

Package ‘rangeModelMetadata’

March 14, 2020

Type Package

Title Provides Templates for Metadata Files Associated with Species
Range Models

Version 0.1.3

Author Cory Merow, Brian Maitner, Hannah Owens, Jamie Kass, Brian Enquist, Rob Guralnick, Damairis Zurrel, Christian Koenig

Maintainer Cory Merow <cory.merow@gmail.com>

Description Range Modeling Metadata Standards (RMMS) address three challenges: they (i) are designed for convenience to encourage use, (ii) accommodate a wide variety of applications, and (iii) are extensible to allow the community of range modelers to steer it as needed. RMMS are based on a data dictionary that specifies a hierarchical structure to catalog different aspects of the range modeling process. The dictionary balances a constrained, minimalist vocabulary to improve standardization with flexibility for users to provide their own values. Merow et al. (2019) <DOI:10.1111/geb.12993> describe the standards in more detail. Note that users who prefer to use the R package 'ecospat' can obtain it from <<https://github.com/ecospat/ecospat>>.

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

Depends

Suggests BIEN, biomod2, dismo, ecospat, ENMeval, googlesheets, knitr, rmarkdown

Imports dplyr, jsonlite, MASS, raster, rgbif, rgdal, rgeos, shiny, sp, spatstat, spocc, spThin, utils

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

Date/Publication 2020-03-14 16:50:03 UTC

R topics documented:

cleanForCSV	2
csvToRMM	3
rmmAutofillBIEN	4
rmmAutofillENMeval	5
rmmAutofillEnvironment	6
rmmAutofillPackageCitation	7
rmmAutofillspocc	8
rmmCheckEmpty	9
rmmCheckFinalize	10
rmmCheckMissingNames	11
rmmCheckName	12
rmmCheckShiny	13
rmmCheckValue	14
rmmCleanNULLs	15
rmmDataDictionary	16
rmmFamilies	17
rmmSuggest	17
rmmTemplate	18
rmmToCSV	18
Index	20

cleanForCSV	<i>Helper function for non-string metadata in rmmToCSV</i>
-------------	--

Description

Cleans up metadata instances that get messy if one tries to write them directly to csv tables (i.e. extent objects, bibtex objects.)

Usage

```
cleanForCSV(x = NULL)
```

Arguments

x An rmm entry that returned to the rmmToCSV function.

Details

This is a utility function for use by rmmToCSV.

Value

Reformatted element for use in rmmToCSV function.

Author(s)

Hannah Owens <hannah.owens@gmail.com>, Cory Merow <cory.merow@gmail.com>

See Also

Other csvConversion: [csvToRMM\(\)](#), [rmmToCSV\(\)](#)

csvToRMM

Create rangeModelMetaData ('rmm') object from a .csv File

Description

Takes user-input .csv file and converts it to a rangeModelMetaData ('rmm') object.

Usage

```
csvToRMM(csv, family = NULL)
```

Arguments

csv	A character file path to the csv file.
family	character string; specifies an application profile (use case) by specifying the families of entities that should be included. Specifying NULL includes all entities. Use rmmFamilies() to see supported values.

Details

See Examples.

Value

An rmm object that was read from the supplied .csv text file.

Author(s)

Hannah Owens <hannah.owens@gmail.com>

See Also

Other csvConversion: [cleanForCSV\(\)](#), [rmmToCSV\(\)](#)

Examples

```
csv <- "somePathOnYourMachine/rmm_example.csv";  
## Not run: temp <- csvToRMM(csv);
```

rmmAutofillBIEN	<i>Add occurrence metadata from a BIEN query to an rmm object</i>
-----------------	---

Description

This function populates occurrence field in an rmm object with output from a BIEN_occurrence_... query

Usage

```
rmmAutofillBIEN(rmm, occurrences)
```

Arguments

rmm	an rmm list
occurrences	an occurrence data.frame obtained from a BIEN occurrence query

Details

See Examples.

Value

a range model metadata list

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

See Also

[BIEN_occurrence_species](#)

Other autofill: [rmmAutofillENMeval\(\)](#), [rmmAutofillEnvironment\(\)](#), [rmmAutofillPackageCitation\(\)](#), [rmmAutofillspocc\(\)](#)

Examples

```
## Not run:  
rmm <- rmmTemplate()  
xs <- BIEN::BIEN_occurrence_species(species="Xanthium strumarium")  
rmmAutofillBIEN(rmm = rmm, occurrences = xs)  
  
## End(Not run)
```

rmmAutofillENMeval *Fill in relevant rmm fields from an ENMevaluation object.*

Description

Fill in relevant rmm fields from an ENMevaluation object.

Usage

```
rmmAutofillENMeval(rmm, e, selectionCriteria, optimalModelIndex)
```

Arguments

rmm	an rmm list
e	an ENMevaluation object
selectionCriteria	a character string indicating the model selection rules used (e.g., "first chose models with lowest MTP omission rate, then chose the model with highest average test AUC")
optimalModelIndex	a numeric value indicating the row number of the model chosen by the user (e.g., if you chose the model corresponding to row 5 in the results table, this number would be 5); multiple models may be selected in theory (for the purposes of model averaging, etc.), but selecting one is preferable to reduce confusion

Details

See Examples.

Value

a range model metadata list

Author(s)

Jamie M. Kass <jamie.m.kass@gmail.com>

See Also

Other autofill: [rmmAutofillBIEN\(\)](#), [rmmAutofillEnvironment\(\)](#), [rmmAutofillPackageCitation\(\)](#), [rmmAutofillspocc\(\)](#)

Examples

```
#see vignette('rmm_workflow')
```

 rmmAutofillEnvironment

Add relevant environmental data information to an rmm object

Description

This can be used with environmental layers used for fitting or transferring

Usage

```
rmmAutofillEnvironment(rmm, env, transfer)
```

Arguments

rmm	an rmm list
env	a raster stack
transfer	0 if not transfer, 1:n for n environments that you're transferring to

Details

See Examples.

Value

a range model metadata list

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

See Also

Other autofill: [rmmAutofillBIEN\(\)](#), [rmmAutofillENMeval\(\)](#), [rmmAutofillPackageCitation\(\)](#), [rmmAutofillspocc\(\)](#)

Examples

```
## Not run:
rmm=rmmTemplate()
rasterFiles=list.files(path=paste(system.file(package='dismo'), '/ex', sep=''),
                      pattern='grd', full.names=TRUE)
#make a stack of the rasters
env=raster::stack(rasterFiles)
# for fitting environment
rmm=rmmAutofillEnvironment(rmm,env,transfer=0)
# for the first environment that you're transferring to
rmm=rmmAutofillEnvironment(rmm,env,transfer=1)
# for the second environment that you're transferring to, etc.
```

```
rmm=rmmAutofillEnvironment(rmm,env,transfer=2)
## End(Not run)
```

rmmAutofillPackageCitation
Add all package citations to an rmm object

Description

Using bibtex citations

Usage

```
rmmAutofillPackageCitation(rmm, packages)
```

Arguments

rmm	an rmm list
packages	a vector of quoted package names

Details

See Examples.

Value

a range model metadata list

Author(s)

Brian Maitner <bmailto:bmailto@gmail.com>, Cory Merow <cory.merow@gmail.com>

See Also

Other autofill: [rmmAutofillBIEN\(\)](#), [rmmAutofillENMeval\(\)](#), [rmmAutofillEnvironment\(\)](#), [rmmAutofillspocc\(\)](#)

Examples

```
rmm=rmmTemplate()
rmm=rmmAutofillPackageCitation(rmm,c('raster','sp'))
```

rmmAutofillspocc	<i>Add occurrence metadata from a spocc query to an rmm object</i>
------------------	--

Description

This function populates occurrence field in an rmm object with output from a spocc query

Usage

```
rmmAutofillspocc(rmm, occ)
```

Arguments

rmm	an rmm list
occ	Output from occ

Details

See Examples.

Value

a range model metadata list

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

See Also

[occ](#)

Other autofill: [rmmAutofillBIEN\(\)](#), [rmmAutofillENMeval\(\)](#), [rmmAutofillEnvironment\(\)](#), [rmmAutofillPackageCitation\(\)](#)

Examples

```
## Not run:  
rmm=rmmTemplate()  
xs <- spocc::occ("Xanthium strumarium")  
rmmAutofillspocc(rmm = rmm, occ = xs)  
  
## End(Not run)
```

`rmmCheckEmpty`*Check an rmm object for empty fields*

Description

Identify empty fields in an rmm object and classify these into obligate and optional fields.

Usage

```
rmmCheckEmpty(rmm, family = c("base"))
```

Arguments

<code>rmm</code>	a range model metadata list
<code>family</code>	an rmm family, "base" by default

Details

See Examples.

Value

A dataframe containing empty fields labelled as obligate, optional, or suggested.

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

See Also

Other check: [rmmCheckFinalize\(\)](#), [rmmCheckMissingNames\(\)](#), [rmmCheckName\(\)](#), [rmmCheckValue\(\)](#), [rmmCleanNULLs\(\)](#)

Examples

```
#First, make an empty rmm object:
rmm<-rmmTemplate()
#Next, we check for empty fields:
empties1<-rmmCheckEmpty(rmm = rmm)
#If looks like there are quite a few empty obligate fields. Let's populate a few:
rmm$data$occurrence$taxon<-"Acer rubrum"
rmm$data$environment$variableNames<-"Bio1"
#Now, if we run rmmCheckEmpty again, we see there are 2 fewer empty, obligate fields
empties2<-rmmCheckEmpty(rmm = rmm)
```

rmmCheckFinalize *Run a final check of an rmm object*

Description

Check an rmm object for non-standard and missing values and fields

Usage

```
rmmCheckFinalize(rmm, family = c("base"))
```

Arguments

rmm	a range model metadata list
family	The rmm family to check the rmm against

Details

See Examples.

Value

Prints feedback to point out possible errors.

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

See Also

Other check: [rmmCheckEmpty\(\)](#), [rmmCheckMissingNames\(\)](#), [rmmCheckName\(\)](#), [rmmCheckValue\(\)](#), [rmmCleanNULLs\(\)](#)

Examples

```
rmm<-rmmTemplate() # Make an empty template  
rmmCheckFinalize(rmm)
```

rmmCheckMissingNames *Check for missing fields*

Description

Identify obligate fields that are missing

Usage

```
rmmCheckMissingNames(rmm, family = c("base"))
```

Arguments

rmm	a range model metadata list
family	The rmm family to check the rmm against

Details

See Examples.

Value

A vector of names that are missing from the rmm object.

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

See Also

Other check: [rmmCheckEmpty\(\)](#), [rmmCheckFinalize\(\)](#), [rmmCheckName\(\)](#), [rmmCheckValue\(\)](#), [rmmCleanNULLs\(\)](#)

Examples

```
rmm<-rmmTemplate() # Make an empty template
```

rmmCheckName	<i>Check field names of a range model metadata list against conventions</i>
--------------	---

Description

Identify nonstandard fields

Usage

```
rmmCheckName(  
  rmm,  
  cutoff_distance = 3,  
  returnData = F,  
  interactiveCorrections = FALSE  
)
```

Arguments

rmm	a range model metadata list
cutoff_distance	number of allowed different characters to match standardized names
returnData	logical. If FALSE, the function will return the (possibly) corrected rmm object. If TRUE, the function will return a data.frame containing information on incorrect names.
interactiveCorrections	logical. If TRUE, the user will be prompted to indicate whether the proposed correction should be accepted, thereby modifying the 'rmm' object. If FALSE, suggestions will just be printed to the screen and users can edit them manually.

Details

See Examples.

Value

Either an rmm list object (returnData=F) or a data.frame containing information on possible name errors (returnData=T).

Note

Names returned by this check may be either incorrectly named or correctly named but missing from the data dictionary.

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

See Also

Other check: [rmmCheckEmpty\(\)](#), [rmmCheckFinalize\(\)](#), [rmmCheckMissingNames\(\)](#), [rmmCheckValue\(\)](#), [rmmCleanNULLs\(\)](#)

Examples

```
rmm<-rmmTemplate() # Make an empty template
rmm$dataPrep$biological$taxonomicHarmonization$taxonomy_source<-"The Plant List"
# Add a new, non-standard field
rmm.1=rmmCheckName(rmm)
# Checking the names should identify the new, non-standard field we've added ("taxonomy_source")
```

rmmCheckShiny

RangeModelMetadata Check in Shiny

Description

Run shiny app to visualize rmm check functions

Usage

```
rmmCheckShiny()
```

Details

See Examples.

Value

None

Note

This function launches a shiny app in the default web browser

Author(s)

Jamie Kass <jamie.m.kass@gmail.com>

Examples

```
## Not run:
rmm1=rmmTemplate()
rmm1=rmmAutofillPackageCitation(rmm1,c('raster','sp'))
rasterFiles=list.files(path=paste(system.file(package='dismo'), '/ex', sep=''),
                        pattern='grd', full.names=TRUE)

make a stack of the rasters
env=raster::stack(rasterFiles)
# for fitting environment
rmm1=rmmAutofillEnvironment(rmm1,env,transfer=0)
# for transfer environment 1 (assuming different than for fitting)
rmm1=rmmAutofillEnvironment(rmm1,env,transfer=1)
# for transfer environment 2 (assuming different than 1)
rmm1=rmmAutofillEnvironment(rmm1,env,transfer=2)

## End(Not run)
## Not run: rmmCheckShiny(rmm1)
```

rmmCheckValue	<i>Check values of a range model metadata list against commonly used values</i>
---------------	---

Description

Identify nonstandard values

Usage

```
rmmCheckValue(rmm, cutoff_distance = 3, returnData = F)
```

Arguments

rmm	a range model metadata list
cutoff_distance	The maximum allowable similarity (Levenshtein (edit) distance) for use in fuzzy matching.
returnData	Should a dataframe containing information on matched and unmatched values be returned? Default is FALSE

Details

See Examples.

Value

Text describing identical, similar and non-matched values for rmm entities with suggested values. If `returnData = T`, a dataframe is returned containing 5 columns: `field` (the rmm entity), `exact_match` (values that appear correct), `partial_match` (values that are partial_match to common values), `not_matched` (values that are dissimilar from accepted values), `partial_match_suggestions` (suggested values for partial_match values).

Note

Names returned by this check may be either incorrectly named or correctly named but missing from the data dictionary.

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

See Also

Other check: [rmmCheckEmpty\(\)](#), [rmmCheckFinalize\(\)](#), [rmmCheckMissingNames\(\)](#), [rmmCheckName\(\)](#), [rmmCleanNULLs\(\)](#)

Examples

```
rmm<-rmmTemplate() #First, we create an empty rmm template
rmm$data$environment$variableNames<- c("bio1", "bio 2", "bio3", "cromulent")
#We add 3 of the bioclim layers, including a spelling error (an extra space) in bio2,
# and a word that is clearly not a climate layer, 'cromulent'.
rmmCheckValue(rmm = rmm)
#Now, when we check the values, we see that bio1 and bio2 are reported as exact matches,
#while 'bio 2' is flagged as a partial match with a suggested value of 'bio2',
# and cromulent is flagged as not matched at all.
#If we'd like to return a dataframe containing this information in a perhaps more useful format:
rmmCheckValue_output<-rmmCheckValue(rmm = rmm,returnData = TRUE)
```

rmmCleanNULLs

Remove NULL entries range model metadata list

Description

Check if fields are NULL in a range model metadata list and toss

Usage

```
rmmCleanNULLs(rmm)
```

Arguments

rmm a range model metadata list

Details

See Examples.

Value

printout to the console

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

See Also

Other check: [rmmCheckEmpty\(\)](#), [rmmCheckFinalize\(\)](#), [rmmCheckMissingNames\(\)](#), [rmmCheckName\(\)](#), [rmmCheckValue\(\)](#)

Examples

```
# see vignette('rmm_vignette')
```

rmmDataDictionary *Open range model metadata dictionary.*

Description

For viewing only

Usage

```
rmmDataDictionary(excel = F)
```

Arguments

excel logical; open in excel?

Examples

```
dd=rmmDataDictionary()
```

rmmFamilies	<i>Print supported family names for rmm objects</i>
-------------	---

Description

Used to see options to for specifying an rmm object template

Usage

```
rmmFamilies()
```

Examples

```
rmmFamilies()
```

rmmSuggest	<i>Suggest inputs for a range model metadata list</i>
------------	---

Description

Supply fields to receive suggested inputs

Usage

```
rmmSuggest(charString, fullFieldDepth = FALSE)
```

Arguments

charString	string referencing fields of the form 'field1\$field2' or 'field1\$field2\$field3', etc.
fullFieldDepth	print all fields below the current field depth

```
rmm1=rmmTemplate() rmmSuggest('dataPrep',fullFieldDepth=FALSE) rmm-
Suggest('dataPrep',fullFieldDepth=TRUE) rmmSuggest('dataPrep$errors$duplicateRemoval')
rmmSuggest('dataPrep$errors$duplicateRemoval$rule') rmmSuggest('model') rmm-
Suggest('modelFit$algorithmSettings$') rmmSuggest('modelFit$algorithmSettings$maxent$')
rmmSuggest('$modelFit$algorithmSettings$maxent$featureSet')
```

Details

See Examples.

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>,

rmmTemplate	<i>Range modeling metadata</i>
-------------	--------------------------------

Description

Make an empty metadata list

Usage

```
rmmTemplate(family = NULL)
```

Arguments

family character string; specifies an application profile (use case) by specifying the families of entities that should be included. Specifying NULL includes all entities. Use 'rmmFamilies' to see supported values.

Details

See Examples.

Value

a range model metadata list

Author(s)

Cory Merow <cory.merow@gmail.com>, Brian Maitner <bmaitner@gmail.com>

Examples

```
rmm1=rmmTemplate()  
rmm2=rmmTemplate(family=c('base'))  
str(rmm2)
```

rmmToCSV	<i>Create .csv File From rangeModelMetaData Object</i>
----------	--

Description

Takes user-input rangeModelMetaData object and from it generates a .csv file that can be used to document range model metadata for a variety of applications.

Usage

```
rmmToCSV(x = rmmTemplate(family = NULL), filename = NULL)
```

Arguments

x An object of class rmm that the user wishes transposed into a .csv file.
filename The name of the transcription .csv file.

Details

See Examples.

Value

An data frame containing all the information from an rmm object.

Author(s)

Hannah Owens <hannah.owens@gmail.com>, Cory Merow <cory.merow@gmail.com>

See Also

Other csvConversion: [cleanForCSV\(\)](#), [csvToRMM\(\)](#)

Examples

```
rmm=rmmTemplate()
rasterFiles=list.files(path=paste(system.file(package='dismo'), '/ex', sep=''),
                       pattern='grd', full.names=TRUE)
#make a stack of the rasters
env=raster::stack(rasterFiles)
# for fitting environment
rmm=rmmAutofillEnvironment(rmm,env,transfer=0)
# for the first environment that you're transferring to
rmm=rmmAutofillEnvironment(rmm,env,transfer=1)
# for the second environment that you're transferring to, etc.
rmm=rmmAutofillEnvironment(rmm,env,transfer=2)
## Not run:
tmp=rmmToCSV(rmm,file='somePathOnYourMachine/rmm_example.csv')

## End(Not run)
```

Index

BIEN_occurrence_species, [4](#)

cleanForCSV, [2](#), [3](#), [19](#)

csvToRMM, [3](#), [3](#), [19](#)

occ, [8](#)

rmmAutofillBIEN, [4](#), [5–8](#)

rmmAutofillENMeval, [4](#), [5](#), [6–8](#)

rmmAutofillEnvironment, [4](#), [5](#), [6](#), [7](#), [8](#)

rmmAutofillPackageCitation, [4–6](#), [7](#), [8](#)

rmmAutofillspocc, [4–7](#), [8](#)

rmmCheckEmpty, [9](#), [10](#), [11](#), [13](#), [15](#), [16](#)

rmmCheckFinalize, [9](#), [10](#), [11](#), [13](#), [15](#), [16](#)

rmmCheckMissingNames, [9](#), [10](#), [11](#), [13](#), [15](#), [16](#)

rmmCheckName, [9–11](#), [12](#), [15](#), [16](#)

rmmCheckShiny, [13](#)

rmmCheckValue, [9–11](#), [13](#), [14](#), [16](#)

rmmCleanNULLs, [9–11](#), [13](#), [15](#), [15](#)

rmmDataDictionary, [16](#)

rmmFamilies, [17](#)

rmmSuggest, [17](#)

rmmTemplate, [18](#)

rmmToCSV, [3](#), [18](#)