

# Package ‘COSTdbe’

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**Title** Design-based estimates package for COST.

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**Date** 2009

**Author** COST Team and various contributors.

**Description** COSTdbe is a package dealing with Design Based Estimates, i.e. considering two sets of methods, analytical issued from the sampling theory (Cochran, 1977) and resampling making use of the bootstrap (Efron and Tibshirani, 1993).

**Depends** R(>= 2.8.1), COSTcore, lattice, boot, methods, tcltk

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**License** GPL 2 or above

**LazyLoad** Yes

**LazyData** Yes

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InterCatch\_output      *Create InterCatch Exchange Format file*

---

## Description

Converts a COST dbOutput object of numbers at length or age into InterCatch Exchange Format Version 1.4 file

## Usage

```
makeICdf(dbOutput, filename=NA, output.df = TRUE, append = FALSE, CANUMtype = "length",
         Country, Species = NA, ReportingCategory, Usage = NA, DataToFrom = NA,
         SamplesOrigin, InfoFleet = NA, InfoStockCoordinator = NA, InfoGeneral = NA,
         Sex = "N", PlusGroup = -9, unitMeanWeight = "g", unitCANUM = "n", Maturity = NA)
```

```
makeICfile(ICdfs, filename, append=FALSE)
```

## Arguments

dbOutput	A COST dbOutput object of numbers by length and/or age
ICdfs	list of 3 dataframes corresponding to InterCatch HI, SI and SD record types
filename	filename for output, if NA no file is written
output.df	logical, should list of dataframes be output
append	logical, should output be appended to existing file
CANUMtype	"age" for numbers at age, "lngt" or "length" for numbers at length
Country	The remaining arguments are character elements that match the Inter-Catch format description and are transferred directly to the output file
Species	If species is NA then it is taken from the dbOutput, but note this is likely to be scientific name and InterCatch expects FAO code
ReportingCategory	

## Usage

DataToFrom

SamplesOrigin

InfoFleet

InfoStockCoordinator

InfoGeneral

Sex

PlusGroup  
unitMeanWeight

unitCANUM  
Maturity

### Details

makeICdf creates a list of 3 dataframes corresponding to InterCatch HI, SI and SD record types then if filename is not NA makeICfile is called and a CSV file output to filename.

The process can be split into two parts by using makeICdf first, storing the list of dataframes and then calling makeICfile on the list.

We expect the function to develop as InterCatch develops and expect more of the fields to be automatically filled in future versions.

### Value

A list of 3 dataframes if output.df = TRUE A csv file if filename is not NA

### Author(s)

David Maxwell

### References

InterCatch Exchange Format Version 1.4 <http://www.ices.dk/datacentre/InterCatch/IC-ExchFormat1-0\%20Doc1-4.pdf>

### See Also

dbeOutput

### Examples

```
# load example data set
data("LEMexample")
# Setup object for output
LEM.dbeOut.an = dbeObject(desc="Example",species="Microstomus kitt,param="landings",
                          strataDesc=LEM.strat, catchCat="LAN",methodDesc="analytical")

## Run vesselRaise function
LEM.dbeOut.an = vesselRaise.an (csObject = LEM.CScon, clObject = LEM.CLcon, dbeOutp = LEM.dbeOut.an)

# In two steps
# Create list with HI, SI, SD dataframes
LEM.ICdf <- makeICdf (LEM.dbeOut.an, Country = "UKE", Species = "LEM", ReportingCategory = "R",
                     SamplesOrigin = "M")
# edit dataframes in LEM.ICdf if required then write InterCatch file
# Not run
makeICfile (LEM.ICdf, filename = "IC_LEM.csv")

# In one step, straight to file. output.df=F stops dataframes being saved within R
# Not run
makeICdf (LEM.dbeOut.an, filename = "IC_LEM.csv", output.df = FALSE, Country = "UKE",
```

```
Species = "LEM", ReportingCategory = "R", SamplesOrigin = "M")
```

---

LEM.objects	<i>ToDo</i>
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---

### Description

ToDo

### Usage

LEM.CE

### Format

ToDo

### Details

ToDo

### WARNING

This data is provided is for testing only and should not be used for any other purpose.

### Source

ToDo

### Examples

```
data(LEMexample)
```

---

RaiseAge	<i>Estimation of total numbers-at-age from market sampling</i>
----------	--

---

### Description

Estimation of total numbers-at-age from market sampling

### Usage

```
RaiseAge(dbeOutput, csObject, clObject, ...)
```

**Arguments**

<code>dbeOutput</code>	A <i>dbeOutput</i> object.
<code>csObject</code>	A <i>csDataCons</i> object matching 'dbeOutput' specifications.
<code>clObject</code>	Optionnal. A <i>clDataCons</i> object matching 'dbeOutput' specifications (only required if <code>type="direct"</code> ).
<code>...</code>	Further arguments such as:
<code>type</code>	Character. Specification of the raising method : "p" (default value), "fixedK", "propK", "agesK", or "direct".
<code>sex</code>	Character. Sex specification, basically "M", "F" or <code>as.character(NA)</code> (default value) for no restriction.

**Details**

Method used for estimates and variance calculation of total numbers at age is specified by *type* input parameter. If "direct", calculations are based on a stratified simple random sampling (see *Type1SimpleRandomSampling.doc* file in COSTdbe package's doc folder for methodology), and raising process is made within *clObject* input data. If "p", "fixedK", "propK" or "agesK", estimates are similarly computed following Kimura (see *references* section). In these cases, as calculation requires total numbers-at-length estimates, *RaiseLgth* method must be run beforehand to update input *dbeOutput* object with needed information. Contrary to estimates, variances computation differs between these 4 methods. "fixedK" is computing within an "age subsample fixed" strategy expectation, "propK" within an "age subsample random" strategy, "agesK" within a "random sample with ages only" strategy (see Kimura for those methodologies), and finally, "p" default method is based on "random sample with ages and lengths" strategy.

**Value**

An updated object of class *dbeOutput*. Slots `nSamp$age` & `nMeas$age` with number of samples and measurements, `ageStruc$estim` with numbers-at-age estimates, `ageVar` with the variance of numbers-at-age .

**Author(s)**

Mathieu Merzereaud & Marcel Machiels

**References**

D.K. Kimura, Statistical assessment of the age-length key, J. Fish. Res. Board Can. 34 (1977)

**See Also**

`dbeOutput`, `dbeObject`, `RaiseAgeBoot`, `RaiseLgth`, `csDataCons`, `clDataCons`

**Examples**

```
data(sole)
#stratification
strD <- strIni(timeStrata="quarter",techStrata="commCat")
#only market sampling data and biological parameters are kept
csObject <- csDataCons(csDataVal(subset(sole.cs,sampType%in%c("M","V"))),strD)
clObject <- clDataCons(clDataVal(sole.cl),strD)
```

```
#initializing the output object
dbeOutput <- dbeObject(species="Solea solea",catchCat="LAN",strataDesc=strD)

# total numbers at length
dbeOutput <- RaiseLgth (dbeOutput, csObject, clObject)

# total numbers at age
dbeOutput <- RaiseAge (dbeOutput, csObject)
```

---

RaiseAgeBoot	<i>Estimation of numbers-at-age from market sampling with bootstrap variance</i>
--------------	--

---

## Description

RaiseAgeBoot follows the approach of RaiseAge to calculate numbers-at-age by strata from market sampling data. A set of bootstrap estimates is created to calculate the variance. This method requires RaiseLgthBoot to have been run to estimate the length structure and define the number of bootstrap replicates.

## Usage

```
RaiseAgeBoot(dbeOutput, csObject, type="p", sex=as.character(NA), bootMethod = "samples", .
```

## Arguments

<code>dbeOutput</code>	A <i>dbeOutput</i> object containing output from RaiseLgthBoot.
<code>csObject</code>	A <i>csDataCons</i> object matching 'dbeOutput' specifications.
<code>type</code>	Allocation strategy used to establish the age-length data, one of "p", "fixedK", "propK" or "agesK" (see <i>RaiseAge</i> )
<code>sex</code>	Sex
<code>bootMethod</code>	"samples" (the default) or "otoliths"
<code>...</code>	Further arguments

## Details

If `bootMethod="samples"` then samples in the data are defined by `PSUId` and `SSUId` and these samples are selected with replacement to create bootstrap estimates.

If `bootMethod="otoliths"` then individual age observations within each length class (i.e. row of the ALK) are resampled instead. This makes the assumption that individual otoliths are independent. In other words, that for age-given-length, fish in the same sample are not more similar than fish in different samples.

## Value

An updated object of class *dbeOutput*. Slot `methodDesc` with bootstrap samples or bootstrap otoliths, `nSamp$age` & `nMeas$age` with number of samples and measurements, `ageStruc$rep` with bootstrap replicates for numbers-at-age, `iter=0` is assigned the estimates from the original data, `ageStruc$estim` with the mean of the bootstrap replicates, `ageVar` with the variance of the bootstrap replicates

**Author(s)**

David Maxwell & Mathieu Merzereaud

**See Also**

dbeOutput, dbeObject, csDataCons, clDataCons, RaiseAge, RaiseLgthBoot

**Examples**

```
data(sole)
strD <- strIni(timeStrata="quarter",techStrata="commCat")
csObject <- csDataCons(csDataVal(subset(sole.cs,sampType%in%c("M","V"))),strD)
clObject <- clDataCons(clDataVal(sole.cl),strD)
dbeOutput <- dbeObject(species="Solea solea",catchCat="LAN",strataDesc=strD)

# Analytical estimates
sol.dbe.an <- RaiseLgth (dbeOutput, csObject, clObject)

# Bootstrap estimates. B set to a very low number of iterations for demonstration only.
# Several thousand iterations recommended for final run, which will take some time.
sol.dbe.boot <- RaiseLgthBoot (dbeOutput, csObject, clObject, B=10)

sol.dbe.boot <- RaiseAgeBoot (dbeOutput = sol.dbe.boot, csObject = csObject, type="p")
```

---

RaiseLgth

*Estimation of total numbers-at-length from market sampling*

---

**Description**

This method calculates total numbers-at-length by strata from market sampling data.

**Usage**

```
RaiseLgth(dbeOutput,csObject,clObject,spp,taxon,sex=as.character(NA),...)
```

**Arguments**

<code>dbeOutput</code>	A <i>dbeOutput</i> object.
<code>csObject</code>	A <i>csDataCons</i> object matching 'dbeOutput' specifications.
<code>clObject</code>	A <i>clDataCons</i> object matching 'dbeOutput' specifications. If not specified, data is only raised to trips.
<code>spp</code>	Species, if missing this is set to <code>dbeOutput@species</code>
<code>taxon</code>	Taxon, if missing this is set to <code>dbeOutput@species</code>
<code>sex</code>	Sex
<code>...</code>	Further arguments

**Value**

An updated object of class *dbeOutput*. Slots `nSamp$len` & `nMeas$len` with number of samples and measurements, `totalW$estim` with total weight, `lenStruc$estim` with numbers-at-length estimates, `lenVar` with the variance of numbers-at-length.

**Author(s)**

Mathieu Merzereaud

**See Also**

dbeOutput, dbeObject, RaiseAge, csDataCons, clDataCons

**Examples**

```

data(sole)
#stratification
strD <- strIni(timeStrata="quarter",techStrata="commCat")
#only market sampling data and biological parameters are kept
csObject <- csDataCons(csDataVal(subset(sole.cs,sampType%in%c("M","V"))),strD)
clObject <- clDataCons(clDataVal(sole.cl),strD)
#initializing the output object
dbeOutput <- dbeObject(species="Solea solea",catchCat="LAN",strataDesc=strD)

# total numbers at length
dbeOutput <- RaiseLgth (dbeOutput, csObject, clObject)

```

---

 RaiseLgthBoot

*Estimation of numbers-at-length from market sampling with bootstrap variance*


---

**Description**

RaiseLgthBoot follows the approach of RaiseLgth to calculate numbers-at-length by strata from market sampling data. The data are resampled with replacement to create B bootstrap estimates that are used to calculate the variance.

**Usage**

```
RaiseLgthBoot(dbeOutput,csObject,clObject,spp,taxon,sex=as.character(NA),B,...)
```

**Arguments**

<code>dbeOutput</code>	A <i>dbeOutput</i> object.
<code>csObject</code>	A <i>csDataCons</i> object matching 'dbeOutput' specifications.
<code>clObject</code>	A <i>clDataCons</i> object matching 'dbeOutput' specifications.
<code>spp</code>	Species, if missing this is set to <code>dbeOutput@species</code>
<code>taxon</code>	Taxon, if missing this is set to <code>dbeOutput@species</code>
<code>sex</code>	Sex
<code>B</code>	Number of bootstrap iterations
<code>...</code>	Further arguments



**Value**

An updated object of class *dbeOutput*. Slots *nSamp\$len* & *nMeas\$len* with number of samples and measurements, *methodDesc* with "bootstrap", *totalW\$estim* with total weight, *lenStruc\$rep* & *totalN\$rep* with bootstrap replicates for numbers-at-length and total numbers, *iter=0* is assigned the estimates from the original data, *lenStruc\$estim* & *totalN\$estim* with the mean of the bootstrap replicates, *lenVar* & *totalNvar* with the variance of the bootstrap replicates

**Author(s)**

David Maxwell & Mathieu Merzereaud

**See Also**

`dbeOutput`, `dbeObject`, `csDataCons`, `c1DataCons`, `RaiseLgth`

**Examples**

```
data(sole)
strD <- strIni(timeStrata="quarter",techStrata="commCat")
csObject <- csDataCons(csDataVal(subset(sole.cs,sampType%in%c("M","V"))),strD)
c1Object <- c1DataCons(c1DataVal(sole.c1),strD)
dbeOutput <- dbeObject(species="Solea solea",catchCat="LAN",strataDesc=strD)

# Analytical estimates
sol.dbe.an <- RaiseLgth (dbeOutput, csObject, c1Object)

# Bootstrap estimates. B set to a very low number of iterations for demonstration only.
# Several thousand iterations recommended for final run, which will take some time.
sol.dbe.boot <- RaiseLgthBoot (dbeOutput, csObject, c1Object, B=10)
```

---

alkLgthRec

*Method for managing gaps in age-length keys*

---

**Description**

This function proposes various methods to solve alk gaps problems inherent to a 'csDataCons' object. Input object is updated according to chosen method(s) (grouped/recoded length classes, addition of 'virtual' individuals,...)

**Usage**

```
alkLgthRec(object,type="stepIncr",value,preview=FALSE,postview=TRUE,update=FALSE,...)
```

**Arguments**

<code>object</code>	A <i>csDataCons</i> object with ca information.
<code>type</code>	Character for chosen method. Values are :
"stepIncr"	Default parameter. Length class step is increased to specified <i>value</i> parameter (default value=10)

"fillMiss"	All gaps (with size $\leq$ value) are filled out with the sum of surrounding recorded classes (default value=1)
"sFillMiss"	The 'value' empty classe(s) prior to first recorded length class is filled out with the latter (default value=1)
"lFillMiss"	The 'value' empty classe(s) following last recorded length class is filled out with the latter (default value=1)
value	Numerical parameter for chosen method (see 'type').
preview	Logical. If TRUE, original age length key is displayed.
postview	Logical. If TRUE, new age length key is displayed.
update	Logical. If TRUE, 'csDataCons' object is updated in accordance with chosen method, and then returned. If FALSE, descriptive elements about updated alk are returned (see 'values'), but input object remains unchanged.
...	Further arguments, and particularly a <i>start</i> numerical parameter specifying the first considered length class when recoding (only useful for 'type="stepIncr"). Default value is the minimum aged length class in <i>ca</i> table.

### Value

If `update=FALSE`, returned elements are : `$alk` is the raw resulting age-length key, `$propMiss` are short statistics about gaps (see 'propMissLgthCons' method), `$lgthCls` is a description of length classes recoding for 'stepIncr', 'sExtrGrp' and 'lExtrGrp' methods and `$addIndTab` is a description of added virtual individuals for other methods.

### Author(s)

Mathieu Merzereaud

### See Also

`viewGapsAlkCons`, `propMissLgthCons`

### Examples

```
data(sole)
#restriction to "27.7.d" & "27.7.e" areas
csRaw <- subset(sole.cs,area%in%c("27.7.d","27.7.e"),table="hh")
#consolidation process
conSole.cs <- csDataCons(csDataVal(csRaw),strIni(timeStrata="quarter",spaceStrata="area"))

res1 <- alkLgthRec(conSole.cs,type="stepIncr",value=20)
names(res1)

res1$missProp #updated statistics about missing length classes

res1$lgthCls #updated Length Classes
#if it's allright, consolidated object can be updated --> conSole.cs1
conSole.cs1 <- alkLgthRec(conSole.cs,type="stepIncr",value=20,postview=FALSE,update=TRUE)
```

bpBoot

*Bootstrap estimates of biological parameters***Description**

This method implements a non-parametric bootstrap procedure to estimate empirical estimates of weight-at-length, maturity-at-length, sex-ratio-at-length, weight-at-age, maturity-at-age, sex-ratio-at-age and their associated variances. It requires a *csDataCons* object and a *dbeOutput* object.

**Usage**

```
bpBoot(dbeOutput,object,mat.scale=list(immature=c(0,1),mature=c(2:8)),
       sample.boot=FALSE,nboot=1000,...)
```

**Arguments**

<code>dbeOutput</code>	A <i>dbeOutput</i> object.
<code>object</code>	A <i>csDataCons</i> object.
<code>mat.scale</code>	List containing the maturity stages for immature and mature individuals. The codes must match with maturity scale of <i>csDataCons</i> object.
<code>sample.boot</code>	Logical value. If FALSE, the resampling unit is the individual. If TRUE, the resampling unit is the sample.
<code>nboot</code>	Single positive integer indicating the number of bootstrap replicates.
<code>...</code>	Any additional arguments.

**Details**

This method uses the non-parametric bootstrap techniques to estimate the variation in biological parameters (mean weight, maturity and sex-ratio) based on the original data provided at the slot *ca* of a consolidated *COST* object.

It is assumed that the biological sampling is representative of the catches. If the number of samples by defined strata is lower than ten, variance estimates should not be considered reliable.

The results of this method are included as components of the object of class "dbeObject".

**Author(s)**

Paz Sampedro

**References**

B. Efron and R. Tibshirani (1993). *An Introduction to the Bootstrap*. Chapman & Hall.

**See Also**

`dbeOutput`, `dbeOutput`, `dbeOutput`

## Examples

```
## Mean weight-at-length/age and variance for IFREMER sole data
## Estimates are made by quarter and area
#
#data (sole)
#sole.str <- strIni(timeStrata="quarter",spaceStrata="area")
#sole.cons <- csDataCons(csDataVal(sole.cs),sole.str)
#sole.dbeOutput <- dbeObject(desc="Results of design based estimates",species="Solea solea",
#                             param="weight",strataDesc=sole.str,methodDesc="Bootstrap")
#sole.Weight <- bpBoot(sole.dbeOutput,sole.cons, sample.boot=TRUE)
```

---

 bpEstim

*Analytical estimates of biological parameters*


---

## Description

This method implements analytical estimates of empirical weight-at-length/age, maturity-at-length/age, sex-ratio-at-length/age and variances. The needed parameters are from input 'dbeOutput' slots. Estimates-at-age can be calculated by injecting the length distribution resultin from 3 different sampling data : *ca* table or *hl* table from input consolidated object, or total number-at-length from an input *dbeOutput* object. In the latter case, *totalN* and *totalW* slots are also inserted in output *dbeOutput* object.

## Usage

```
bpEstim(dbeOutput,object,dbeLD,adjust=TRUE,immature.scale=1,...)
```

## Arguments

<code>dbeOutput</code>	A <i>dbeOutput</i> object.
<code>object</code>	A <i>csDataCons</i> object.
<code>dbeLD</code>	Optionnal. A <i>dbeOutput</i> object with total numbers-at-length data (possibly resulting from <i>RaiseLgth</i> method). If missing, injected length distribution for estimates-at-age calculation is created within input consolidated object. In that case, the source table is specified with <i>adjust</i> parameter.
<code>adjust</code>	Logical. Only useful if <i>dbeLD</i> parameter is missing. If FALSE, length distribution in <i>object</i> 's CA table is supposed to be representative of the catch (all calculations are made within CA). If TRUE (default value), estimates-at-age are calculated by injecting <i>object</i> 's HL information.
<code>immature.scale</code>	Numeric or character. Specifies the value(s) in <i>matStage</i> field (from ca table in <i>object</i> ) for which the individuals are defined as immature.
<code>...</code>	Further arguments.

## Author(s)

Mathieu Merzereaud

## See Also

`dbeOutput`, `dbeOutput`

## Examples

```

data(sole)
#stratification object
strDef <- strIni(timeStrata="quarter",spaceStrata="area")
#consolidated object
object <- csDataCons(csDataVal(sole.cs),strDef)
#dbeOutput initial object with needed parameters
dbeOutput <- dbeObject(desc="My object",species="Solea solea",param="weight",
                      strataDesc=strDef,methodDesc="analytical")

lWeight <- bpEstim(dbeOutput,object)

```

---

dBeCalc

*CI and CV calculation*


---

## Description

Method for calculating coefficients of variation or confidence intervals from 'dbeOutput' object estimates. Input object can optionally be updated with resulting table.

## Usage

```
dBeCalc(object,type="CI",vrbl="l",probs=c(0.025,0.975),replicates=FALSE,update=TRUE,...)
```

## Arguments

<b>object</b>	A <i>dbeOutput</i> object.
<b>type</b>	Character. "CI" for confidence interval calculation, or "CV" for coefficients of variation.
<b>vrbl</b>	Character specifying 'dbeOutput' estimates on which calculation is applied : "l" for length structure, "a" for age structure, "n" for total number estimates, "w" for total weight estimates.
<b>probs</b>	Numeric vector of probabilities with values in [0,1]. Defines CI bounds (relevant only if type="CI"). See <i>quantile</i> .
<b>replicates</b>	Logical. If TRUE, calculation is made from @...\$rep elements ; if FALSE, @...\$estim and @...Var 'dbeOutput' data are used.
<b>update</b>	Logical. If TRUE, updated 'dbeOutput' object is returned ; if FALSE, only resulting dataframe is returned
<b>...</b>	Further arguments used as ' <i>quantile</i> method input parameter (if type="CI" and besides probs parameter).

## Details

If calculation is made from replicates (see *replicates* parameter), confidence interval is estimated using *quantile* fonction with *probs* and ... parameters. If calculation is made from estimates, normal distribution of total estimates is assumed to compute confidence intervals. Possible resulting negative bounds are automatically replaced by 0 in output object.

**Author(s)**

Mathieu Merzereaud

**See Also**

dbeOutput, dbePlot, quantile

**Examples**

```

data(sole)
#stratification
strD <- strIni(timeStrata="quarter",techStrata="commCat")
#only market sampling data and biological parameters are kept
csObject <- csDataCons(csDataVal(subset(sole.cs,sampType%in%c("M","V"))),strD)
clObject <- clDataCons(clDataVal(sole.cl),strD)
#initializing the output object
dbeOutput <- dbeObject(species="Solea solea",catchCat="LAN",strataDesc=strD)

# total numbers at length
dbeOutput <- RaiseLgth (dbeOutput, csObject, clObject)
#object is updated with cv-at-length
dbeOutput <- dbeCalc(dbeOutput,type="CV")

```

---

**dbeCorrPlot**
*Levelplot of a correlation matrix between estimates at age (replicates)*


---

**Description**

Method for plotting an image of the correlation matrix between estimates at age, from *dbeOutput* 'ageStruc' slot replicates.

**Usage**

```
dbeCorrPlot(object,dispKey=TRUE,...)
```

**Arguments**

<b>object</b>	A <i>dbeOutput</i> object with replicates information in 'ageStruc' slot.
<b>dispKey</b>	Logical. If TRUE, a legend is drawn
<b>...</b>	Further graphical arguments.

**Author(s)**

Mathieu Merzereaud

**See Also**

dbeOutput

---

dbeObject	<i>Initialized 'dbeOutput' object creator</i>
-----------	---

---

### Description

This function returns an initialized *dbeOutput* object that can be used as input object for 'COSTdbe' package methods.

### Usage

```
dbeObject(desc, species, catchCat, param, strataDesc, methodDesc, ...)
```

### Arguments

desc	'desc' slot of returned 'dbeOutput' object.
species	'species' slot of returned 'dbeOutput' object.
catchCat	'catchCat' slot of returned 'dbeOutput' object.
param	'param' slot of returned 'dbeOutput' object.
strataDesc	'strataDesc' slot of returned 'dbeOutput' object.
methodDesc	'methodDesc' slot of returned 'dbeOutput' object.
...	Further arguments.

### Author(s)

Mathieu Merzereaud

### See Also

dbeOutput

### Examples

```
obj <- dbeObject(desc="My object",species="Solea solea",catchCat="DIS",methodDesc="analytical")
```

---

dbeOutput-class	<i>Class "dbeOutput"</i>
-----------------	--------------------------

---

### Description

Outcome object from *COSTdbe* methods

### Slots

slot	desc	elements	class	description
desc			character	Descriptive slot
species			character	Species
catchCat			character	Catch category (eg "LAN", "DIS" or "all")
param			character	Parameter estimated (eg "maturity","sex-ratio",...)
strataDesc			strIni	Stratification considered
methodDesc			character	Used method (eg "analytical","bootstrap" or "Bayesian")

All the following slots contain numerics or dataframes that will be generated by COSTdbe methods :

<b>nSamp</b>		list	Number of samples
	len	data.frame	Number of length samples.
	age	data.frame	Number of age samples.
	<b>nMes</b>	list	Number of individual measured
	len	data.frame	Number of individual measured for length data.
	age	data.frame	Number of individual measured for age data.
<b>lenStruc</b>		list	Estimates of the length structure
	estim	data.frame	Final estimates ( <i>length</i> field added).
	rep	data.frame	Resampling replicates ( <i>length</i> and <i>iter</i> fields added).
	<b>lenVar</b>	data.frame	Estimates of the variance of 'lenStruc'
<b>lenNum</b>		list	Precision estimates for length structure
	ci	data.frame	Confidence intervals.
	cv	data.frame	Coefficients of variation.
	DCRcvIndicator	numeric	Weighted global cv.
<b>ageStruc</b>		list	Estimates of the age structure
	estim	data.frame	Final estimates ( <i>age</i> field added).
	rep	data.frame	Resampling replicates ( <i>age</i> and <i>iter</i> fields added).
	<b>ageVar</b>	data.frame	Estimates of the variance of 'ageStruc'
<b>ageNum</b>		list	Precision estimates for age structure
	ci	data.frame	Confidence intervals.
	cv	data.frame	Coefficients of variation.
	DCRcvIndicator	numeric	Weighted global cv.
<b>totalN</b>		list	Estimates of the total number of the parameters
	estim	data.frame	Final estimates.
	rep	data.frame	Resampling replicates ( <i>iter</i> field added).
	<b>totalNvar</b>	data.frame	Estimates of the variance of 'totalN'
<b>totalNnum</b>		list	Precision estimates for total numbers
	ci	data.frame	Confidence intervals.
	cv	data.frame	Coefficients of variation.
	DCRcvIndicator	numeric	Weighted global cv.
<b>totalW</b>		list	Estimates of the total weight of the parameters
	estim	data.frame	Final estimates.
	rep	data.frame	Resampling replicates ( <i>iter</i> field added).
	<b>totalWvar</b>	data.frame	Estimates of the variance of 'totalW'
<b>totalWnum</b>		list	Precision estimates for total weights
	ci	data.frame	Confidence intervals.
	cv	data.frame	Coefficients of variation.
	DCRcvIndicator	numeric	Weighted global cv.

### Author(s)

Mathieu Merzereaud

### See Also

totVolume, dbePlot

### Examples

```
showClass("dbeOutput")
```



---

dbePlot	<i>Graphical display of 'dbeOutput' final estimates</i>
---------	---

---

## Description

Method for plotting final estimates from an input 'dbeOutput' object.

## Usage

```
dbePlot(object, elmt, type="bar", Xstratum=NULL, step=NA, dispKey=TRUE, indScale=FALSE, ...)
```

## Arguments

<code>object</code>	A <i>dbeOutput</i> object.
<code>elmt</code>	Character specifying an element (a dataframe) of <i>dbeOutput</i> 'object'. For example, "lenStruc\$estim", "ageVar" or "totalNnum\$cv". 'rep' elements are not accepted ; see <i>dbePlotRep</i> .
<code>type</code>	Character specifying the type of the drawn plot. To be chosen between "bar" (default value), "point" and "line".
<code>Xstratum</code>	Stratum displayed on x-axis if 'elmt' doesn't point at length or age structure information. To be chosen between "time", "space", "technical" and NULL (default value).
<code>step</code>	Numeric. If given, empty length or age classes will be considered and displayed, according to specified value.
<code>dispKey</code>	Logical. If TRUE, a describing key is displayed
<code>indScale</code>	Logical. If TRUE, y-axis scale is specific to each panel. If FALSE, the same limits are used for every panel.
<code>...</code>	Further graphical arguments such as <i>col</i> , <i>lwd</i> , <i>lty</i> , <i>pch</i> , <i>cex</i> , <i>font</i> , <i>rot</i> ,...

## Author(s)

Mathieu Merzereaud

## See Also

dbeOutput, dbePlotRep

## Examples

```
data(sole)

#stratification object
strDef <- strIni(timeStrata="quarter",spaceStrata="area")
#consolidated object
object <- csDataCons(csDataVal(sole.cs),strDef)
#dbeOutput initial object with needed parameters
dbeOutput <- dbeObject(desc="My object",species="Solea solea",param="weight",
                      strataDesc=strDef,methodDesc="analytical")

lW <- bpEstim(dbeOutput,object)
```

```
dbPlot(1W,elmt="ageStruc$estim",step=1,ylab="Mean weight (g)")
```

---

dbePlotRep

*Graphical display of 'dbeOutput' replicates*


---

## Description

Method for plotting replicates data from an input 'dbeOutput' object (distribution of total estimates replicates, description of length or age structure replicates).

## Usage

```
dbPlotRep(object,Slot,probs=c(0.05,0.95),step=NA,origin=TRUE,dispKey=TRUE,
           KurtSkew=FALSE,...)
```

## Arguments

<b>object</b>	A <i>dbeOutput</i> object with replicates information.
<b>Slot</b>	A <i>dbeOutput</i> slot with a 'rep' element (eg "totalW" or "lenStruc").
<b>probs</b>	Numeric with 2 elements (or NA for no display) : quantiles defining displayed confidence intervals for each set of replicates (per stratum and length/age class). Only useful for "lenStruc" or "ageStruc" <i>Slot</i> parameter
<b>step</b>	Numeric. If given, empty length or age classes will be considered and displayed, according to specified value. Only useful for "lenStruc" or "ageStruc" <i>Slot</i> parameter.
<b>origin</b>	Logical. Only useful for "lenStruc" or "ageStruc" <i>Slot</i> parameter. If TRUE, original raw estimates, stored in 'rep' object for <i>iter</i> value at 0, are displayed.
<b>dispKey</b>	Logical. If TRUE, a legend is drawn
<b>KurtSkew</b>	Logical. If TRUE, skewness and kurtosis values are calculated for each set of replicates (per stratum and length/age class) and as specific plot is displayed. Only useful for "lenStruc" or "ageStruc" <i>Slot</i> parameter.
<b>...</b>	Further graphical arguments.

## Details

This method provides 3 types of graphical outputs. If *Slot* is "totalN" or "totalW", a frequency histogram of total estimates replicates is displayed. If *Slot* is "lenStruc" or "ageStruc", then means at length/age calculated from replicates are showed with confidence interval (if *probs* is given) and raw estimates (if *origin* is TRUE). If *KurtSkew* is TRUE, skewness and kurtosis values at length/age are calculated from replicates, and drawn.

## Author(s)

Mathieu Merzereaud

## See Also

dbOutput

---

plus-dbeOutput	<i>Addition of 'dbeOutput' objects</i>
----------------	--

---

### Description

This method implements addition of 'dbeOutput' objects provided by COSTdbe package.

### Details

Every dataframe are summed, except "num" elements that are set to NA.

### Methods

```
signature(e1 = "dbeOutput", e2 = "dbeOutput")
```

---

propMissLgthCons	<i>Proportions of empty length classes in an age-length key</i>
------------------	---

---

### Description

This method calculates empty length classes proportion in an age-length key obtained from a 'csDataCons' object (ca table). 'pEmpty' element describes the proportion of missing LC per alk within hl table. 'pEmptyExtr' submits the proportion of extrema missing LC (among all missing LC) per alk within hl table.

### Usage

```
propMissLgthCons(object, ...)
```

### Arguments

object	A <i>csDataCons</i> object.
...	Further arguments.

### Author(s)

Mathieu Merzereaud

### See Also

alkLgthRec, viewGapsAlkCons, csDataCons

### Examples

```
data(sole)
#subset to "27.7.d" & "27.7.e" areas
csSub <- subset(sole.cs, area%in%c("27.7.d", "27.7.e"), table="hh")
conSole.cs <- csDataCons(csDataVal(csSub), strIni(spaceStrata="area"))

propMissLgthCons(conSole.cs)
```

---

rbind2-dbeOutput	<i>rbind2 for 'dbeOutput' objects</i>
------------------	---------------------------------------

---

### Description

This method implements rbind2 for the 'dbeOutput' class provided by COSTdbe package.

### Details

Only dataframes are combined in the output object. Its descriptive slots are the same as *x*'s, and *dcrCVIndicator* elements are set to NA.

### Methods

```
signature(x = "dbeOutput", y = "dbeOutput")
```

---

sampStrDef	<i>Definition of the sampling strategy</i>
------------	--

---

### Description

This method defines from 'csData' or 'csDataVal' datasets what is the sampling strategy at haul level (one value per *hh* row) and at trip level (one value per *tr* row).

### Usage

```
sampStrDef(x, species, fraction="LAN", fishAct="foCatEu5", sampPar=TRUE, ...)
```

### Arguments

<b>x</b>	A <i>csData</i> or <i>csDataVal</i> object.
<b>species</b>	Character specifying species for which sampling strategy must be defined
<b>fraction</b>	Character specifying catch category for which sampling strategy must be defined. To be chosen between "LAN" (default value) for landings and "DIS" for discards.
<b>fishAct</b>	Character specifying fishing activity field taken into account for sampling strategy definition. To be chosen between "foCatEu5" (default value), "foCatEu6" and "focatNat".
<b>sampPar</b>	Logical. Checks if given species is considered to be automatically sampled (TRUE, default value) or not (FALSE) during the sampling process.
<b>...</b>	Further arguments.

**Value**

Returned elements are `$sampStrategyTR` that describes the sampling strategy at trip level, and `$sampStrategyHH` for sampling strategy at haul level. Used codification is :

1	Sampling for length in fishing trips - Unsorted catch
2	Sampling for length in fishing trips - Commercial Categories
3	Sampling for length in Commercial categories
4	Sampling for age in fishing trips - Unsorted catch
5	Sampling for age in fishing trips - Commercial Categories
6	Sampling for age in commercial categories
0	No sampling or undefined strategy
9	Several defined strategies (trip level)

**Author(s)**

Mathieu Merzereaud

**See Also**

`csData`, `csDataVal`

**Examples**

```
data(sole)
sampStrDef(sole.cs,species="Solea solea")
```

---

sampledFO

*Sampled haul index*

---

**Description**

Method returning from a 'csDataCons' object an index of sampled hauls for a given species and a given fraction.

**Usage**

```
sampledFO(x,species,fraction="LAN",sampPar=TRUE,...)
```

**Arguments**

<code>x</code>	A <i>csDataCons</i> object.
<code>species</code>	Given species for which sampling must be considered.
<code>fraction</code>	Given catch category for which sampling must be considered. To be chosen between "LAN" (default value) and "DIS".
<code>sampPar</code>	logical specifying if given species is considered to be automatically sampled during the sampling process (default value is TRUE).
<code>...</code>	Further arguments.

**Value**

A list with 2 vectors of the same length as HH table from input 'csDataCons' object. `$sampWt` is the index for weight sampling, `$sampLg` is for length sampling (numbers). 1 means that the haul is sampled/measured and the species is caught in the fraction, 0 means that the haul is sampled/measured but the species is not caught in the fraction (0-values), and NA means that the haul is not sampled/measured.

**Author(s)**

Mathieu Merzereaud

**See Also**

`csDataCons`

**Examples**

```
data(sole)
x <- csDataCons(csDataVal(sole.cs))
sampledFO(x,species="Solea solea",fraction="LAN")
```

---

`stratAggreg`

*Aggregation of 'dbeOutput' table*

---

**Description**

This method is aggregating (summing in case of number or weight estimates, or averaging as to mean parameters) input 'dbeOutput' object tables over chosen stratification(s).

**Usage**

```
stratAggreg(object,timeStrata=TRUE,spaceStrata=TRUE,techStrata=FALSE,wt="totalW",...)
```

**Arguments**

<code>object</code>	A <i>dbeOutput</i> object.
<code>timeStrata</code>	Logical. If TRUE, aggregation is made over time strata.
<code>spaceStrata</code>	Logical. If TRUE, aggregation is made over space strata.
<code>techStrata</code>	Logical. If TRUE, aggregation is made over technical strata.
<code>wt</code>	Character. Input <i>object</i> slot with which a weighted mean over strata is computed (only if <i>param</i> slot is "weight", "maturity" or "sex"). Possible values are "totalW" or "totalN". Check that specified slot is not empty, otherwise resulting table of estimates will also be empty.
<code>...</code>	Further arguments

**Details**

Aggregating process is only applied to these tables : `nSamp`, `nMeas`, `lenVar`, `ageVar`, `totalNvar`, `totalWvar`, and all `estim` and `rep` list elements. Other tables in output object are empty (so, for example, 'dbeCalc' method must be called to calculate and insert `cv` table in this new object). **WARNING** : summing variances requires some strong probability assumptions within strata, such as uncorrelated variables. In the 'variance at age' case, this can be problematic since the same age-length key is used for every technical strata.

**Value**

An updated object of class `dbeOutput`.

**Author(s)**

Mathieu Merzereaud

**See Also**

`dbeOutput`, `dbeObject`

---

`tkFillGaps`

*Addition of virtual individuals in age-length keys*

---

**Description**

This method displays stratified ALKs from a `csDataCons` object in a GUI table that allows to add 'virtual' individuals. Input object is then updated and returned (see *Value* section).

**Usage**

```
tkFillGaps(object)
```

**Arguments**

`object`            A `csDataCons` object with `ca` information.

**Details**

See `viewGapsAlkCons` for a description of the codification used in displayed ALKs. Interface has been computed with `tcltk` package.

**Value**

An updated `csDataCons` object. `CA` table is updated with new individuals (one per line). New `PSUid` and `trpCode` values are then created, and `tr` table is also updated with those new 'virtual trips'.

**Author(s)**

Mathieu Merzereaud

**See Also**

csDataCons, viewGapsAlkCons

**Examples**

```
data(sole)
#subset to "27.7.d" & "27.7.e" areas
csSub <- subset(sole.cs,area%in%c("27.7.d","27.7.e"),table="hh")
object <- csDataCons(csDataVal(csSub),strIni(spaceStrata="area"))
#obj <- tkFillGaps(object)
#tail(obj)
```

---

totVolume	<i>Estimation of total volume of discards or/and landings (weight, number or number-at-length)</i>
-----------	--

---

**Description**

Generic function to estimate total volume of discards or/and landings (weight, number or number-at-length) based on various raising methods.

**Usage**

```
totVolume(dbeOutput,csObject,ceObject,clObject,...)
```

**Arguments**

dbeOutput	A <i>dbeOutput</i> object. All necessary information for calculation process are taken in the first slots (species, catch category,...). See <i>dbeObject</i> method for object initialization.
csObject	A <i>csDataCons</i> object matching 'dbeOutput' specifications.
ceObject	A <i>ceDataCons</i> object matching 'dbeOutput' specifications.
clObject	An optionnal <i>clDataCons</i> object matching 'dbeOutput' specifications. If specified, raising is made with ratio-to-landings method.
...	Further arguments such as:
type	Specification of the raising method : "trip" (default value) for raising by trip, "fo" for raising by fishing operations, "fd" for raising by fishing days,"landings" for ratio-to-total landings raising method, and "time" for ratio-to-fishing duration raising method.
val	Estimated parameter. To be chosen between "weight" (default value), "number" and "nAtLength".
sampPar	logical specifying if given species is considered to be automatically sampled during the sampling process (default value is TRUE).
landSpp	character vector describing the species considered in the 'volume of landings' variable if chosen raising method is ratio-to-landings (see 'clObject' description).

**Value**

An updated object of class *dbeOutput*.



**Author(s)**

Mathieu Merzereaud

**References**

Vigneau, J. (2006) *Raising procedures for discards : Sampling theory (Toward agreed methodologies for calculating precision in the discard programmes)*. Working document in support of PGCCDBS (Rostock, 2006).

**See Also**

dbeOutput, dbeObject, csDataCons, ceDataCons, clDataCons

**Examples**

```
data(sole)

#consolidated datasets are built
strDef <- strIni(timeStrata="quarter",techStrata="foCatEu5")
csObject <- csDataCons(csDataVal(sole.cs),strDef)
clObject <- clDataCons(clDataVal(sole.cl),strDef)
ceObject <- ceDataCons(ceDataVal(sole.ce),strDef)

#dbeOutput initial object
obj <- dbeObject(desc="My object",species="Solea solea",catchCat="DIS",strataDesc=strDef,
                 methodDesc="analytical")

##raising by trip
newObj <- totVolume(obj,csObject,ceObject)
newObj
```

---

vesselRaise

---

*Estimate numbers-at-age and numbers-at-length*


---

**Description**

Estimate numbers-at-age and numbers-at-length from market sampling data with Sampling strategy: Length + ALK, Commercial categories within Trips Sampling source: Auction/Market/Harbour Landed fraction vesselRaise.boot provides variance estimates by bootstrapping the age and length samples. vesselRaise.an provides analytical variance estimates derived from the proportions in the ALK and variation in numbers per kg in the length samples.

**Usage**

```
vesselRaise.an(csObject, clObject, dbeOutp, age.plus = -1)
vesselRaise.boot(csObject, clObject, dbeOutp, B, age.plus = -1, bootMethod = "samples")
```

**Arguments**

<code>csObject</code>	A <i>csDataCons</i> object of sampling data
<code>clObject</code>	A <i>clDataCons</i> object of landings data
<code>dbeOutp</code>	A <i>dbeOutput</i> object that provides sample information and stores the function's results.
<code>B</code>	numeric, length=1. Number of bootstrap iterations
<code>age.plus</code>	numeric, length=1. All ages greater than <code>age.plus</code> are set to <code>age.plus</code> to form a plus group
<code>bootMethod</code>	only acceptable value is "samples" to bootstrap samples.

**Details**

Estimates by length are provided for each combination of the space, time and technical strata specified in `dbeOutp`. Estimates by age are provided for each combination of the space and time strata because the biological data (*ca* table) does not include technical stratification. Estimation for mixed species landings is not implemented; the species in the biological data must match the *taxon* field in the landings data. Similarly, estimates are not given by sex if unsexed length data and sexed age data are used. Either use combined-sex length and age data or single-sex length and age data. If *clDataCons* includes adjustments to the landed weight these are applied as:  $\text{Total Landings} = \text{Official Landings} * \text{Multiplier} + \text{Unallocated Catch} + \text{Misallocated Catch}$  If the multiplier field is NA it is assumed to be one, if unallocated catch and misallocated catch are NA they are assumed to be zero.

**Value**

The following slots of `dbeOutp` are filled:

<code>methodDesc</code>	Method of estimation
<code>nSamp</code>	Number of length samples by technical strata and number of age samples where technical is output as "AgeSamples"
<code>nMes</code>	Number of length measurements by technical strata and number of age measurements where technical is output as "Otoliths"
<code>lenStruc</code>	Numbers-at-length. For <code>vesselRaise.boot</code> bootstrap replicates are also given and <code>iter=0</code> contains estimates from the original data.
<code>lenVar</code>	Variance of numbers-at-length.
<code>ageStruc</code>	Numbers-at-age. For <code>vesselRaise.boot</code> bootstrap replicates are also given and <code>iter=0</code> contains estimates from the original data.
<code>ageVar</code>	Variance of numbers-at-age.
<code>totalN</code>	Total numbers. For <code>vesselRaise.boot</code> bootstrap replicates are also given and <code>iter=0</code> contains estimates from the original data.
<code>totalNvar</code>	Variance of total numbers.
<code>totalW</code>	Total landed weight (kg)

**Note**

You should check the number of samples and age-length data are suitable before calculating estimates. `vesselRaise.an` stops if there are length classes with no age information. `vesselRaise.boot` fills in gaps that are 1 or 2 length groups wide with ages from surrounding length groups, see `alkLgthRec(type="fillMiss", value=2)`.

**Author(s)**

David Maxwell

**References**<http://wwz.ifremer.fr/cost>**See Also**

dbeOutput, dbOutput, dbOutput, dbOutput, dbOutput

**Examples**

```

# load example data set
data("LEMexample")
# Setup objects for output
# LEM.strat was defined when creating consolidated object
LEM.dbeOut = dbObject(desc="Example",species="Microstomus kitt",param="landings",
                      strataDesc=LEM.strat, catchCat="LAN",methodDesc="bootstrap samples")
LEM.dbeOut.an = dbObject(desc="Example",species="Microstomus kitt",param="landings",
                        strataDesc=LEM.strat, catchCat="LAN",methodDesc="analytical")

# Run vesselRaise.boot function. B set to a very low number of iterations for demonstration only.
# example data set is very small so it generates warnings about the number of samples.
LEM.dbeOut = vesselRaise.boot (csObject = LEM.CScon, clObject = LEM.CLcon,
                              dbeOutp = LEM.dbeOut, B = 3 )
dbePlotRep(LEM.dbeOut,"lenStruc") # outputs to 2 pages turn graph history on, to see the first page

# Run vesselRaise.an function
LEM.dbeOut.an = vesselRaise.an (csObject = LEM.CScon, clObject = LEM.CLcon, dbeOutp = LEM.dbeOut.an)
# CV (see function dbCalc for full implementation of calculating CV and confidence intervals)
100*sqrt(LEM.dbeOut.an@ageVar$value)/LEM.dbeOut.an@ageStruc$estim$value

```

viewGapsAlkCons

*Calculation and display of age-length keys with gaps underlining***Description**

This method calculates and underlines empty length classes in an age-length key from a given 'csDataCons' object (ca table). '.' shows length classes that are not recorded in hl for the specified stratum. '-' shows length classes that are recorded in hl but not in ca, for the specified stratum.

**Usage**

viewGapsAlkCons(object,...)

**Arguments**

object            A *csDataCons* object.  
 ...              Further arguments.

**Author(s)**

Mathieu Merzereaud

**See Also**

alkLgthRec, propMissLgthCons, csDataCons

**Examples**

```
data(sole)
  #subset to "27.7.d" & "27.7.e" areas
csSub <- subset(sole.cs,area%in%c("27.7.d","27.7.e"),table="hh")
conSole.cs <- csDataCons(csDataVal(csSub),strIni(spaceStrata="area"))

viewGapsAlkCons(conSole.cs)
```

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