

Package: mmstat4 (via r-universe)

November 6, 2024

Title Access to Teaching Materials from a ZIP File or GitHub

Version 0.2.3

Author Sigbert Klinke [aut, cre]

(<<https://orcid.org/0000-0003-3337-1863>>), Jekaterina Zukovska
[ctb] (<<https://orcid.org/0000-0002-7753-9210>>)

Maintainer Sigbert Klinke <sigbert@hu-berlin.de>

Description Provides access to teaching materials for various statistics courses, including R and Python programs, Shiny apps, data, and PDF/HTML documents. These materials are stored on the Internet as a ZIP file (e.g., in a GitHub repository) and can be downloaded and displayed or run locally. The content of the ZIP file is temporarily or permanently stored. By default, the package uses the GitHub repository 'sigbertklinke/mmstat4.data.' Additionally, the package includes 'association_measures.R' from the archived package 'ryouready' by Mark Heckman and some auxiliary functions.

License GPL-3

Encoding UTF-8

Roxygen list(markdown = TRUE)

Depends reticulate

Imports crayon, digest, httr, knitr, tcltk, rappdirs, rio, rstudioapi,
shiny, stringdist, tools

Suggests rmarkdown

VignetteBuilder knitr

RoxygenNote 7.3.2

Config/pak/sysreqs make libpng-dev libssl-dev python3 libx11-dev
zlib1g-dev

Repository <https://sigbertklinke.r-universe.dev>

RemoteUrl <https://github.com/sigbertklinke/mmstat4>

RemoteRef HEAD

RemoteSha a30188c8de42097751505849d8eb7eac6639105e

Contents

askUser	2
association	3
cdf	6
checkFiles	7
defaultApp	8
dupFiles	9
getList	10
getMMstat	10
getText	11
gh	11
ghappAddin	12
ghc	13
ghdecompose	13
ghfile	14
ghget	15
ghinstall	16
ghlist	16
ghopenAddin	18
ghpath	18
ghquery	19
ghrepos	20
ghzip	20
isLocal	21
normpathes	21
note	22
openFile	23
pkglist	23
pkgMissing	24
py_env	25
toInt	25
toNum	26
urlExists	26
Index	28

 askUser

askUser

Description

askUser provides a way to ask the user a yes/no/cancel question (default). A * after a number indicates the default option.

Usage

```
askUser(
  msg,
  choices = c("Yes", "No", "Cancel"),
  default = 1,
  col = crayon::black
)
```

Arguments

<code>msg</code>	character: the prompt message for the user
<code>choices</code>	character: vector of choices (default: <code>c("Yes", "No", "Cancel")</code>)
<code>default</code>	character/integer: default option if only Enter pressed (default: 1)
<code>col</code>	function: a color function (default: <code>crayon::black</code>)

Value

the integer number chosen by the user

Examples

```
if (interactive())
  askUser("Do you want to use askUser?")
```

association

Association measures

Description

Various association coefficients for nominal and ordinal data; the input formats follows `stats::chisq.test()`.

- `concordant` concordant pairs
- `discordant` discordant pairs
- `ties.row` pairs tied on rows
- `ties.col` pairs tied on columns
- `nom.phi` Phi Coefficient
- `nom.cc` Contingency Coefficient (Pearson's C) and Sakoda's Adjusted Pearson's C
- `nom.TT` Tshuprow's T (not meaningful for non-square tables)
- `nom.CV` Cramer's V (for 2 x 2 tables $V = \text{Phi}$)
- `nom.lambda` Goodman and Kruskal's Lambda with
 - `lambda.cr` The row variable is used as independent, the column variable as dependent variable.
 - `lambda.rc` The column variable is used as independent, the row variable as dependent variable.

- `lambda.symmetric` Symmetric Lambda (the mean of both above).
- `nom.uncertainty` Uncertainty Coefficient (Theil's U) with
 - `ucc.cr` The row variable is used as independent, the column variable as dependent variable.
 - `uc.rc` The column variable is used as independent, the row variable as dependent variable.
 - `uc.symmetric` Symmetric uncertainty coefficient.
- `ord.gamma` Gamma coefficient
- `ord.tau` a vector with Kendall-Stuart Tau's
 - `tau.a` Tau-a (for quadratic tables only)
 - `tau.b` Tau-b
 - `tau.c` Tau-c
- `ord.somers.d` Somers' d
- `eta` Eta coefficient for nominal/interval data

Usage

`concordant(x, y = NULL)`

`discordant(x, y = NULL)`

`ties.row(x, y = NULL)`

`ties.col(x, y = NULL)`

`nom.phi(x, y = NULL)`

`nom.cc(x, y = NULL)`

`nom.TT(x, y = NULL)`

`nom.CV(x, y = NULL)`

`nom.lambda(x, y = NULL)`

`nom.uncertainty(x, y = NULL)`

`ord.gamma(x, y = NULL)`

`ord.tau(x, y = NULL)`

`ord.somers.d(x, y = NULL)`

`eta(x, y, breaks = NULL)`

Arguments

x	a numeric vector, table or matrix. x and y can also both be factors. For eta the independent nominal variable (factor or numeric).
y	a numeric vector; ignored if x is a table or matrix. If x is a factor, y should be a factor of the same length. For eta the dependent interval variable (numeric).
breaks	either a numeric vector of two or more unique cut points or a single number (greater than or equal to 2) giving the number of intervals into which x is to be cut (only for eta).

Value

the association coefficient(s)

Source

From the [archived ryouready package](#) by Mark Heckmann. The code for the calculation of `nom.lambda`, `nom.uncertainty`, `ord.gamma`, `ord.tau`, `ord.somers.d` was supplied by Marc Schwartz (under GPL 2) and checked against SPSS results.

Examples

```
## Nominal data
# remove gender from the table
hec <- apply(HairEyeColor, 1:2, sum)
nom.phi(hec)
nom.cc(hec)
nom.TT(hec)
nom.CV(hec)
nom.lambda(hec)
nom.uncertainty(hec)
## Ordinal data
# create a fake data set
ordx <- sample(5, size=100, replace=TRUE)
ordy <- sample(5, size=100, replace=TRUE)
concordant(ordx, ordy)
discordant(ordx, ordy)
ties.row(ordx, ordy)
ties.col(ordx, ordy)
ord.gamma(ordx, ordy)
ord.tau(ordx, ordy)
ord.somers.d(ordx, ordy)
## Interval/nominal data
eta(iris$Species, iris$Sepal.Length)
```

`cdf`*Generates and plots a cumulative distribution function.*

Description

Generates and plots a cumulative distribution function.

Usage

```
cdf(x, ...)  
  
## Default S3 method:  
cdf(x, y, discrete = TRUE, ...)  
  
## S3 method for class 'cdf'  
plot(x, y, ..., col.01line = "black", pch = 19)
```

Arguments

<code>x</code>	numeric: x-values
<code>...</code>	further parameters given to <code>graphics::plot()</code>
<code>y</code>	numeric: y-values
<code>discrete</code>	logical: if distribution is discrete
<code>col.01line</code>	color: color of horizontal lines at 0 and 1 (default: black)
<code>pch</code>	point type: See <code>graphics::points()</code> for possible values and their interpretation (default: 19)

Value

returns a cdf object

Examples

```
# Binomial distribution  
x <- cdf(0:10, pbinom(0:10, 10, 0.5))  
plot(x)  
# Exponential distribution  
x <- seq(0, 5, by=0.01)  
x <- cdf(x, pexp(x), discrete=FALSE)  
plot(x)
```

`checkFiles`*Checks whether all specified files are valid R or Python files*

Description

`checkFiles` verifies whether all specified files are valid source files that can be executed independently of each other. If an error occurs, the following actions are taken:

1. If `open` is either a function name or a function with a `file` parameter, then `checkFiles` will attempt to open the faulty source file; otherwise, it will not.
2. The execution of `checkFiles` is stopped.

If you do not want the faulty source file to be opened immediately, use `open=0`.

Three modes are available for checking a file:

1. `exist`: Does the source file exist?
2. `parse`: (default) Is `parse(file)` (in R) or `python -m py_compile "file"` (in Python) successful?
3. `run`: Is `Rscript "file"` (in R) or `reticulate::py_run_file(file)` (in Python) successful?

If source files have side effects, e.g., generating an image or producing other outputs, and `mode == "parse"`, these side effects will occur during the check. To prevent a script from being executed during the check, add a `## Not check: comment` at the top of the script.

Usage

```
checkFiles(  
  files,  
  index = seq_along(files),  
  path = NULL,  
  open = openFile,  
  mode = c("parse", "run", "exist"),  
  ...  
)
```

```
Rsolo(  
  files,  
  index = seq_along(files),  
  path = NULL,  
  open = openFile,  
  mode = c("parse", "run", "exist"),  
  ...  
)
```

Arguments

files	character: file name(s)
index	integer(s): if length(index)==1 the files from index to length(files) are checked (default: seq_along(files)) otherwise the files with values in index are checked.
path	character: path to start from (default: getwd())
open	function: function or function name to call after an error occurs (default: openFile)
mode	character which check to do
...	further parameters given to the function in open

Value

nothing

Examples

```
if (interactive()) {
  files <- list.files(pattern="*(R|py)", full.names=TRUE, recursive=TRUE)
  checkFiles(files)
}
```

defaultApp

defaultApp

Description

Tries to open the given file with the default application of the operating system using `base::system2()`. Only Windows (windows), macOS (darwin), Linux (linux) and FreeBSD (freebsd) is supported.

Usage

```
defaultApp(file, wait = FALSE, ...)
```

Arguments

file	character: file name
wait	logical: indicates whether the R interpreter should wait for the command to finish, or run it asynchronously (default: FALSE)
...	further arguments passed to system2

Value

Result of `try(system2, ...)`, invisibly

See Also

[berryFunctions::openFile\(\)](#)

Examples

```
if (interactive()) {  
  ghget()  
  defaultApp(ghlist("dataanalysis.pdf", full.names = TRUE))  
}
```

dupFiles

Find duplicate files

Description

dupFiles computes checksums to find duplicate files.

Usage

```
dupFiles(files, ...)
```

```
Rdups(files, ...)
```

Arguments

files character: file name(s)

... further parameters given to [digest::digest\(\)](#)

Value

a list of file names with the same checksum or NULL

Examples

```
if (interactive()) {  
  files <- list.files(pattern="*.R$", full.names=TRUE, recursive=TRUE)  
  dupFiles(files)  
}
```

getList *getList*

Description

Creates a list with element names replaced by `link{getText}`.

Usage

```
getList(...)
```

Arguments

... named elements of a list

Value

renamed list

Examples

```
getList(BOSTON=1, MTCARS=2)
```

getMMstat *getMMstat*

Description

Allows to access the package internal `mmstat` environment.

Usage

```
getMMstat(...)
```

Arguments

... elements

Value

the choosen element

Examples

```
getMMstat('version')
```

getText	<i>getText</i>
---------	----------------

Description

Translates a given message into another language.

Usage

```
getText(msg)
```

Arguments

msg character vector

Value

vector of translated messages

Examples

```
getText('Test')
```

gh	<i>gh functions</i>
----	---------------------

Description

The function `gh` carries out the following operation on a file named `x`. It searches for a match for `x` within the active repository, utilizing fuzzy string matching. If no unique match is identified, an error is thrown along with suggestions for potential "best" matches. Otherwise, the following operation are performed:

- `gh(x, 'open')` or `ghopen(x)`: Opens a file in the local browser if the file extension is `html` or `pdf`, otherwise in the RStudio editor.
- `gh(x, 'load')` or `ghload(x)`: Loads the contents of a file with `import` and `trust=TRUE`.
- `gh(x, 'source')` or `ghsource(x)`: Executes the contents of a file with `source`.
- `gh(x, 'app')` or `ghapp(x)`: Tries to open the file with the default application of the OS, see [defaultApp\(\)](#).
- `ghdata(x, pkg)`: Helper function to load data sets from R packages into Python, simulates `pkg::x`.

Usage

```
gh(x, what = c("open", "load", "source", "app"), ..., .call = NULL)
```

```
ghopen(x, ...)
```

```
ghload(x, ...)
```

```
ghsource(x, ...)
```

```
ghapp(x, ...)
```

Arguments

x	character(1): name of the file, app or data set
what	character or function: a name of a predefined function or another function. The function must have a formal parameter file.
...	further parameters used in <code>utils::browseURL()</code> , <code>openFile()</code> , <code>rio::import()</code> , or <code>base::source()</code> .
.call	the original function call (default: NULL)

Value

invisibly the result of `utils::browseURL`, `openFile()`, `rio::import()`, or `base::source()`.

Examples

```
if (interactive()) {  
  x <- ghopen("bank2.SAV")  
  x <- ghload("bank2.SAV")  
  str(x)  
  x <- ghsource("univariate/example_ecdf.R")  
}
```

ghappAddin

ghappAddin

Description

Runs a Shiny app from the downloaded zip file.

Usage

```
ghappAddin()
```

Value

nothing

Examples

```
if (interactive()) ghappAddin()
```

ghc	<i>Creates a ghdecompose pbject</i>
-----	-------------------------------------

Description

ghc creates from a list of file names using [ghdecompose\(\)](#) and deletes mssing files.

Usage

```
ghc(...)
```

Arguments

```
...          list(s) of filenmaes
```

Value

a ghdecompose pbject

Examples

```
ghc(list.files(system.file(package="mmstat4"), recursive=TRUE))
```

ghdecompose	<i>ghdecompose</i>
-------------	--------------------

Description

Decomposes a path of a set of files (or dirs) in several parts:

Usage

```
ghdecompose(files, dirs = FALSE)
```

Arguments

```
files          character vector: path of files
dirs           logical: directory or files names (default: FALSE)
```

Details

- `outpath` the path part which is common to all files (basically the place where the ZIP file was extracted)
- `inpath` the path part which is not necessary for a unique address in teh ZIP file
- `minpath` the minimal path part such that all files addressable in unique manner,
- `filename` the basename of the file, and
- `source` the input to `shortpath`.

Value

a data frame with five variables

Examples

```
ghget("local")
pdf <- ghdecompose(ghlist(full.names=TRUE))
pdf
```

ghfile

ghfile

Description

Finds either a unique match in the list of files or throws an error with possible candidate files.

Usage

```
ghfile(x, n = 6, silent = FALSE, msg = "%s")
```

Arguments

<code>x</code>	character: a single file name
<code>n</code>	logical: if <code>x</code> can not be found how many best matches should be returned (default: 6)
<code>silent</code>	logical: if no (unique) match is found, then NULL is returned, otherwise an error is thrown (default: FALSE, throw error)
<code>msg</code>	character: error message how to put the file name(s) (default: %s)

Value

the full matching file

Examples

```
ghfile("data/BANK2.sav")
if (interactive()) ghfile("data/BANK2.SAV") # throws an error
```

 ghget

ghget

Description

Makes a repository the active repository and downloads it if necessary. The parameter `.tempdir` is TRUE (default) then the repository is stored in the temporary directory `tempdir()` else in the application directory `rappdirs::user_data_dir()` for mmstat4. The parameter `.tempdir` is not logical then the value will be used as installation path.

Usage

```
ghget(..., .force = FALSE, .tempdir = TRUE, .quiet = !interactive())
```

Arguments

<code>...</code>	parameters to set and activate a repository
<code>.force</code>	logical: download and unzip in any case? (default: FALSE)
<code>.tempdir</code>	logical or character: store download temporary or permanently (default: <code>getOption("mmstat4.tempdir")</code>)
<code>.quiet</code>	logical: show repository read attempts (default: <code>!interactive()</code>)

- if `.tempdir==TRUE` then the downloaded zip file will be stored temporarily in `tempdir()`
- if `.tempdir==FALSE` then the downloaded zip file will be stored temporarily in `rappdirs::user_data_dir()`
- otherwise it is assumed that you give the name of an existing directory to store the downloaded zip file

Details

Note, the list of repository names, directories and urls is stored in the installation directory, too.

Value

the name of the current key or nothing if unsuccessful

Examples

```
if (interactive()) {
  # get one of the default ZIP file from internet
  ghget("hu.data")
  # get a locally stored zip file
  ghget(dummy2=system.file("zip", "mmstat4.dummy.zip", package="mmstat4"))
  # get from an URL
  ghget(dummy.url="https://github.com/sigbertklinke/mmstat4.dummy/archive/refs/heads/main.zip")
}
```

 ghinstall

ghinstall

Description

If the user agrees, it installs additional software necessary for running a script. Currently, only `type=="py"` for Python scripts and `type=="R"` for R scripts are supported. When a repository is downloaded, `ghinstall` is called once. If the user calls `ghinstall` for an update, the parameter `force=TRUE` must be set.

Usage

```
ghinstall(type = c("py", "R"), force = FALSE)
```

Arguments

<code>type</code>	character: programm type (default: py)
<code>force</code>	logical: should the installation really done (default: 'NA')

Details

R `mmstat4_init.R` is opened if present in the active repository.

py `mmstat4` internally utilizes a virtual environment named `mmstat4.xxxx`, where `xxxx`, varies depending on the repository. When `ghinstall` is invoked, it verifies the existence of the virtual environment `mmstat4.xxxx`. If it does not exist, it is opened if present in the active repository.

Value

NULL if type is not found, otherwise type

Examples

```
# to delete the virtual environment use
# reticulate::virtualenv_remove('mmstat4')
if (interactive()) ghinstall()
```

 ghlist

ghgrep, ghlist

Description

Both functions return unique (short) names for accessing each file in the repository according to a regular expression. For details about regular expressions, see [base::regex](#).

Usage

```

ghlist(
  pattern = ".",
  ignore.case = FALSE,
  perl = FALSE,
  fixed = FALSE,
  useBytes = FALSE,
  full.names = FALSE
)

ghgrep(
  pattern = ".",
  ignore.case = FALSE,
  perl = FALSE,
  fixed = FALSE,
  useBytes = FALSE,
  full.names = FALSE
)

```

Arguments

pattern	character string containing a regular expression (or character string for fixed = TRUE) to be matched in the given character vector. Coerced by as.character to a character string if possible. If a character vector of length 2 or more is supplied, the first element is used with a warning. Missing values are allowed except for <code>regexpr</code> , <code>gregexpr</code> and <code>regexec</code> .
ignore.case	if FALSE, the pattern matching is <i>case sensitive</i> and if TRUE, case is ignored during matching.
perl	logical. Should Perl-compatible regexps be used?
fixed	logical. If TRUE, pattern is a string to be matched as is. Overrides all conflicting arguments.
useBytes	logical. If TRUE the matching is done byte-by-byte rather than character-by-character. See 'Details'.
full.names	logical: should full names returned instead of short names (default: FALSE)

Value

character vector of short names

Examples

```
if (interactive()) ghgrep()
```

ghopenAddin *ghopenAddin*

Description

A RStudio addin to open a file from the downloaded zip file.

Usage

```
ghopenAddin()
```

Value

nothing

Examples

```
if (interactive()) ghopenAddin()
```

ghpath *ghpath*

Description

Returns a path for files based on ghdecompose.

Usage

```
ghpath(df, from = c("outpath", "inpath", "minpath", "filename"))
```

Arguments

df	data frame: returned from ghdecompose
from	character: either inpath (default), outpath, minpath, or filename

Value

a character vector with file paths

Examples

```
ghget("dummy")
pdf <- ghdecompose(ghlist(full.names=TRUE))
ghpath(pdf)
ghpath(pdf, 'o') # equals the input to ghdecompose
ghpath(pdf, 'i')
ghpath(pdf, 'm')
ghpath(pdf, 'f')
```

ghquery	<i>ghquery</i>
---------	----------------

Description

Queries the unique (short) names for each file in the repository. Several query methods are available, see Details.

Usage

```
ghquery(
  query,
  n = 6,
  full.names = FALSE,
  method = c("fpdist", "overlap", "tfidf"),
  costs = NULL,
  counts = FALSE,
  useBytes = FALSE
)
```

Arguments

query	character: query string
n	integer: maximal number of matches to return
full.names	logical: should full names used instead of short names (default: FALSE)
method	character: method to be used (default: fpdist)
costs	a numeric vector or list with names partially matching 'insertions', 'deletions' and 'substitutions' giving the respective costs for computing the Levenshtein distance, or NULL (default) indicating using unit cost for all three possible transformations.
counts	a logical indicating whether to optionally return the transformation counts (numbers of insertions, deletions and substitutions) as the "counts" attribute of the return value.
useBytes	a logical. If TRUE distance computations are done byte-by-byte rather than character-by-character.

Details

The following query methods are available:

- fpdist uses a partial backward matching distance based on `utils::adist()`
- overlap uses the **overlap distance** for query and file names

Value

character vector of short names fitting best to the query

Examples

```
if (interactive()) ghquery("bank")
```

```
ghrepos
```

```
ghrepos
```

Description

If key is NULL, then it returns the known repositories and where they are stored. If key is not NULL, then possible addresses for a repository are returned .

Usage

```
ghrepos(key = NULL)
```

Arguments

key character: "name" of the repository to find (default: NULL)

Value

a data frame with the data about the repositories

Examples

```
ghrepos()
```

```
ghzip
```

```
Creates a ZIP file or directory with files
```

Description

ghzip creates a ZIP file (if dest has an extension zip) or copies to the destination directory. If dest is NULL then a temporary directory will be used. Please note that neither the ZIP file is deleted nor the target directory is cleaned beforehand if it already exists.

Usage

```
ghzip(files, dest = NULL)
```

Arguments

files ghdecompose object or character: list of files to copy

dest character: ZIP file name of destination directory (default: NULL)

Value

the name of the destination directory or the ZIP file

Examples

```
if (interactive()) {
  zipfile <- tempfile(fileext='.zip')
  files <- list.files(system.file(package="mmstat4"), recursive=TRUE)
  ghzip(files, zipfile)
}
```

isLocal

isLocal

Description

Checks if a Shiny app runs locally or on a server

Usage

```
isLocal()
```

Value

logical

Examples

```
isLocal()
```

normpathes

normpathes

Description

Returns a list with normalized pathes.

Usage

```
normpathes(x)
```

Arguments

x file pathes

Value

A list of the same length as `x`, the *i*-th element of which contains the vector of splits of `x[i]`.

Examples

```
normpaths("CRAN/./mmstat4/python/./ghdist.R")
```

note

Create and display a note

Description

`note` internally stores a colored message, while `display` utilizes `base::cat()` to present them and reset the internal message stack.

Usage

```
note(msg, col = crayon::green)
```

```
display()
```

Arguments

`msg` character: message

`col` function: a color function (default: `crayon::green`)

Value

`note` returns invisibly the number of notes

Examples

```
notetest <- function(msg) {  
  on.exit({ display() })  
  note(msg)  
  # do some complex computation  
  x <- 1+1  
}  
notetest("Hello world!")
```

openFile	<i>openFile</i>
----------	-----------------

Description

The function attempts to open a file either in RStudio or in a text editor, depending on the environment. If the session is interactive, it tries to open the file in RStudio using `rstudioapi::navigateToFile()`. If RStudio is not available or the attempt fails, it opens the file in a text editor using `utils::edit()`. If the session is not interactive, it simply returns the contents of the file.

Usage

```
openFile(file, ...)
```

Arguments

file	character: name of the file
...	further parameters give to <code>rstudioapi::navigateToFile()</code> or <code>utils::edit()</code>

Value

invisibly the result from `try(rstudioapi::navigateToFile(file))` or `try(utils::edit(file))`.

Examples

```
openFile(system.file("rstudio", "addins.dcf", package = "mmstat4"))
```

pkglist	<i>Extract library and require calls in R and import calls from Python</i>
---------	--

Description

`pkglist` counts the number of `library/require/import` calls for R and Python commands within the files. It checks the availability of a package/module via `utils::available.packages()` (for R) and via PyPI (for Python). If `code=TRUE` is set, it returns R/Python code for installing packages/modules. Otherwise, a table with the number of `library` or `import` calls is returned.

Usage

```
pkglist(files, code = TRUE, repos = getOption("repos"))
```

```
Rlibs(files, code = TRUE, repos = getOption("repos"))
```

```
modlist(files, code = TRUE, repos = getOption("repos"))
```

Arguments

files	character: file name(s)
code	logical: should names given back or code for init scrips? (default: TRUE)
repos	character: the base URL(s) of the repositories to use (default: <code>getOption("repos")</code>)

Value

a table how frequently the packages are called or R Code to install them

Examples

```
if (interactive()) {
  files <- list.files(pattern="*(R|py)$", full.names=TRUE, recursive=TRUE)
  pkglist(files)
}
```

pkgMissing

pkgMissing

Description

Checks if a package is available.

Usage

```
pkgMissing(package)
```

Arguments

package	character: string naming the package/name space to load.
---------	--

Value

a logical value

Examples

```
pkgMissing("tools")
pkgMissing("A3")
```

py_env	<i>py_env</i>
--------	---------------

Description

Name of the currently used virtual environment.

Usage

```
py_env()
```

Value

the name of the virtual Python environment currently used by mmsstat4

Examples

```
py_env()
```

toInt	<i>toInt</i>
-------	--------------

Description

Converts `x` to an integer. If the conversion fails or the integer is outside `min` and `max` then `NA_integer_` is returned

Usage

```
toInt(x, min = -Inf, max = +Inf)
```

Arguments

<code>x</code>	input object
<code>min</code>	numeric: minimal value
<code>max</code>	numeric: maximal value

Value

a single integer value

Examples

```
toInt(3.0)
toInt("3.0")
toInt("test")
```

toNum *toNum*

Description

Converts *x* to a numeric. If the conversion fails or the value is outside *min* and *max* then NA is returned

Usage

```
toNum(x, min = -Inf, max = +Inf)
```

Arguments

<i>x</i>	input object
<i>min</i>	numeric: minimal value
<i>max</i>	numeric: maximal value

Value

a single integer value

Examples

```
toNum(3.0)  
toNum("3.0")  
toNum("test")
```

urlExists *urlExists*

Description

Verifies whether a provided *url* is downloadable, without detecting redirections in the URL.

Usage

```
urlExists(url)
```

Arguments

<i>url</i>	a vector of text URLs
------------	-----------------------

Value

TRUE if URL exists otherwise FALSE

Examples

```
if (interactive()) {  
    urlExists("https://hu-berlin.de/sk")  
    urlExists("https://huglawurza.de")  
}
```

Index

as.character, [17](#)
askUser, [2](#)
association, [3](#)

base::cat(), [22](#)
base::regex, [16](#)
base::source(), [12](#)
base::system2(), [8](#)

cdf, [6](#)
checkFiles, [7](#)
concordant (association), [3](#)

defaultApp, [8](#)
defaultApp(), [11](#)
digest::digest(), [9](#)
discordant (association), [3](#)
display (note), [22](#)
dupFiles, [9](#)

eta (association), [3](#)

getList, [10](#)
getMMstat, [10](#)
getText, [11](#)
gh, [11](#)
ghapp (gh), [11](#)
ghappAddin, [12](#)
ghc, [13](#)
ghdata (gh), [11](#)
ghdecompose, [13](#)
ghdecompose(), [13](#)
ghfile, [14](#)
ghget, [15](#)
ghgrep (ghlist), [16](#)
ghinstall, [16](#)
ghlist, [16](#)
ghload (gh), [11](#)
ghopen (gh), [11](#)
ghopenAddin, [18](#)
ghpath, [18](#)

ghquery, [19](#)
ghrepos, [20](#)
ghsource (gh), [11](#)
ghzip, [20](#)
graphics::plot(), [6](#)
graphics::points(), [6](#)

isLocal, [21](#)

modlist (pkglist), [23](#)

nom.cc (association), [3](#)
nom.CV (association), [3](#)
nom.lambda (association), [3](#)
nom.lambda (association), [3](#)
nom.phi (association), [3](#)
nom.TT (association), [3](#)
nom.uncertainty (association), [3](#)
normpathes, [21](#)
note, [22](#)

openFile, [23](#)
openFile(), [12](#)
ord.gamma (association), [3](#)
ord.somers.d (association), [3](#)
ord.tau (association), [3](#)

pkglist, [23](#)
pkgMissing, [24](#)
plot.cdf (cdf), [6](#)
py_env, [25](#)

rappdirs::user_data_dir(), [15](#)
Rdups (dupFiles), [9](#)
regular expression, [17](#)
rio::import(), [12](#)
Rlibs (pkglist), [23](#)
Rsolo (checkFiles), [7](#)
rstudioapi::navigateToFile(), [23](#)

stats::chisq.test(), [3](#)

`tempdir()`, [15](#)
`ties.col` (association), [3](#)
`ties.row` (association), [3](#)
`toInt`, [25](#)
`toNum`, [26](#)

`urlExists`, [26](#)
`utils::adist()`, [19](#)
`utils::available.packages()`, [23](#)
`utils::browseURL`, [12](#)
`utils::browseURL()`, [12](#)
`utils::edit()`, [23](#)