Package ‘quadcleanR’

July 22, 2025

Title Cleanup and Visualization of Quadrat Data

Version 1.1.0

Description A tool that can be customized to aid in the clean up of ecological data collected using quadrats and can crop quadrats to ensure comparability between quadrats collected under different methodologies.

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Encoding UTF-8

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URL `https://github.com/DominiqueMaucieri/quadcleanR`,

`https://dominiquemaucieri.com/quadcleanR/`

BugReports `https://github.com/DominiqueMaucieri/quadcleanR/issues`

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Contents

`add_data` *Add data to existing data frame.*

Description

Using key identifying columns, add additional columns to an existing data frame. This function allows you to match new columns based on specified IDs and you can choose what columns to add. Additionally you can specify the column number at which to add the new columns, so they are not added to the end of the data frame. Helpful for adding environmental or taxonomic data to your quadrat data.

Usage

```
add_data(data, add, cols, data_id, add_id, number = FALSE)
```

Arguments

`data`	A data frame you want to add columns to.
`add`	A data frame with columns you want to add to `data`.
`cols`	The column names from `add` that you wish to add to `data`.
`data_id`	The ID column in `data` that will be used to match rows in `add`.
`add_id`	The ID column in `add` that will be used to match rows in `data`.

`number`	The column number to start at to add the new columns, so they are not added to the end of the data frame. If not specified they will be added to the end of the data frame by default.

Value

A data frame with added columns.

Examples

```
Sites <- as.factor(c("One", "One", "One", "Two", "Two", "Three"))
Transect <- as.factor(c("1-Deep", "1-Shallow", "2-Shallow", "1-Shallow", "1-Deep", "1"))
coral_name <- c("Acropora.sp", "Leptastrea.sp", "Sinularia.sp", "Psammocora.sp", "
    Psammocora.sp", "Leptastrea.sp")
prop_cover <- c(0.1, 0.6, 0.4, 0.9, 0.2, 0.5)
coral_cover <- data.frame(Sites, Transect, coral_name, prop_cover)

corals <- c("Acropora.sp", "Leptastrea.sp", "Psammocora.sp")
lifehistory <- c("compeditive", "weedy",  "stresstolerant")
functionalgroup <- c("hardcoral", "hardcoral", "hardcoral")
coral_info <- data.frame(corals, lifehistory, functionalgroup)

add_data(data = coral_cover, add = coral_info, cols = c("lifehistory", "functionalgroup"),
         data_id = "coral_name", add_id = "corals", number = 4)
```

`categorize` *Categorize data based on contents of a column*

Description

Using a column within the data frame, categorize rows in a binary of yes or no, or customize with a set of category names. Data can be categorized based on the inclusion or lack of inclusion of parts of characters, or based on exact characters. Especially useful for turning ID tags into useful categories for analysis such as morphology, bleaching, taxonomy etc.

Usage

```
categorize(data, column, values, name, binary = TRUE, exact = TRUE, categories)
```

Arguments

`data`	The data frame.
`column`	The column name which contains the data on which to categorize rows.
`values`	The characters or parts of characters to use to classify rows.
`name`	The name of the now column of categories.

`binary`	If `binary = TRUE`, the `name` column will be returned with "Yes" denoting that characters ,or parts of characters specified by `values` are present in the row, while "No" denotes that there are no characters or parts of characters specified in `values` present in the row. If `binary = FALSE` there must be `categories` provided which will be used to classify the presence of characters or parts of characters specified in `values`.
`exact`	If `exact = TRUE` only exact matches will be selected. If `exact = FALSE` matches will be selected if they contain the characters in the `values` vector and will not be limited by exact matches.
`categories`	The factor names denoting the presence of the characters or parts of characters specified by `values`. These must be specified in the same order as the corresponding element in `values`.

Value

A data frame with new categorization column.

Examples

```
Sites <- as.factor(c("One", "One", "One", "Two", "Two", "Three"))
Transect <- as.factor(c("1-Deep", "1-Shallow", "2-Shallow", "1-Shallow", "1-Deep", "1-Deep"))
Acropora.sp <- c(0.1, 0.6, 0.4, 0.9, 0.2, 0.5)
Gardineroseris.sp <- c(0.4, 0.9, 0.5, 0.23, 0.5, NA)
Psammocora.sp <- c(0.9, 0.6, 0.5, 0.8, 0.1, 0.4)
Leptastrea.sp <- c(0.5, 0.7, 0.4, 0.8, 0.2, NA)
Notes <- c(NA, NA, "saw octopus", NA, "white balance corrected", NA)
coral_cover <- data.frame(Sites, Transect, Acropora.sp, Gardineroseris.sp,
                          Psammocora.sp, Leptastrea.sp, Notes)

# Classify shallow transects in a binary column
categorize(data = coral_cover, column = "Transect", values = "Shallow",
    name = "Shallow", binary = TRUE, exact = FALSE)

# Classify depth of transect in a new column based on transect name
categorize(data = coral_cover, column = "Transect", values = c("Shallow", "Deep"),
    name = "Depth", binary = FALSE, categories = c("S", "D"), exact = FALSE)
```

`change_names` *Change names of columns*

Description

Using a new data frame of labels, change column names in one function. Helpful if column names are shorthands or contain spaces and characters that are not supported in column names in R.

Usage

```
change_names(data, labelset, from, to)
```

Arguments

`data`	The data frame that you want to change the column names of.
`labelset`	The data frame containing column names that you want to change and what you want them to be changed to.
`from`	The name of the column in the label set data frame containing the original column names.
`to`	The name of the column in the label set data frame containing new column names that the original column names will be changed to.

Value

A data frame containing new column names.

Examples

```
#creating data set
Sites <- c("One", "Two", "Three", "Four", "Five")
Acrop <- c(0.1, 0.4, 0.9, 0.2, 0.5)
Gardin <- c(0.4, 0.9, 0.5, 0.23, 0.8)
Psam <- c(0.9, 0.5, 0.8, 0.1, 0.4)
Lepta <- c(0.5, 0.7, 0.8, 0.2, 0.9)
coral_cover <- data.frame(Sites, Acrop, Gardin, Psam, Lepta)

#creating label data frame
species_short <- c("Acrop", "Gardin", "Psam", "Lepta")
species_long <- c("Acropora", "Gardineroseris", "Psammocora", "Leptastrea")
coral_labels <- data.frame(species_short, species_long)

change_names(coral_cover, coral_labels, "species_short", "species_long")
```

`change_values` *Change values within a column*

Description

Using two vectors, change the values in one column to a new set of values. Helpful if you need to change many values at once, like updating changes to site names or taxonomy.

Usage

```
change_values(data, column, from, to)
```

Arguments

`data`	A data frame.
`column`	The column in which to change values.
`from`	A vector containing the values you wish to change.
`to`	A vector contain the values you want to change to, ensuring these occur in the same order as the `from` vector.

Value

A data frame containing new values within the specified column.

Examples

```
Sites <- c("One.jpg", "Two.jpg", "Three.jpg", "Four.jpg", "Five.jpg")
Dominant_Coral <- c("Acropora.sp", "Leptastrea.spp", "Acropora.sp",
                    "Acropora.sp", "Acropora.sp")
Dominant_Cover <- c(0.1, 0.4, 0.9, 0.2, 0.5)
Largest_Coral <- c("Acropora.sp", "Acropora.sp", "Psammocora.sp",
                   "Acropora.sp","Gardineroseris.spp")

coral_cover <- data.frame(Sites, Dominant_Coral, Dominant_Cover, Largest_Coral)

change_values(coral_cover, "Dominant_Coral",
    c("Acropora.sp","Leptastrea.spp"), c("Acropora_tabulate", "Leptastrea.purpurea"))
```

`corals` *Simple Coral Quadrat Data*

Description

A `data_frame` that can be used with the Simple Examples of Functions vignette to learn how the cleaning functions in quadcleanR work. Data was collected by the Baum Lab and Kiritimati Field Teams. Data is the uncleaned version of data found in Maucieri and Baum 2021. Biological Conservation. doi:10.1016/j.biocon.2021.109328 The data are from photo quadrats (1m by 1m) which were randomly annotated with 100 random points each. At each of these annotated points, the substrate was identified. Photo quadrats were collected on Kiritimati Island in the Republic of Kiribati and document coral cover over time and space. The annotations and output of the `data_frame` were produced using CoralNet and all annotations were done manually, by trained researchers.

Usage

```
corals
```

Format

A `data_frame` with 14 columns, which are:

Field.Season Field season ID.

Site Site number.

Quadrat Quadrat ID.

AcCor Percent of total annotated points annotated for Acropora (corymbose morphology).

AcDig Percent of total annotated points annotated for Acropora (digitate morphology).

AcroTab Percent of total annotated points annotated for Acropora (tabulate morphology).

Monta Percent of total annotated points annotated for Montastraea.

Lepta Percent of total annotated points annotated for Leptastrea.

Sinu Percent of total annotated points annotated for Sinularia.

Clad Percent of total annotated points annotated for Cladiella.

Lobph Percent of total annotated points annotated for Lobophora.

Sarco Percent of total annotated points annotated for Sarcophyton.

Unc Percent of total annotated points annotated for unclear.

SHAD Percent of total annotated points annotated for shadow.

`coral_labelset` *Labelset for Corals*

Description

A `data_frame` that can be used with the Simple Cleaning Quadrat Data vignette to rename columns in quadrat data and add functional group data, to produce easy to analyze data frames. The short names were used to identify substrate using CoralNet and are included in the output from CoralNet.

Usage

```
coral_labelset
```

Format

A `data_frame` with 5 columns, which are:

short_name The short name ID used to annotate the photo quadrats.

full_name The long name and definition for each short name ID.

taxonomic_name The taxonomic grouping name for each short name ID.

functional_group The functional group for each ID.

life_history The life history category for each coral ID.

`cover_calc` *Calculate species cover*

Description

Convert the number of observations for each species or non-species to proportion or percent cover within each row based on the total number of observations in each row. Useful for quadrats with varying numbers of observations to calculate each row's percent cover all at once.

Usage

```
cover_calc(data, spp, prop = TRUE, total = FALSE)
```

Arguments

`data`	A data frame with each row representing a sampling unit (ex. a quadrat or photo).
`spp`	The column names containing all observations to be used in the proportion calculation. It is important to note that the proportions will be scaled to the total observations in these columns for each quadrat.
`prop`	If `prop` = `TRUE`, the resulting cover will be proportions. If `prop` = `FALSE`, the resulting cover will be in percentages.
`total`	If `total` = `TRUE`, a column containing the total number of observations at each sampling unit will be returned in a new column called `total_pts`. This will not be returned if `total` = `FALSE`.

Value

A data frame containing scaled observation cover.

Examples

```
#create data set for example
Sites <- as.factor(c("One", "One", "Two", "Two", "Three", "Three"))
Transect <- as.factor(c("1-Shallow", "2-Shallow", "1-Shallow", "2-Shallow",
    "1-Shallow", "2-Shallow"))
Acropora.sp <- c(1, 2, 3, 4, 5, 6)
Gardineroseris.sp <- c(6, 1, 2, 3, 4, 5)
Psammocora.sp <- c(5, 6, 1, 2, 3, 4)
Leptastrea.sp <- c(4, 5, 6, 1, 2, 3)
coral_cover <- data.frame(Sites, Transect, Acropora.sp, Gardineroseris.sp,
                          Psammocora.sp, Leptastrea.sp)

cover_calc(data = coral_cover, spp = names(coral_cover[3:6]), prop = TRUE, total = TRUE)

cover_calc(data = coral_cover, spp = names(coral_cover[3:6]), prop = FALSE, total = FALSE)
```

`crop_area` *Crop quadrats based on area*

Description

Using the location of annotated points within quadrats and the size of the quadrat, crop quadrat data to a smaller area, while maintaining the spatial relationships between points. Useful for making different sized quadrat data comparable.

Usage

```
crop_area(
  data,
  row,
  column,
  id,
  dim,
  obs_rm = FALSE,
  obs_range,
  res = FALSE,
  res_dim_x,
  res_dim_y
)
```

Arguments

`data`	A data frame containing annotations, in long format, such that all observations are contained in one column.
`row`	The column name in `data` which contains the row locations of the annotated points.
`column`	The column name in `data` which contains the column location of the annotated points.
`id`	The column name in `data` which contains the quadrat ID for the annotated points.
`dim`	A vector with length of 2, containing the proportion of the row and columns to crop. First element will be the proportion of the rows and the second will be the proportion of the columns.
`obs_rm`	If `obs_rm = FALSE`, no quadrats will be removed from the returned data set. If `obs_rm = TRUE`, quadrats will be removed from the returned data set based on the number of annotated observations in the cropped area as specified by `obs_range`.
`obs_range`	A vector with length of 2, specifying the min and max accepted number of annotated observations to retain in the data set.

`res`	If `res = TRUE` if the dimensions of each quadrat are known. These must be the same units as the row and column locations. If dimensions are not known, specify `res = FALSE`, and the function will estimate the max dimensions based off the max row and column location for the annotated points.
`res_dim_x`	The column name in `data` which contains the max column dimension for each quadrat.
`res_dim_y`	The column name in `data` which contains the max row dimension for each quadrat.

Value

A data frame in of quadrat annotations with a subset of annotated points.

Examples

```
#Creating the data file
tags <- c("Clad", "Sinu", "Sarco", "Loph")

site <- c(rep("Site1", times = 100),
         rep("Site2", times = 100),
         rep("Site3", times = 100),
         rep("Site4", times = 100))
row <- c(sample(x = c(1:2000), size = 100, replace = TRUE),
        sample(x = c(1:2000), size = 100, replace = TRUE),
        sample(x = c(1:2000), size = 100, replace = TRUE),
        sample(x = c(1:2000), size = 100, replace = TRUE))
column <- c(sample(x = c(1:2000), size = 100, replace = TRUE),
           sample(x = c(1:2000), size = 100, replace = TRUE),
           sample(x = c(1:2000), size = 100, replace = TRUE),
           sample(x = c(1:2000), size = 100, replace = TRUE))
label <- c(sample(x = tags, size = 100, replace = TRUE),
          sample(x = tags, size = 100, replace = TRUE),
          sample(x = tags, size = 100, replace = TRUE),
          sample(x = tags, size = 100, replace = TRUE))
coral_annotations <- data.frame(site, row, column, label)

crop_area_coral <- crop_area(data = coral_annotations, row = "row",
                            column = "column", id = "site", dim = c(0.5, 0.5))

coral_annotations$col_dim <- 2000
coral_annotations$row_dim <- 2000

crop_area_coral_2 <- crop_area(data = coral_annotations, row = "row",
                              column = "column", id = "site", dim = c(0.5, 0.5),
                              res = TRUE, res_dim_x = "col_dim", res_dim_y = "row_dim")
```

`environmental_data` *Sample Environmental Data for Cleaning Vignettes*

Description

A `data_frame` that can be used with the Simple Cleaning Quadrat Data vignette to show how environmental data can be easily added to quadrat data. Data was collected and collated by the Baum Lab. Data was originally published with coral quadrat data in Maucieri and Baum 2021. Biological Conservation doi:10.1016/j.biocon.2021.109328.

Usage

```
environmental_data
```

Format

A `data_frame` with 7 columns, which are:

Site Site number.

HD_Cat Estimate of local human disturbance at each site as a categorical variable.

HD_Cont Estimate of local human disturbance at each site as a continuous variable.

NPP Max net primary productivity at each site (mg C m^-2 day^-1).

WE If the sampling site is on the sheltered or windward side of the atoll.

Region Region of the atoll.

WaveEnergy Wave energy at each site (kW m^-1).

`final_cleaned` *Final cleaned quadrat data*

Description

A `data_frame` that was created with the Cleaning Quadrat Data from CoralNet. This is an example data frame of how the `quadcleanR` package can be useful in cleaning quadrat data.

Usage

```
final_cleaned
```

Format

A `data_frame` with 14 columns, which are:

Field.Season Field season ID.

TimeBlock If the sampling season was before, during or after the El Niño event.

Site Site number.

Quadrat Quadrat ID.

HD_Cat Estimate of local human disturbance at each site as a categorical variable.

HD_Cont Estimate of local human disturbance at each site as a continuous variable.

NPP Max net primary productivity at each site (mg C m^-2 day^-1).

WE If the sampling site is on the sheltered or windward side of the atoll.

Region Region of the atoll.

WaveEnergy Wave energy at each site (kW m^-1).

Taxonomic_Name Taxonomic name for each substrate.

functional_group Functional group for each substrate.

life_history Life history classification for each substrate.

prop_cover The proportion cover for each substrate.

`keep_rm` *Keep or remove rows and columns from data frame*

Description

Using a character, or part of character select rows or columns of the data frame to either keep or remove. A more customizable way to subset your data as you can keep or remove based on partial matches, or cells containing select characters.

Usage

```
keep_rm(
  data,
  values,
  select,
  keep = TRUE,
  drop_levels = TRUE,
  exact = TRUE,
  colname
)
```

Arguments

`data`	A data frame.
`values`	A vector containing the characters or parts of characters to base selection off of.
`select`	If `select = "row"`, rows containing the `values` will be selected for either being kept, or being removed, as specified by `keep`. If `select = "col"`, columns with names containing the `values` will either be kept or removed, as specified by `keep`.
`keep`	If `keep = TRUE` the presence of the `values` will cause the selected rows or columns to be kept. If `keep = FALSE` the presence of the `values` will cause the selected rows or columns to be removed.
`drop_levels`	If `drop_levels = TRUE`, factor levels that have been removed will be dropped. Only applicable when `select = "row"`
`exact`	If `exact = TRUE` only exact matches will be selected. If `exact = FALSE` matches will be selected if they contain the characters in the `values` vector and will not be limited to exact matches only.
`colname`	If `select = "row"`, `colname` will specify the column to select rows from.

Value

A data frame containing new selection of data.

Examples

```
# create data frame
Sites <- as.factor(c("One", "One", "One", "Two", "Two", "Three"))
Transect <- as.factor(c("1-Deep", "1-Shallow", "2-Shallow", "1-Shallow", "1-Deep", "1-Deep"))
Acropora.sp <- c(0.1, 0.6, 0.4, 0.9, 0.2, 0.5)
Gardineroseris.sp <- c(0.4, 0.9, 0.5, 0.23, 0.5, NA)
Psammocora.sp <- c(0.9, 0.6, 0.5, 0.8, 0.1, 0.4)
Leptastrea.sp <- c(0.5, 0.7, 0.4, 0.8, 0.2, NA)
Notes <- c(NA, NA, "saw octopus", NA, "white balance corrected", NA)
coral_cover <- data.frame(Sites, Transect, Acropora.sp, Gardineroseris.sp,
                          Psammocora.sp, Leptastrea.sp, Notes)

#Removing Notes column
keep_rm(data = coral_cover, values = c("Notes") , select = "col",
   keep = FALSE, drop_levels = FALSE, exact = TRUE)

#Selecting site One and dropping extra levels
Site_One <- keep_rm(data = coral_cover, values = c("One") , select = "row",
   keep = TRUE, drop_levels = TRUE, exact = TRUE, "Sites")
levels(Site_One$Sites)

#Removing Deep sites
Shallow_Sites <- keep_rm(data = coral_cover, values = c("-Shallow") , select ="row",
   keep = FALSE, drop_levels = TRUE, exact = FALSE, "Transect")

#Selecting only species data
Species <- keep_rm(data = coral_cover, values = c(".sp") , select ="col",
```

```
    keep = TRUE, drop_levels = TRUE, exact = FALSE)
```

`rm_chr` *Remove characters from data frame*

Description

Parts of characters can be removed based on a vector of removal characters. When these characters are present in the data frame they will be removed. Selection area can include the full data frame or a subset of columns. When working with images, this can be helpful to remove extra characters from image IDs, or anywhere else where you want to remove specific characters from your data.

Usage

```
rm_chr(data, rm, full_selection = TRUE, cols)
```

Arguments

`data`	A data frame.
`rm`	The parts of characters to be removed from the data frame. Can be a single element or a vector of elements.
`full_selection`	If `full_selection` = `TRUE` parts of characters matching the `rm` argument will be removed from entire data frame. If `full_selection` = `FALSE` only the specified columns will have the parts of characters matching the `rm` argument removed.
`cols`	If `full_selection` = `FALSE` this argument will specify which columns to have characters matching the `rm` argument removed.

Value

A data frame containing the selected parts of characters removed.

Examples

```
# creating data set
Sites <- c("One.jpg", "Two.jpg", "Three.jpg", "Four.jpg", "Five.jpg")
Dominant_Coral <- c("Acropora.sp", "Leptastrea.spp", "Acropora.sp",
    "Acropora.sp", "Acropora.sp")
Dominant_Cover <- c(0.1, 0.4, 0.9, 0.2, 0.5)
Largest_Coral <- c("Acropora.sp", "Acropora.sp", "Psammocora.sp",
    "Acropora.sp","Gardineroseris.spp")

coral_cover <- data.frame(Sites, Dominant_Coral, Dominant_Cover, Largest_Coral)

# removing a character from select columns
coral_cover_nospp <- rm_chr(coral_cover, c(".spp"), full_selection = FALSE,
    cols = c("Largest_Coral", "Dominant_Coral"))

# removing multiple characters from all columns
coral_cover_clean <- rm_chr(coral_cover, c(".jpg", ".spp", ".sp"))
```

`sample_size` *Calculate sample sizes*

Description

Specify which columns to use to produce a table with sample sizes. Helpful to visualize number of samples in your data.

Usage

```
sample_size(data, dim_1, dim_2, count)
```

Arguments

`data`	The data frame you want to calculate sample sizes for.
`dim_1`	The first dimension to calculate sample sizes for. This will be the resulting row names. This must be the column name within `data`.
`dim_2`	The second dimension to calculate sample sizes for. This will be the resulting column names. This must be the column name within `data`.
`count`	The column name within `data` that you wish to count the length of in order to calculate the sample sizes.

Value

A data frame of sample sizes.

Examples

```
Year <- c("2000", "2000", "2000", "2000", "2000", "2001", "2001", "2001", "2001",
"2002", "2002", "2002", "2002", "2003", "2003", "2003", "2003", "2003", "2003")
Site <- c("site1", "site1", "site2", "site2", "site2","site1", "site1", "site2",
          "site2", "site1", "site1", "site2", "site2","site1", "site1", "site2",
          "site2", "site2", "site2")
Quadrat <- c("Q1", "Q2", "Q3", "Q4", "Q5", "Q6", "Q7", "Q8", "Q9", "Q10", "Q11",
             "Q12", "Q13", "Q14", "Q15", "Q16", "Q17", "Q18", "Q19")
Cover <- sample(x = seq(from = 0, to = 1, by = 0.01), 19, replace = TRUE)
coral_cover <- data.frame(Year, Site, Quadrat, Cover)

sample_size(coral_cover, dim_1 = "Site", dim_2 = "Year", count = "Quadrat")
```

`softcoral_annotations` *Sample Annotation Data for Cropping Vignette*

Description

A `data_frame` that can be used with the Why to Crop Quadrats by Area vignette to show how quadrat data can be cropped while maintaining spatial relationships between observations. Data was collected by the Baum Lab and Kiritimati Field Teams. Data is the uncleaned version of data found in Maucieri and Baum 2021. Biological Conservation. doi:10.1016/j.biocon.2021.109328 The data are from photo quadrats (1m by 1m) which were randomly annotated with 100 random points each. At each of these annotated points, the substrate was identified. Photo quadrats were collected on Kiritimati Island in the Republic of Kiribati and document coral cover over time and space. The annotations and output of the `data_frame` were produced using CoralNet and all annotations were done manually, by trained researchers.

Usage

```
softcoral_annotations
```

Format

A `data_frame` with 4 columns, which are:

Name Unique identification code for each quadrat.

Row The pixel row where the annotation occurred in the photo of the quadrat.

Column The pixel column where the annotation occurred in the photo of the quadrat.

Label The identification for the substrate below the annotation location.

`softcoral_LQuads` *Sample Quadrat Data (1m by 1m)*

Description

A `data_frame` that can be used with the cleaning vignette to show how quadrat data can be cleaned to produce easy to analyze data frames. Data was collected by the Baum Lab and Kiritimati Field Teams. Data is the uncleaned version of data found in Maucieri and Baum 2021. Biological Conservation. doi:10.1016/j.biocon.2021.109328 The data are from photo quadrats (1m by 1m) which were randomly annotated with 100 random points each. At each of these annotated points, the substrate was identified. Photo quadrats were collected on Kiritimati Island in the Republic of Kiribati and document coral cover over time and space. The annotations and output of the `data_frame` were produced using CoralNet and all annotations were done manually, by trained researchers.

Usage

```
softcoral_LQuads
```

Format

A `data_frame` with 135 columns, which are:

Image.ID Photo quadrat image ID from CoralNet.

Image.name The photo quadrat image name.

Annotation.status If the quadrat has been completely annotated, or if there are more annotations to occur.

Points The total number of annotation points in the quadrat.

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AcDig Percent of total annotated points annotated for Acropora (digitate morphology).

Acr_arb Percent of total annotated points annotated for Acropora (arborescent morphology).

Acrop Percent of total annotated points annotated for Acropora.

AcroTab Percent of total annotated points annotated for Acropora (tabulate morphology).

Astreo Percent of total annotated points annotated for Astreopora.

B_Acr_arb Percent of total annotated points annotated for bleached Acropora (arborescent morphology)

B_Acro Percent of total annotated points annotated for bleached Acropora.

B_Astre Percent of total annotated points annotated for bleached Astreopora.

BAT Percent of total annotated points annotated for bleached Acropora (tabulate morphology).

B_Cosc Percent of total annotated points annotated for bleached Coscinarea.

B_Echin Percent of total annotated points annotated for bleached Echinophyllia.

B_FavHal Percent of total annotated points annotated for bleached Favites halicora.

B_Favia Percent of total annotated points annotated for bleached_Favia.

B_FaviaM Percent of total annotated points annotated for bleached Favia matthaii.

B_FaviaS Percent of total annotated points annotated for bleached Favia speciosa.

B_FaviaSt Percent of total annotated points annotated for bleached Goniastrea stelligera.

B_Favites Percent of total annotated points annotated for bleached Favites.

B_FavPent Percent of total annotated points annotated for bleached Favites pentagona.

B_Fung Percent of total annotated points annotated for bleached Fungia.

BGard Percent of total annotated points annotated for bleached Gardineroseris.

B_GonEd Percent of total annotated points annotated for bleached Goniastrea edwardsi.

B_Herpo Percent of total annotated points annotated for bleached Herpolitha.

B_HYDNO Percent of total annotated points annotated for bleached Hydnophora.

B_HyExe Percent of total annotated points annotated for bleached Hydnophora exesa.

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B_Lepta Percent of total annotated points annotated for bleached Leptastrea.

B_Lepto Percent of total annotated points annotated for bleached Leptoseris.

Blisop Percent of total annotated points annotated for bleached Isopora.

B_Lobo Percent of total annotated points annotated for bleached Lobophyllia.

BlTurbFol Percent of total annotated points annotated for bleached Turbinaria (foliose morphology).

B_MOEN Percent of total annotated points annotated for bleached Montipora (encrusting morphology).

B_MOFO Percent of total annotated points annotated for bleached Montipora (foliose morphology).

B_Monta Percent of total annotated points annotated for bleached Montastraea.

B_Monti Percent of total annotated points annotated for bleached Montipora.

B_Oxyp Percent of total annotated points annotated for bleached Oxypora.

B_Paly Percent of total annotated points annotated for bleached Palythoa.

B_PaveDUER Percent of total annotated points annotated for bleached Pavona duerdeni.

B_Pavona Percent of total annotated points annotated for bleached Pavona.

B_PEYDO Percent of total annotated points annotated for bleached Pocillopora eydouxi.

B_Plat Percent of total annotated points annotated for bleached Platygyra.

B_PMEAN Percent of total annotated points annotated for bleached Pocillopora meandrina.

B_Pocillo Percent of total annotated points annotated for bleached Pocillopora.

B_Porit Percent of total annotated points annotated for bleached Porites.

B_Psam Percent of total annotated points annotated for bleached Psammocora.

B_PVAR Percent of total annotated points annotated for bleached Pavona varians.

B_Sando Percent of total annotated points annotated for bleached Sandolitha.

B_UnkCoral Percent of total annotated points annotated for bleached unknown hard coral.

Cirr Percent of total annotated points annotated for Cirrhipathes.

COSC Percent of total annotated points annotated for Coscinaraea.

ECHIN Percent of total annotated points annotated for Echinophyllia.

Fav Percent of total annotated points annotated for Favites.

FavHal Percent of total annotated points annotated for Favites halicora.

Favites halicora Percent of total annotated points annotated for Favia.

FaviaM Percent of total annotated points annotated for Dipsastraea matthaii.

FaviaS Percent of total annotated points annotated for Favia speciosa.

FaviaSt Percent of total annotated points annotated for Favia stelligera.

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ANEM Percent of total annotated points annotated for sea anemone.

B_Clad Percent of total annotated points annotated for bleached Cladiella.

B_Sinu Percent of total annotated points annotated for bleached Sinularia.

Clad Percent of total annotated points annotated for Cladiella.

EncBry Percent of total annotated points annotated for encrusting Bryozoan.

EUR Percent of total annotated points annotated for sea urchin.

HYDCO Percent of total annotated points annotated for Hydrocoral.

Hydra Percent of total annotated points annotated for Hydroid.

Mille Percent of total annotated points annotated for Millepora.

MOBI Percent of total annotated points annotated for bivalves.

Sarco Percent of total annotated points annotated for Sarcophyton.

SECO Percent of total annotated points annotated for sea cucumber.

Sinu Percent of total annotated points annotated for Sinularia.

Sponge Percent of total annotated points annotated for sponge.

Stylas Percent of total annotated points annotated for Stylaster.

UnkTUN Percent of total annotated points annotated for unknown Tunicate.

XmasW Percent of total annotated points annotated for Christmas Tree Worm.

ZOAN Percent of total annotated points annotated for Zoanthid.

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SCRO Percent of total annotated points annotated for consolidated rock.

B_Loph Percent of total annotated points annotated for bleached Lobophytum.

CYAN Percent of total annotated points annotated for Cyanobacteria films.

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Rubble Percent of total annotated points annotated for broken coral rubble.

SHAD Percent of total annotated points annotated for shadow.

Trans Percent of total annotated points annotated for transect hardware.

Unc Percent of total annotated points annotated for unclear.

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TURFH Percent of total annotated points annotated for turf algae on hard substrate.

Unidentified Percent of total annotated points annotated that were unidentified.

`softcoral_SQuads` *Sample Quadrat Data (0.6m by 0.9m)*

Description

A `data_frame` that can be used with the Simple Cleaning Quadrat Data and the Cleaning and Cropping Quadrat Data vignettes to show how quadrat data can be cleaned to produce easy to analyze data frames. Data was collected by the Baum Lab and Kiritimati Field Teams. Data is the uncleaned version of data found in Maucieri and Baum 2021. Biological Conservation. doi:10.1016/j.biocon.2021.109328 The data are from photo quadrats (0.9m by 0.6m) which were randomly annotated with 54 random points each. At each of these annotated points, the substrate was identified. Photo quadrats were collected on Kiritimati Island in the Republic of Kiribati and document coral cover over time and space. The annotations and output of the `data_frame` were produced using CoralNet and all annotations were done manually, by trained researchers.

Usage

```
softcoral_SQuads
```

Format

A `data_frame` with 135 columns, which are:

Image.ID Photo quadrat image ID from CoralNet.

Image.name The photo quadrat image name.

Annotation.status If the quadrat has been completely annotated, or if there are more annotations to occur.

Points The total number of annotation points in the quadrat.

AcCor Percent of total annotated points annotated for Acropora (corymbose morphology).

AcDig Percent of total annotated points annotated for Acropora (digitate morphology).

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Unidentified Percent of total annotated points annotated that were unidentified.

`sum_cols` *Sum columns based on matching names*

Description

Select columns and attach a vector of their new names, then columns with matching names will have each row summed. This is helpful to simplify your data quickly, like simplifying at a higher taxonomic group.

Usage

```
sum_cols(data, from, to)
```

Arguments

`data`	A data frame.
`from`	The column names in `data`.
`to`	A vector of new names, with matching names being the columns where each row will be summed.

Value

A data frame with summed columns.

Examples

```
Sites <- as.factor(c("One", "One", "One", "Two", "Two", "Three"))
Transect <- as.factor(c("1-Deep", "1-Shallow", "2-Shallow", "1-Shallow", "1-Deep", "1-Deep"))
Acropora.tabulate <- c(0.1, 0.6, 0.4, 0.9, 0.2, 0)
Acropora.corymbose <- c(0.4, 0, 0.1, 0, 0.3, 0.5)
Gardineroseris.sp <- c(0.4, 0.9, 0.5, 0.23, 0.5, 0.6)
Psammocora.sp <- c(0.9, 0.6, 0.5, 0.8, 0.1, 0.4)
Leptastrea.sp <- c(0.5, 0.7, 0.4, 0.8, 0.2, 0.3)
coral_cover <- data.frame(Sites, Transect, Acropora.tabulate, Acropora.corymbose,
```

```
                         Gardineroseris.sp, Psammocora.sp, Leptastrea.sp)

new_names <- c("Acropora.spp", "Acropora.spp", "Gardineroseris.sp",
               "Psammocora.sp", "Leptastrea.sp")

sum_cols(data = coral_cover, from = colnames(coral_cover[,3:7]),
         to = new_names)
```

`usable_obs` *Extract usable observations*

Description

Sum columns containing unusable observations and remove rows that contain more than the specified cutoff number of unusable points. Helpful if there are annotations that were unidentifiable and you want to remove them from the total usable observations, and you can remove quadrats with too many unusable observations.

Usage

```
usable_obs(
  data,
  unusable,
  max = FALSE,
  cutoff,
  above_cutoff = FALSE,
  rm_unusable = TRUE
)
```

Arguments

`data`	A data frame with each row representing a sampling unit (ex. a quadrat or photo).
`unusable`	A vector of column names containing unusable observations.
`max`	If `max = FALSE`, no threshold will be examined. If `max = TRUE`, a threshold cutoff needs to be provided where rows containing more than the `cutoff` will be removed from the data frame.
`cutoff`	The threshold number where rows containing more unusable observations than the `cutoff` will be removed from the data frame.
`above_cutoff`	If `above_cutoff = TRUE`, the data frame returned will be the rows containing more unusable observations than the cutoff. If `above_cutoff = FALSE` the data frame returned will be the rows containing equal to or less unusable observations than the cutoff.
`rm_unusable`	If `rm_unusable = TRUE`, the columns named in the unusable vector will be removed from the data frame. These columns will not be removed if `rm_unusable = FALSE`, though duplicate data will remain.

Value

A data frame containing summed unusable points.

Examples

```
#create data set for example
Sites <- as.factor(c("One", "One", "Two", "Two", "Three", "Three"))
Transect <- as.factor(c("1-Shallow", "2-Shallow", "1-Shallow", "2-Shallow",
    "1-Shallow", "2-Shallow"))
Acropora.sp <- c(1, 2, 3, 4, 5, 6)
Gardineroseris.sp <- c(6, 1, 2, 3, 4, 5)
Psammocora.sp <- c(5, 6, 1, 2, 3, 4)
Leptastrea.sp <- c(4, 5, 6, 1, 2, 3)
Blurry <- c(3, 4, 5, 6, 1, 2)
Unk <- c(2, 3, 4, 5, 6, 1)
coral_cover <- data.frame(Sites, Transect, Acropora.sp, Gardineroseris.sp,
                          Psammocora.sp, Leptastrea.sp, Blurry, Unk)


usable_obs(coral_cover, c("Blurry", "Unk"))

usable_obs(coral_cover, c("Blurry", "Unk"), above_cutoff = TRUE)

usable_obs(coral_cover, c("Blurry", "Unk"), rm_unusable = FALSE)

usable_obs(coral_cover, c("Blurry", "Unk"), max = TRUE, cutoff = 8)

usable_obs(coral_cover, c("Blurry", "Unk"), max = TRUE, cutoff = 8, above_cutoff = TRUE)
```

`visualize_app` *Visualize cleaned data*

Description

Using an interactive shiny app, visualize and explore cleaned quadrat data.

Usage

```
visualize_app(data, xaxis, yaxis)
```

Arguments

`data`	A data frame containing cleaned quadrat data.
`xaxis`	The xaxis variable column names found in `data`.
`yaxis`	The yaxis variable column names found in `data`.

Value

A shiny app launched in your browser.

Examples

```
year <- sample(x = seq(from = 2000, to = 2020, by = 1), 1000, replace = TRUE)
site <- sample(x = c("site1", "site2", "site3", "site4", "site5"), 1000, replace = TRUE)
transect <- sample(x = c("transect1", "transect2", "transect3", "transect4"),
    1000, replace = TRUE)
species <- sample(x = c("Acropora", "Gardineroseris", "Psammocora", "Leptastrea"),
    1000, replace = TRUE)
cover <- sample(x = seq(from = 0, to = 1, by = 0.01), 1000, replace = TRUE)

coral <- data.frame(year, site, transect, species, cover)

if (interactive()) {
visualize_app(data = coral, xaxis = colnames(coral[,1:4]), yaxis = "cover")
}
```

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