

Package ‘quadcleanR’

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Title Cleanup and Visualization of Quadrat Data

Version 1.0.0

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.

License GPL (>= 3)

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<https://dominiquemaucieri.com/quadcleanR/>

BugReports <https://github.com/DominiqueMaucieri/quadcleanR/issues>

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add_data	<i>Add data to existing data frame.</i>
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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")
lifecycle <- c("competitive", "weedy", "stresstolerant")
functionalgroup <- c("hardcoral", "hardcoral", "hardcoral")
coral_info <- data.frame(corals, lifecycle, functionalgroup)

add_data(data = coral_cover, add = coral_info, cols = c("lifecycle", "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 new column of categories.
binary	If <code>binary = TRUE</code> , 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 <code>binary = FALSE</code> 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

<code>data</code>	A data frame.
<code>column</code>	The column in which to change values.
<code>from</code>	A vector containing the values you wish to change.
<code>to</code>	A vector contain the values you which to change to, ensuring these occur in the same order as the <code>from</code> 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"))
```

<code>coral_labelset</code>	<i>Labelset for Corals</i>
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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	<i>Calculate species cover</i>
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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](https://doi.org/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 ($\text{mg C m}^{-2} \text{ day}^{-1}$).

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}).

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	<i>Calculate sample sizes</i>
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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")
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")
```

simple_cleaned *Simple cleaned quadrat data*

Description

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

Usage

```
simple_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 ($\text{mg C m}^{-2} \text{ day}^{-1}$).

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.

softcoral_annotatons *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_annotatons
```

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	<i>Sample Quadrat Data (1m by 1m)</i>
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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](https://doi.org/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.

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

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*.
- BIacro-Cor** Percent of total annotated points annotated for bleached *Acropora* (corymbose morphology).
- 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*.
- BITurbFol** 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_PFYDO 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.
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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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Sand Percent of total annotated points annotated for sand.
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SCRO Percent of total annotated points annotated for consolidated rock.
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CYAN Percent of total annotated points annotated for Cyanobacteria films.

- Loph** Percent of total annotated points annotated for Lobophytum.
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- CCA** Percent of total annotated points annotated for crustose coralline algae.
- Dict** Percent of total annotated points annotated for Dictyota.
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- Hali** Percent of total annotated points annotated for Halimeda.
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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](https://doi.org/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).

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.

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 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,  
  print_max = FALSE,  
  rm_unusable = TRUE  
)
```

Arguments

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