

Package ‘intSDM’

October 20, 2023

Title Reproducible Integrated Species Distribution Models Across Norway using 'INLA'

Description Integration of disparate datasets is needed in order to make efficient use of all available data and thereby address the issues currently threatening biodiversity. Data integration is a powerful modeling framework which allows us to combine these datasets together into a single model, yet retain the strengths of each individual dataset. We therefore introduce the package, 'intSDM': an R package designed to help ecologists develop a reproducible workflow of integrated species distribution models, using data both provided from the user as well as data obtained freely online. An introduction to data integration 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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Author Philip Mostert [aut, cre],
Angeline Bruls [aut],
Ragnhild {Bjørkås} [aut],
Wouter Koch [aut],
Ellen Martin [aut]

Maintainer Philip Mostert <philip.s.mostert@ntnu.no>

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R topics documented:

formatStructured	2
generateAbsences	3
obtainArea	3
obtainCovariate	4
obtainGBIF	4
sdmWorkflow	5
species_model	6
startWorkflow	19

Index **21**

formatStructured	<i>formatStructured: Function to add structured data into the workflow.</i>
------------------	---

Description

Function used to format structure data into a coherent framework.

Usage

```
formatStructured(dataOCC, type, varsOld, varsNew, projection, boundary)
```

Arguments

dataOCC	The species occurrence data. May be either a SpatialPointsDataFrame, sf or data.frame object.
type	The type of observation model for the data. May be either: PO, PA or Counts.
varsOld	The names of the old variables in the model which need to be converted to something new.
varsNew	The name of the new variables in the model which will be used in the full model.
projection	The CRS object to add to the species occurrence data.
boundary	An sf object of the boundary of the study area, used to check if the data points are over the region.

Value

An sf object containing the locations of the species.

generateAbsences *Function to generate absences for data that comes from checklist data.*

Description

Function used to generate absences for data coming from lists. This function takes all the sampling locations from all the species obtained from a given dataset, and generates an absence if a species does not occur at a given location.

Usage

```
generateAbsences(dataList, datasetName, speciesName, responseName, Projection)
```

Arguments

dataList	A List of data objects for the dataset.
datasetName	The name of the dataset.
speciesName	The name of the species variable name.
responseName	The name of the response variable name.
Projection	Coordinate reference system used.

obtainArea *obtainArea: Function to obtain a boundary for a specified country.*

Description

Function to obtain a sf boundary object around a specified country.

Usage

```
obtainArea(names, projection, ...)
```

Arguments

names	A vector of names of countries used in the analysis.
projection	Coordinate reference system used.
...	Additional arguments passed to gisco_get_countries .

Value

An sf object of the boundary of the specified country.

obtainCovariate	<i>obtainCovariate: Function to obtain a covariate later for a specified country.</i>
-----------------	---

Description

Function to obtain covariate layers from *WorldClim* around a specified area.

Usage

```
obtainCovariate(covariates, res, projection, path)
```

Arguments

covariates	A vector of covariate names to obtain.
res	Resolution of the worldclim variable. Valid options are: 10, 5, 2.5 or 0.5 (minutes of a degree).
projection	Coordinate reference system to use in analysis.
path	The path where the covariate will be saved.

Value

A `spatialRaster` object of the covariates across the specified area.

obtainGBIF	<i>obtainGBIF: Function to obtain occurrence data from GBIF.</i>
------------	--

Description

Function used to obtain species observations from *GBIF*.

Usage

```
obtainGBIF(query, geometry, projection, datasettype, ...)
```

Arguments

query	The scientific name of the species for which observations need to be obtained.
geometry	An <code>sf</code> object surrounding the study area where observations need to be obtained.
projection	The coordinate reference system used for the observations and geometry.
datasettype	The type of dataset that is obtained from <i>GBIF</i> . Can be one of: PO, PA, Counts.
...	Additional arguments to pass to <code>occ_download</code> .

Value

An `sf` object containing the locations and other relevant information of the species obtained from *GBIF*.

`sdmWorkflow``sdmWorkflow: Function to compile the reproducible workflow.`

Description

This function is used to compile the reproducible workflow from the R6 object created with `startFunction`. Depending on what was specified before, this function will estimate the integrated species distribution model, perform cross-validation, create predictions from the model and plot these predictions.

Usage

```
sdmWorkflow(Workflow = NULL)
```

Arguments

`Workflow` The R6 object created from `startWorkflow`. This object should contain all the data and model information required to estimate and specify the model.

Value

The return of the function depends on the argument `Save` from the `startWorkflow` function. If this argument is `FALSE` then the objects will be saved to the specified directory. If this argument is `TRUE` then a list of different outcomes from the workflow will be returned.

Examples

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

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))
workflow$addArea(countryName = 'Sweden')

workflow$addGBIF(datasetName = 'exampleGBIF',
                 datasetType = 'PA',
                 limit = 10000,
                 coordinateUncertaintyInMeters = '0,50')
workflow$addMesh(cutoff = 20000,
                 max.edge=c(60000, 80000),
                 offset= 100000)
workflow$workflowOutput('Model')

Model <- sdmWorkflow(workflow)

}

## End(Not run)
```

`species_model`*R6 class for creating a species_model object.*

Description

An object containing the data, covariates and other relevant information to be used in the reproducible workflow. The function `startWorkflow` acts as a wrapper in creating one of these objects. This object has additional slot functions within, which allow for further specification and customization of the reproducible workflow.

Methods

Public methods:

- `species_model$new()`
- `species_model$print()`
- `species_model$plot()`
- `species_model$addStructured()`
- `species_model$addMesh()`
- `species_model$addGBIF()`
- `species_model$addCovariates()`
- `species_model$addArea()`
- `species_model$crossValidation()`
- `species_model$modelOptions()`
- `species_model$specifySpatial()`
- `species_model$biasFields()`
- `species_model$workflowOutput()`
- `species_model$obtainMeta()`
- `species_model$clone()`

Method `new()`: initialize the species_model object.

Usage:

```
species_model$new(  
  Countries,  
  Species,  
  nameProject,  
  Save,  
  Directory,  
  Projection,  
  Quiet = TRUE  
)
```

Arguments:

`Countries` Name of the countries to include in the workflow.

`Species` Name of the species to include in the workflow.

nameProject Name of the project for the workflow.
Save Logical argument indicating if the model outputs should be saved.
Directory Directory where the model outputs should be saved.
Projection The coordinate reference system used in the workflow.
Quiet Logical variable indicating if the workflow should provide messages throughout the estimation procedure.

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

Usage:

```
species_model$print(...)
```

Arguments:

... Not used.

Examples:

```
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))
```

```
workflow$print()
```

Method plot(): Makes a plot of the features used in the integrated model.

Usage:

```
species_model$plot(
  Mesh = FALSE,
  Boundary = TRUE,
  Species = FALSE,
  Covariates = FALSE
)
```

Arguments:

Mesh Add the mesh to the plot.

Boundary Add the boundary to the plot.

Species Add the species location data to the plot.

Covariates Add the spatial covariates to the plot.

Returns: A ggplot object.

Examples:

```
\dontrun{
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))
```

```
#Add boundary
workflow$addArea(countryName = 'Germany')
workflow$plot(Boundary = TRUE)
}
```



```

workflow$addStructured(dataStructured = speciesData, datasetType = 'PA',
                      datasetName = 'xx', responseName = 'Response',
                      speciesName = 'Name', coordinateNames = c('X', 'Y'))
}

```

Method addMesh(): Function to add an `inla.mesh` object to the workflow. The user may either add their own mesh to the workflow, or use the arguments of this function to help create one.

Usage:

```
species_model$addMesh(Object, ...)
```

Arguments:

Object An `inla.mesh` object to add to the workflow.

... Additional arguments to pass to INLA's `inla.mesh.2d`. Use `?inla.mesh.2d` to find out more about the different arguments.

Examples:

```

if (requireNamespace('INLA')) {
  \dontrun{
    workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                             Projection = '+proj=longlat +ellps=WGS84',
                             Save = FALSE,
                             saveOptions = list(projectName = 'example'))

    #Add boundary
    workflow$addArea(countryName = 'Sweden')
    workflow$addMesh(cutoff = 20000,
                    max.edge=c(60000, 80000),
                    offset= 100000)

  }
}

```

Method addGBIF(): Function to add species occurrence records from GBIF (using the `rgbif` package) to the reproducible workflow. The arguments for this function are used to either filter the GBIF records, or to specify the characteristics of the observation model.

Usage:

```

species_model$addGBIF(
  Species = "All",
  datasetName = NULL,
  datasetType = "PO",
  responseCounts = "individualCount",
  responsePA = "occurrenceStatus",
  removeDuplicates = FALSE,
  generateAbsences = FALSE,
  ...
)

```

Arguments:

Species The names of the species to include in the workflow (initially specified using [startWorkflow](#)). Defaults to ALL, which will find occurrence records for all specie specified in [startWorkflow](#).

datasetName The name to give the dataset obtained from GBIF. Cannot be NULL.

datasetType The data type of the dataset. Defaults to PO, but may also be PA or Counts.

responseCounts Name of the response variable for the counts data. Defaults to the standard Darwin core value `individualCounts`.

responsePA Name of the response variable for the PA data. Defaults to the standard Darwin core value `occurrenceStatus`.

removeDuplicates Argument used to remove duplicate observations for a species across datasets. May take a long time if there are many observations obtained across multiple datasets. Defaults to FALSE.

generateAbsences Generates absences for 'PA' data. This is done by combining all the sampling locations for all the species, and creating an absence where a given species does not occur.

... Additional arguments to specify the [occ_data](#) function from `rgbif`. See `?occ_data` for more details.

Examples:

```
\dontrun{
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))
workflow$addArea(countryName = 'Sweden')

workflow$addGBIF(datasetName = 'exampleGBIF',
                 datasetType = 'PA',
                 limit = 10000,
                 coordinateUncertaintyInMeters = '0,50')
}
```

Method `addCovariates()`: Function to add spatial covariates to the workflow. The covariates may either be specified by the user, or they may come from `worldClim` obtained with the `geodata` package.

Usage:

```
species_model$addCovariates(
  Object = NULL,
  worldClim = NULL,
  res = 2.5,
  Months = "All",
  Function = "mean",
  ...
)
```

Arguments:

Object A object of class: `spatRaster`, `SpatialPixelsDataFrame` or `raster` containing covariate information across the area. Note that this function will check if the covariates span

the boundary area, so it may be preferable to add your own boundary using ``. $addArea`` if this argument is specified.

`worldClim` Name of the worldClim to include in the model. See `?worldclim_country` from the `geodata` package for more information.

`res` Resolution of the worldclim variable. Valid options are: 10, 5, 2.5 or 0.5 (minutes of a degree).

`Months` The months to include the covariate for. Defaults to All which includes covariate layers for all months.

`Function` The function to aggregate the temporal data into one layer. Defaults to mean.

... Not used.

Examples:

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

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

#Add boundary
workflow$addArea(countryName = 'Sweden')
workflow$addCovariates(worldClim = 'tavg', res = '10')

}
}
```

Method `addArea()`: Function to add a boundary around the study area. This function allows the user to either add their own boundary object, or obtain a country's boundary using [gisco_get_countries](#) from the `giscoR` package.

Usage:

```
species_model$addArea(Object = NULL, countryName = NULL, ...)
```

Arguments:

`Object` A `sf` or `SpatialPolygons` object of the boundary surrounding the study area.

`countryName` Name of the countries to obtain a boundary for. This argument will then use the [gisco_get_countries](#) function from the `giscoR` package to obtain a boundary.

... Additional arguments passed to [gisco_get_countries](#).

Examples:

```
\dontrun{
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

#Add boundary
workflow$addArea(countryName = 'Sweden')
}
```

Method `crossValidation()`: Function to add a spatial cross validation method to the workflow.

Usage:

```
species_model$crossValidation(
  Method,
  blockOptions = list(k = 5, rows_cols = c(4, 4), plot = FALSE, seed = NULL)
)
```

Arguments:

Method The spatial cross-validation methods to use in the workflow. May be at least one of `spatialBlock` or `Loo` (leave-one-out). See the `PointedSDMs` package for more details.

blockOptions A list of options to specify the spatial block cross-validation. Must be a named list with arguments specified for: `k`, `rows_cols`, `plot`, `seed`. See `blockCV::cv_spatial` for more information.

Examples:

```
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

workflow$crossValidation(Method = 'Loo')
```

Method `modelOptions()`: Function to specify model options for the INLA and `PointedSDMs` parts of the model.

Usage:

```
species_model$modelOptions(ISDM = list(), INLA = list())
```

Arguments:

ISDM Arguments to specify in `intModel` from the `PointedSDMs` function. This argument needs to be a named list of the following options: `pointCovariates`, `pointsIntercept`, `pointsSpatial` or `copyModel`. See `?intModel` for more details.

INLA Options to specify in `INLA` from the `inla` function. See `?inla` for more details.

Examples:

```
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

workflow$modelOptions(INLA = list(control.inla=list(int.strategy = 'eb')),
                      ISDM = list(pointsIntercept = FALSE))
```

Method `specifySpatial()`: Function to specify pc priors for the shared random field in the model. See `?INLA::inla.spde2.pcmatern` for more details.

Usage:

```
species_model$specifySpatial(...)
```

Arguments:

... Arguments passed on to `inla.spde2.pcmatern`.

Examples:

```

\dontrun{
if (requireNamespace('INLA')) {
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

#Add boundary
workflow$addArea(countryName = 'Sweden')
workflow$addMesh(cutoff = 20000,
                 max.edge=c(60000, 80000),
                 offset= 100000)
workflow$specifySpatial(prior.range = c(200000, 0.05),
                       prior.sigma = c(5, 0.1))
}
}

```

Method `biasFields()`: Function to add bias fields to the model.

Usage:

```
species_model$biasFields(datasetName, ...)
```

Arguments:

`datasetName` Name of the dataset to add a bias field to.

`...` Additional arguments passed on to [inla.spde2.pcmatern](#) to customize the priors for the pc matern for the bias fields.

Examples:

```

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

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))
workflow$addArea(countryName = 'Sweden')

workflow$addGBIF(datasetName = 'exampleGBIF',
                 datasetType = 'PA',
                 limit = 10000,
                 coordinateUncertaintyInMeters = '0,50')
workflow$biasFields(datasetName = 'exampleGBIF')
}
}

```

Method `workflowOutput()`: Function to specify the workflow output from the model. This argument must be at least one of: 'Model', 'Prediction', 'Richness', 'Maps' and 'Cross-validation'.

Usage:

```
species_model$workflowOutput(Output)
```

Arguments:

Output The names of the outputs to give in the workflow. Must be at least one of: 'Model', 'Prediction', 'Richness', 'Maps' and 'Cross-validation'.

Examples:

```
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))
workflow$workflowOutput('Predictions')
```

Method obtainMeta(): Obtain metadata from the workflow.

Usage:

```
species_model$obtainMeta(Number = TRUE, Citations = TRUE)
```

Arguments:

Number Print the number of observations per dataset. Defaults to TRUE.

Citations Print the citations for the GBIF obtained datasets. Defaults to TRUE.

Examples:

```
\dontrun{
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))
workflow$addArea(countryName = 'Sweden')

workflow$addGBIF(datasetName = 'exampleGBIF',
                 datasetType = 'PA',
                 limit = 10000,
                 coordinateUncertaintyInMeters = '0,50')
workflow$obtainMeta()
}
```

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

Usage:

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

Arguments:

deep Whether to make a deep clone.

Examples

```
## -----
## Method `species_model$print`
## -----

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
```

```

        Save = FALSE,
        saveOptions = list(projectName = 'example'))

workflow$print()

## -----
## Method `species_model$plot`
## -----

## Not run:
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

#Add boundary
workflow$addArea(countryName = 'Germany')
workflow$plot(Boundary = TRUE)

## End(Not run)

## -----
## Method `species_model$addStructured`
## -----

## Not run:
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

#Add boundary
workflow$addArea(countryName = 'Sweden')

#Generate random species
speciesData <- data.frame(X = runif(1000, 12, 24),
                          Y = runif(1000, 56, 68),
                          Response = sample(c(0,1), 1000, replace = TRUE),
                          Name = 'Fraxinus_excelsior')
workflow$addStructured(dataStructured = speciesData, datasetType = 'PA',
                      datasetName = 'xx', responseName = 'Response',
                      speciesName = 'Name', coordinateNames = c('X', 'Y'))

## End(Not run)

## -----
## Method `species_model$addMesh`
## -----

if (requireNamespace('INLA')) {
## Not run:
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',

```

```

        Save = FALSE,
        saveOptions = list(projectName = 'example'))

#Add boundary
workflow$addArea(countryName = 'Sweden')
workflow$addMesh(cutoff = 20000,
                 max.edge=c(60000, 80000),
                 offset= 100000)

## End(Not run)
}

## -----
## Method `species_model$addGBIF`
## -----

## Not run:
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))
workflow$addArea(countryName = 'Sweden')

workflow$addGBIF(datasetName = 'exampleGBIF',
                 datasetType = 'PA',
                 limit = 10000,
                 coordinateUncertaintyInMeters = '0,50')

## End(Not run)

## -----
## Method `species_model$addCovariates`
## -----

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

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

#Add boundary
workflow$addArea(countryName = 'Sweden')
workflow$addCovariates(worldClim = 'tavg', res = '10')

}

## End(Not run)

## -----
## Method `species_model$addArea`

```



```

## -----

## Not run:
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

#Add boundary
workflow$addArea(countryName = 'Sweden')

## End(Not run)

## -----
## Method `species_model$crossValidation`
## -----

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

workflow$crossValidation(Method = 'Loo')

## -----
## Method `species_model$modelOptions`
## -----

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = '+proj=longlat +ellps=WGS84',
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))

workflow$modelOptions(INLA = list(control.inla=list(int.strategy = 'eb')),
                      ISDM = list(pointsIntercept = FALSE))

## -----
## Method `species_model$specifySpatial`
## -----

## Not run:
if (requireNamespace('INLA')) {
  workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                            Projection = '+proj=longlat +ellps=WGS84',
                            Save = FALSE,
                            saveOptions = list(projectName = 'example'))

#Add boundary
workflow$addArea(countryName = 'Sweden')
workflow$addMesh(cutoff = 20000,
                 max.edge=c(60000, 80000),
                 offset= 100000)
workflow$specifySpatial(prior.range = c(200000, 0.05),

```

```

        prior.sigma = c(5, 0.1))
    }

## End(Not run)

## -----
## Method `species_model$biasFields`
## -----

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

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                        Projection = '+proj=longlat +ellps=WGS84',
                        Save = FALSE,
                        saveOptions = list(projectName = 'example'))
workflow$addArea(countryName = 'Sweden')

workflow$addGBIF(datasetName = 'exampleGBIF',
                datasetType = 'PA',
                limit = 10000,
                coordinateUncertaintyInMeters = '0,50')
workflow$biasFields(datasetName = 'exampleGBIF')
}

## End(Not run)

## -----
## Method `species_model$workflowOutput`
## -----

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                        Projection = '+proj=longlat +ellps=WGS84',
                        Save = FALSE,
                        saveOptions = list(projectName = 'example'))
workflow$workflowOutput('Predictions')

## -----
## Method `species_model$obtainMeta`
## -----

## Not run:
workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                        Projection = '+proj=longlat +ellps=WGS84',
                        Save = FALSE,
                        saveOptions = list(projectName = 'example'))
workflow$addArea(countryName = 'Sweden')

workflow$addGBIF(datasetName = 'exampleGBIF',
                datasetType = 'PA',
                limit = 10000,
                coordinateUncertaintyInMeters = '0,50')
workflow$obtainMeta()

```

```
## End(Not run)
```

startWorkflow	startWorkflow: <i>function to commence the integrated species distribution model workflow.</i>
---------------	--

Description

Function to initialize the reproducible workflow using integrated species distribution models. The arguments for this function are used to specify which species and countries are to be studied, as well as how the results of the model should be saved (either as an R object or saved to some directory). This function outputs an R6 object with additional slot functions to help further customize the model specification. See ?species_model for more details on these functions.

Usage

```
startWorkflow(
  Countries,
  Species,
  Projection,
  Save = TRUE,
  saveOptions = list(projectDirectory = NULL, projectName = NULL),
  Quiet = FALSE
)
```

Arguments

Countries	A vector of country names to complete the analysis over. If missing, a boundary object (of class Spatial or sf) has to be added to the model using <code>.\$addArea</code> before any analysis is completed.
Species	A vector of Species names (scientific) to include in the analysis. Names should be given carefully since the names provided will be used to obtain <i>GBIF</i> observations.
Projection	The coordinate reference system used in the workflow.
Save	Logical argument indicating if the model objects and outputs should be saved as <code>.rds</code> files. Defaults to TRUE. If FALSE then the output of the workflow will be a list of objects at each step of the workflow.
saveOptions	A list containing two items: <code>projectDirectory</code> indicating where the objects should be saved (defaults to NULL), and <code>projectName</code> which indicates the name for the folder in the relevant directory. The latter argument is required, regardless of the value given to Save.
Quiet	Logical argument indicating if the workflow should provide the user messages during the setup and estimation process. Defaults to TRUE.

Value

An R6 object of class `species_model`. This object contains a collection of slot functions to assist the user in customizing their workflow.

Examples

```
##Start a workflow without saving objects

workflow <- startWorkflow(Species = 'Fraxinus excelsior',
                          Projection = "+proj=longlat +ellps=WGS84",
                          Save = FALSE,
                          saveOptions = list(projectName = 'example'))
```

Index

`formatStructured`, [2](#)

`generateAbsences`, [3](#)

`gisco_get_countries`, [3](#), [11](#)

INLA, [12](#)

`inla.spde2.pcmatern`, [12](#), [13](#)

`intModel`, [12](#)

`obtainArea`, [3](#)

`obtainCovariate`, [4](#)

`obtainGBIF`, [4](#)

`occ_data`, [10](#)

`occ_download`, [4](#)

`sdmWorkflow`, [5](#)

`species_model`, [6](#)

`startWorkflow`, [6](#), [10](#), [19](#)