Package ‘quadcleanR’

June 17, 2022

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)

Encoding UTF-8

RoxygenNote 7.2.0

URL https://github.com/DominqueMaucieri/quadcleanR,
https://dominiquemaucieri.com/quadcleanR/

BugReports https://github.com/DominqueMaucieri/quadcleanR/issues

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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

```r
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

```r
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

```r
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 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.
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**

```r
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**

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

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 which 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"))

---

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 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.
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.

The column name in `data` which contains the max column dimension for each quadrat.

The column name in `data` which contains the max row dimension for each quadrat.

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

#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).

**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**

```r
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**

```r
# create data frame
Sites <- as.factor(c("One", "One", "One", "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 = TRUE)
```
rem_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

rem_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 <- rem_chr(coral_cover, c(".spp"), full_selection = FALSE, cols = c("Largest_Coral", "Dominant_Coral"))

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

```r
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

```r
Site <- c("site1", "site1", "site2", "site2", "site1", "site1", "site2", "site2", "site1", "site1", "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")
```
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 (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.

# 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.

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.
- **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.

**B_Acro-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.

**BFturFol** 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.
### Percent of total annotated points annotated for bleached corals

<table>
<thead>
<tr>
<th>Coral</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>B_Pavona</strong></td>
<td>Percent of total annotated points annotated for bleached Pavona.</td>
</tr>
<tr>
<td><strong>B_PEYDO</strong></td>
<td>Percent of total annotated points annotated for bleached Pocillopora eydouxi.</td>
</tr>
<tr>
<td><strong>B_Plat</strong></td>
<td>Percent of total annotated points annotated for bleached Platygyra.</td>
</tr>
<tr>
<td><strong>B_Pocillo</strong></td>
<td>Percent of total annotated points annotated for bleached Pocillopora meandrina.</td>
</tr>
<tr>
<td><strong>B_Porit</strong></td>
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</tr>
<tr>
<td><strong>B_Pmeandrica</strong></td>
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<td><strong>B_UnkCoral</strong></td>
<td>Percent of total annotated points annotated for bleached unknown hard coral.</td>
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<td>Percent of total annotated points annotated for Cirrhipathes.</td>
</tr>
<tr>
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<td>Percent of total annotated points annotated for Coscinaraea.</td>
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<tr>
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Turf  Percent of total annotated points annotated for turf algae.
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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).
- **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 Favites.
- **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_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.
- **BLAcro-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.
<table>
<thead>
<tr>
<th>Coral Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blisop</td>
<td>Percent of total annotated points annotated for bleached Isopora.</td>
</tr>
<tr>
<td>B_Lobo</td>
<td>Percent of total annotated points annotated for bleached Lobophyllia.</td>
</tr>
<tr>
<td>BF_TurbFol</td>
<td>Percent of total annotated points annotated for bleached Turbinaria (foliose morphology).</td>
</tr>
<tr>
<td>B_MOEN</td>
<td>Percent of total annotated points annotated for bleached Montipora (encrusting morphology).</td>
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<td>B_MOFO</td>
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<td>B_Monta</td>
<td>Percent of total annotated points annotated for bleached Montastraea.</td>
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<tr>
<td>B_Oxyp</td>
<td>Percent of total annotated points annotated for bleached Oxypora.</td>
</tr>
<tr>
<td>B_Paly</td>
<td>Percent of total annotated points annotated for bleached Palythoa.</td>
</tr>
<tr>
<td>B_PaveDUER</td>
<td>Percent of total annotated points annotated for bleached Pavona duerdeni.</td>
</tr>
<tr>
<td>B_Pavona</td>
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</tr>
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<td>B_PEYDO</td>
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<tr>
<td>HYDNO</td>
<td>Percent of total annotated points annotated for Hydnophora.</td>
</tr>
<tr>
<td>Name</td>
<td>Description</td>
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<td>-----------------------------------------------------------------------------</td>
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<tr>
<td>HyExe</td>
<td>Percent of total annotated points annotated for Hydnophora exesa.</td>
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<tr>
<td>Isopora</td>
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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

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.
print_max    If print_max = TRUE, the data frame returned will be the rows containing more unusable observations than the cutoff. If print_max = 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

```r
# 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)
```

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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

```r
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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