Package 'mads'

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Depends mrds, stats

Suggests testthat

Type Package

Title Multi-Analysis Distance Sampling

Version 0.1.5

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Description Performs distance sampling analyses on a number of species
accounting for unidentified sightings, model uncertainty and covariate
uncertainty.

BugReports https://github.com/DistanceDevelopment/mads/issues

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Collate 'accumulate.results.R' 'calculate.dht.R'
'check.bootstrap.options.r' 'check.convergence.R'
'check.fitted.R' 'check.covar.uncertainty.R'
'check.ddf.models.R' 'check.species.code.definitions.R'
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'summary.ma.species.R' 'summary.ma.unid.R'

NeedsCompilation no

Repository CRAN

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R topics documented:

---

accumulate.results   *Enters the prorated results into the bootstrap.results array*

Description

Enters the prorated results into the bootstrap.results array

Usage

```
accumulate.results(n, bootstrap.results, formatted.results, clusters)
```

Arguments

`n`	index of the current bootstrap iteration
`bootstrap.results`	
	list of 4-dimensional arrays containing the bootstrap results
`formatted.results`	
	list of data objects similar to the dht class
`clusters`	boolean are the observations clusters of individuals bootstrap results

Value

list of 4-dimensional arrays containing the updated

Author(s)

Laura Marshall

---

calculate.dht	*Calculates the abundance for each species code including the unidentified codes if supplied.*

Description

Calculates the abundance for each species code including the unidentified codes if supplied.

Usage

```
calculate.dht(species.name, species.field.name, model.index, ddf.results,
  region.table, sample.table, obs.table, dht.options)
```

Arguments

`species.name`	character vector of species codes
`species.field.name`	
	character vector giving the field name of the ddf data that contains the species codes
`model.index`	named character vector which acts as a look up table for duplicate detection function models
`ddf.results`	a list of ddf objects
`region.table`	dataframe of region records - Region.Label and Area
`sample.table`	dataframe of sample records - Region.Label, Sample.Label, Effort
`obs.table`	dataframe of observation records with fields object, Region.Label, and Sample.Label which give links to sample.table, region.table and the data records used in `model`
`dht.options`	a list of the options to be supplied to mrds::dht

Value

a list of dht objects, one for each species code

Author(s)

Laura Marshall

See Also

`mrds::dht`

---

check.convergence   *Checks whether the model has converged*

Description

Checks whether the model has converged

Usage

```
check.convergence(ddf.model)
```

Arguments

ddf.model   ddf object

Value

boolean

Author(s)

Laura Marshall

---

check.covar.uncertainty

Performs checks on the covariate.uncertainty dataframe

Description

Ensures that where necessary the values are characters and that only supported sampling distributions have been selected.

Usage

```
check.covar.uncertainty(covariate.uncertainty)
```

Arguments

covariate.uncertainty

> dataframe containing information used to parametrically resample data or NULL if not required

Value

verified covariate.uncertainty dataframe

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

See Also

```
execute.multi.analysis
```

---

check.ddf.models   *Checks the list of model names supplied by the user*

Description

Performs various checks on the models and model names supplied by the user, including checking that the data in each model are the same across species codes to ensure valid comparison using the AIC/AICc/BIC selection criteria.

Usage

```
check.ddf.models(model.names, ddf.models)
```

Arguments

`model.names`	a list of vectors of model names. Each list element is named according to the species code.
`ddf.models`	a list of ddf objects named in model.names

Details

In addition, this routine establishes whether the analyses are double observer or not and whether the observations are individuals of clusters.

Value

list of two boolean values relating to cluster size and double observer analyses.

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

See Also

`execute.multi.analysis`

`check.fitted`	*Checks whether the model's fitted values make sense*

Description

Checks whether the model's fitted values make sense

Usage

```
check.fitted(ddf.model)
```

Arguments

`ddf.model`	ddf object

Value

boolean

Author(s)

Laura Marshall

check.species.code.definitions

Checks the list of species code deifinitions supplied by the user

Description

Firstly, it checks that there are not multiple definitions for the same species code. Secondly, it checks that the names of the ddf models correspond to the names in the species code definitions. Lastly, it checks that definitions are provided for all species codes and if not it adds the missing definitions assuming they correspond to identified categories

Usage

```
check.species.code.definitions(species.code.definitions, species.name)
```

Arguments

species.code.definitions

a list with an element for each unidentified code which contains a vector of corresponding identified species codes or NULL if not required

species.name   a vector of species names for which model names were supplied in the ddf.models list passed to execute.multi.analysis by the user.

Value

updated species.code.definitions list

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

See Also

execute.multi.analysis

---

check.species.presence

Checks the list of species presence definitions supplied by the user

---

Description

Performs a numer of checks to ensure the list has been defined correctly. If no list was specified one is created assuming all species are present in all strata.

Usage

```
check.species.presence(species.presence, species.name, strata.name)
```

Arguments

species.presence

a list with an element for each strata which contains a vector of corresponding species codes for those species which occur in that strata or NULL if it is to be data driven.

species.name   a vector of species names for which model names were supplied in the ddf.models list passed to execute.multi.analysis by the user.

strata.name   character vector of strata names

Value

updated species.presence list

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

See Also

execute.multi.analysis

---

create.obs.table *Creates a subsetted observation table*

Description

Subsets the obs.table dataframe supplied to only contain the observations of interest.

Usage

```
create.obs.table(obs.table, ddf.data, subset.variable, subset.value)
```

Arguments

obs.table	dataframe of observation records with fields object, Region.Label, and Sample.Label which give links to sample.table, region.table and the data records used in model
ddf.data	dataframe containing the observations
subset.variable	
	variable name supplied as a character
subset.value	character value on which to subset the data

Value

dataframe containing the subset of the obs.table

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

---

create.param.arrays *Creates a list of arrays for storing the ddf results*

Description

Creates a list of arrays. These are used to store the parameter estimates, a record of convergence, selection criteria values and which model was selected in the case of model uncertainty.

Usage

```
create.param.arrays(model.names, ddf.models, n, criteria)
```

Arguments

`model.names`	a list of character vectors of model names with the elements named by species code
`ddf.models`	a list of all the ddf models named in model.names.
`n`	the number of bootstrap iterations to be completed.
`criteria`	the name of the model selection criteria.

Value

list of arrays

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

`create.result.arrays`   *Creates a list of arrays for storing the dht results*

Description

Creates a list of arrays. These are used to store the summary, abundance and density outputs of the dht routine called from `mrds`.

Usage

```
create.result.arrays(species.name, species.code.definitions, region.table,
  clusters, n)
```

Arguments

`species.name`	a list of all the species in the analysis
`species.code.definitions`	
	a list with an element for each unidentified code which contains a vector of corresponding identified species codes or NULL if not required
`region.table`	dataframe of region records - Region.Label and Area
`clusters`	boolean, TRUE if observations are of cluster, FALSE if observations are of individuals.
`n`	the number of bootstrap iterations to be completed.

Value

list of arrays

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

---

execute.multi.analysis

Performs Multiple Analyses on Distance Data

Description

Analyses are performed for multiple species contained within the same dataset. Individual detection function analyses of each species must have already been completed using the ddf function in the mrds library. This function may then perform additional tasks such as assessing variance via a non-parametric bootstrap, including covariate variability via a parametric bootstrap, including model uncertainty and dealing with species codes which relate to unidentified sightings.

Usage

```
execute.multi.analysis(species.code, unidentified.sightings = NULL,
  species.presence = NULL, covariate.uncertainty = NULL,
  models.by.species.code, ddf.model.objects,
  ddf.model.options = list(criterion = "AIC", species.field.name = "species"),
  region.table, sample.table, obs.table, dht.options = list(convert.units =
  1), bootstrap, bootstrap.options = list(resample = "samples", n = 1,
  quantile.type = 7), silent = FALSE)
```

Arguments

species.code   vector of all the species codes to be included in the analysis

unidentified.sightings

a list with an element for each unidentified code which contains a vector of corresponding identified species codes or NULL if not required

species.presence

must be specified if species.code.definitions is specified. A list with an element for each strata which contains the vector of species codes present in that strata

covariate.uncertainty

a dataframe detailing the variables to be resampled - variable.layer, variable.name, cor.factor.layer, cor.factor.name , uncertainty.layer, uncertainty.name, uncertainty.measure, sampling.distribution. or NULL if not required

models.by.species.code

a list of character vectors of model names with the elements named by species code

ddf.model.objects

> a list of all the ddf models named in models.by.species.code

ddf.model.options

> a list of options 1) selection.criterion either "AIC", "AICc" or "BIC" 2) species.field.name describing the field name in the ddf dataset containing species codes.

region.table   dataframe of region records - Region.Label and Area

sample.table   dataframe of sample records - Region.Label, Sample.Label, Effort

obs.table   dataframe of observation records with fields object, Region.Label, and Sample.Label which give links to sample.table, region.table and the data records used in model

dht.options   list containing option for dht: convert.units indicated if the distance measurement units are different from shapefile and transect coordinate units.

bootstrap   if TRUE resamples data to obtain variance estimate

bootstrap.options

> a list of options that can be set 1) n: number of repetitions 2) resample: how to resample data ("samples", "observations")

silent   boolean used to surpress some warning messages

Details

This is a new package with limited testing on real data, please drop me a line if you plan on using it (lhm[at]st-and.ac.uk).

The model fitting code in this function obtains its data and the model descriptions from the ddf objects passed in via the ddf.models argument.

If you wish to include model uncertainty then each model which you wish to be included in the analyses must have already been run and should be provided in the ddf.models argument. The model.names argument tells this function which "ddf" objects are associated with which species code in the dataset. This object must be constructed as a list of vectors. Each element in the list must be named corresponding to one of the species codes in the dataset and contain a character vector of object names.

For the majority of analyses the variance will be estimated using a non-parametric bootstrap, indicated by the bootstrap argument. You may select options for the bootstrap using the bootstrap.options argument. This is a list with elements specifying the number of repetitions and whether to resample samples within strata ($resample = "samples") or observations withing strata ($resample = "observations"). In addition, the bootstrap.covariates is a boolean argument specifying whether or not a parametric bootstrap should be performed on any of the covariates. The details of which variables should be resampled and from which distributions should be entered in the covariate.uncertainty dataframe. This dataframe should contain 7 columns with the following names: variable.layer, variable.name, cor.factor.layer, cor.factor.name, uncertainty.layer, uncertainty.name, uncertainty.measure and sampling.distribution. [Currently this is only implemented for the observation layer]. The variable.name and uncertainty.name should be the names of the variable in the dataset giving the covariate to be resampled and the variable containing the uncertainty respectively. The cor.factor.layer specifies the data layer which contains the correction factor variable, although alternatively "numeric" can be entered. The cor.factor.name specifies the name of the correction factor variable or the correction factor value if "numeric" was specified for the correction factor layer. The uncertainty.name should specify what values the uncertainty

variable contains and should be one of ″sd″, ″var″ or ″CV″. The `sampling.distribution` should specify one of the following distributions to parametrically resample from ″Normal″, ″Normal.Absolute″, ″Lognormal.BC″, ″Poisson″ or ″TruncPoissonBC″. The remaning column in this dataset, `variable.correction.factos.` allows the user to specify a value by which the variable should be scaled. If this is not reqied this should be set to 1.

If there are unidentified sightings in the dataset then the `unidentified.sightings` argument should be `true` and a `species.code.definitions` list should be provided. This list must contain one element for every unidentified species code which should be named according to this code. Each element will contain a vector of identified species codes corresponding to those species which the unidentified code could have potentially been. This function uses this information to prorate the abundance estimated from the unidentified species codes to the relevant abundances from the identified codes. The prorating is done individually for each strata. The function can be forced not to prorate to any given species in any selected strata using the `species.presence` argument. This is a list containing one element for each strata, each must be named using the appropriate strata name. Each element should contain a vector of identified species codes corresponding to which species are present in each strata.

Value

object of class "ma" which consists of a list of objects of class "ma.element". Each "ma.element" consists of the following elements:

`individuals`	Summary, N (abundance) and D (density) tables
`clusters`	Summary, N (abundance) and D (density) tables
`Expected.S`	Expected cluster size table
`ddf`	Model details including a summary of convergence and selection as well as parameter estimates for selected models.

Author(s)

Laura Marshall

References

Marques, F.F.C. and S.T. Buckland. 2004. Covariate models for the detection function. In: Advanced Distance Sampling, eds. S.T. Buckland, D.R.Anderson, K.P. Burnham, J.L. Laake, D.L. Borchers, and L. Thomas. Oxford University Press. Gerrodette, T. and Forcada, J. 2005 Non-recovery of two spotted and spinner dolphin populations in the eastern tropical Pacific Ocean. Marine Ecology Progress Series, 291:1-21.

Examples

```
## Not run:

ex.filename<-system.file("testData/input_checks/ddf_dat.robj", package="mads")
load(ex.filename)
ex.filename<-system.file("testData/input_checks/obs_table.robj", package="mads")
load(ex.filename)
ex.filename<-system.file("testData/input_checks/region_table.robj", package="mads")
```

```
load(ex.filename)
ex.filename<-system.file("testData/input_checks/sample_table.robj", package="mads")
load(ex.filename)

#run ddf analyses
ddf.1 <- ddf(dsmodel = ~mcds(key = "hn", formula = ~ size),
             method='ds', data=ddf.dat,meta.data=list(width=4))
ddf.2 <- ddf(dsmodel = ~mcds(key = "hr", formula = ~ size),
             method='ds', data=ddf.dat,meta.data=list(width=4))

model.names <- list("CD"=c("ddf.1","ddf.2"), "WD"=c("ddf.1","ddf.2"),
                    "UnidDol"=c("ddf.1","ddf.2"))
ddf.models  <- list("ddf.1" = ddf.1, "ddf.2" = ddf.2)

unidentified.code.definitions <- list("UnidDol" = c("CD","WD"))
bootstrap.options             <- list(resample="samples", n=10, quantile.type = 7)

results<- execute.multi.analysis(
            species.code = names(model.names),
            unidentified.sightings = unidentified.code.definitions,
            models.by.species.code = model.names,
            ddf.model.objects = ddf.models,
            ddf.model.options = list(criterion="AIC"),
            region.table = region.table,
            sample.table = sample.table,
            obs.table = obs.table,
            bootstrap = TRUE,
            bootstrap.option = bootstrap.options)


## End(Not run)
```

---

fit.ddf.models   *Refits the detection functions to the resampled data*

Description

Fits all the models named in model.names to the associated data supplied in ddf.dat.working. If more than one model is supplied for any species the model with the minimum selection crieteria will be selected.

Usage

```
fit.ddf.models(ddf.dat.working, model.names, ddf.models, criterion,
  bootstrap.ddf.statistics, rep.no, MAE.warnings)
```

Arguments

ddf.dat.working

        list of dataframes containing the data to which the models will be fitted

`model.names`	list of unique character vectors giving the names of the ddf objects for each species.
`ddf.models`	a list of ddf objects
`criterion`	character option specifying the model selection criteria - "AIC", "AICc" or "BIC".
`bootstrap.ddf.statistics`	
	array storing parameter estimates
`rep.no`	numeric value indicating iteration number
`MAE.warnings`	character vector of warning messages

Value

list of ddf objects

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

`format.dht.results`	*Formats the estimated abundances of all species categories, to be consistent with the prorated results.*

Description

Formats the estimated abundances of all species categories, to be consistent with the prorated results.

Usage

```
## S3 method for class 'dht.results'
format(dht.results, species.name, clusters)
```

Arguments

`dht.results`	a list of objects of class dht
`species.name`	a character vectors detailing the species codes
`clusters`	boolean whether observations are clusters of individuals

Value

a list of results with an element for each species

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

---

get.datasets   *Extracts the data and models from the ddf objects*

Description

Compiles a list of unique model combinations, which are stored as character vectors within the list. The associated data for the models in each of the elements of this list are also obtained (these will only be one per set of models as each model group must use the same data). It also constructs a look up table in the from of a named character vector to relate species code to models as these have now been reduced to unique model combinations only.

Usage

```
get.datasets(model.names, ddf.models)
```

Arguments

model.names   a list of character vectors of model names with the elements named by species
               code
ddf.models   a list of the ddf models named in model.names

Value

list with the following elements: unique.model.names - a list of unique model combinations ddf.dat.master - a list of dataframes containing the data used to fit the unique models combinations defined in unique.model.names model.index - named character vector indicating which model is to be used for each species.

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

---

mae.warning *Warning function*

Description

Writes or stores messages for various situations that can occur

Usage

```
mae.warning(warning.msg = NULL, warning.mode = "store", MAE.warnings)
```

Arguments

`warning.msg`	the message to be stored/printed (optional)
`warning.mode`	report or print errors (default report)
`MAE.warnings`	character vector of existing warning messages

Value

None

Author(s)

Dave Miller & Laura Marshall

---

model.description *Extracts the model description*

Description

Returns a description of the model fitted in the ddf object.

Usage

```
model.description(model)
```

Arguments

`model`	a ddf object

Value

mod.str a string descibing the fitted model

Author(s)

Jeff Laake & Laura Marshall

---

process.bootstrap.results

Summarises the bootstrap results.

Description

Creates summary statistics for each species. These consist of dataframes relating to summaries, abundance (N) and density (D) for both individuals and clusters. In addition, summary statistics for expected cluster size (Expected.S) are also calculated.

Usage

```
process.bootstrap.results(bootstrap.results, model.index, clusters,
  bootstrap.ddf.statistics, quantile.type, analysis.options = list(bootstrap,
  n, covariate.uncertainty, clusters, double.observer, unidentified.species,
  species.code.definitions, model.names))
```

Arguments

bootstrap.results
:   list of arrays containing results from the repeated analyses.

model.index
:   named character vector which acts as a look up table for duplicate detection function models.

clusters
:   boolean whether observations are clusters of individuals

bootstrap.ddf.statistics
:   array storing parameter estimates from ddf models

quantile.type
:   numeric value describing which quantile algorithm to use

analysis.options
:   list describing the type of analysis carried out

Value

ma object a list of summary statistics for each species

Note

Internal functions not intended to be called by user.

Author(s)

Laura Marshall

---

process.warnings   *Summarises warnings*

Description

Sumarises warnings generated during the bootstrap and removes the MAE.warnings global object.

Usage

```
process.warnings(MAE.warnings)
```

Arguments

MAE.warnings   character vector of warning messages

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

---

prorate.unidentified   *Prorate the estimated abundances of the unidentified sightings to the other identified species categories.*

Description

The prorating is done individually for each strata. It will prorate the unidentified abundance between the species as defined in the species.code.definitions except where specified that a given species is not present in that strata as defined in the species.presence argument.

Usage

```
prorate.unidentified(dht.results, species.code.definitions, species.presence,
  clusters)
```

Arguments

dht.results   a list of objects of class dht
species.code.definitions
                a list of character vectors detailing the species codes associated with the unidentified code given as the element name.
species.presence
                a list of character vectors defining the species present in each strata.
clusters   boolean whether observations are clusters of individuals of identified species codes corresponding to which species are present in each strata.

Value

a list of proprated results with an element for each species

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

---

renumber.duplicates   *Renumbers the object IDs for the duplicate observations generated when bootstrapping*

Description

Find the largest object ID and renumbers all duplicate IDs starting form this value. The information for the duplicates is also added to the obs.table

Usage

```
renumber.duplicates(ddf.dat, obs.table, double.observer)
```

Arguments

`ddf.dat`	dataframe containing a single dataset with duplicate observations
`obs.table`	dataframe of observation records with fields object, Region.Label, and Sample.Label which give links to sample.table, region.table and the data records used in `model`
`double.observer`	
	boolean indicating if it is a double observer survey

Value

list with 2 elements: ddf.dat dataframe containing a single dataset with new and unique observation IDs obs.table the updated obs.table dataframe containing the new observation IDs

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

See Also

resample.data

---

resample.covariates *Parametrcally resamples selected variables in the dataset.*

Description

Parametricelly resamples specified variables in the dataset based on a measure of uncertainty and a sampling distribution supplied by the user.

Usage

```
resample.covariates(ddf.dat.working, covariate.uncertainty, MAE.warnings)
```

Arguments

ddf.dat.working
: a list of datasets to be used in the analyses

covariate.uncertainty
: a dataframe detailing the variables to be resampled - variable.layer, variable.name, cor.factor.layer, cor.factor.name , uncertainty.layer, uncertainty.name, uncertainty.measure, sampling.distribution.

MAE.warnings
: character vector of warning messages

Details

This function may also apply a correction factor. If numeric is specified the same value will be applied to all observations. If a data layer is specified then this function looks for a variable name in the specified layer of the dataset and applies this as a correction factor.

Value

list of dataframes containing the parametrically resampled data

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

---

resample.data   *Resamples the data for the bootstrap*

Description

Can either resample samples within strata or observations within samples

Usage

```
resample.data(resample, obs.table, sample.table, ddf.dat.master,
  double.observer, subset.variable = "species")
```

Arguments

resample	if "samples" resample samples within strata, if "observations" resample observations within samples.
obs.table	dataframe of observation records with fields object, Region.Label, and Sample.Label which give links to sample.table, region.table and the data records used in model
sample.table	dataframe of sample records - Region.Label, Sample.Label, Effort
ddf.dat.master	list of complete/original datasets
double.observer	
	boolean indicating if it is a double observer survey
subset.variable	
	character describing which variable in the dataset should be used in subsetting the data.

Details

Once the observations have been resampled duplicates are given a different object id and the obs.table is updated appropriately.

Value

a list with 2 elements: ddf.dat.working a list of resampled datasets to be used in the analyses obs.table an updated obs.table with additional entries for data replicates

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

---

rtpois   *Ramdonly generates values from a zero-truncated Poisson distribution*

Description

Generates values from a zero-truncated Poisson distribution with mean equal to that specified. It uses a look up table to check which value of lambda will give values with the requested mean.

Usage

```
rtpois(N, mean = NA)
```

Arguments

N	number of values to randomly generate
mean	mean of the generated values

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

---

store.param.ests   *Updates bootstrap.ddf.statistics*

Description

#' Updates bootstrap.ddf.statistics with the latest parameter estimates from the ddf object supplied.

Usage

```
store.param.ests(bootstrap.ddf.statistics, species.name, model.name, ddf.model,
  rep.no)
```

Arguments

bootstrap.ddf.statistics	
	a list containing various arrays and vectors storing model details.
species.name	name of species the model relates to
model.name	name of ddf object
ddf.model	ddf object
rep.no	iteration number of the bootstrap

Value

bootstrap.ddf.statistics the updated list

Note

Internal function not intended to be called by user.

Author(s)

Laura Marshall

See Also

`create.param.arrays`

---

summary.ma   *Summary of multi-analysis object*

Description

Provides asummary of the fitted detection probability model parameters, model selection criterion, and optionally abundance in the covered (sampled) region and its standard error for all species.

Usage

```
## S3 method for class 'ma'
summary(object, description = FALSE, glossary = FALSE, ...)
```

Arguments

`object`	an object of class ma
`description`	boolean if you would like
`glossary`	a ma model object would like a glossary to be displayed
`...`	unspecified and unused arguments for S3 consistency

Value

list of extracted and summarized objects

Note

This function is called by the generic function `summary` for any `ma` object.

Author(s)

Laura Marshall

---

summary.ma.allspecies   *Summary of multi-analysis object*

Description

Provides asummary of the fitted detection probability model parameters, model selection criterion, and optionally abundance in the covered (sampled) region and its standard error for all species.

Usage

```
## S3 method for class 'ma.allspecies'
summary(object, ...)
```

Arguments

object   a ma model object

...   unspecified and unused arguments for S3 consistency

Value

list of extracted and summarized objects

Note

This function is called by the generic function summary for any ma object.

Author(s)

Laura Marshall

---

summary.ma.allunid   *Summary of multi-analysis object*

Description

Provides asummary of the fitted detection probability model parameters, model selection criterion, and optionally abundance in the covered (sampled) region and its standard error for all species.

Usage

```
## S3 method for class 'ma.allunid'
summary(object, ...)
```

Arguments

object   a ma model object

...   unspecified and unused arguments for S3 consistency

Value

list of extracted and summarized objects

Note

This function is called by the generic function summary for any ma object.

Author(s)

Laura Marshall

---

summary.ma.analysis   *Summary of multi-analysis object*

Description

Provides asummary of the fitted detection probability model parameters, model selection criterion, and optionally abundance in the covered (sampled) region and its standard error for all species.

Usage

```
## S3 method for class 'ma.analysis'
summary(object, ...)
```

Arguments

object   a ma model object

...   unspecified and unused arguments for S3 consistency

Value

list of extracted and summarized objects

Note

This function is called by the generic function summary for any ma object.

Author(s)

Laura Marshall

---

summary.ma.species   *Print a summary of an element of a multi-analysis result correcpond-ing to a single species included in the analyses.*

Description

Provides a summary of the fitted detection probability model parameters, model selection criterion, and optionally abundance in the covered (sampled) region and its standard error. What is printed depends on the corresponding call to summary.

Usage

```
## S3 method for class 'ma.species'
summary(object, species = NULL, ...)
```

Arguments

object	a summary of ma model object
species	optional character value giving the species name, solely for display purposes
...	unspecified and unused arguments for S3 consistency

Author(s)

Laura Marshall

See Also

summary.ma

---

summary.ma.unid   *Summary of multi-analysis object*

Description

Provides asummary of the fitted detection probability model parameters, model selection criterion, and optionally abundance in the covered (sampled) region and its standard error for all species.

Usage

```
## S3 method for class 'ma.unid'
summary(object, species = NULL, ...)
```

Arguments

`object`	an object of class `ma.unid`
`species`	optional character value giving the species name, solely for display purposes
`...`	unspecified and unused arguments for S3 consistency

Value

list of extracted and summarized objects

Note

This function is called by the generic function `summary` for any `ma` object.

Author(s)

Laura Marshall

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