

Package ‘PointedSDMs’

July 21, 2025

Type Package

Title Fit Models Derived from Point Processes to Species Distributions
using 'inlabru'

Version 2.1.3

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URL <https://github.com/PhilipMostert/PointedSDMs>

BugReports <https://github.com/PhilipMostert/PointedSDMs/issues>

Description Integrated species distribution modeling is a rising field in quantitative ecology thanks to significant rises in the quantity of data available, increases in computational speed and the proven benefits of using such models. Despite this, the general software to help ecologists construct such models in an easy-to-use framework is lacking.

We therefore introduce the R package 'PointedSDMs': which provides the tools to help ecologists set up integrated models and perform inference on them.

There are also functions within the package to help run spatial cross-validation for model selection, as well as generic plotting and predicting functions.

An introduction to these methods is discussed in Issac, Jarzyna, Keil, Dambly, Boersch-Supan, Browning, Freeman, Golding, Guillera-Aroita, Henrys, Jarvis, Lahoz-Monfort, Pagel, Pescott, Schmucki, Simmonds and O'Hara (2020) <[doi:10.1016/j.tree.2019.08.006](https://doi.org/10.1016/j.tree.2019.08.006)>.

Depends R (>= 4.1), stats, sf, inlabru (>= 2.12.0), R6 (>= 2.5),
methods,

Imports terra, ggplot2, fmesher, raster, sp (>= 1.4-5), R.devices,
blockCV (>= 3.0.0), FNN

Suggests testthat (>= 3.0.0), sn, INLA (>= 21.08.31), rasterVis,
ggmap, RColorBrewer, cowplot, knitr, kableExtra, rmarkdown,
spocc, covr

Additional_repositories <https://inla.r-inla-download.org/R/testing>

RoxygenNote 7.3.2

License GPL (>= 3)

VignetteBuilder knitr

Config/testthat/edition 3

LazyData false

Encoding UTF-8

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-01-13 17:50:22 UTC

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BBA

Dataset of setophaga caerulescens obtained from the Pennsylvania Atlas of Breeding Birds.

Description

Dataset of setophaga caerulescens obtained from the Pennsylvania Atlas of Breeding Birds.

References

<https://ebird.org/atlaspa/home>

BBS	<i>Dataset of setophaga caerulescens obtained from the North American Breeding Bird survey across Pennsylvania state.</i>
-----	---

Description

Dataset of setophaga caerulescens obtained from the North American Breeding Bird survey across Pennsylvania state.

References

<https://www.pwrc.usgs.gov/bbs/>

BBSColinusVirginianus	<i>Dataset of Colinus Virginianus obtained from the North American Breeding Bird survey across Alabama state.</i>
-----------------------	---

Description

Dataset of Colinus Virginianus obtained from the North American Breeding Bird survey across Alabama state.

References

<https://www.pwrc.usgs.gov/bbs/>

blockedCV	<i>blockedCV: run spatial blocked cross-validation on the integrated model.</i>
-----------	---

Description

This function is used to perform spatial blocked cross-validation with regards to model selection for the integrated model. It does so by leaving out a block of data in the full model, running a model with the remaining data, and then calculating the deviance information criteria (DIC) as a score of model fit.

Usage

```
blockedCV(
  data,
  options = list(),
  method = "DIC",
  predictName = NULL,
  datasetCombs = NULL
)
```

Arguments

data	An object produced by either <code>startISDM</code> or <code>startSpecies</code> . Requires the slot function, <code>.\$spatialBlock</code> to be run first in order to specify how the data in the model is blocked.
options	A list of INLA or inlabru options to be used in the model. Defaults to <code>list()</code> .
method	Which cross-validation method to perform. Must be one of 'DIC' or 'Predict'. If 'DIC' then the DIC values for each block are obtained. If 'Predict' then predictions are made on a dataset in the left out block. For this to work, please specify the argument <code>methodOptions</code> .
predictName	Name of the dataset to predict onto if <code>method = 'Predict'</code> .
datasetCombs	A list of vectors containing dataset combinations to include in each model run if <code>method = 'Prediction'</code> . If NULL then all combinations of the dataset will be estimated.

Value

An object of class `blockedCV`, which is essentially a list of DIC values obtained from each iteration of the model.

Examples

```
## Not run:
if(requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,
                             responsePA = 'Present',
                             Projection = proj)

  #Set up spatial block
  organizedData$spatialBlock(k = 2, rows = 2, cols = 1)

  #Run spatial block cross-validation
  blocked <- blockedCV(organizedData)

  #Print summary
  blocked

}

## End(Not run)
```

blockedCV-class	<i>Export class blockedCV</i>
-----------------	-------------------------------

Description

Export class blockedCV

blockedCVpred-class	<i>Export class blockedCVpred</i>
---------------------	-----------------------------------

Description

Export class blockedCVpred

bruSDM-class	<i>Export bru_sdm class</i>
--------------	-----------------------------

Description

Export bru_sdm class

bruSDM_predict-class	<i>Export class predict_bru_sdm</i>
----------------------	-------------------------------------

Description

Export class predict_bru_sdm

changeCoords	changeCoords: <i>function used to change coordinate names.</i>
--------------	--

Description

An internal function used to change the coordinate names for datasets.

Usage

```
changeCoords(data, oldcoords, newcoords)
```

Arguments

data	A list of datasets.
oldcoords	The old coordinate names.
newcoords	The new coordinate names.

Value

A list of data.frame or spatial objects with the coordinate names changed.

checkCoords	checkCoords: <i>function used to check coordinate names.</i>
-------------	--

Description

An internal function used to check if all the coordinates are the same.

Usage

```
checkCoords(data, coords)
```

Arguments

data	A list of datasets.
coords	A vector of length 2 of the coordinate names.

Value

A logical variable.

checkVar	checkVar: <i>Function used to check variable names.</i>
----------	---

Description

Internal function used to check if variable is in dataset.

Usage

```
checkVar(data, var)
```

Arguments

data	A list of datasets.
var	A variable name.

Value

A logical variable

data2ENV	data2ENV: <i>function used to move objects from one environment to another.</i>
----------	---

Description

Internal function: used to assign objects specified in bruSDM to the dataSDM/blockedCV function environments.

Usage

```
data2ENV(data, env)
```

Arguments

data	bruSDM data file to be used in the integrated model.
env	Environment where the objects should be assigned.

Value

Assignment of the relevant spatial fields to the specified environment.

dataOrganize*R6 class to assist in reformatting the data to be used in dataSDM.*

Description

Internal functions used to temporarily store data and other information before adding to dataSDM.

Methods

Public methods:

- `dataOrganize$makeData()`
- `dataOrganize$makeSpecies()`
- `dataOrganize$makeMultinom()`
- `dataOrganize$makeFormulas()`
- `dataOrganize$makeComponents()`
- `dataOrganize$makeLhoods()`
- `dataOrganize$clone()`

Method `makeData()`:

Usage:

```
dataOrganize$makeData(  
  datapoints,  
  datanames,  
  coords,  
  proj,  
  marktrialname,  
  paresp,  
  countsresp,  
  trialname,  
  speciesname,  
  marks,  
  pointcovnames,  
  markfamily,  
  temporalvar,  
  offsetname  
)
```

Method `makeSpecies()`:

Usage:

```
dataOrganize$makeSpecies(speciesname, repl = FALSE)
```

Method `makeMultinom()`:

Usage:

```
dataOrganize$makeMultinom(multinomVars, return, oldVars, repl = FALSE)
```

Method makeFormulas():*Usage:*

```
dataOrganize$makeFormulas(  
  spatcovs,  
  speciesname,  
  paresp,  
  countresp,  
  marks,  
  marksspatial,  
  speciesintercept,  
  speciesenvironment,  
  spatial,  
  intercept,  
  temporalname,  
  speciesindependent,  
  markintercept,  
  pointcovs,  
  speciesspatial,  
  biasformula,  
  covariateformula  
)
```

Method makeComponents():*Usage:*

```
dataOrganize$makeComponents(  
  spatial,  
  intercepts,  
  datanames,  
  marks,  
  speciesname,  
  multinomnames,  
  pointcovariates,  
  covariatenames,  
  covariateclass,  
  marksspatial,  
  marksintercept,  
  temporalname,  
  speciesspatial,  
  speciesenvironment,  
  speciesintercept,  
  numtime,  
  temporalmodel,  
  offsetname,  
  copymodel,  
  speciesindependent,  
  biasformula,  
  covariateformula,  
  marksCopy
```

```
)
```

Method makeLhoods():

Usage:

```
dataOrganize$makeLhoods(
  mesh,
  ips,
  paresp,
  ntrialsvar,
  markstrialsvar,
  speciesname
)
```

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
dataOrganize$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

dataSet	<i>Internal function used to standardize datasets, as well as assign meta-data.</i>
---------	---

Description

Internal function used to assist in structuring the data.

Usage

```
dataSet(
  datapoints,
  datanames,
  coords = c("CoordLoc1", "CoordLoc2"),
  proj,
  pointcovnames,
  paresp,
  countsresp,
  trialname,
  speciesname,
  marks,
  marktrialname,
  markfamily,
  temporalvar,
  offsetname
)
```

Arguments

<code>datapoints</code>	A list of datasets as sf objects
<code>datanames</code>	A vector of the names of the datasets.
<code>coords</code>	Names of the coordinates used in the model.
<code>proj</code>	The projection reference system used in the model.
<code>pointcovnames</code>	Name of the point covariates used in the model.
<code>paresp</code>	Name of the response variable used by the presence absence datasets.
<code>countsresp</code>	Name of the response variable used by the counts data.
<code>trialname</code>	Name of the trial variable used by the presence absence datasets.
<code>speciesname</code>	Name of the species name variable.
<code>marks</code>	Name of the marks considered in the model.
<code>marktrialname</code>	Name of the trial variable used by the binomial marks.
<code>markfamily</code>	A vector describing the distribution of the marks.
<code>temporalvar</code>	Name of the temporal variable.
<code>offsetname</code>	Name of the offset column in the datasets.

Value

A list of relevant metadata

<code>datasetOut</code>	<i>datasetOut: function that removes a dataset out of the main model, and calculates some cross-validation score.</i>
-------------------------	---

Description

This function calculates the difference in covariate values between a full integrated model and a model with one dataset left out, as well as some cross-validation score, which is used to obtain a score of the relative importance of the dataset in the full model. The score is calculated as follows:

1. Running a new model with one less dataset (from the main model) – resulting in a reduced model,
2. predicting the intensity function at the locations of the left-out dataset with the reduced model,
3. using the predicted values as an offset in a new model,
4. finding the difference between the marginal-likelihood of the main model (ie the model with all the datasets considered) and the marginal-likelihood of the offset model.

Usage

```
datasetOut(model, dataset, predictions = TRUE)
```

Arguments

model	Model of class modISDM run with multiple datasets.
dataset	Names of the datasets to leave out. If missing, will run for all datasets used in the full model.
predictions	Will new models be used for predictions. If TRUE returns marginals and bru_info in model. Defaults to TRUE.

Value

A list of inlabru models with the specified dataset left out. If predictions is FALSE, these objects will be missing their bru_info and call lists.

Examples

```
## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,
                             Projection = proj,
                             responsePA = 'Present')

  ##Run the model
  modelRun <- fitISDM(organizedData,
                      options = list(control.inla = list(int.strategy = 'eb'))))

  #Choose dataset to leave out
  eBirdOut <- datasetOut(modelRun, dataset = 'eBird')

  #Print datasetOut summary
  eBirdOut

}

## End(Not run)
```

datasetOut-class	<i>Export class bru_sdm_leave_one_out</i>
------------------	---

Description

Export class bru_sdm_leave_one_out

eBird	<i>data.frame object containing solitary tinamou observations from eBird</i>
-------	--

Description

data.frame object containing solitary tinamou observations from eBird

References

<http://ebird.org/>

elev_raster	<i>Raster object containing the elevation across Pennsylvania state.</i>
-------------	--

Description

Raster object containing the elevation across Pennsylvania state.

References

<https://cran.r-project.org/package=elevatr>

fitISDM	fitISDM: <i>function used to run the integrated model.</i>
---------	--

Description

This function takes a `intModel` object and produces an `inlabru` model object with additional lists and meta-data added.

Usage

```
fitISDM(data, options = list())
```

Arguments

<code>data</code>	A <code>intModel</code> object to be used in the integrated model.
<code>options</code>	A list of INLA options used in the model. Defaults to <code>list()</code> .

Value

An `inlabru` model with additional lists containing some more metadata attached.

Examples

```
## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                           Projection = proj, responsePA = 'Present')

  ##Run the model
  modelRun <- fitISDM(organizedData,
                     options = list(control.inla = list(int.strategy = 'eb'))))

  #Print summary of model
  modelRun

}

## End(Not run)
```

Gbif	<i>data.frame</i> object containing solitary tinamou observations from Gbif
------	---

Description

data.frame object containing solitary tinamou observations from Gbif

Source

<https://www.gbif.org/>

intModel	<i>intModel: Function used to initialize the integrated species distribution model.</i>
----------	---

Description

This function is depreciated. Please use one of [startISDM](#) or [startSpecies](#).

Usage

```
intModel(
  ...,
  spatialCovariates = NULL,
  Coordinates,
  Projection,
  Mesh,
  IPS = NULL,
  Boundary = NULL,
  speciesSpatial = "copy",
  speciesIndependent = FALSE,
  markNames = NULL,
  markFamily = NULL,
  pointCovariates = NULL,
  pointsIntercept = TRUE,
  marksIntercept = TRUE,
  speciesEffects = list(randomIntercept = FALSE, Environmental = TRUE),
  Offset = NULL,
  pointsSpatial = "copy",
  marksSpatial = TRUE,
  responseCounts = "counts",
  responsePA = "present",
  trialsPA = NULL,
  trialsMarks = NULL,
  speciesName = NULL,
```

```

temporalName = NULL,
temporalModel = list(model = "ar1"),
copyModel = list(beta = list(fixed = FALSE)),
Formulas = list(covariateFormula = NULL, biasFormula = NULL)
)

```

Arguments

...	The datasets to be used in the model. May come as either <code>sf</code> , <code>data.frame</code> or <code>SpatialPoints*</code> objects, or as a list of objects with these classes. The classes of the datasets do not necessarily need to be standardized, however the variable names within them often have to be.
spatialCovariates	The spatial covariates used in the model. These covariates must be measured at every location (pixel) in the study area, and must be a <code>Raster*</code> , <code>SpatialPixelsDataFrame</code> or <code>SpatialRaster</code> object. Can be either numeric, factor or character data.
Coordinates	A vector of length 2 containing the names (class character) of the coordinate variables used in the model.
Projection	The coordinate reference system used by both the spatial points and spatial covariates. Must be of class character.
Mesh	An <code>fm_mesh_2d</code> object required for the spatial random fields and the integration points in the model (see fm_mesh_2d_inla from the fmesh package for more details).
IPS	The integration points to be used in the model (that is, the points on the map where the intensity of the model is calculated). See fm_int from the fmesh package for more details regarding these points; however defaults to <code>NULL</code> which will create integration points from the <code>Mesh</code> object.
Boundary	A <code>sf</code> object of the study area. If not missing, this object is used to help create the integration points.
speciesSpatial	Argument to specify if each species should have their own spatial effect with different hyperparameters to be estimated using INLA 's "replicate" feature, or if a the field's should be estimated per species copied across datasets using INLA 's "copy" feature. Possible values include: 'replicate', 'copy', 'shared' or <code>NULL</code> if no species-specific spatial effects should be estimated.
speciesIndependent	Logical argument: Should species effects be made independent of one another. Defaults to <code>FALSE</code> which creates effects for each species independently.
markNames	A vector with the mark names (class character) to be included in the integrated model. Marks are variables which are used to describe the individual points in the model (for example, in the field of ecology the size of the species or its feeding type could be considered). Defaults to <code>NULL</code> , however if this argument is non- <code>NULL</code> , the model run will become a marked point process. The marks must be included in the same data object as the points.
markFamily	A vector with the statistical families (class character) assumed for the marks. Must be the same length as <code>markNames</code> , and the position of the mark in the vector <code>markName</code> is associated with the position of the family in <code>markFamily</code> . Defaults to <code>NULL</code> which assigns each mark as "Gaussian".

pointCovariates	The non-spatial covariates to be included in the integrated model (for example, in the field of ecology the distance to the nearest road or time spent sampling could be considered). These covariates must be included in the same data object as the points.
pointsIntercept	Logical argument: should the points be modeled with intercepts. Defaults to TRUE. Note that if this argument is non-NULL and pointsIntercepts is missing, pointsIntercepts will be set to FALSE.
marksIntercept	Logical argument: should the marks be modeled with intercepts. Defaults to TRUE.
speciesEffects	List specifying if intercept terms and environments effects should be made for the species. Defaults to <code>list(randomIntercept = FALSE, Environmental = TRUE)</code> . <code>randomIntercept</code> may take on three values: TRUE which creates a random intercept for each species, FALSE which creates fixed intercepts for each species, or NULL which removes all species level intercepts. Note that if <code>randomIntercept = NULL</code> and <code>pointsIntercept = TRUE</code> , dataset specific intercept terms will be created.
Offset	Name of the offset variable (class character) in the datasets. Defaults to NULL; if the argument is non-NULL, the variable name needs to be standardized across datasets (but does not need to be included in all datasets). The offset variable will be transformed onto the log-scale in the integrated model.
pointsSpatial	Argument to determine whether the spatial field is shared between the datasets, or if each dataset has its own unique spatial field. The datasets may share a spatial field with INLA 's "copy" feature if the argument is set to copy. May take on the values: "shared", "individual", "copy", "correlation" or NULL if no spatial field is required for the model. Defaults to "copy".
marksSpatial	Logical argument: should the marks have their own spatial field. Defaults to TRUE.
responseCounts	Name of the response variable in the counts/abundance datasets. This variable name needs to be standardized across all counts datasets used in the integrated model. Defaults to 'counts'.
responsePA	Name of the response variable (class character) in the presence absence/detection non-detection datasets. This variable name needs to be standardized across all present absence datasets. Defaults to 'present'.
trialsPA	Name of the trials response variable (class character) for the presence absence datasets. Defaults to NULL.
trialsMarks	Name of the trials response variable (class character) for the binomial marks (if included). Defaults to NULL.
speciesName	Name of the species variable name (class character). Specifying this argument turns the model into a stacked species distribution model, and calculates covariate values for the individual species, as well as a species group model in the shared spatial field. Defaults to NULL. Note that if this argument is non-NULL and pointsIntercepts is missing, pointsIntercepts will be set to FALSE.
temporalName	Name of the temporal variable (class character) in the model. This variable is required to be in all the datasets. Defaults to NULL.

temporalModel	List of model specifications given to the control.group argument in the time effect component. Defaults to <code>list(model = 'ar1')</code> ; see <code>control.group</code> from the INLA package for more details.
copyModel	List of model specifications given to the hyper parameters for the "copy" model. Defaults to <code>list(beta = list(fixed = FALSE))</code> .
Formulas	A named list with two objects. The first one, <code>covariateFormula</code> , is a formula for the covariates and their transformations for the distribution part of the model. Defaults to <code>NULL</code> which includes all covariates specified in <code>spatialCovariates</code> into the model. The second, <code>biasFormula</code> , specifies which covariates are used for the PO datasets. Defaults to <code>NULL</code> which includes no covariates for the PO datasets.

Value

A `specifyISDM` object (class R6). Use `?specifyISDM` to get a comprehensive description of the slot functions associated with this object.

Note

The idea with this function is to describe the full model: that is, all the covariates and spatial effects will appear in all the formulas for the datasets and species. If some of these terms should not be included in certain observation models in the integrated model, they can be thinned out using the `.$updateFormula` function. Note: the point covariate and mark terms will only be included in the formulas for where they are present in a given dataset, and so these terms do not need to be thinned out if they are not required by certain observation models.

Examples

```
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set base model up
  baseModel <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                        Projection = proj, responsePA = 'Present')

  #Print summary
  baseModel

  #Set up model with dataset specific spatial fields

  indSpat <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                      Projection = proj, pointsSpatial = 'individual', responsePA = 'Present')

  #Model with offset variable
```

```

offSet <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                  Projection = proj, Offset = 'area', responsePA = 'Present')

#Assume area as a mark
markModel <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                     Projection = proj, markNames = 'area', markFamily = 'gamma',
                     responsePA = 'Present')

}

```

Koala

Dataset of Eucalyptus globulus (common name: blue gum) sightings collected across the Koala conservation reserve on Phillip island (Australia) between 1993 and 2004. Two marks are considered from this dataset: "koala" which describes the number of koala visits to each tree, and "food" which is some index of the palatability of the leaves.

Description

Dataset of Eucalyptus globulus (common name: blue gum) sightings collected across the Koala conservation reserve on Phillip island (Australia) between 1993 and 2004. Two marks are considered from this dataset: "koala" which describes the number of koala visits to each tree, and "food" which is some index of the palatability of the leaves.

Format

eucTrees is a data.frame object (1284 observations; 6 variables) with the following columns:

E Latitude of the observation.

N Longitude of the observation.

FOOD Some value of the palatability of the leaves of the trees.

koala The number of koala sightings per tree.

nitrogen Total nitrogen (mg.g-1 DM).

dbh Diameter at breast height of the trees (cm).

References

Moore, B.D., Lawler, I.R., Wallis, I.R., Collin, B.M. and Foley, W.J. (2010). Palatability mapping: a koala's eye view of spatial variation in habitat quality. Ecology 91 (11): 3165-3176.

makeFormulaComps	makeFormulaComps: <i>function to make components for the covariate and bias Formulas.</i>
------------------	---

Description

An internal function used to make the formula components required for inlabru.

Usage

```
makeFormulaComps(form, species, speciesnames, type)
```

Arguments

form	The formula which needs to be changed into a component.
species	Logical indicating if species occur in the model.
speciesnames	The names of the species occurring in the model.
type	What type of component is being created: one for the covariate formula or the bias formula.

Value

A vector of components required for inlabru.

makeLhoods	makeLhoods: <i>function to make likelihoods.</i>
------------	--

Description

Function to make the datasets into likelihoods.

Usage

```
makeLhoods(
  data,
  formula,
  family,
  mesh,
  ips,
  paresp,
  ntrialsvar,
  markstrialsvar,
  speciesname,
  speciesindex,
  samplers,
  pointcovs = NULL
)
```

Arguments

data	A list of sf objects containing the datasets for which likelihoods need to be constructed.
formula	A list of formulas to add to the likelihoods.
family	A list of vectors containing the families within each dataset.
mesh	An fm_mesh_2d object.
ips	Integration points used.
paresp	The response variable name for the presence absence datasets.
ntrialsvar	The trials variable name for the presence absence datasets.
markstrialsvar	The trial variable name for the binomial marks.
speciesname	The name of the species variable used.
speciesindex	A vector containing the numeric index of where the species occurs in the data
samplers	A list of integration domains for the datasets.
pointcovs	A vector of the point covariates used in the model.

modISDM-class	<i>Export modISDM class</i>
---------------	-----------------------------

Description

Export modISDM class

modISDM_predict-class	<i>Export class predict.modISDM</i>
-----------------------	-------------------------------------

Description

Export class predict.modISDM

modMarks-class	<i>Export modMarks class</i>
----------------	------------------------------

Description

Export modMarks class

modMarks_predict-class	<i>Export class predict_modMarks</i>
------------------------	--------------------------------------

Description

Export class predict_modMarks

modSpecies-class	<i>Export modSpecies class</i>
------------------	--------------------------------

Description

Export modSpecies class

modSpecies_predict-class	<i>Export class predict_modSpecies</i>
--------------------------	--

Description

Export class predict_modSpecies

nameChanger	<i>nameChanger: function to change a variable name.</i>
-------------	---

Description

An internal function used to change the name of a variable.

Usage

nameChanger(data, oldName, newName)

Arguments

- | | |
|---------|------------------------|
| data | A list of datasets. |
| oldName | The old variable name. |
| newName | The new variable name. |

Value

A list of data.frame or spatial objects with the name of the variable changes.

nearestValue	<i>nearestValue: Match species location data to environmental raster layers</i>
--------------	---

Description

Obtain the nearest covariate value at each of the species locations.

Usage

```
nearestValue(pts, r, ...)
```

Arguments

pts	The species location data
r	The raster file to extract the covariates at.
...	Extra arguments for knnx.index .

NLCD_canopy_raster	<i>Raster object containing the canopy cover across Pennsylvania state.</i>
--------------------	---

Description

Raster object containing the canopy cover across Pennsylvania state.

References

<https://cran.r-project.org/package=FedData>

Parks	<i>data.frame object containing solitary tinamou observations from Parks</i>
-------	--

Description

data.frame object containing solitary tinamou observations from Parks

Source

<https://www.gbif.org/>

plot.bruSDM_predict	<i>Generic plot function for predict_bru_sdm.</i>
---------------------	---

Description

Plot for predict_bru_sdm
 Plot for modISDM_predict
 Plot for modMarks_predict
 Plot for modSpecies_predict

Usage

```
## S3 method for class 'bruSDM_predict'
plot(
  x,
  whattoplot = c("mean"),
  cols = NULL,
  layout = NULL,
  colourLow = NULL,
  colourHigh = NULL,
  plot = TRUE,
  ...
)

## S3 method for class 'modISDM_predict'
plot(x, variable = "mean", plot = TRUE, ...)

## S3 method for class 'modMarks_predict'
plot(x, variable = "mean", plot = TRUE, ...)

## S3 method for class 'modSpecies_predict'
plot(x, variable = "mean", plot = TRUE, ...)
```

Arguments

x	A modSpecies_predict object.
whattoplot	One of the following statistics to plot: "mean", "sd", "q0.025", "median", "q0.975", "smin", "smax", "cv", "var"
cols	Number of columns required for the plotting. Used by inlabru's multiplot function.
layout	Layout of the plots. Used by inlabru's multiplot function.
colourLow	Colour for the low values in the predictions (see ?scale_colour_gradient from ggplot2). Defaults to NULL. If non-NULL, colourHigh is required.
colourHigh	Colour for the high values in the predictions (see ?scale_colour_gradient from ggplot2). Defaults to NULL. If non-NULL, colourLow is required.

plot	Should the plots be printed, defaults to TRUE. If FALSE will produce a list of ggplot objects.
...	Argument not used
variable	One of the following statistics to plot: "mean", "sd", "q0.025", "median", "q0.975", "smin", "smax", "cv", "var"

Value

A ggplot2 object.

A ggplot2 object.

A ggplot2 object.

A ggplot2 object.

Examples

Not run:

```
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                           Projection = proj, responsePA = 'Present')

  ##Run the model
  modelRun <- fitISDM(organizedData, options = list(control.inla = list(int.strategy = 'eb'))))

  #Predict spatial field on linear scale
  predictions <- predict(modelRun, mesh = mesh, spatial = TRUE, fun = 'linear')

  #Make generic plot of predictions
  plot(predictions, colourHigh = 'red', colourLow = 'orange')

}
```

End(Not run)

Not run:

```
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
```

```

data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set model up
organizedData <- startISDM(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                           Projection = proj, responsePA = 'Present')

##Run the model
modelRun <- fitISDM(organizedData, options = list(control.inla = list(int.strategy = 'eb'))))

#Predict spatial field on linear scale
predictions <- predict(modelRun, mesh = mesh, spatial = TRUE, fun = 'linear')

#Make generic plot of predictions
plot(predictions, colourHigh = 'red', colourLow = 'orange')

}

## End(Not run)

## Not run:

if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set model up
organizedData <- startMarks(data, Mesh = mesh,
                           Projection = proj, responsePA = 'Present',
                           markNames = 'speciesName',
                           markFamily = 'multinomial')

##Run the model
modelRun <- fitISDM(organizedData, options = list(control.inla = list(int.strategy = 'eb',
                                                                    diagonal = 1)))

#Predict spatial field on linear scale
predictions <- predict(modelRun, mesh = mesh, spatial = TRUE, fun = 'linear')

#Make generic plot of predictions
plot(predictions)

}

## End(Not run)

## Not run:

```

```

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datssets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startSpecies(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                                Projection = proj, responsePA = 'Present')

  ##Run the model
  modelRun <- fitISDM(organizedData, options = list(control.inla = list(int.strategy = 'eb'))))

  #Predict spatial field on linear scale
  predictions <- predict(modelRun, mesh = mesh, spatial = TRUE, fun = 'linear')

  #Make generic plot of predictions
  plot(predictions, colourHigh = 'red', colourLow = 'orange')

}

## End(Not run)

```

predict.bruSDM

Generic predict function for bru_SDM objects.

Description

Predict function for the object produced by `fitISDM`. Should act identically to **inlabru**'s generic predict function if wanted, but has additional arguments to help predict certain components created by the model. This is needed since `intModel` creates variable names which might not be directly apparent to the user.

Predict function for the object produced by `fitISDM`. Should act identically to **inlabru**'s generic predict function if wanted, but has additional arguments to help predict certain components created by the model. This is needed since `startISDM` creates variable names which might not be directly apparent to the user.

Predict function for the object produced by `fitISDM`. Should act identically to **inlabru**'s generic predict function if wanted, but has additional arguments to help predict certain components created by the model. This is needed since `startMarks` creates variable names which might not be directly apparent to the user.

Predict function for the object produced by `fitISDM`. Should act identically to **inlabru**'s generic predict function if wanted, but has additional arguments to help predict certain components created by the model. This is needed since `startSpecies` creates variable names which might not be directly apparent to the user.

Usage

```
## S3 method for class 'bruSDM'
predict(
  object,
  data = NULL,
  formula = NULL,
  mesh = NULL,
  mask = NULL,
  temporal = FALSE,
  covariates = NULL,
  spatial = FALSE,
  intercepts = FALSE,
  datasets = NULL,
  species = NULL,
  marks = NULL,
  biasfield = FALSE,
  biasnames = NULL,
  predictor = FALSE,
  fun = "linear",
  format = "sf",
  ...
)

## S3 method for class 'modISDM'
predict(
  object,
  data = NULL,
  formula = NULL,
  mesh = NULL,
  mask = NULL,
  covariates = NULL,
  spatial = FALSE,
  intercepts = FALSE,
  datasets = NULL,
  bias = FALSE,
  biasnames = NULL,
  predictor = FALSE,
  fun = "linear",
  ...
)

## S3 method for class 'modMarks'
predict(
  object,
  data = NULL,
  formula = NULL,
  mesh = NULL,
  mask = NULL,
```

```

    covariates = NULL,
    spatial = FALSE,
    intercepts = FALSE,
    datasets = NULL,
    marks = NULL,
    bias = FALSE,
    biasnames = NULL,
    predictor = FALSE,
    fun = "linear",
    ...
)

## S3 method for class 'modSpecies'
predict(
  object,
  data = NULL,
  formula = NULL,
  mesh = NULL,
  mask = NULL,
  covariates = NULL,
  spatial = FALSE,
  intercepts = FALSE,
  datasets = NULL,
  species,
  bias = FALSE,
  biasnames = NULL,
  predictor = FALSE,
  fun = "linear",
  ...
)

```

Arguments

object	A modSpecies object.
data	Data containing points of the map with which to predict on. May be NULL if one of mesh or mask is NULL.
formula	Formula to predict. May be NULL if other arguments: covariates, spatial, intercepts are not NULL.
mesh	An fm_mesh_2d object.
mask	A mask of the study background. Defaults to NULL.
temporal	Make predictions for the temporal component of the model.
covariates	Name of covariates to predict.
spatial	Logical: include spatial effects in prediction. Defaults to FALSE.
intercepts	Logical: include intercept terms in prediction. Defaults to FALSE.
datasets	Names of the datasets to include intercept and spatial term.

species	Names of the species to predict. Default of NULL results in all species being predicted.
marks	Names of the marks to include intercept and spatial term.
biasfield	Logical include bias field in prediction. Defaults to FALSE.
biasnames	Names of the datasets to include bias term. Defaults to NULL. Note: the chosen dataset needs to be run with a bias field first; this can be done using <code>.\$addBias</code> with the object produced by <code>startSpecies</code> .
predictor	Should all terms (except the bias terms) included in the linear predictor be used in the predictions. Defaults to FALSE.
fun	Function used to predict. Set to 'linear' if effects on the linear scale are desired.
format	Class of the data for which to predict on. Must be one of 'sp', 'sf' or 'terra'. Defaults to 'sf'.
...	Additional arguments used by the inlabru predict function.
bias	Logical include bias field in prediction. Defaults to FALSE.

Details

Predict for bru_sdm

Predict for modISDM

Predict for modMarks

Predict for modSpecies

Value

A list of inlabru predict objects.

A list of inlabru predict objects.

A list of inlabru predict objects.

A list of inlabru predict objects.

Examples

```
## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                           Projection = proj, responsePA = 'Present')
```

```

##Run the model
modelRun <- fitISDM(organizedData, options = list(control.inla = list(int.strategy = 'eb'))))

#Predict spatial field on linear scale
predictions <- predict(modelRun, mesh = mesh, spatial = TRUE, fun = 'linear')

}

## End(Not run)

## Not run:

if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set model up
organizedData <- startISDM(data, Mesh = mesh,
                           Projection = proj,
                           responsePA = 'Present')

##Run the model
modelRun <- fitISDM(organizedData, options = list(control.inla = list(int.strategy = 'eb'))))

#Predict spatial field on linear scale
predictions <- predict(modelRun, mesh = mesh, spatial = TRUE, fun = 'linear')

}

## End(Not run)

## Not run:

if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
data <- lapply(data, function(x) {x$mark = runif(nrow(x));x})
mesh$crs <- proj

#Set model up
organizedData <- startMarks(data, Mesh = mesh, markNames = 'mark',

```

```

        markFamily = 'gaussian',
        Projection = proj, responsePA = 'Present')

##Run the model
modelRun <- fitISDM(organizedData, options = list(control.inla = list(int.strategy = 'eb',
                                                                    diagonal = 1)))

#Predict spatial field on linear scale
predictions <- predict(modelRun, mesh = mesh, marks = 'mark', fun = 'linear')

}

## End(Not run)

## Not run:

if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set model up
organizedData <- startSpecies(data, Mesh = mesh, speciesName = 'speciesName',
                             Projection = proj, responsePA = 'Present')

##Run the model
modelRun <- fitISDM(organizedData, options = list(control.inla = list(int.strategy = 'eb',
                                                                    diagonal = 1)))

#Predict spatial field on linear scale
predictions <- predict(modelRun, mesh = mesh, spatial = TRUE, fun = 'linear')

}

## End(Not run)

```

print.blockedCV

Print function for blockedCV.

Description

Print for blockedCV

Usage

```
## S3 method for class 'blockedCV'  
print(x, ...)
```

Arguments

x	A blockedCV object.
...	Unused argument.

print.blockedCVpred	<i>Print function for blockedCV.</i>
---------------------	--------------------------------------

Description

Print for blockedCVpred

Usage

```
## S3 method for class 'blockedCVpred'  
print(x, ...)
```

Arguments

x	A blockedCV object.
...	Unused argument.

print.bruSDM	<i>Generic print function for bruSDM.</i>
--------------	---

Description

Print method for bru_sdm

Usage

```
## S3 method for class 'bruSDM'  
print(x, ...)
```

Arguments

x	bruSDM object.
...	Un used argument.

print.bruSDM_predict *Generic print function for bru_sdm_predict.*

Description

Generic print function for bru_sdm_predict.

Usage

```
## S3 method for class 'bruSDM_predict'  
print(x, ...)
```

Arguments

x	bruSDM_predict object
...	Not used.

print.datasetOut *Generic print function for datasetOut.*

Description

Print for bru_sdm_leave_one_out

Usage

```
## S3 method for class 'datasetOut'  
print(x, ...)
```

Arguments

x	datasetOut object.
...	Unused argument.

<code>print.modISDM</code>	<i>Generic print function for modISDM.</i>
----------------------------	--

Description

Print method for modISDM

Usage

```
## S3 method for class 'modISDM'  
print(x, ...)
```

Arguments

- `x` modISDM object.
- `...` Not used.

<code>print.modMarks</code>	<i>Generic print function for modMarks.</i>
-----------------------------	---

Description

Print method for modMarks

Usage

```
## S3 method for class 'modMarks'  
print(x, ...)
```

Arguments

- `x` modMarks object.
- `...` Not used.

print.modSpecies	<i>Generic print function for modSpecies.</i>
------------------	---

Description

Print method for modSpecies

Usage

```
## S3 method for class 'modSpecies'  
print(x, ...)
```

Arguments

x	modSpecies object.
...	Not used.

reduceComps	<i>reduceComps: Reduce the components of the model.</i>
-------------	---

Description

reduceComps: Reduce the components of the model.

Usage

```
reduceComps(componentsOld, pointsCopy, biasCopy, datasetName, reducedTerms)
```

Arguments

componentsOld	The old components in the model.
pointsCopy	Logical: is the spatial model for the points copy.
biasCopy	Logical: is the bias model copy.
datasetName	Name of the dataset of interest.
reducedTerms	Terms to include in the new components.

Value

New components.

region	<i>sf object containing the boundary region for solitary tinamouc</i>
--------	---

Description

sf object containing the boundary region for solitary tinamouc

Source

<https://github.com/oharar/PointedSDMs>

removeFormula	<i>removeFormula: Function to remove term from a formula.</i>
---------------	---

Description

formulaChanger: Internal function used to remove formula terms.

Usage

```
removeFormula(formulaRemove, oldFormula)
```

Arguments

formulaRemove	The formula with all the components to remove.
oldFormula	The formula which needs to change.

runModel	<i>runModel: function used to run the integrated model. Note that this function is depreciated, and will be removed in a later version of the package.</i>
----------	--

Description

This function takes a intModel object and produces an inlabru model object with additional lists and meta-data added.

Usage

```
runModel(data, options = list())
```

Arguments

data A `intModel` object to be used in the integrated model.

options A list of INLA options used in the model. Defaults to `list()`.

Value

An `inlabru` model with additional lists containing some more metadata attached.

Examples

```
## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                           Projection = proj, responsePA = 'Present')

  ##Run the model
  modelRun <- runModel(organizedData,
                      options = list(control.inla = list(int.strategy = 'eb'))))

  #Print summary of model
  modelRun

}

## End(Not run)
```

SetophagaData

List of all data objects used for the Setophaga vignette.

Description

List of all data objects used for the Setophaga vignette.

SolitaryTinamou	<i>List of all data objects used for the solitary tinamou vignette.</i>
-----------------	---

Description

List of all data objects used for the solitary tinamou vignette.

SolTinCovariates	<i>spatRaster object containing covariate values</i>
------------------	--

Description

spatRaster object containing covariate values

Source

<https://github.com/oharar/PointedSDMs>

specifyISDM	<i>R6 class for creating a startISDM object.</i>
-------------	--

Description

A data object containing the data and the relevant information about the integrated model. The function `startISDM` acts as a wrapper in creating one of these objects. The output of this object has additional functions within the object which allow for further specification and customization of the integrated model.

Methods

Public methods:

- `specifyISDM$help()`
- `specifyISDM$print()`
- `specifyISDM$plot()`
- `specifyISDM$addBias()`
- `specifyISDM$updateFormula()`
- `specifyISDM$changeComponents()`
- `specifyISDM$priorsFixed()`
- `specifyISDM$specifySpatial()`
- `specifyISDM$changeLink()`
- `specifyISDM$spatialBlock()`

- `specifyISDM$addSamplers()`
- `specifyISDM$specifyRandom()`
- `specifyISDM$new()`
- `specifyISDM$samplingBias()`

Method `help()`: Function to provide documentation for a `specifyISDM` object.

Usage:

```
specifyISDM$help(...)
```

Arguments:

... Not used

Returns: Documentation.

Method `print()`: Prints the datasets, their data type and the number of observations, as well as the marks and their respective families.

Usage:

```
specifyISDM$print(...)
```

Arguments:

... Not used.

Method `plot()`: Makes a plot of the points surrounded by the boundary of the region where they were collected. The points may either be plotted based on which dataset they come from, or which species group they are part of (if `speciesName` is non-NULL in [intModel](#)).

Usage:

```
specifyISDM$plot(datasetNames, Boundary = TRUE, ...)
```

Arguments:

`datasetNames` Name of the datasets to plot. If this argument is missing, the function will plot all the data available to the model.

`Boundary` Logical: should a boundary (created using the Mesh object) be used in the plot. Defaults to TRUE.

... Not used.

Returns: A ggplot object.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    library(ggplot2)
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj

    #Set model up
```

```

organizedData <- startISDM(data, Mesh = mesh,
                           Projection = proj,
                           responsePA = 'Present')

#Create plot of data
organizedData$plot()

}
}

```

Method `addBias()`: Function used to add additional spatial fields (called *bias fields*) to a selected dataset present in the integrated model. *Bias fields* are typically used to account for sampling biases in opportunistic citizen science data in the absence of any covariate to do such.

Usage:

```

specifyISDM$addBias(
  datasetNames = NULL,
  allPO = FALSE,
  biasField = NULL,
  copyModel = TRUE,
  shareModel = FALSE,
  temporalModel = list(model = "ar1")
)

```

Arguments:

`datasetNames` A vector of dataset names (class character) for which a bias field needs to be added to. If NULL (default), then `allPO` has to be TRUE.

`allPO` Logical: should a bias field be added to all datasets classified as presence only in the integrated model. Defaults to FALSE.

`biasField` An `inla.spde` object used to describe the bias field. Defaults to NULL which uses [inla.spde2.matern](#) to create a Matern model for the field.

`copyModel` Create copy models for all the of the datasets specified with either `datasetNames` or `allPO`. The first dataset in the vector will have its own spatial effect, and the other datasets will "copy" the effect with shared hyperparameters. Defaults to TRUE.

`shareModel` Share a bias field across the datasets specified with `datasetNames`. Defaults to FALSE.

`temporalModel` List of model specifications given to the `control.group` argument in the time effect component. Defaults to `list(model = 'ar1')`; see [control.group](#) from the **INLA** package for more details. `temporalName` needs to be specified in `intModel` prior.

Returns: A bias field to the model.

Examples:

```

\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
  }
}

```

```

mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set model up
organizedData <- startISDM(data, Mesh = mesh,
                           Projection = proj,
                           responsePA = 'Present')

#Add bias field to eBird records
organizedData$addBias(datasetNames = 'eBird')

}
}

```

Method `updateFormula()`: Function used to update the formula for a selected observation model. The function is designed to work similarly to the generic update formula, and should be used to thin terms out of a process from the full model specified in `intModel`. The function also allows the user to add their own formula to the model, such that they can include non-linear components in the model. The function can also be used to print out the formula for a process by not specifying the `Formula` or `newFormula` arguments.

Usage:

```

specifyISDM$updateFormula(
  datasetName = NULL,
  Formula,
  newFormula,
  processLevel = FALSE
)

```

Arguments:

`datasetName` Name of the dataset (class character) for which the formula needs to be changed.

`Formula` An updated formula to give to the process. The syntax provided for the formula in this argument should be identical to the formula specification as in base **R**. Should be used to thin terms out of a formula but could be used to add terms as well. If adding new terms not specified in `intModel`, remember to add the associated component using `.$changeComponents` as well.

`newFormula` Completely change the formula for a process – primarily used to add non-linear components into the formula. Note: all terms need to be correctly specified here.

`processLevel` Logical argument: if TRUE changes the formulas for all of the processes in a dataset. Defaults to FALSE.

Returns: An updated formula.

Examples:

```

\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"

```

```

data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj
Forest <- terra::rast(
  system.file(
    'extdata/SolitaryTinamouCovariates.tif',
    package = "PointedSDMs"))$Forest

#Set model up
organizedData <- startISDM(data, Mesh = mesh,
                           spatialCovariates = Forest,
                           Projection = proj,
                           responsePA = 'Present',
                           pointsSpatial = 'individual')

#Remove Forest from eBird
organizedData$updateFormula(datasetName = 'eBird', Formula = ~ . - Forest)

#Add some scaling to Forest for Parks
organizedData$updateFormula('Parks', newFormula = ~ I(. +(Forest+1e-6)*scaling))

#Now add scaling to components
organizedData$changeComponents(addComponent = 'scaling')

}
}

```

Method `changeComponents()`: Function to add and specify custom components to model, which are required by **inlabru**. The main purpose of the function is to re-specify or completely change components already in the model, however the user can also add completely new components to the model as well. In this case, the components need to be added to the correct formulas in the model using the `.$updateFormula` function. If `addComponent` and `removeComponent` are both missing, the function will print out the components to be supplied to **inlabru**'s `bru` function.

Usage:

```
specifyISDM$changeComponents(addComponent, removeComponent, print = TRUE)
```

Arguments:

`addComponent` Component to add to the integrated model. Note that if the user is re-specifying a component already present in the model, they do not need to remove the old component using `removeComponent`.

`removeComponent` Component (or just the name of a component) present in the model which should be removed.

`print` Logical: should the updated components be printed. Defaults to TRUE.

Returns: An updated components list.

Examples:

```
\dontrun{
```

```

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,
                             spatialCovariates = Forest,
                             Projection = proj, responsePA = 'Present')

  #Remove Forest from components
  organizedData$changeComponents(removeComponent = 'Forest')

}

}

```

Method `priorsFixed()`: Function to change priors for the fixed (and possibly random) effects of the model.

Usage:

```

specifyISDM$priorsFixed(
  Effect,
  datasetName = NULL,
  mean.linear = 0,
  prec.linear = 0.001
)

```

Arguments:

Effect Name of the fixed effect covariate to change the prior for. Can take on 'intercept', which will change the specification for an intercept (specified by one of species or datasetName).

datasetName Name of the dataset for which the prior of the intercept should change (if fixed-Effect = 'intercept'). Defaults to NULL which will change the prior effect of the intercepts for all the datasets in the model.

mean.linear Mean value for the prior of the fixed effect. Defaults to 0.

prec.linear Precision value for the prior of the fixed effect. Defaults to 0.001.

Returns: New priors for the fixed effects.

Examples:

```

\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startISDM(data, Mesh = mesh,
                               spatialCovariates = Forest,
                               Projection = proj, responsePA = 'Present',
                               pointsSpatial = 'individual')

    #Add prior to Forest
    organizedData$priorsFixed(Effect = 'Forest', mean.linear = 2, prec.linear = 0.1)

  }
}

```

Method `specifySpatial()`: Function to specify random fields in the model using penalizing complexity (PC) priors for the parameters.

Usage:

```

specifyISDM$specifySpatial(
  sharedSpatial = FALSE,
  datasetName,
  Bias,
  PC = TRUE,
  Remove = FALSE,
  ...
)

```

Arguments:

`sharedSpatial` Logical: specify the shared spatial field in the model. Requires `pointsSpatial` == 'shared' in [intModel](#). Defaults to FALSE.

`datasetName` Name of which of the datasets' spatial fields to be specified. Requires `pointsSpatial` = 'individual' in [intModel](#).

`Bias` Name of the dataset for which the bias field to be specified.

`PC` Logical: should the Matern model be specified with pc priors. Defaults to TRUE, which uses [inla.spde2.pcmatern](#) to specify the model; otherwise uses [inla.spde2.matern](#).

`Remove` Logical: should the chosen spatial field be removed. Requires one of `sharedSpatial`, `species`, `mark` or `bias` to be non-missing, which chooses which field to remove.

... Additional arguments used by **INLA**'s `inla.spde2.pcmatern` or `inla.spde2.matern` function, dependent on the value of PC.

Returns: A new model for the spatial effects.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$d datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startISDM(data, Mesh = mesh,
                               spatialCovariates = Forest,
                               Projection = proj, responsePA = 'Present')

    #Specify the shared spatial field
    organizedData$specifySpatial(sharedSpatial = TRUE,
                                 prior.range = c(1,0.001),
                                 prior.sigma = c(1,0.001))

  }
}
```

Method `changeLink()`: Function used to change the link function for a given process.

Usage:

```
specifyISDM$changeLink(datasetName, Link)
```

Arguments:

`datasetName` Name of the dataset for which the link function needs to be changed.

`Link` Name of the link function to add to the process. If missing, will print the link function of the specified dataset.

Returns: A new link function for a process.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
```

```

proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj
Forest <- terra::rast(
  system.file(
    'extdata/SolitaryTinamouCovariates.tif',
    package = "PointedSDMs"))$Forest

#Set model up
organizedData <- startISDM(data, Mesh = mesh,
                           spatialCovariates = Forest,
                           Projection = proj, responsePA = 'Present')

#Specify the shared spatial field
organizedData$changeLink('Parks', 'logit')

}
}

```

Method `spatialBlock()`: Function to spatially block the datasets, which will then be used for model cross-validation with `blockedCV`. See the `spatialBlock` function from **blockCV** for how the spatial blocking works and for further details on the function's arguments.

Usage:

```
specifyISDM$spatialBlock(k, rows_cols, plot = FALSE, seed = 1234, ...)
```

Arguments:

`k` Integer value reflecting the number of folds to use.

`rows_cols` Integer value by which the area is divided into longitudinal and latitudinal bins.

`plot` Plot the cross-validation folds as well as the points across the boundary. Defaults to FALSE.

`seed` Seed used by **blockCV**'s `spatialBlock` to make the spatial blocking reproducible across different models. Defaults to 1234.

`...` Additional arguments used by **blockCV**'s `spatialBlock`.

Returns: If `plot = TRUE`, a plot of the grid.

Examples:

```

if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj
Forest <- terra::rast(

```

```

system.file(
  'extdata/SolitaryTinamouCovariates.tif',
  package = "PointedSDMs"))$Forest

#Set model up
organizedData <- startISDM(data, Mesh = mesh,
                           spatialCovariates = Forest,
                           Projection = proj, responsePA = 'Present',
                           pointsSpatial = 'individual')

#Specify the spatial block
organizedData$spatialBlock(k = 2, rows = 2, cols = 1, plot = FALSE)

}

```

Method `addSamplers()`: Function to add an integration domain for the PO datasets.

Usage:

```
specifyISDM$addSamplers(datasetName, Samplers)
```

Arguments:

`datasetName` Name of the dataset for the samplers.

`Samplers` A `Spatial*` object representing the integration domain.

Returns: New samplers for a process.

Examples:

```

\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj

    #Set model up
    organizedData <- startISDM(data, Mesh = mesh,
                               Projection = proj,
                               responsePA = 'Present')

    #Add integration domain for the eBird records
    organizedData$addSamplers(datasetName = 'eBird', Samplers = SolitaryTinamou$region)

  }
}

```

Method `specifyRandom()`: Function to specify the models and priors for the random effects included in the model.

Usage:

```
specifyISDM$specifyRandom(
  temporalModel = list(model = "ar1"),
  copyModel = list(beta = list(fixed = FALSE)),
  copyBias = list(beta = list(fixed = FALSE))
)
```

Arguments:

temporalModel List of model specifications given to the `control.group` argument in the time effect component. Defaults to `list(model = 'ar1')`; see [control.group](#) from the **INLA** package for more details.

copyModel List of model specifications given to the hyper parameters for the "copy" model. Defaults to `list(beta = list(fixed = FALSE))`.

copyBias List of model specifications given to the hyper parameters for the "copy" bias model. Defaults to `list(beta = list(fixed = FALSE))`.

Returns: An updated component list.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj

    #Set model up
    organizedData <- startISDM(data, Mesh = mesh,
                               Projection = proj,
                               responsePA = 'Present',
                               pointsSpatial = copy)

    #Add integration domain for the eBird records
    organizedData$specifyRandom(copyModel = list(beta = list(fixed = TRUE)))

  }
}
```

Method new():*Usage:*

```
specifyISDM$new(
  data,
  projection,
  Inlamesh,
  initialnames,
  responsecounts,
```

```

    responsepa,
    pointcovariates,
    trialspa,
    spatial,
    intercepts,
    spatialcovariates,
    boundary,
    ips,
    temporal,
    temporalmodel,
    offset,
    copymodel,
    formulas
  )

```

Method samplingBias():

Usage:

```
specifyISDM$samplingBias(datasetName, Samplers)
```

Examples

```

## -----
## Method `specifyISDM$plot`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  library(ggplot2)
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datssets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,
                             Projection = proj,
                             responsePA = 'Present')

  #Create plot of data
  organizedData$plot()

}

## End(Not run)

## -----
## Method `specifyISDM$addBias`
## -----

```

```

## Not run:
if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set model up
organizedData <- startISDM(data, Mesh = mesh,
                           Projection = proj,
                           responsePA = 'Present')

#Add bias field to eBird records
organizedData$addBias(datasetNames = 'eBird')

}

## End(Not run)

## -----
## Method `specifyISDM$updateFormula`
## -----

## Not run:
if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj
Forest <- terra::rast(
system.file(
'extdata/SolitaryTinamouCovariates.tif',
package = "PointedSDMs"))$Forest

#Set model up
organizedData <- startISDM(data, Mesh = mesh,
                           spatialCovariates = Forest,
                           Projection = proj,
                           responsePA = 'Present',
                           pointsSpatial = 'individual')

#Remove Forest from eBird
organizedData$updateFormula(datasetName = 'eBird', Formula = ~ . - Forest)

#Add some scaling to Forest for Parks

```

```

organizedData$updateFormula('Parks', newFormula = ~ I(. +(Forest+1e-6)*scaling))

#Now dd scaling to components
organizedData$changeComponents(addComponent = 'scaling')

}

## End(Not run)

## -----
## Method `specifyISDM$changeComponents`
## -----

## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,
                             spatialCovariates = Forest,
                             Projection = proj, responsePA = 'Present')

  #Remove Forest from components
  organizedData$changeComponents(removeComponent = 'Forest')

}

## End(Not run)

## -----
## Method `specifyISDM$priorsFixed`
## -----

## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets

```

```

mesh <- SolitaryTinamou$mesh
mesh$crs <- proj
Forest <- terra::rast(
  system.file(
    'extdata/SolitaryTinamouCovariates.tif',
    package = "PointedSDMs"))$Forest

#Set model up
organizedData <- startISDM(data, Mesh = mesh,
                           spatialCovariates = Forest,
                           Projection = proj, responsePA = 'Present',
                           pointsSpatial = 'individual')

#Add prior to Forest
organizedData$priorsFixed(Effect = 'Forest', mean.linear = 2, prec.linear = 0.1)

}

## End(Not run)

## -----
## Method `specifyISDM$specifySpatial`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,
                             spatialCovariates = Forest,
                             Projection = proj, responsePA = 'Present')

  #Specify the shared spatial field
  organizedData$specifySpatial(sharedSpatial = TRUE,
                               prior.range = c(1,0.001),
                               prior.sigma = c(1,0.001))

}

## End(Not run)

```

```

## -----
## Method `specifyISDM$changeLink`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,
                             spatialCovariates = Forest,
                             Projection = proj, responsePA = 'Present')

  #Specify the shared spatial field
  organizedData$changeLink('Parks', 'logit')

}

## End(Not run)

## -----
## Method `specifyISDM$spatialBlock`
## -----

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,

```

```

        spatialCovariates = Forest,
        Projection = proj, responsePA = 'Present',
        pointsSpatial = 'individual')

#Specify the spatial block
organizedData$spatialBlock(k = 2, rows = 2, cols = 1, plot = FALSE)

}

## -----
## Method `specifyISDM$addSamplers`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datssets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,
                             Projection = proj,
                             responsePA = 'Present')

  #Add integration domain for the eBird records
  organizedData$addSamplers(datasetName = 'eBird', Samplers = SolitaryTinamou$region)

}

## End(Not run)

## -----
## Method `specifyISDM$specifyRandom`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datssets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startISDM(data, Mesh = mesh,
                             Projection = proj,

```

```

        responsePA = 'Present',
        pointsSpatial = copy)

#Add integration domain for the eBird records
organizedData$specifyRandom(copyModel = list(beta = list(fixed = TRUE)))

}

## End(Not run)

```

specifyMarks

R6 class for creating a specifyMarks object.

Description

A data object containing the data and the relevant information about the integrated model. The function `startMarks` acts as a wrapper in creating one of these objects. The output of this object has additional functions within the object which allow for further specification and customization of the integrated model.

Methods

Public methods:

- `specifyMarks$help()`
- `specifyMarks$print()`
- `specifyMarks$plot()`
- `specifyMarks$addBias()`
- `specifyMarks$updateFormula()`
- `specifyMarks$changeComponents()`
- `specifyMarks$priorsFixed()`
- `specifyMarks$specifySpatial()`
- `specifyMarks$changeLink()`
- `specifyMarks$spatialBlock()`
- `specifyMarks$addSamplers()`
- `specifyMarks$specifyRandom()`
- `specifyMarks$new()`
- `specifyMarks$samplingBias()`

Method `help()`: Function to provide documentation for a specifyMarks object.

Usage:

```
specifyMarks$help(...)
```

Arguments:

... Not used

Returns: Documentation.

Method `print()`: Prints the datasets, their data type and the number of observations, as well as the marks and their respective families.

Usage:

```
specifyMarks$print(...)
```

Arguments:

... Not used.

Method `plot()`: Makes a plot of the points surrounded by the boundary of the region where they were collected. The points may either be plotted based on which dataset they come from, or which species group they are part of (if `speciesName` is non-NULL in [intModel](#)).

Usage:

```
specifyMarks$plot(datasetNames, Boundary = TRUE, ...)
```

Arguments:

`datasetNames` Name of the datasets to plot. If this argument is missing, the function will plot all the data available to the model.

`Boundary` Logical: should a boundary (created using the `Mesh` object) be used in the plot. Defaults to `TRUE`.

... Not used.

Returns: A `ggplot` object.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    library(ggplot2)
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj

    #Set organizedData up
    organizedData <- startMarks(data, Mesh = mesh,
                                Projection = proj, responsePA = 'Present',
                                markNames = 'speciesName',
                                markFamily = 'multinomial')

    #Create plot of data
    organizedData$plot()

  }
}
```

Method `addBias()`: Function used to add additional spatial fields (called *bias fields*) to a selected dataset present in the integrated model. *Bias fields* are typically used to account for sampling biases in opportunistic citizen science data in the absence of any covariate to do such.

Usage:

```
specifyMarks$addBias(
  datasetNames = NULL,
  allPO = FALSE,
  biasField = NULL,
  copyModel = TRUE,
  shareModel = FALSE,
  temporalModel = list(model = "ar1")
)
```

Arguments:

datasetNames A vector of dataset names (class character) for which a bias field needs to be added to. If NULL (default), then **allPO** has to be TRUE.

allPO Logical: should a bias field be added to all datasets classified as presence only in the integrated model. Defaults to FALSE.

biasField An `inla.spde` object used to describe the bias field. Defaults to NULL which uses [inla.spde2.matern](#) to create a Matern model for the field.

copyModel Create copy models for all the of the datasets specified with either **datasetNames** or **allPO**. The first dataset in the vector will have its own spatial effect, and the other datasets will "copy" the effect with shared hyperparameters. Defaults to TRUE.

shareModel Share a bias field across the datasets specified with **datasetNames**. Defaults to FALSE.

temporalModel List of model specifications given to the `control.group` argument in the time effect component. Defaults to `list(model = 'ar1')`; see [control.group](#) from the **INLA** package for more details. **temporalName** needs to be specified in `intModel` prior.

Returns: A bias field to the model.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj

    #Set model up
    organizedData <- startMarks(data, Mesh = mesh,
                                Projection = proj, responsePA = 'Present',
                                markNames = 'speciesName',
                                markFamily = 'multinomial')

    #Add bias field to eBird records
    organizedData$addBias(datasetNames = 'eBird')

  }
}
```



```

#Remove Forest from eBird
organizedData$updateFormula(datasetName = 'eBird', Mark = 'speciesName', Formula = ~ . - Forest)

}
}

```

Method `changeComponents()`: Function to add and specify custom components to model, which are required by **inlabru**. The main purpose of the function is to re-specify or completely change components already in the model, however the user can also add completely new components to the model as well. In this case, the components need to be added to the correct formulas in the model using the `$.updateFormula` function. If `addComponent` and `removeComponent` are both missing, the function will print out the components to be supplied to **inlabru**'s `bru` function.

Usage:

```
specifyMarks$changeComponents(addComponent, removeComponent, print = TRUE)
```

Arguments:

`addComponent` Component to add to the integrated model. Note that if the user is re-specifying a component already present in the model, they do not need to remove the old component using `removeComponent`.

`removeComponent` Component (or just the name of a component) present in the model which should be removed.

`print` Logical: should the updated components be printed. Defaults to TRUE.

Examples:

```

\dontrun{

  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- SolitaryTinamou$covariates$Forest

    #Set model up
    organizedData <- startMarks(data, Mesh = mesh,
                                Projection = proj, responsePA = 'Present',
                                markNames = 'speciesName',
                                markFamily = 'multinomial')

    #Remove Forest from components
    organizedData$changeComponents(removeComponent = 'Forest')

  }

}

```

Method priorsFixed(): Function to change priors for the fixed (and possibly random) effects of the model.

Usage:

```
specifyMarks$priorsFixed(
  Effect,
  datasetName = NULL,
  mean.linear = 0,
  prec.linear = 0.001
)
```

Arguments:

Effect Name of the fixed effect covariate to change the prior for. Can take on 'intercept', which will change the specification for an intercept (specified by one of species or datasetName).

datasetName Name of the dataset for which the prior of the intercept should change (if fixed-Effect = 'intercept'). Defaults to NULL which will change the prior effect of the intercepts for all the datasets in the model.

mean.linear Mean value for the prior of the fixed effect. Defaults to 0.

prec.linear Precision value for the prior of the fixed effect. Defaults to 0.001.

Returns: New priors for the fixed effects.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startMarks(data, Mesh = mesh, marksIntercept = FALSE,
                                Projection = proj, responsePA = 'Present',
                                markNames = 'speciesName',
                                markFamily = 'multinomial')

    #Add prior to Forest
    organizedData$priorsFixed(Effect = 'Intercept', mean.linear = 2, prec.linear = 0.1)

  }
}
```

Method `specifySpatial()`: Function to specify random fields in the model using penalizing complexity (PC) priors for the parameters.

Usage:

```
specifyMarks$specifySpatial(
  sharedSpatial = FALSE,
  datasetName,
  Mark,
  Bias,
  PC = TRUE,
  Remove = FALSE,
  ...
)
```

Arguments:

`sharedSpatial` Logical: specify the shared spatial field in the model. Requires `pointsSpatial == 'shared'` in `intModel`. Defaults to FALSE.

`datasetName` Name of which of the datasets' spatial fields to be specified. Requires `pointsSpatial = 'individual'` in `intModel`.

`Mark` Name of the marks to specify the spatial field for. If TRUE changes the spatial effect for all marks.

`Bias` Name of the dataset for which the bias field to be specified.

`PC` Logical: should the Matern model be specified with pc priors. Defaults to TRUE, which uses `inla.spde2.pcmatern` to specify the model; otherwise uses `inla.spde2.matern`.

`Remove` Logical: should the chosen spatial field be removed. Requires one of `sharedSpatial`, `species`, `mark` or `bias` to be non-missing, which chooses which field to remove.

`...` Additional arguments used by **INLA**'s `inla.spde2.pcmatern` or `inla.spde2.matern` function, dependent on the value of PC.

Returns: A new model for the spatial effects.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startMarks(data, Mesh = mesh,
                                Projection = proj, responsePA = 'Present',
```

```

        markNames = 'speciesName',
        markFamily = 'multinomial')

#Specify the shared spatial field
organizedData$specifySpatial(sharedSpatial = TRUE,
                             prior.range = c(1,0.001),
                             prior.sigma = c(1,0.001))

}
}

```

Method `changeLink()`: Function used to change the link function for a given process.

Usage:

```
specifyMarks$changeLink(datasetName, Mark, Link, ...)
```

Arguments:

`datasetName` Name of the dataset for which the link function needs to be changed.

`Mark` Name of the mark for which the link function needs to be changed.

`Link` Name of the link function to add to the process. If missing, will print the link function of the specified dataset.

`...` Not used

`Species` Name of the species for which the link function needs to be changed.

Examples:

```

\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startMarks(data, Mesh = mesh,
                                Projection = proj, responsePA = 'Present',
                                markNames = 'speciesName',
                                markFamily = 'multinomial')

    #Specify the shared spatial field
    organizedData$changeLink(datasetName = 'Parks',
                             Mark = 'speciesName',
                             Link = 'logit')
  }
}

```

```
}
}
```

Method `spatialBlock()`: Function to spatially block the datasets, which will then be used for model cross-validation with `blockedCV`. See the `spatialBlock` function from **blockCV** for how the spatial blocking works and for further details on the function's arguments.

Usage:

```
specifyMarks$spatialBlock(k, rows_cols, plot = FALSE, seed = 1234, ...)
```

Arguments:

`k` Integer value reflecting the number of folds to use.

`rows_cols` Integer value by which the area is divided into longitudinal and latitudinal bins.

`plot` Plot the cross-validation folds as well as the points across the boundary. Defaults to FALSE.

`seed` Seed used by **blockCV**'s `spatialBlock` to make the spatial blocking reproducible across different models. Defaults to 1234.

`...` Additional arguments used by **blockCV**'s `spatialBlock`.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- SolitaryTinamou$covariates$Forest

    #Set model up
    organizedData <- startMarks(data, Mesh = mesh,
                                Projection = proj, responsePA = 'Present',
                                markNames = 'speciesName',
                                markFamily = 'multinomial')

    #Specify the spatial block
    organizedData$spatialBlock(k = 2, rows = 2, cols = 1, plot = FALSE)

  }
}
```

Method `addSamplers()`: Function to add an integration domain for the PO datasets.

Usage:

```
specifyMarks$addSamplers(datasetName, Samplers)
```

Arguments:

datasetName Name of the dataset for the samplers.

Samplers A `Spatial*` object representing the integration domain.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj

    #Set model up
    organizedData <- startMarks(data, Mesh = mesh,
                                Projection = proj, responsePA = 'Present',
                                markNames = 'speciesName',
                                markFamily = 'multinomial')

    #Add integration domain for the eBird records
    organizedData$addSamplers(datasetName = 'eBird', Samplers = SolitaryTinamou$region)

  }
}
```

Method `specifyRandom()`: Function to specify the models and priors for the random effects included in the model.

Usage:

```
specifyMarks$specifyRandom(
  temporalModel = list(model = "ar1"),
  copyModel = list(beta = list(fixed = FALSE)),
  copyBias = list(beta = list(fixed = FALSE))
)
```

Arguments:

temporalModel List of model specifications given to the `control.group` argument in the time effect component. Defaults to `list(model = 'ar1')`; see [control.group](#) from the **INLA** package for more details.

copyModel List of model specifications given to the hyper parameters for the "copy" model. Defaults to `list(beta = list(fixed = FALSE))`.

copyBias List of model specifications given to the hyper parameters for the "copy" bias model. Defaults to `list(beta = list(fixed = FALSE))`.

Returns: An updated component list.

Examples:

```
\dontrun{
```

```

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startMarks(data, Mesh = mesh,
                              Projection = proj, responsePA = 'Present',
                              markNames = 'speciesName',
                              markFamily = 'multinomial')

  #Add integration domain for the eBird records
  organizedData$specifyRandom(copyModel = list(beta = list(fixed = TRUE)))

}
}

```

Method new():

Usage:

```

specifyMarks$new(
  data,
  coordinates,
  projection,
  Inlamesh,
  initialnames,
  responsecounts,
  responsepa,
  marksnames,
  marksfamily,
  pointcovariates,
  trialspa,
  trialsmarks,
  marksspatial,
  spatial,
  intercepts,
  spatialcovariates,
  marksintercepts,
  boundary,
  ips,
  temporal,
  temporalmodel,
  offset,
  copymodel,
  formulas
)

```

Method samplingBias():

Usage:

```
specifyMarks$samplingBias(datasetName, Samplers)
```

Examples

```
## -----
## Method `specifyMarks$plot`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  library(ggplot2)
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set organizedData up
  organizedData <- startMarks(data, Mesh = mesh,
                              Projection = proj, responsePA = 'Present',
                              markNames = 'speciesName',
                              markFamily = 'multinomial')

  #Create plot of data
  organizedData$plot()

}

## End(Not run)

## -----
## Method `specifyMarks$addBias`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startMarks(data, Mesh = mesh,
                              Projection = proj, responsePA = 'Present',
```

```

                                markNames = 'speciesName',
                                markFamily = 'multinomial')

#Add bias field to eBird records
organizedData$addBias(datasetNames = 'eBird')

}

## End(Not run)

## -----
## Method `specifyMarks$updateFormula`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datssets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- SolitaryTinamou$covariates$Forest

  #Set model up
  organizedData <- startMarks(data, Mesh = mesh,
                              Projection = proj, responsePA = 'Present',
                              markNames = 'speciesName',
                              markFamily = 'multinomial')

  #Remove Forest from eBird
  organizedData$updateFormula(datasetName = 'eBird', Mark = 'speciesName', Formula = ~ . - Forest)

}

## End(Not run)

## -----
## Method `specifyMarks$changeComponents`
## -----

## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datssets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

```

```

Forest <- SolitaryTinamou$covariates$Forest

#Set model up
organizedData <- startMarks(data, Mesh = mesh,
                           Projection = proj, responsePA = 'Present',
                           markNames = 'speciesName',
                           markFamily = 'multinomial')

#Remove Forest from components
organizedData$changeComponents(removeComponent = 'Forest')

}

## End(Not run)

## -----
## Method `specifyMarks$priorsFixed`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up
  organizedData <- startMarks(data, Mesh = mesh, marksIntercept = FALSE,
                             Projection = proj, responsePA = 'Present',
                             markNames = 'speciesName',
                             markFamily = 'multinomial')

  #Add prior to Forest
  organizedData$priorsFixed(Effect = 'Intercept', mean.linear = 2, prec.linear = 0.1)

}

## End(Not run)

## -----
## Method `specifyMarks$specifySpatial`
## -----

```



```

        markFamily = 'multinomial')

#Specify the shared spatial field
organizedData$changeLink(datasetName = 'Parks',
                          Mark = 'speciesName',
                          Link = 'logit')

}

## End(Not run)

## -----
## Method `specifyMarks$spatialBlock`
## -----

## Not run:
if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datssets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj
Forest <- SolitaryTinamou$covariates$Forest

#Set model up
organizedData <- startMarks(data, Mesh = mesh,
                            Projection = proj, responsePA = 'Present',
                            markNames = 'speciesName',
                            markFamily = 'multinomial')

#Specify the spatial block
organizedData$spatialBlock(k = 2, rows = 2, cols = 1, plot = FALSE)

}

## End(Not run)

## -----
## Method `specifyMarks$addSamplers`
## -----

## Not run:
if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datssets
mesh <- SolitaryTinamou$mesh

```

```

mesh$crs <- proj

#Set model up
organizedData <- startMarks(data, Mesh = mesh,
                             Projection = proj, responsePA = 'Present',
                             markNames = 'speciesName',
                             markFamily = 'multinomial')

#Add integration domain for the eBird records
organizedData$addSamplers(datasetName = 'eBird', Samplers = SolitaryTinamou$region)

}

## End(Not run)

## -----
## Method `specifyMarks$specifyRandom`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$d datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startMarks(data, Mesh = mesh,
                              Projection = proj, responsePA = 'Present',
                              markNames = 'speciesName',
                              markFamily = 'multinomial')

  #Add integration domain for the eBird records
  organizedData$specifyRandom(copyModel = list(beta = list(fixed = TRUE)))

}

## End(Not run)

```

specifySpecies

R6 class for creating a startSpecies object.

Description

A data object containing the data and the relevant information about the integrated model. The function `startSpecies` acts as a wrapper in creating one of these objects. The output of this object has additional functions within the object which allow for further specification and customization of the integrated model.

Methods

Public methods:

- `specifySpecies$help()`
- `specifySpecies$print()`
- `specifySpecies$plot()`
- `specifySpecies$addBias()`
- `specifySpecies$updateFormula()`
- `specifySpecies$changeComponents()`
- `specifySpecies$priorsFixed()`
- `specifySpecies$specifySpatial()`
- `specifySpecies$changeLink()`
- `specifySpecies$spatialBlock()`
- `specifySpecies$addSamplers()`
- `specifySpecies$specifyRandom()`
- `specifySpecies$new()`
- `specifySpecies$samplingBias()`

Method `help()`: Function to provide documentation for a `specifySpecies` object.

Usage:

```
specifySpecies$help(...)
```

Arguments:

... Not used

Returns: Documentation.

Method `print()`: Prints the datasets, their data type and the number of observations, as well as the marks and their respective families.

Usage:

```
specifySpecies$print(...)
```

Arguments:

... Not used.

Method `plot()`: Makes a plot of the points surrounded by the boundary of the region where they were collected.

Usage:

```
specifySpecies$plot(datasetNames, Species = TRUE, Boundary = TRUE, ...)
```

Arguments:

`datasetNames` Name of the datasets to plot. If this argument is missing, the function will plot all the data available to the model.

`Species` Logical: should the points be plotted based on the species name. Defaults to TRUE.

`Boundary` Logical: should a boundary (created using the Mesh object) be used in the plot. Defaults to TRUE.

... Not used.

Returns: A ggplot object.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    library(ggplot2)
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj

    #Set model up
    organizedData <- startSpecies(data, Mesh = mesh,
                                   speciesName = 'speciesName',
                                   Projection = proj,
                                   responsePA = 'Present')

    #Create plot of data
    organizedData$plot()

  }
}
```

Method `addBias()`: Function used to add additional spatial fields (called *bias fields*) to a selected dataset present in the integrated model. *Bias fields* are typically used to account for sampling biases in opportunistic citizen science data in the absence of any covariate to do such.

Usage:

```
specifySpecies$addBias(
  datasetNames = NULL,
  allPO = FALSE,
  biasField = NULL,
  copyModel = TRUE,
  shareModel = FALSE,
  temporalModel = list(model = "ar1")
)
```

Arguments:

`datasetNames` A vector of dataset names (class character) for which a bias field needs to be added to. If NULL (default), then `allPO` has to be TRUE.

`allPO` Logical: should a bias field be added to all datasets classified as presence only in the integrated model. Defaults to FALSE.

`biasField` An `inla.spde` object used to describe the bias field. Defaults to NULL which uses [inla.spde2.matern](#) to create a Matern model for the field.

`copyModel` Create copy models for all the of the datasets specified with either `datasetNames` or `allPO`. The first dataset in the vector will have its own spatial effect, and the other datasets will "copy" the effect with shared hyperparameters. Defaults to TRUE.

shareModel Share a bias field across the datasets specified with **datasetNames**. Defaults to FALSE.

temporalModel List of model specifications given to the **control.group** argument in the time effect component. Defaults to `list(model = 'ar1')`; see [control.group](#) from the **INLA** package for more details. **temporalName** needs to be specified in **intModel** prior.

Returns: A bias field to the model.

Examples:

```
\dontrun{
if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set model up
organizedData <- startSpecies(data, Mesh = mesh,
                             speciesName = 'speciesName',
                             Projection = proj,
                             responsePA = 'Present')

#Add bias field to eBird records
organizedData$addBias(datasetNames = 'eBird')

}
}
```

Method `updateFormula()`: Function used to update the formula for a selected observation model. The function is designed to work similarly to the generic update formula, and should be used to thin terms out of a process from the full model specified in [intModel](#). The function also allows the user to add their own formula to the model, such that they can include non-linear components in the model. The function can also be used to print out the formula for a process by not specifying the **Formula** or **newFormula** arguments.

Usage:

```
specifySpecies$updateFormula(
  datasetName = NULL,
  speciesName = NULL,
  Formula,
  processLevel = FALSE,
  newFormula
)
```

Arguments:

datasetName Name of the dataset (class character) for which the formula needs to be changed.

speciesName Name of the species for which to change a formula for. Defaults to NULL which changes the formula for all species present in **datasetName**.

Formula An updated formula to give to the process. The syntax provided for the formula in this argument should be identical to the formula specification as in base **R**. Should be used to thin terms out of a formula but could be used to add terms as well. If adding new terms not specified in `intModel`, remember to add the associated component using `.$changeComponents` as well.

processLevel Logical argument: if TRUE changes the formulas for all of the processes in a dataset. Defaults to FALSE.

newFormula Completely change the formula for a process – primarily used to add non-linear components into the formula. Note: all terms need to be correctly specified here.

Returns: An updated formula.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startSpecies(data, Mesh = mesh, speciesName = 'speciesName',
                                   spatialCovariates = Forest,
                                   Projection = proj, responsePA = 'Present',
                                   pointsSpatial = 'individual')

    #Remove Forest from eBird
    organizedData$updateFormula(datasetName = 'eBird', Formula = ~ . - Forest)

    #Add some scaling to Forest for Parks
    organizedData$updateFormula(datasetName = 'Parks', newFormula = ~ I(. +(Forest+1e-6)*scaling))

    #Now add scaling to components
    organizedData$changeComponents(addComponent = 'scaling')

  }
}
```

Method `changeComponents()`: Function to add and specify custom components to model, which are required by **inlabru**. The main purpose of the function is to re-specify or completely change components already in the model, however the user can also add completely new components to the model as well. In this case, the components need to be added to the correct formulas

in the model using the `.$updateFormula` function. If `addComponent` and `removeComponent` are both missing, the function will print out the components to be supplied to **inlabru**'s `bru` function.

Usage:

```
specifySpecies$changeComponents(addComponent, removeComponent, print = TRUE)
```

Arguments:

`addComponent` Component to add to the integrated model. Note that if the user is re-specifying a component already present in the model, they do not need to remove the old component using `removeComponent`.

`removeComponent` Component (or just the name of a component) present in the model which should be removed.

`print` Logical: should the updated components be printed. Defaults to TRUE.

Returns: An updated components list.

Examples:

```
\dontrun{

  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$d datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startSpecies(data, Mesh = mesh,
                                   speciesName = 'speciesName',
                                   spatialCovariates = Forest,
                                   Projection = proj,
                                   responsePA = 'Present')

    #Remove Forest from components
    organizedData$changeComponents(removeComponent = 'speciesSpatial')

  }

}
```

Method `priorsFixed()`: Function to change priors for the fixed (and possibly random) effects of the model.

Usage:

```
specifySpecies$priorsFixed(
  Effect,
  Species = NULL,
  datasetName = NULL,
  mean.linear = 0,
  prec.linear = 0.001
)
```

Arguments:

Effect Name of the fixed effect covariate to change the prior for. Can take on 'intercept', which will change the specification for an intercept (specified by one of species or datasetName).

Species Name of the species (class character) for which the prior should change. Defaults to NULL which will change the prior for all species added to the model.

datasetName Name of the dataset for which the prior of the intercept should change (if fixed-Effect = 'intercept'). Defaults to NULL which will change the prior effect of the intercepts for all the datasets in the model.

mean.linear Mean value for the prior of the fixed effect. Defaults to 0.

prec.linear Precision value for the prior of the fixed effect. Defaults to 0.001.

Returns: New priors for the fixed effects.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startSpecies(data, Mesh = mesh,
                                   speciesName = 'speciesName',
                                   spatialCovariates = Forest,
                                   Projection = proj, responsePA = 'Present',
                                   pointsSpatial = 'individual')

    #Add prior to Forest
    organizedData$priorsFixed(Effect = 'Forest', mean.linear = 2, prec.linear = 0.1)

  }
}
```



```

        spatialCovariates = Forest,
        Projection = proj, responsePA = 'Present')

#Specify the shared spatial field
organizedData$specifySpatial(sharedSpatial = TRUE, PC = TRUE,
                             prior.range = c(1,0.001),
                             prior.sigma = c(1,0.001))

}
}

```

Method `changeLink()`: Function used to change the link function for a given process.

Usage:

```
specifySpecies$changeLink(datasetName, Link, ...)
```

Arguments:

`datasetName` Name of the dataset for which the link function needs to be changed.

`Link` Name of the link function to add to the process. If missing, will print the link function of the specified dataset.

Returns: A new link function for a process.

Examples:

```

\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startSpecies(data, Mesh = mesh,
                                   speciesName = 'speciesName',
                                   spatialCovariates = Forest,
                                   Projection = proj, responsePA = 'Present')

    #Specify the shared spatial field
    organizedData$changeLink('Parks', 'logit')

  }
}

```

Method `spatialBlock()`: Function to spatially block the datasets, which will then be used for model cross-validation with `blockedCV`. See the `spatialBlock` function from **blockCV** for how the spatial blocking works and for further details on the function's arguments.

Usage:

```
specifySpecies$spatialBlock(k, rows_cols, plot = FALSE, seed = 1234, ...)
```

Arguments:

`k` Integer value reflecting the number of folds to use.

`rows_cols` Integer value by which the area is divided into longitudinal and latitudinal bins.

`plot` Plot the cross-validation folds as well as the points across the boundary. Defaults to FALSE.

`seed` Seed used by **blockCV**'s `spatialBlock` to make the spatial blocking reproducible across different models. Defaults to 1234.

`...` Additional arguments used by **blockCV**'s `spatialBlock`.

Returns: If `plot = TRUE`, a plot of the grid.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj
    Forest <- terra::rast(
      system.file(
        'extdata/SolitaryTinamouCovariates.tif',
        package = "PointedSDMs"))$Forest

    #Set model up
    organizedData <- startSpecies(data, Mesh = mesh,
                                   speciesName = 'speciesName',
                                   spatialCovariates = Forest,
                                   Projection = proj, responsePA = 'Present',
                                   pointsSpatial = 'individual')

    #Specify the spatial block
    organizedData$spatialBlock(k = 2, rows = 2, cols = 1, plot = FALSE)

  }
}
```

Method `addSamplers()`: Function to add an integration domain for the PO datasets.

Usage:

```
specifySpecies$addSamplers(datasetName, Samplers)
```

Arguments:

datasetName Name of the dataset for the samplers.

Samplers A Spatial* object representing the integration domain.

Returns: New samplers for a process.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datasets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj

    #Set model up
    organizedData <- startSpecies(data, Mesh = mesh,
                                   speciesName = 'speciesName',
                                   Projection = proj, responsePA = 'Present')

    #Add integration domain for the eBird records
    organizedData$addSamplers(datasetName = 'eBird', Samplers = SolitaryTinamou$region)

  }
}
```

Method `specifyRandom()`: Function to specify the models and priors for the random effects included in the model.

Usage:

```
specifySpecies$specifyRandom(
  temporalModel = list(model = "ar1"),
  copyModel = list(beta = list(fixed = FALSE)),
  copyBias = list(beta = list(fixed = FALSE)),
  speciesCopy = list(beta = list(fixed = FALSE)),
  speciesIntercepts = list(prior = "loggamma", param = c(1, 5e-05)),
  speciesGroup = list(model = "iid", hyper = list(prec = list(prior = "loggamma", param =
    c(1, 5e-05))))
)
```

Arguments:

temporalModel List of model specifications given to the `control.group` argument in the time effect component. Defaults to `list(model = 'ar1')`; see [control.group](#) from the **INLA** package for more details.

copyModel List of model specifications given to the hyper parameters for the "copy" model. Defaults to `list(beta = list(fixed = FALSE))`.

copyBias List of model specifications given to the hyper parameters for the "copy" bias model. Defaults to `list(beta = list(fixed = FALSE))`.

speciesCopy List of model specifications given to the hyper parameters for the species "copy" model. Defaults to `list(beta = list(fixed = FALSE))`.

speciesIntercepts Prior distribution for precision parameter for the random species intercept term. Defaults to INLA's default choice.

speciesGroup Prior distribution for the precision parameter for the iid group model. Defaults to INLA's default. #' @return An updated component list.

Examples:

```
\dontrun{
  if (requireNamespace('INLA')) {

    #Get Data
    data("SolitaryTinamou")
    proj <- "+proj=longlat +ellps=WGS84"
    data <- SolitaryTinamou$datssets
    mesh <- SolitaryTinamou$mesh
    mesh$crs <- proj

    #Set model up
    organizedData <- startSpecies(data, Mesh = mesh,
                                   speciesName = 'speciesName',
                                   Projection = proj,
                                   responsePA = 'Present',
                                   pointsSpatial = copy)

    #Add integration domain for the eBird records
    organizedData$specifyRandom(copyModel = list(beta = list(fixed = TRUE)))

  }
}
```

Method new():

Usage:

```
specifySpecies$new(
  data,
  projection,
  Inlamesh,
  initialnames,
  responsecounts,
  responsepa,
  pointcovariates,
  speciesintercept,
  trialspa,
  spatial,
  intercepts,
  spatialcovariates,
  boundary,
  ips,
  temporal,
```

```

    temporalmodel,
    offset,
    copymodel,
    formulas,
    speciesindependent,
    speciesname,
    speciesenvironment,
    speciesspatial
  )

```

Method samplingBias():

Usage:

```
specifySpecies$samplingBias(datasetName, Samplers)
```

Examples

```

## -----
## Method `specifySpecies$plot`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  library(ggplot2)
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set model up
  organizedData <- startSpecies(data, Mesh = mesh,
                                speciesName = 'speciesName',
                                Projection = proj,
                                responsePA = 'Present')

  #Create plot of data
  organizedData$plot()

}

## End(Not run)

## -----
## Method `specifySpecies$addBias`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data

```

```

data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set model up
organizedData <- startSpecies(data, Mesh = mesh,
                             speciesName = 'speciesName',
                             Projection = proj,
                             responsePA = 'Present')

#Add bias field to eBird records
organizedData$addBias(datasetNames = 'eBird')

}

## End(Not run)

## -----
## Method `specifySpecies$updateFormula`
## -----

## Not run:
if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj
Forest <- terra::rast(
system.file(
'extdata/SolitaryTinamouCovariates.tif',
package = "PointedSDMs"))$Forest

#Set model up
organizedData <- startSpecies(data, Mesh = mesh, speciesName = 'speciesName',
                             spatialCovariates = Forest,
                             Projection = proj, responsePA = 'Present',
                             pointsSpatial = 'individual')

#Remove Forest from eBird
organizedData$updateFormula(datasetName = 'eBird', Formula = ~ . - Forest)

#Add some scaling to Forest for Parks
organizedData$updateFormula(datasetName = 'Parks', newFormula = ~ I(. +(Forest+1e-6)*scaling))

#Now dd scaling to components
organizedData$changeComponents(addComponent = 'scaling')

```

```

}

## End(Not run)

## -----
## Method `specifySpecies$changeComponents`
## -----

## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$d datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up
  organizedData <- startSpecies(data, Mesh = mesh,
                                speciesName = 'speciesName',
                                spatialCovariates = Forest,
                                Projection = proj,
                                responsePA = 'Present')

  #Remove Forest from components
  organizedData$changeComponents(removeComponent = 'speciesSpatial')

}

## End(Not run)

## -----
## Method `specifySpecies$priorsFixed`
## -----

## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$d datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(

```

```

system.file(
  'extdata/SolitaryTinamouCovariates.tif',
  package = "PointedSDMs"))$Forest

#Set model up
organizedData <- startSpecies(data, Mesh = mesh,
                             speciesName = 'speciesName',
                             spatialCovariates = Forest,
                             Projection = proj, responsePA = 'Present',
                             pointsSpatial = 'individual')

#Add prior to Forest
organizedData$priorsFixed(Effect = 'Forest', mean.linear = 2, prec.linear = 0.1)

}

## End(Not run)

## -----
## Method `specifySpecies$specifySpatial`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up
  organizedData <- startSpecies(data, Mesh = mesh,
                               speciesName = 'speciesName',
                               spatialCovariates = Forest,
                               Projection = proj, responsePA = 'Present')

  #Specify the shared spatial field
  organizedData$specifySpatial(sharedSpatial = TRUE, PC = TRUE,
                              prior.range = c(1,0.001),
                              prior.sigma = c(1,0.001))

}

## End(Not run)

```

```

## -----
## Method `specifySpecies$changeLink`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up
  organizedData <- startSpecies(data, Mesh = mesh,
                                speciesName = 'speciesName',
                                spatialCovariates = Forest,
                                Projection = proj, responsePA = 'Present')

  #Specify the shared spatial field
  organizedData$changeLink('Parks', 'logit')

}

## End(Not run)

## -----
## Method `specifySpecies$spatialBlock`
## -----

## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
  Forest <- terra::rast(
    system.file(
      'extdata/SolitaryTinamouCovariates.tif',
      package = "PointedSDMs"))$Forest

  #Set model up

```

```

organizedData <- startSpecies(data, Mesh = mesh,
                             speciesName = 'speciesName',
                             spatialCovariates = Forest,
                             Projection = proj, responsePA = 'Present',
                             pointsSpatial = 'individual')

#Specify the spatial block
organizedData$spatialBlock(k = 2, rows = 2, cols = 1, plot = FALSE)

}

## End(Not run)

## -----
## Method `specifySpecies$addSamplers`
## -----

## Not run:
if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datssets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set model up
organizedData <- startSpecies(data, Mesh = mesh,
                             speciesName = 'speciesName',
                             Projection = proj, responsePA = 'Present')

#Add integration domain for the eBird records
organizedData$addSamplers(datasetName = 'eBird', Samplers = SolitaryTinamou$region)

}

## End(Not run)

## -----
## Method `specifySpecies$specifyRandom`
## -----

## Not run:
if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$datssets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

```

```

#Set model up
organizedData <- startSpecies(data, Mesh = mesh,
                             speciesName = 'speciesName',
                             Projection = proj,
                             responsePA = 'Present',
                             pointsSpatial = copy)

#Add integration domain for the eBird records
organizedData$specifyRandom(copyModel = list(beta = list(fixed = TRUE)))

}

## End(Not run)

```

startISDM	<i>startISDM: Function used to initialize the integrated species distribution model.</i>
-----------	--

Description

This function is used to create an object containing all the data, metadata and relevant components required for the integrated species distribution model and **INLA** to work. As a result, the arguments associated with this function are predominantly related to describing variable names within the datasets that are relevant, and arguments related to what terms should be included in the formula for the integrated model. The output of this function is an R6 object, and so there are a variety of public methods within the output of this function which can be used to further specify the model (see ?specifyISDM or .\$help() for a comprehensive description of these public methods).

Usage

```

startISDM(
  ...,
  spatialCovariates = NULL,
  Projection,
  Mesh,
  IPS = NULL,
  Boundary = NULL,
  pointCovariates = NULL,
  Offset = NULL,
  pointsIntercept = TRUE,
  pointsSpatial = "copy",
  responseCounts = "counts",
  responsePA = "present",
  trialsPA = NULL,
  temporalName = NULL,
  Formulas = list(covariateFormula = NULL, biasFormula = NULL)
)

```

Arguments

...	The datasets to be used in the model. Must come as either <i>sf</i> objects, or as a list of named <i>sf</i> objects.
spatialCovariates	The spatial covariates used in the model. These covariates must be measured at every location (pixel) in the study area, and must be a <i>SpatialRaster</i> object. Can be either numeric, factor or character data. Defaults to <i>NULL</i> which includes no spatial effects in the model.
Projection	The coordinate reference system used by both the spatial points and spatial covariates. Must be of class character.
Mesh	An <i>fm_mesh_2d</i> object required for the spatial random fields and the integration points in the model (see <i>fm_mesh_2d_inla</i> from the fmesh package for more details).
IPS	The integration points to be used in the model (that is, the points on the map where the intensity of the model is calculated). See <i>fm_int</i> from the fmesh package for more details regarding these points; however defaults to <i>NULL</i> which will create integration points from the Mesh and Boundary objects.
Boundary	A <i>sf</i> object of the study area. If not missing, this object is used to help create the integration points.
pointCovariates	The non-spatial covariates to be included in the integrated model (for example, in the field of ecology the distance to the nearest road or time spent sampling could be considered). These covariates must be included in the same data object as the points, and do not necessarily need to be present in all datasets.
Offset	Name of the offset variable (class character) in the datasets. Defaults to <i>NULL</i> ; if the argument is non- <i>NULL</i> , the variable name needs to be standardized across datasets (but does not need to be included in all datasets). The offset variable will be transformed onto the log-scale in the integrated model.
pointsIntercept	Logical argument: should the points be modeled with intercepts. Defaults to <i>TRUE</i> .
pointsSpatial	Argument to determine whether the spatial field is shared between the datasets, or if each dataset has its own unique spatial field. The datasets may share a spatial field with INLA 's "copy" feature if the argument is set to copy. May take on the values: "shared", "individual", "copy" or <i>NULL</i> if no spatial field is required for the model. Defaults to "copy".
responseCounts	Name of the response variable in the counts/abundance datasets. This variable name needs to be standardized across all counts datasets used in the integrated model. Defaults to 'counts'.
responsePA	Name of the response variable (class character) in the presence absence/detection non-detection datasets. This variable name needs to be standardized across all present absence datasets. Defaults to 'present'.
trialsPA	Name of the trials response variable (class character) for the presence absence datasets. Defaults to <i>NULL</i> .

temporalName	Name of the temporal variable (class character) in the model. This variable is required to be in all the datasets. Defaults to NULL.
Formulas	A named list with two objects. The first one, covariateFormula, is a formula for the covariates and their transformations for the distribution part of the model. Defaults to NULL which includes all covariates specified in spatialCovariates into the model. The second, biasFormula, specifies which covariates are used for the PO datasets. Defaults to NULL which includes no covariates for the PO datasets.

Value

A `specifyISDM` object (class R6). Use `?specifyISDM` to get a comprehensive description of the slot functions associated with this object.

Note

The idea with this function is to describe the full model: that is, all the covariates and spatial effects will appear in all the formulas for the datasets and species. If some of these terms should not be included in certain observation models in the integrated model, they can be thinned out using the `$.updateFormula` function. Note: the point covariate will only be included in the formulas for where they are present in a given dataset, and so these terms do not need to be thinned out if they are not required by certain observation models.

Examples

```
## Not run:
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

  #Set base model up
  baseModel <- startISDM(data, Mesh = mesh,
                        Projection = proj, responsePA = 'Present')

  #Print summary
  baseModel

  #Set up model with dataset specific spatial fields
  indSpat <- startISDM(data, Mesh = mesh,
                      Projection = proj, pointsSpatial = 'individual', responsePA = 'Present')

  #Model with offset variable
  offSet <- startISDM(data, Mesh = mesh,
                    Projection = proj, Offset = 'area', responsePA = 'Present')

  #Add own formula
```

```
quadModel <- startISDM(data, Mesh = mesh,
  Projection = proj, pointsSpatial = 'copy', responsePA = 'Present',
  Formulas = list(covariateFormula = ~ NPP + I(NPP^2)))

}

## End(Not run)
```

startMarks

startMarks: *Function used to initialize a marked-point process model.*

Description

This function is used to create an object containing all the data, metadata and relevant components required for the integrated species distribution model and **INLA** to work. As a result, the arguments associated with this function are predominantly related to describing variable names within the datasets that are relevant, and arguments related to what terms should be included in the formula for the integrated model. The output of this function is an R6 object, and so there are a variety of public methods within the output of this function which can be used to further specify the model (see ?specifyMarks for a comprehensive description of these public methods).

Usage

```
startMarks(
  ...,
  spatialCovariates = NULL,
  Projection,
  Mesh,
  IPS = NULL,
  Boundary = NULL,
  markNames = NULL,
  markFamily = NULL,
  marksSpatial = TRUE,
  pointCovariates = NULL,
  pointsIntercept = TRUE,
  marksIntercept = TRUE,
  Offset = NULL,
  pointsSpatial = "copy",
  responseCounts = "counts",
  responsePA = "present",
  trialsPA = NULL,
  trialsMarks = NULL,
  temporalName = NULL,
  Formulas = list(covariateFormula = NULL, biasFormula = NULL)
)
```

Arguments

...	The datasets to be used in the model. Must come as either <i>sf</i> objects, or as a list of named <i>sf</i> objects.
spatialCovariates	The spatial covariates used in the model. These covariates must be measured at every location (pixel) in the study area, and must be a <i>SpatialRaster</i> object. Can be either numeric, factor or character data. Defaults to <code>NULL</code> which includes no spatial effects in the model.
Projection	The coordinate reference system used by both the spatial points and spatial covariates. Must be of class character.
Mesh	An <i>fm_mesh_2d</i> object required for the spatial random fields and the integration points in the model (see fm_mesh_2d_inla from the fmesh package for more details).
IPS	The integration points to be used in the model (that is, the points on the map where the intensity of the model is calculated). See fm_int from the fmesh package for more details regarding these points; however defaults to <code>NULL</code> which will create integration points from the Mesh and Boundary objects.
Boundary	A <i>sf</i> object of the study area. If not missing, this object is used to help create the integration points.
markNames	A vector with the mark names (class character) to be included in the integrated model. Marks are variables which are used to describe the individual points in the model (for example, in the field of ecology the size of the species or its feeding type could be considered). Defaults to <code>NULL</code> , however if this argument is non- <code>NULL</code> , the model run will become a marked point process. The marks must be included in the same data object as the points.
markFamily	A vector with the statistical families (class character) assumed for the marks. Must be the same length as <code>markNames</code> , and the position of the mark in the vector <code>markName</code> is associated with the position of the family in <code>markFamily</code> . Defaults to <code>NULL</code> which assigns each mark as "Gaussian".
marksSpatial	Logical argument: should the marks have their own spatial field. Defaults to <code>TRUE</code> .
pointCovariates	The non-spatial covariates to be included in the integrated model (for example, in the field of ecology the distance to the nearest road or time spent sampling could be considered). These covariates must be included in the same data object as the points.
pointsIntercept	Logical argument: should the points be modeled with intercepts. Defaults to <code>TRUE</code> . Note that if this argument is non- <code>NULL</code> and <code>pointsIntercepts</code> is missing, <code>pointsIntercepts</code> will be set to <code>FALSE</code> .
marksIntercept	Logical argument: should the marks be modeled with intercepts. Defaults to <code>TRUE</code> .
Offset	Name of the offset variable (class character) in the datasets. Defaults to <code>NULL</code> ; if the argument is non- <code>NULL</code> , the variable name needs to be standardized across datasets (but does not need to be included in all datasets). The offset variable will be transformed onto the log-scale in the integrated model.

pointsSpatial	Argument to determine whether the spatial field is shared between the datasets, or if each dataset has its own unique spatial field. The datasets may share a spatial field with INLA 's "copy" feature if the argument is set to copy. May take on the values: "shared", "individual", "copy" or NULL if no spatial field is required for the model. Defaults to "shared".
responseCounts	Name of the response variable in the counts/abundance datasets. This variable name needs to be standardized across all counts datasets used in the integrated model. Defaults to 'counts'.
responsePA	Name of the response variable (class character) in the presence absence/detection non-detection datasets. This variable name needs to be standardized across all present absence datasets. Defaults to 'present'.
trialsPA	Name of the trials response variable (class character) for the presence absence datasets. Defaults to NULL.
trialsMarks	Name of the trials response variable (class character) for the binomial marks (if included). Defaults to NULL.
temporalName	Name of the temporal variable (class character) in the model. This variable is required to be in all the datasets. Defaults to NULL.
Formulas	A named list with two objects. The first one, covariateFormula, is a formula for the covariates and their transformations for the distribution part of the model. Defaults to NULL which includes all covariates specified in spatialCovariates into the model. The second, biasFormula, specifies which covariates are used for the PO datasets. Defaults to NULL which includes no covariates for the PO datasets.

Value

A `specifyMarks` object (class R6). Use `?specifyMarks` or `.$help()` to get a comprehensive description of the slot functions associated with this object.

Note

The idea with this function is to describe the full model: that is, all the covariates and spatial effects will appear in all the formulas for the datasets and species. If some of these terms should not be included in certain observation models in the integrated model, they can be thinned out using the `.$updateFormula` function. Note: the point covariate and mark terms will only be included in the formulas for where they are present in a given dataset, and so these terms do not need to be thinned out if they are not required by certain observation models.

Examples

```
if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- "+proj=longlat +ellps=WGS84"
  data <- SolitaryTinamou$datasets
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj
}
```

```
#Set base model up
baseModel <- startMarks(data, Mesh = mesh,
                        Projection = proj, responsePA = 'Present',
                        markNames = 'speciesName',
                        markFamily = 'multinomial')

}
```

startSpecies	startSpecies: <i>Function used to initialize a multi-species integrated species distribution model.</i>
--------------	---

Description

This function is used to create an object containing all the data, metadata and relevant components required for the multi-species integrated species distribution model and **INLA** to work. As a result, the arguments associated with this function are predominantly related to describing variable names within the datasets that are relevant, and arguments related to what terms should be included in the formula for the integrated model. The output of this function is an R6 object, and so there are a variety of public methods within the output of this function which can be used to further specify the model (see `?specifySpecies` or `.$help()` for a comprehensive description of these public methods).

Usage

```
startSpecies(
  ...,
  spatialCovariates = NULL,
  Projection,
  Mesh,
  speciesSpatial = "replicate",
  speciesIntercept = TRUE,
  speciesEnvironment = TRUE,
  speciesName,
  IPS = NULL,
  Boundary = NULL,
  pointCovariates = NULL,
  Offset = NULL,
  pointsIntercept = TRUE,
  pointsSpatial = "copy",
  responseCounts = "counts",
  responsePA = "present",
  trialsPA = NULL,
  temporalName = NULL,
  Formulas = list(covariateFormula = NULL, biasFormula = NULL)
)
```

Arguments

...	The datasets to be used in the model. Must come as either sf objects, or as a list of named sf objects.
spatialCovariates	The spatial covariates used in the model. These covariates must be measured at every location (pixel) in the study area, and must be a SpatialRaster object. Can be either numeric, factor or character data. Defaults to NULL which includes no spatial effects in the model.
Projection	The coordinate reference system used by both the spatial points and spatial covariates. Must be of class character.
Mesh	An fm_mesh_2d object required for the spatial random fields and the integration points in the model (see fm_mesh_2d_inla from the fmesh package for more details).
speciesSpatial	Argument to specify if each species should have their own spatial effect with different hyperparameters to be estimated using INLA 's "replicate" feature, or if a the field's should be estimated per species copied across datasets using INLA 's "copy" feature. Possible values include: 'replicate', 'copy', 'shared' or NULL if no species-specific spatial effects should be estimated.
speciesIntercept	Argument to control the species intercept term. Defaults to TRUE which creates a random intercept term, FALSE creates a fixed intercept term, and NULL removes the intercept term.
speciesEnvironment	Argument to control the species environmental term. Defaults to TRUE which creates species level environmental effects. To create shared effects across the species, use FALSE.
speciesName	Name of the species variable name (class character). Specifying this argument turns the model into a stacked species distribution model, and calculates covariate values for the individual species, as well as a species group model in the shared spatial field. Defaults to NULL. Note that if this argument is non-NULL and pointsIntercepts is missing, pointsIntercepts will be set to FALSE.
IPS	The integration points to be used in the model (that is, the points on the map where the intensity of the model is calculated). See fm_int from the fmesh package for more details regarding these points; however defaults to NULL which will create integration points from the Mesh object.
Boundary	A sf object of the study area. If not missing, this object is used to help create the integration points.
pointCovariates	The non-spatial covariates to be included in the integrated model (for example, in the field of ecology the distance to the nearest road or time spent sampling could be considered). These covariates must be included in the same data object as the points.
Offset	Name of the offset variable (class character) in the datasets. Defaults to NULL; if the argument is non-NULL, the variable name needs to be standardized across datasets (but does not need to be included in all datasets). The offset variable will be transformed onto the log-scale in the integrated model.

pointsIntercept	Logical argument: should the points be modeled with intercepts. Defaults to TRUE. Note that if this argument is non-NULL and pointsIntercepts is missing, pointsIntercepts will be set to FALSE.
pointsSpatial	Argument to determine whether the spatial field is shared between the datasets, or if each dataset has its own unique spatial field. The datasets may share a spatial field with INLA 's "copy" feature if the argument is set to copy. May take on the values: "shared", "individual", "copy", "correlate" or NULL if no spatial field is required for the model. Defaults to "copy".
responseCounts	Name of the response variable in the counts/abundance datasets. This variable name needs to be standardized across all counts datasets used in the integrated model. Defaults to 'counts'.
responsePA	Name of the response variable (class character) in the presence absence/detection non-detection datasets. This variable name needs to be standardized across all present absence datasets. Defaults to 'present'.
trialsPA	Name of the trials response variable (class character) for the presence absence datasets. Defaults to NULL.
temporalName	Name of the temporal variable (class character) in the model. This variable is required to be in all the datasets. Defaults to NULL.
Formulas	A named list with two objects. The first one, covariateFormula, is a formula for the covariates and their transformations for the distribution part of the model. Defaults to NULL which includes all covariates specified in spatialCovariates into the model. The second, biasFormula, specifies which covariates are used for the PO datasets. Defaults to NULL which includes no covariates for the PO datasets.

Value

A [specifySpecies](#) object (class R6). Use ?specifySpecies to get a comprehensive description of the slot functions associated with this object.

Note

The idea with this function is to describe the full model: that is, all the covariates and spatial effects will appear in all the formulas for the datasets and species. If some of these terms should not be included in certain observation models in the integrated model, they can be thinned out using the `$.updateFormula` function. Note: the point covariate will only be included in the formulas for where they are present in a given dataset, and so these terms do not need to be thinned out if they are not required by certain observation models.

Examples

```
## Not run:
if (requireNamespace('INLA')) {

##REDO WITH OTHER DATA

#Get Data
```

```

data("SolitaryTinamou")

proj <- "+proj=longlat +ellps=WGS84"
data <- SolitaryTinamou$dats
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

#Set base model up
baseModel <- startSpecies(data, Mesh = mesh,
                          Projection = proj, responsePA = 'Present',
                          speciesName = 'speciesName')

#Print summary
baseModel

#Set up model with dataset specific spatial fields

indSpat <- startSpecies(data, Mesh = mesh,
                        Projection = proj, pointsSpatial = 'individual',
                        responsePA = 'Present', speciesName = 'speciesName')

#Model with offset variable
offSet <- startSpecies(data, Mesh = mesh,
                       Projection = proj,
                       Offset = 'area',
                       responsePA = 'Present',
                       speciesName = 'speciesName')

#Non-random effects for the species
speciesInt <- startSpecies(data, Mesh = mesh,
                           Projection = proj,
                           speciesIntercept = FALSE,
                           responsePA = 'Present',
                           speciesName = 'speciesName')

#Turn off species level field

speciesInt <- startSpecies(data, Mesh = mesh,
                           Projection = proj,
                           speciesSpatial = NULL,
                           responsePA = 'Present',
                           speciesName = 'speciesName')

}

## End(Not run)

```

Description

Summary for bru_sdm
Summary for modSpecies
Summary for modISDM
Summary for modMarks

Usage

```
## S3 method for class 'bruSDM'  
summary(object, ...)  
  
## S3 method for class 'modSpecies'  
summary(object, ...)  
  
## S3 method for class 'modISDM'  
summary(object, ...)  
  
## S3 method for class 'modMarks'  
summary(object, ...)
```

Arguments

object	modMarks object.
...	Not used argument

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