

# Package ‘PointedSDMs’

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**Type** Package

**Title** Fit Models Derived from Point Processes to Species Distributions  
using ‘inlabru’

**Version** 1.2.1

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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-Arroita, 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)>.

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**Imports** R6, sp (>= 1.4-5), raster, R.devices, blockCV (>= 3.0.0)

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Altitude	<i>SpatialPixelsDataFrame containing Altitude covariate</i>
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**Description**

SpatialPixelsDataFrame containing Altitude covariate

**Source**

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

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BBA	<i>Dataset of setophaga caerulescens obtained from the Pennsylvania Atlas of Breeding Birds.</i>
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**Description**

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

**References**

<http://www.pabirdatlas.psu.edu>

---

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

**Description**

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

**References**

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

---

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

---

### 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())
```

### Arguments

data	An object produced by <a href="#">intModel</a> . 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 <b>INLA</b> or <b>inlabru</b> options to be used in the model. Defaults to <code>list()</code> .

### 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 <- CRS("+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)

  #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>
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**Description**

Export class blockedCV

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

Export bru\_sdm class

---

bruSDM\_predict-class    *Export class predict\_bru\_sdm*

---

### Description

Export class predict\_bru\_sdm

---

changeCoords            *changeCoords: function used to change coordinate names.*

---

### 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: function used to check coordinate names.*

---

### 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,  
  parest,  
  countsresp,  
  trialname,  
  speciesname,  
  marks,  
  pointcovnames,  
  markfamily,  
  temporalvar,  
  offsetname  
)
```

**Method** `makeSpecies()`:

*Usage:*

```
dataOrganize$makeSpecies(speciesname)
```

**Method** `makeMultinom()`:

*Usage:*

```
dataOrganize$makeMultinom(multinomVars, return, oldVars)
```



**Method** makeFormulas():*Usage:*

```
dataOrganize$makeFormulas(  
  spatcovs,  
  speciesname,  
  parest,  
  countresp,  
  marks,  
  marksspatial,  
  spatial,  
  intercept,  
  temporalname,  
  markintercept,  
  pointcovs,  
  speciesspatial  
)
```

**Method** makeComponents():*Usage:*

```
dataOrganize$makeComponents(  
  spatial,  
  intercepts,  
  datanames,  
  marks,  
  speciesname,  
  multinomnames,  
  pointcovariates,  
  covariatenames,  
  covariateclass,  
  marksspatial,  
  marksintercept,  
  temporalname,  
  speciesspatial,  
  numtime,  
  temporalmodel,  
  offsetname,  
  copymodel  
)
```

**Method** makeLhoods():*Usage:*

```
dataOrganize$makeLhoods(  
  mesh,  
  ips,  
  parest,  
  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.

---

dataSDM

*R6 class for creating a dataSDM object.*

---

## Description

A data object containing the data and the relevant information about the integrated model. The function `intModel` 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:

- `dataSDM$print()`
- `dataSDM$plot()`
- `dataSDM$addData()`
- `dataSDM$addBias()`
- `dataSDM$updateFormula()`
- `dataSDM$changeComponents()`
- `dataSDM$priorsFixed()`
- `dataSDM$specifySpatial()`
- `dataSDM$changeLink()`
- `dataSDM$spatialBlock()`
- `dataSDM$addSamplers()`
- `dataSDM$new()`
- `dataSDM$samplingBias()`

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

*Usage:*

```
dataSDM$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:*

```
dataSDM$plot(datasetNames, Species = FALSE, 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 FALSE.

`Boundary` Logical: should a boundary (created using the Mesh object) be used in the plot. Defaults to TRUE. Note that the output of this function is a gg object, and so a boundary surrounding the points may be added using standard **ggplot2** syntax and the `gg` function provided in the **inlabru** package.

... Not used.

*Returns:* A ggplot object.

*Examples:*

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

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

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

  #Create plot of data
  organizedData$plot()

}
```

**Method** `addData()`: Function used to add additional datasets to the `dataSDM` object. This function should be used if the user would like to add any additional datasets to the integrated model, but do not have the same standardized variable names as those added initially with `intModel`. Use `?intModel` for a more comprehensive description on what each argument in this function is used for.

*Usage:*

```
dataSDM$addData(
  ...,
  responseCounts,
  responsePA,
  trialsPA,
  markNames,
```

```

    markFamily,
    pointCovariates,
    trialsMarks,
    speciesName,
    temporalName,
    Coordinates,
    Offset
  )

```

*Arguments:*

... The datasets to be added to the integrated model: should be either `data.frame` or `SpatialPoints*` objects, or a list of objects from these classes.

`responseCounts` The name of the response variable for the counts data.

`responsePA` The name of the response variable for the presence absence data.

`trialsPA` The name of the trials variable for the presence absence data.

`markNames` The names of the marks found in the data.

`markFamily` The associated distributions of the marks.

`pointCovariates` The additional, non-spatial covariates describing the data.

`trialsMarks` The name of the trials variable for the binomial marks.

`speciesName` The name of the species variable included in the data. Used to make a stacked species distribution model.

`temporalName` The name of the temporal variable in the datasets.

`Coordinates` A vector of length 2 describing the names of the coordinates of the data.

`Offset` Name of the offset column in the dataset

*Examples:*

```

if (requireNamespace('INLA')) {

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

  #Only select eBird data
  ebird <- SolitaryTinamou$datasets$eBird
  mesh <- SolitaryTinamou$mesh
  mesh$crs <- proj

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

  #Print summary
  organizedData

  #Add new dataset
  Parks = SolitaryTinamou$datasets$Parks
  organizedData$addData(Parks, responsePA = 'Present')
}

```

```

#Print summary
organizedData

}

```

**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:*

```

dataSDM$addBias(
  datasetNames = NULL,
  allPO = FALSE,
  biasField = NULL,
  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.

`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.

*Examples:*

```

if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")
proj <- CRS("+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')

#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:*

```
dataSDM$updateFormula(
  datasetName = NULL,
  Points = TRUE,
  speciesName = NULL,
  markName = NULL,
  Formula,
  allProcesses = FALSE,
  newFormula
)
```

*Arguments:*

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

`Points` Logical: should the formula be changed for the points (or otherwise, a marked process).

Defaults to TRUE. If FALSE, then `markNames` needs to be non-NULL in `intModel`.

`speciesName` Name of the species (class character) to change the formula for. Defaults to NULL. If NULL and `speciesName` is non-NULL in `intModel`, will update the formula for all species within the dataset. Cannot be non-NULL if `speciesName` is NULL in `intModel`.

`markName` Name of the mark (class character) to change the formula for. Defaults to NULL. If NULL and `markNames` is non-NULL in `intModel`, will update the formula for all marks within the dataset. Cannot be non-NULL if `markNames` is NULL in `intModel`.

`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 `.$addComponents` as well.

`allProcesses` 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:* If `Formula` and `newFormula` are missing, will print out the formula for the specified processes.

*Examples:*

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

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

```

#Set model up
organizedData <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                          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:*

```
dataSDM$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 <- CRS("+proj=longlat +ellps=WGS84")
data <- SolitaryTinamou$datasets
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj
Forest <- SolitaryTinamou$covariates$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:*

```

dataSDM$specifySpatial(
  sharedSpatial = FALSE,
  datasetName,
  Species,
  Mark,
  Bias,
  PC = TRUE,
  Copy = NULL,
  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`.

`Species` Name of which of the species' spatial field to be specified. Requires `speciesName` to be non-NULL in `intModel`.

`Mark` Name of which of the mark' spatial field to be specified. Requires `markNames` to be non-NULL 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.

*Examples:*

```

if (requireNamespace('INLA')) {

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

```

```

mesh$crs <- proj
Forest <- SolitaryTinamou$covariates$Forest

#Set model up
organizedData <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                          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:*

```
dataSDM$changeLink(datasetName, Species, Mark, Link, ...)
```

*Arguments:*

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

`Species` Name of the species 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

*Examples:*

```

\dontrun{

#Create data object
dataObj <- intModel(...)

#Print link function for a process

dataObj$changeLink(Dataset = Dataset, Species = Species)

#Change link function
dataObj$changeLink(Dataset = Dataset, Species = Species,
                   Link = "log")

}

```

**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:*

```
dataSDM$spatialBlock(k, rows, cols, plot = FALSE, seed = 1234, ...)
```

*Arguments:*

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

**rows** Integer value by which the area is divided into latitudinal bins.

**cols** Integer value by which the area is divided into longitudinal 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:*

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

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

  #Set model up
  organizedData <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                           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:*

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

*Arguments:*

**datasetName** Name of the dataset for the samplers.

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

**Method** `new()`:

*Usage:*

```
dataSDM$new(
  coordinates,
```

```

    projection,
    Inlamesh,
    initialnames,
    responsecounts,
    responsepa,
    marksnames,
    marksfamily,
    pointcovariates,
    trialspa,
    trialsmarks,
    speciesname,
    marksspatial,
    spatial,
    intercepts,
    spatialcovariates,
    marksintercepts,
    boundary,
    ips,
    temporal,
    temporalmodel,
    speciesspatial,
    offset,
    copymodel
  )

```

**Method** `samplingBias()`:

*Usage:*

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

### Note

The arguments of this function may be missing (ie not provided) if they have already been specified in `intModel`, and do not need changing. Therefore this function is useful if there are some variable names not standardized across the datasets; this function will thus standardize the variable names to those provided initially in `intModel`.

### Examples

```

## -----
## Method `dataSDM$plot`
## -----

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- CRS("+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')

#Create plot of data
organizedData$plot()

}

## -----
## Method `dataSDM$addData`
## -----

if (requireNamespace('INLA')) {

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

#Only select eBird data
ebird <- SolitaryTinamou$datasets$eBird
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj

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

#Print summary
organizedData

#Add new dataset
Parks = SolitaryTinamou$datasets$Parks
organizedData$addData(Parks, responsePA = 'Present')

#Print summary
organizedData

}

## -----
## Method `dataSDM$addBias`
## -----

if (requireNamespace('INLA')) {

#Get Data
data("SolitaryTinamou")

```

```

proj <- CRS("+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')

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

}

## -----
## Method `dataSDM$updateFormula`
## -----

if (requireNamespace('INLA')) {

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

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

}

## -----
## Method `dataSDM$changeComponents`
## -----

## Not run:

```

```

if (requireNamespace('INLA')) {

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

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

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

}

## End(Not run)

## -----
## Method `dataSDM$priorsFixed`
## -----

if (requireNamespace('INLA')) {

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

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

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

}

## -----
## Method `dataSDM$specifySpatial`

```

```

## -----

if (requireNamespace('INLA')) {

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

  #Set model up
  organizedData <- intModel(data, Mesh = mesh, Coordinates = c('X', 'Y'),
                           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 `dataSDM$changeLink`
## -----

## Not run:

#Create data object
dataObj <- intModel(...)

#Print link function for a process

dataObj$changeLink(Dataset = Dataset, Species = Species)

#Change link function
dataObj$changeLink(Dataset = Dataset, Species = Species,
                  Link = "log")

## End(Not run)

## -----
## Method `dataSDM$spatialBlock`
## -----

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")

```



```
proj <- CRS("+proj=longlat +ellps=WGS84")
data <- SolitaryTinamou$dats
mesh <- SolitaryTinamou$mesh
mesh$crs <- proj
Forest <- SolitaryTinamou$covariates$Forest

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

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

}
```

---

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,
  proj,
  pointcovnames,
  paresp,
  countsresp,
  trialname,
  speciesname,
  marks,
  marktrialname,
  markfamily,
  temporalvar,
  offsetname
)
```

**Arguments**

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

**Value**

A list of relevant metadata

---

datasetOut	<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 <code>bru_sdm</code> 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 <code>bru_info</code> 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 <- CRS("+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')))

  #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	<i>fitISDM: 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 <- CRS("+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)
```

---

Forest	<i>SpatialPixelsDataFrame containing Forest covariate</i>
--------	---

---

**Description**

SpatialPixelsDataFrame containing Forest covariate

**Source**

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

---

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

---

**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 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 ?dataSDM for a comprehensive description of these public methods).

**Usage**

```
intModel(
  ...,
  spatialCovariates = NULL,
  Coordinates,
  Projection,
  Mesh,
  IPS = NULL,
  Boundary = NULL,
  speciesSpatial = TRUE,
  markNames = NULL,
  markFamily = NULL,
  pointCovariates = NULL,
  pointsIntercept = TRUE,
  marksIntercept = TRUE,
  Offset = NULL,
  pointsSpatial = "shared",
  marksSpatial = TRUE,
  responseCounts = "counts",
  responsePA = "present",
  trialsPA = NULL,
  trialsMarks = NULL,
  speciesName = NULL,
  temporalName = NULL,
  temporalModel = list(model = "ar1"),
  copyModel = list(beta = list(fixed = FALSE))
)
```

**Arguments**

...	The datasets to be used in the model. May come as either <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.
<code>spatialCovariates</code>	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> or <code>SpatialPixelsDataFrame</code> object. Can be either numeric or factor\codecharacter data.
<code>Coordinates</code>	A vector of length 2 containing the names (class character) of the coordinate variables used in the model.
<code>Projection</code>	The coordinate reference system used by both the spatial points and spatial covariates. Must be of class <code>CRS</code> (see <code>CRS</code> from the <code>sp</code> package for more details).
<code>Mesh</code>	An <code>inla.mesh</code> object required for the spatial random fields and the integration points in the model (see <code>inla.mesh.2d</code> from the <code>INLA</code> package for more details).
<code>IPS</code>	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 <code>ipoints</code> from the <code>inlabru</code>

	package for more details regarding these points; however defaults to NULL which will create integration points from the Mesh object.
Boundary	A SpatialPolygonsDataFrame object of the study area. If not missing, this object is used to help create the integration points.
speciesSpatial	Logical argument: should the species have their own individual spatial fields in the integrated model. Defaults to TRUE.
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 NULL, however if this argument is non-NULL, 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 markNames, and the position of the mark in the vector markName is associated with the position of the family in markFamily. Defaults to NULL 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.
marksIntercept	Logical argument: should the marks be modeled with intercepts. Defaults to TRUE.
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" or NULL if no spatial field is required for the model. Defaults to "shared".
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
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 <b>INLA</b> 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> .

### Value

A `dataSDM` object (class R6). Use `?dataSDM` 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 <- CRS("+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	<i>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.</i>
-------	---

---

## 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.

---

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

---

### Description

Function to make the datasets into likelihoods.

### Usage

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

### Arguments

data	A list of sp 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 inla.mesh object.
ips	Integration points used.
parest	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.

---

nameChanger	nameChanger: <i>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.

---

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>

---

NPP	<i>SpatialPixelsDataFrame containing NPP covariate</i>
-----	--

---

**Description**

SpatialPixelsDataFrame containing NPP covariate

**Source**

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

---

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

**Usage**

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

**Arguments**

x	A bruSDM_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

**Value**

A ggplot2 object.

**Examples**

```
## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- CRS("+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)
```

---

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.

**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",
  ...
)
```

**Arguments**

object	A bru_sdm objects.
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 inla.mesh 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>intModel</code> .

predictor	Should all terms run in the linear predictor be included in the predictions. Defaults to FALSE.
fun	Function used to predict. Set to 'linear' if effects on the linear scale are desired.
...	Additional arguments used by the inlabru predict function.

**Details**

Predict for bru\_sdm

**Value**

A list of inlabru predict objects.

**Examples**

```
## Not run:

if (requireNamespace('INLA')) {

  #Get Data
  data("SolitaryTinamou")
  proj <- CRS("+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)
```

---

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.bruSDM                    *Generic print function for bruSDM.*

---

**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	<i>Generic print function for datasetOut.</i>
------------------	---

---

**Description**

Print for bru\_sdm\_leave\_one\_out

**Usage**

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

**Arguments**

x	datasetOut object.
...	Unused argument.

---

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

---

**Description**

SpatialPolygons object containing the boundary region for solitary tinamouc

**Source**

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

---

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 <- CRS("+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.

---

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

---

**Description**

Summary for bru\_sdm

**Usage**

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

**Arguments**

object	bruSDM object.
...	Un used argument

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