

Package: soilReports (via r-universe)

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Type Package

Title R Markdown Reports and Convenience Functions for Soil Survey

Description R package container and convenience functions for soil data summary, comparison, and evaluation reports used mainly by NRCS staff.

Version 0.9.1

Author USDA-NRCS Soil Survey Staff

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Depends R (>= 3.5.0)

License GPL (>= 3)

URL <https://github.com/ncss-tech/soilReports>

BugReports <https://github.com/ncss-tech/soilReports/issues>

Suggests rmarkdown, knitr, testthat, scales, clhs, MASS, sharpshootR

Imports remotes

RoxygenNote 7.3.2

Roxygen list(markdown = TRUE)

Config/pak/sysreqs git

Repository <https://ncss-tech.r-universe.dev>

RemoteUrl <https://github.com/ncss-tech/soilReports>

RemoteRef HEAD

RemoteSha ef9ddbdfbb25f10302724921d7e818aa9e5e0e1

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soilReports-package	<i>Soil Reports: R-Markdown reports and convenience functions for soil survey.</i>
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Description

R package container and convenience functions for soil data summary, comparison, and evaluation reports used mainly by USDA-NRCS staff.

[Instructions and project homepage.](#)

Author(s)

Dylan E. Beaudette <dylan.beaudette@ca.usda.gov>

Examples

```
## Not run:
# load this library
library(soilReports)

# list reports in the package
listReports()

# install required packages for a named report
reportSetup(reportName='southwest/mu-comparison')

# copy default configuration file and report to 'MU-comparison' in current working directory
reportInit(reportName='southwest/mu-comparison', outputDir='MU-comparison', overwrite=FALSE)

## End(Not run)
```

appendBelowYAML	<i>Add lines below the YAML header</i>
-----------------	--

Description

Add lines below the YAML header

Usage

```
appendBelowYAML(filepath, what)
```

Arguments

filepath	file path
what	character vector lines to add

Value

logical; TRUE if successful

cLHS_subset	<i>Use cLHS to subset a data.frame using selected variables</i>
-------------	---

Description

Use cLHS to subset a data.frame using selected variables

Usage

```
cLHS_subset(i, n, non.id.vars)
```

Arguments

i	a data.frame
n	number of cLHS samples (rows) to draw
non.id.vars	variables that are non-ID columns

Value

a subset data.frame corresponding to selected cLHS samples (rows)

copyPath	<i>Copy a file from source to output directory</i>
----------	--

Description

Copy a file from source to output directory

Usage

```
copyPath(fname, srcDir, outputDir, overwrite = FALSE)
```

Arguments

fname	file name
srcDir	source directory
outputDir	output directory
overwrite	overwrite? default: FALSE

Value

logical; result of file.copy

custom.bwplot	<i>Title</i>
---------------	--------------

Description

Title

Usage

```
custom.bwplot(x, coef = NA, do.out = FALSE)
```

Arguments

x	vector of values to summarize
coef	Moran's I associated with the current raster
do.out	not used

Value

a list containing elements: stats, n, conf, and out

defineInCodeChunk *Define a parameter in a code chunk*

Description

Define a parameter in a code chunk

Usage

```
defineInCodeChunk(filepath, param.name, param.value)
```

Arguments

filepath	File to add code chunk to
param.name	Parameter name
param.value	Parameter value

Value

logical; TRUE if successful

defineInYAMLHeader *Define a parameter in the YAML header*

Description

Define a parameter in the YAML header

Usage

```
defineInYAMLHeader(filepath, param.name, param.value)
```

Arguments

filepath	File to add code chunk to
param.name	Parameter name
param.value	Parameter value

Value

logical; TRUE if successful

findSafeVars	<i>Return variables with sufficient variation for cLHS</i>
--------------	--

Description

Datasets that are nearly or completely invariant can pose issues for the cLHS algorithm. This function identifies variables that have standard deviation smaller than a specified tolerance. Default: 1e-5

Usage

```
findSafeVars(x, id, tol = 1e-05)
```

Arguments

x	data.frame in wide format
id	vector of IDs variables to exclude from SD test, first element is the group ID
tol	tolerance for near-0 SD test; Default: 1e-5

Value

A character vector of "safe" column names

installRprofile	<i>Install USDA-NRCS SPSD CCE user .Rprofile</i>
-----------------	--

Description

Install USDA-NRCS SPSD CCE user .Rprofile

Usage

```
installRprofile(overwrite = FALSE, user_folder = NULL, home_drive = NULL)
```

Arguments

overwrite	overwrite? Default FALSE
user_folder	User folder name (default NULL; if not null used instead of file.path('C:/Users', Sys.getenv('USERNAME'), 'Documents'))
home_drive	Custom Home Drive (default NULL; if not null replaces "C:")

Value

source() a new .Rprofile set up to redirect R library paths

kdeContours	<i>Calculate kernel density contour lines at specified probability levels Calculate kernel density contour lines at specified probability levels with MASS:kde2d and display with graphics::contour</i>
-------------	---

Description

Calculate kernel density contour lines at specified probability levels Calculate kernel density contour lines at specified probability levels with MASS:kde2d and display with graphics::contour

Usage

```
kdeContours(i, id, prob, cols, m, ...)
```

Arguments

<code>i</code>	a data.frame containing unique ID, x, y
<code>id</code>	a unique ID column name
<code>prob</code>	a vector of probability levels
<code>cols</code>	a vector of colors
<code>m</code>	unique levels of the ID column (used to match colors)
<code>...</code>	additional arguments to graphics::contour

Value

estimated kernel density contours

listReports	<i>List names of available reports</i>
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Description

List names of available reports

Usage

```
listReports(showFullPaths = FALSE)
```

Arguments

<code>showFullPaths</code>	Show full paths to files? Default: FALSE
----------------------------	--

Value

a data.frame containing report names, versions and descriptions for reports available in the currently installed version of the soilReports package.

Examples

```
listReports()
```

```
listReports(showFullPaths = TRUE)
```

pIndex

Indexing for Plotting and Printing

Description

This function creates an index to iterate over when plotting or printing large objects.

Usage

```
pIndex(x, interval = 4)
```

Arguments

x	a data.frame, SoilProfileCollection or table
interval	a value specifying the interval length desired; Default: 4

Value

a numeric vector

Examples

```
x <- as.data.frame(matrix(1:100, ncol = 10))  
pIndex(x, interval = 3)
```

prettySummary	<i>Pretty Quantile Printing</i>
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Description

This function generates a pretty quantile summary for printing.

Usage

```
prettySummary(x, p = c(0, 0.25, 0.5, 0.75, 1), n = TRUE, signif = TRUE)
```

Arguments

x	a numeric vector
p	a numeric vector of percentiles
n	a logical value indicating whether the vector of percentiles should be appended with the number of observations
signif	a logical value indicating whether the percentiles should be rounded to the precision of the data

Value

a character value of quantiles and optionally the number of observations

Author(s)

Stephen Roecker

Examples

```
x <- 1.1:10.1  
prettySummary(x)
```

reportInit	<i>Copy default configuration file and report contents to new directory</i>
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Description

reportInit allows creation new report instances, or updates, from the soilReports R package. soilReports is a container for reports and convenience functions for soil data summary, comparison, and evaluation reports used mainly by USDA-NRCS staff.

Usage

```
reportInit(
  reportName,
  outputDir = NULL,
  overwrite = FALSE,
  updateReport = FALSE
)
```

Arguments

reportName	Name of report, as found in listReports. Format: directory/reportName.
outputDir	Directory to create report instance
overwrite	Overwrite existing directories and files? Default FALSE
updateReport	Only update core report files, leaving configuration unchanged? Specific settings are report-dependent and set in the setup.R manifest.

Value

A time-stamped report instance created in outputDir, and a message summarizing the action(s) completed.

reportSetup	<i>Install packages needed for a report</i>
-------------	---

Description

Install packages needed for a report

Usage

```
reportSetup(reportName, upgrade = TRUE)
```

Arguments

reportName	Name of report, as found in listReports. Format: directory/reportName.
upgrade	Upgrade CRAN packages? Default: TRUE

Value

Installed packages from CRAN and GitHub in user library, as specified in report-specific manifest.

scaled.density	<i>Compute scaled density for a data.frame containing "value"</i>
----------------	---

Description

Gaussian probability densities are re-scaled to $[0, 1]$

Usage

```
scaled.density(d, constantScaling = TRUE)
```

Arguments

d	data.frame containing column "value"
constantScaling	use scales::rescale? Default: TRUE

Value

A data.frame containing (scaled) x and y

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