spTarget" lances

## Description

Plot: Estructura de tallas para "anchoveta "spTarget" lances

## Usage

```
SimpleFrecSp(data = x, sp = "anchoveta", stock = "nc", save = T)
```

## **Arguments**

data	datos del crucero en formato MF
sp	especie objetivo de la evaluación
stock	stock objetivo de la evaluación
save	valor logico: ¿Se deben guardar la matriz de lances en "csv"?

10 validateSp

subsetSurvey

Title

#### **Description**

Title

## Usage

```
subsetSurvey(
  dat = dat,
  col.var = c("biomasa", "abundancia"),
  year.lim = c(1996, 2022),
  col.set = "filter",
  set = "ok",
  col.factor = "season",
  col.label = 2,
  col.date = NA,
  col.month = NA,
  col.sems = "semester",
  col.year = "year"
)
```

#### **Arguments**

col.year

validateSp

Identifica errores y valida la base de datos

## Description

Identifica errores y valida la base de datos

## Usage

```
validateSp(
  data = data,
  sp = "anchoveta",
  stock = NA,
  cout = "outputs",
  file = "validateSp"
)
```

## Arguments

data	datos del crucero en formato MF
sp	especie objetivo de la evaluación
stock	stock objetivo de la evaluación
cout	vector de caracteres que contienen la ruta de salida
file	ector de caracteres que contienen el nombre del archivo

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# Examples

```
\code{validateSp(data = data, sp = "jurel", stock = NA, cout = "outputs",
file = "document.docx")}
```

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