

Package ‘ClimMobTools’

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Type Package

Title API Client for the 'ClimMob' Platform

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BugReports <https://github.com/agrdatasci/ClimMobTools/issues>

Description API client for 'ClimMob', an open source software for decentralized large-N trials with the 'tricot' approach <<https://climmob.net/>>. Developed by van Etten et al. (2019) <[doi:10.1017/S0014479716000739](https://doi.org/10.1017/S0014479716000739)>, it turns the research paradigm on its head; instead of a few researchers designing complicated trials to compare several technologies in search of the best solutions for the target environment, it enables many participants to carry out reasonably simple experiments that taken together can offer even more information. 'ClimMobTools' enables project managers to deep explore and analyse their 'ClimMob' data in R.

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Contents

ClimMobTools	2
exportBlockData	3
exportMeasuredTraits	3
exportTrialMetadata	4
exportTricotRanks	5
exportVariablesDescription	6
getDataCM	6
getProjectProgress	8
getProjectsCM	9
getTraitList	10
randomize	11
rankTricot	13
rmGeoIdentity	14
Index	16

ClimMobTools

API Client for the 'ClimMob' platform in R

Description

API client for 'ClimMob', an open source software for decentralized large-N trials with the 'tricot' approach <https://climmob.net/>. Developed by van Etten et al. (2019) [doi:10.1017/S0014479716000739](https://doi.org/10.1017/S0014479716000739), it turns the research paradigm on its head; instead of a few researchers designing complicated trials to compare several technologies in search of the best solutions for the target environment, it enables many participants to carry out reasonably simple experiments that taken together can offer even more information. 'ClimMobTools' enables project managers to deep explore and analyse their 'ClimMob' data in R.

Author(s)

Kauê de Sousa and Jacob van Etten and Brandon Madriz

See Also

Useful links:

- Development repository: <https://github.com/agrdatasci/ClimMobTools>
- Static documentation: <https://agrdatasci.github.io/ClimMobTools/>
- Report bugs: <https://github.com/agrdatasci/ClimMobTools/issues>
- The tricot user guide: <https://hdl.handle.net/10568/109942>

exportBlockData	<i>Export block-level (participant) data</i>
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Description

Creates a wide-format data.frame of participant (block) data for external export. The output excludes ranking variables and personally identifiable information (PII), such as names, phone numbers, and location metadata. Optionally includes geolocation if available.

Usage

```
exportBlockData(x, ...)
```

Arguments

x	An object of class CM_list containing raw ClimMob trial data.
...	further arguments passed to methods

Value

A data.frame with one row per block (participant), excluding PII and ranking data.

See Also

[rmGeoIdentity](#)

Other export functions: [exportMeasuredTraits\(\)](#), [exportTrialMetadata\(\)](#), [exportTricotRanks\(\)](#), [exportVariablesDescription\(\)](#)

exportMeasuredTraits	<i>Extract and format measured traits</i>
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Description

Extracts non-ranking, plot-level trait data from a ClimMob trial object. The function detects variables ending in "_a", "_b", or "_c", infers the trait and collection moment, and reshapes the data into long format for analysis.

Usage

```
exportMeasuredTraits(x)
```

Arguments

x	An object of class CM_list containing raw ClimMob trial data.
---	---

Details

If no measured traits are found in the data (i.e., no variables ending in "_a", "_b", or "_c"), the function returns an empty CM_df object with valid column names.

Value

A data frame of class CM_df with one row per genotype observation, including block ID, plot, genotype name, collection moment, trait name, value, and value type. Returns an empty CM_df if no measured traits are present.

See Also

Other export functions: [exportBlockData\(\)](#), [exportTrialMetadata\(\)](#), [exportTricotRanks\(\)](#), [exportVariablesDescription\(\)](#)

exportTrialMetadata	<i>Generate metadata for tricot trial export</i>
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Description

Extracts and compiles key metadata from a ClimMob trial object to support standardized data documentation and publication, including fields such as trial identifiers, geographic bounding box, crop and taxon information, and participant statistics.

Usage

```
exportTrialMetadata(x)
```

Arguments

x An object of class CM_list containing raw ClimMob trial data.

Value

A named list containing metadata fields required for tricot data export, including study (trial) name, description, dates, bounding box, participant counts, and institutional information.

See Also

Other export functions: [exportBlockData\(\)](#), [exportMeasuredTraits\(\)](#), [exportTricotRanks\(\)](#), [exportVariablesDescription\(\)](#)

exportTricotRanks	<i>Extract and format tricot rankings for data export</i>
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Description

Processes ClimMob ranking data into a standardized long-format data frame suitable for export to external databases and analysis. For each trait, the function extracts rank positions per genotype and block based on participant responses. Compatible with Dataverse and other FAIR data publication systems.

Usage

```
exportTricotRanks(  
  x,  
  pattern = c("_pos", "_neg"),  
  items = c("package_item_A", "package_item_B", "package_item_C"),  
  nmin = 0.2,  
  ...  
)
```

Arguments

x	An object of class CM_list containing raw ClimMob trial data.
pattern	character, the tricot ranking pattern
items	a character or numerical vector for indexing the column(s) containing the item names in data
nmin	Numeric to define the minimum allowed for complete cases
...	Additional arguments passed to getTraitList().

Value

A data frame in long format containing tricot rankings, with one row per genotype and trait, including the block identifier, plot label (A/B/C), genotype name, trait label, and assigned rank position.

See Also

Other export functions: [exportBlockData\(\)](#), [exportMeasuredTraits\(\)](#), [exportTrialMetadata\(\)](#), [exportVariablesDescription\(\)](#)

`exportVariablesDescription`*Generate descriptions for trial variables*

Description

Extracts metadata for variables found in tricot block data and ranking data, combining question descriptors from the registry and assessments. This function harmonizes variable names and assigns relevant descriptions, value types, and placeholders for ontology and controlled vocabularies.

Usage

```
exportVariablesDescription(x, tricot_ranks, measured_traits, block_data)
```

Arguments

<code>x</code>	An object of class <code>CM_list</code> containing raw ClimMob trial data.
<code>tricot_ranks</code>	A data frame of tricot rankings generated by <code>exportTricotRanks()</code> .
<code>measured_traits</code>	A data frame of plot data generated by <code>exportMeasuredTraits()</code> .
<code>block_data</code>	A data frame of block-level data generated by <code>exportBlockData()</code> .

Value

A data frame describing all trial variables, including name, description, value type, and optional fields for ontology and controlled vocabularies.

See Also

Other export functions: [exportBlockData\(\)](#), [exportMeasuredTraits\(\)](#), [exportTrialMetadata\(\)](#), [exportTricotRanks\(\)](#)

`getDataCM`*Get ClimMob data*

Description

Fetch the data from a ClimMob project using an application programming interface (API) key

Usage

```
getDataCM(
  key,
  project,
  userowner,
  as.data.frame = TRUE,
  as.text = FALSE,
  server = "climmb3",
  ...
)

## S3 method for class 'CM_list'
as.data.frame(x, ..., tidynames = TRUE, pivot.wider = TRUE)
```

Arguments

key	character, the user's API key
project	character, the project id
userowner	character, username of project's owner
as.data.frame	logical, to return a data frame, as.data.frame = FALSE returns a list
as.text	logical, to return a text file that can be parsed to json
server	character, to indicate from which server the data will be retrieved. See details
...	additional arguments passed to methods
x	an object of class CM_list
tidynames	logical, TRUE make clean column names
pivot.wider	logical, if TRUE return a wider object where each tricot package is a row

Details

server: options are: "climmb3" or "1000farms"

Value

An object of class 'CM_list' or a text file or a data.frame with class "CM_df" with the variables:

id	the participant's package id
moment	the data collection moment
variable	the variable name
value	the value for each variable

Author(s)

Kauê de Sousa

See Also

Other GET functions: [getProjectProgress\(\)](#), [getProjectsCM\(\)](#)

Examples

```
# This function only works with an API key
# the API key can be obtained from your ClimMob account

library("ClimMobTools")
my_key = "d39a3c66-5822-4930-a9d4-50e7da041e77"

getDataCM(key = my_key,
           project = "breadwheat",
           userowner = "gosset",
           server = "climmb3")

# get in the long format

getDataCM(key = my_key,
           project = "breadwheat",
           userowner = "gosset",
           server = "climmb3",
           pivot.wider = FALSE)
```

getProjectProgress	<i>Get project progress</i>
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Description

Fetch the progress of a ClimMob project

Usage

```
getProjectProgress(key, project, userowner, server = "climmb3")
```

Arguments

key	character, the user's API key
project	character, the project id
userowner	character, username of project's owner
server	character, to indicate from which server the data will be retrieved. See details

Details

server: the default server is "climmb3" used for clients of <https://climmb3.net/climmb3/>, other options are:

"1000farms" for clients of <https://1000farms.climmb3.net/>

Value

A list with number of submissions per assessment and submissions per assessment per enumerator

Author(s)

Kauê de Sousa

See Also

Other GET functions: [getDataCM\(\)](#), [getProjectsCM\(\)](#)

Examples

```
# This function only works with an API key
# the API key can be obtained from your ClimMob account

library("ClimMobTools")
my_key = "ff05a174-28d0-4a40-ab5a-35dc486133a6"

getProjectProgress(key = my_key,
                   project = "gina2024",
                   userowner = "student",
                   server = "1000FARMS")
```

getProjectsCM

Get ClimMob projects

Description

Fetch the status of ClimMob projects

Usage

```
getProjectsCM(key, server = "climmob3", ...)
```

Arguments

key	character, the user's API key
server	character, to indicate from which server the data will be retrieved. See details
...	additional arguments passed to methods. See details

Details

server: the default server is "climmob" used for clients of <https://climmob.net/climmob3/>, other options are:

"1000farms" for clients of <https://1000farms.climmob.net/>

Value

A data.frame with the variables:

project_id	the ClimMob single id in the server database
project_code	the project's code from the ClimMob user
project_name	the project's name
user_owner	the account name that owns the project
country	the country of project's implementation
status	the current status
creation_date	date where the project was created

Author(s)

Kauê de Sousa

See Also

Other GET functions: [getDataCM\(\)](#), [getProjectProgress\(\)](#)

Examples

```
# This function only works with an API key
# the API key can be obtained from your ClimMob account

my_key = "ff05a174-28d0-4a40-ab5a-35dc486133a6"

getProjectsCM(key = my_key, server = "1000FARMS")
```

getTraitList

Organize trait ranks in a ClimMob data

Description

This function helps in identifying the traits assessed in the tricot project and validates the data returning a list with logical vectors to support the transformation of tricot rankings into a PlackettLuce ranking

Usage

```
getTraitList(data, pattern, trait.labels = NULL, ...)
```

Arguments

data	data.frame, the ClimMob data
pattern	character, the tricot ranking pattern
trait.labels	an optional character with clean trait labels
...	additional arguments, not implemented yet

Value

a list with trait validation data

Examples

```
require("gosset")

data("breadwheat", package = "gosset")

getTraitList(breadwheat, c("_best", "_worst"))
```

randomize

Set an experimental incomplete block design

Description

Generate an incomplete block A-optimal design. The function is optimized for incomplete blocks of three, but it will also work with comparisons of any other number of options. The design strives for approximate A optimality, this means that it is robust to missing observations. It also strives for balance for positions of each option. Options are equally divided between first, second, third, etc. position. The strategy is to create a "pool" of combinations that does not repeat combinations and is A-optimal. Then this pool is ordered to make subsets of consecutive combinations also relatively balanced and A-optimal

Usage

```
randomize(
  npackages,
  itemnames,
  ncomp = 3,
  availability = NULL,
  props = NULL,
  ...
)
```

Arguments

<code>npackages</code>	an integer for the number of incomplete blocks to be generated
<code>itemnames</code>	a character for the name of items tested in the experiment
<code>ncomp</code>	an integer for the number of items to be assigned to each incomplete block
<code>availability</code>	optional, a vector with integers indicating the number of plots available for each <i>itemnames</i>
<code>props</code>	optional, a numeric vector with the desired proportions for each <i>itemnames</i>
<code>...</code>	additional arguments passed to methods

Value

A dataframe with the randomized design

Author(s)

Jacob van Etten

References

Bailey and Cameron (2004). Combinations of optimal designs. <https://webpace.maths.qmul.ac.uk/l.h.soicher/designtheory.org/library/preprints/optimal.pdf>

Examples

```
ncomp = 3
npackages = 20
itemnames = c("apple", "banana", "grape", "mango", "orange")
availability = c(5, 8, 50, 50, 50)

randomize(ncomp = ncomp,
          npackages = npackages,
          itemnames = itemnames)

randomize(ncomp = ncomp,
          npackages = npackages,
          itemnames = itemnames,
          availability = availability)

# run diagnostics to certify that randomization is balanced
# the number of interactions should have the lower sd as possible
# this verification may not work well when technologies are
# tested in different proportions
design = randomize(ncomp = ncomp,
                  npackages = npackages,
                  itemnames = itemnames)

design$best = "A"

design$worst = "C"

# number of times each item is tested in the
# trial design
ntest = table(unlist(design[,c(1:3)]))

ntest

# put into the PlackettLuce structure to check
# number of interactions between items
r = gosset::rank_tricot(design, c(1:3), c(4:5))

bn = gosset::set_binomialfreq(r)
```

```
bn$interactions = bn$win1 + bn$win2

bn = bn[,c(1,2,5)]

bn
```

rankTricot

*Build Plackett-Luce rankings from tricot dataset***Description**

Create an object of class "rankings" from tricot data

Usage

```
rankTricot(
  data,
  items,
  input,
  group = FALSE,
  validate.rankings = FALSE,
  additional.rank = NULL,
  ...
)
```

Arguments

data	a data.frame with columns specified by items and input values
items	a character or numerical vector for indexing the column(s) containing the item names in data
input	a character or numerical vector for indexing the column(s) containing the values in data to be ranked
group	logical, if TRUE return an object of class "grouped_rankings"
validate.rankings	logical, if TRUE implements a check on ranking consistency looking for possible ties, NA or letters other than A, B, C. These entries are set to 0
additional.rank	optional, a data frame for the comparisons between tricot items and the local item
...	additional arguments passed to methods. See details

Details

full.output: logical, to return a list with a "rankings", a "grouped_rankings" and the ordered items

Value

a PlackettLuce "rankings" or "grouped_rankings" object

Author(s)

Kauê de Sousa and Jacob van Etten, with ideas from Heather Turner

Examples

```
# beans data where each observer compares 3 varieties randomly distributed
# from a list of 11 and additionally compares these 3 varieties
# with their local variety
if (require("PlackettLuce")){
  data("beans", package = "PlackettLuce")

  # first build rankings with only tricot items
  # and return an object of class 'rankings'
  R = rankTricot(data = beans,
                 items = c(1:3),
                 input = c(4:5))

  head(R)

#####

# pass the comparison with local item as an additional rankings, then
# each of the 3 varieties are compared separately with the local item
# and return an object of class grouped_rankings
G = rankTricot(data = beans,
               items = c(1:3),
               input = c(4:5),
               group = TRUE,
               additional.rank = beans[c(6:8)])

  head(G)
}
```

rmGeoIdentity

Remove geographical identity

Description

Build a buffer around the a set of geographical coordinates and take a random point around the buffer. The function is used to omit the precise location of tricot participants but keeping a close distance to the trial environment.

Usage

```
rmGeoIdentity(longlat, dist = 0.015, nQuadSegs = 2L, seed = NULL, ...)
```

Arguments

longlat	a data.frame or matrix with geographical coordinates long lat
dist	numeric, buffer distance for all <i>lonlat</i>
nQuadSegs	integer, number of segments per quadrant
seed	integer, the seed for random number generation. If NULL (the default), ClimMobTools will set the seed randomly
...	further arguments passed to sf methods

Value

A data frame with the random coordinates long lat within the buffer

Examples

```
library("sf")

xy = matrix(c(11.097799, 60.801090,
             11.161298, 60.804199,
             11.254428, 60.822457),
            nrow = 3, ncol = 2, byrow = TRUE)

rmGeoIdentity(xy, seed = 1501)

#' the function also handles NAs

xy2 = matrix(c(11.097799, 60.801090,
              NA, NA,
              11.161298, 60.804199,
              11.254428, 60.822457,
              11.254428, NA),
            nrow = 5, ncol = 2, byrow = TRUE)

rmGeoIdentity(xy2)
```

Index

* GET functions

- getDataCM, [6](#)
- getProjectProgress, [8](#)
- getProjectsCM, [9](#)

* export functions

- exportBlockData, [3](#)
- exportMeasuredTraits, [3](#)
- exportTrialMetadata, [4](#)
- exportTricotRanks, [5](#)
- exportVariablesDescription, [6](#)

as.data.frame.CM_list (getDataCM), [6](#)

ClimMobTools, [2](#)

ClimMobTools-package (ClimMobTools), [2](#)

exportBlockData, [3](#), [4–6](#)

exportMeasuredTraits, [3](#), [3](#), [4–6](#)

exportTrialMetadata, [3](#), [4](#), [4](#), [5](#), [6](#)

exportTricotRanks, [3](#), [4](#), [5](#), [6](#)

exportVariablesDescription, [3–5](#), [6](#)

getDataCM, [6](#), [9](#), [10](#)

getProjectProgress, [7](#), [8](#), [10](#)

getProjectsCM, [7](#), [9](#), [9](#)

getTraitList, [10](#)

randomise (randomize), [11](#)

randomize, [11](#)

rankTricot, [13](#)

rmGeoIdentity, [3](#), [14](#)

sf, [15](#)