

Package ‘Rraven’

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Type Package

Title Connecting R and 'Raven' Sound Analysis Software

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Description A tool to exchange data between R and 'Raven' sound analysis software <<http://www.birds.cornell.edu/brp/raven/RavenOverview.html>> (Cornell Lab of Ornithology). Functions work on data formats compatible with the R package 'warbleR'.

License GPL (>= 2)

Imports pbapply, warbleR, utils, stats, vegan, dplyr,kableExtra, doParallel, foreach, pbmcapply

Depends R (>= 3.2.1)

LazyData TRUE

URL <https://github.com/maRce10/Rraven>

BugReports <https://github.com/maRce10/Rraven/issues>

NeedsCompilation no

Suggests knitr

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R topics documented:

exp_raven	2
extract_ts	4
imp_corr_mat	5
imp_raven	7
imp_syrinx	9

match_wav_case	10
raven_batch_detec	11
relabel_colms	13
Rraven	15
run_raven	15
selection_files	17
sort_colms	18
Index	20

exp_raven	<i>Export 'Raven' selections</i>
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Description

exp_raven exports selection tables as 'Raven' selection data in .txt format.

Usage

```
exp_raven(X, path = NULL, file.name = NULL, khz.to.hz = TRUE,
          sound.file.path = NULL, single.file = TRUE)
```

Arguments

X	Data frame containing columns for sound file (sound.files), selection (selec), start and end time of signals ('start' and 'end') and low and high frequency ('bottom.freq' and 'top.freq', optional). See example data 'selec.table' in the warbleR package.
path	A character string indicating the path of the directory in which to save the selection files. If not provided (default) the function saves the file into the current working directory.
file.name	Name of the output .txt file. If NULL then the sound file names are used instead. If multiple selection files are generated (see 'single.file') then the sound files names are added to the provided 'file.name'.
khz.to.hz	Logical. Controls if frequency variables should be converted from kHz (the unit used by other bioacoustic analysis R packages like warbleR) to Hz (the unit used by Raven). Default is TRUE.
sound.file.path	A character string indicating the path of the directory containing the sound file(s). Providing this information allows to open both sound file and selection table simultaneously. This can be done by using the 'File > Open selection table' option in 'Raven' (or drag/drop the selection file into Raven). Default is NULL. This argument is required when exporting selections from multiple sound files.

`single.file` Logical. Controls whether a single selection file (TRUE; default) or multiple selection files for each sound files (FALSE, hence, only applicable when several sound files are included in 'X') are generated. Note that 'sound.file.path' must be provided when exporting several sound files into a single selection file as the duration of the sound files is required.

Details

The function exports selection tables (as the ones used in the R package [warbleR](#)) into the 'Raven' selection file format ('.txt'). This can be useful to obtain additional Raven measurements on existing selections by adding new measurements to the selection table once in Raven. Note that selection labels must be numeric and unduplicated when exporting them to Raven. If that is not the case the function will relabeled the selections and the previous selection labels will be retained in a new column('old.selec').

Value

The function saves a selection table in '.txt' format that can be directly opened in Raven. If several sound files are available users can either export them as a single selection file or as multiple selection files (one for each sound file). No objects are returned in the R environment.

Author(s)

Marcelo Araya-Salas (<araya-salas@cornell.edu>)

See Also

[imp_raven](#); [imp_syrinx](#)

Examples

```
# Load data
library(warbleR)
data(list = c("Phae.long1", "Phae.long2", "Phae.long3", "Phae.long4", "selec.table"))

# Select data for a single sound file
st1 <- selec.table[selec.table$sound.files == "Phae.long1.wav",]

# Export data of a single sound file
exp_raven(st1, file.name = "Phaethornis 1")

writeWave(Phae.long1, "Phae.long1.wav", extensible = FALSE) #save sound files
writeWave(Phae.long2, "Phae.long2.wav", extensible = FALSE)
writeWave(Phae.long3, "Phae.long3.wav", extensible = FALSE)
writeWave(Phae.long4, "Phae.long4.wav", extensible = FALSE)

exp_raven(X = selec.table, file.name = "Phaethornis multiple sound files",
  single.file = TRUE, sound.file.path = getwd())
```

 extract_ts

Extract time series parameters from data imported from 'Raven'

Description

extract_ts extracts time series parameters from data imported from 'Raven' bioacoustic software.

Usage

```
extract_ts(X, ts.column, equal.length = FALSE, as.time.series = FALSE,
length.out = 30)
```

Arguments

X	Data frame imported from Raven. It should include at least columns for: sound file names, selection labels, a parameters encoded as a time series (e.g. several numbers separated by semicolon)
ts.column	Name of the column with the time series data to be extracted. Default is NULL.
equal.length	Logical. Controls whether time series are kept as in the original data (most of the time with unequal lengths) or numbers are interpolated to equalize series length (using the approx function). All series will be interpolated to match the length of the longest series in the data. Default is FALSE.
as.time.series	Logical. Controls if data is converted to the time series format (using the as.ts function). Default is FALSE.
length.out	A numeric vector of length 1 giving the number of measurements to be interpolated (the length of the time series). default is 30. Ignored if equal.length is FALSE.

Details

The function extracts parameters encoded as time series in 'Raven' selection files. The resulting data frame can be directly input into functions for time series analysis of acoustic signals as [dfDTW](#).

Value

A data frame with columns for sound file name (sound.files), selection label (selec) and the time series for each selection.

Author(s)

Marcelo Araya-Salas (<araya-salas@cornell.edu>)

See Also

[imp_raven](#); [exp_raven](#)

Examples

```
# Load data
data(selection_files)

#save 'Raven' selection tables in the temporary directory
writeLines(selection_files[[5]], con = names(selection_files)[5])

# import data to R
rvn.dat <- imp_raven(all.data = TRUE)

# Peak freq dif length
extract_ts(X = rvn.dat, ts.column = "Peak.Freq.Contour..Hz.")

# Peak freq equal length
extract_ts(X = rvn.dat, ts.column = "Peak.Freq.Contour..Hz.", equal.length = T)

# Peak freq equal length 10 measurements
extract_ts(X = rvn.dat, ts.column = "Peak.Freq.Contour..Hz.",
equal.length = TRUE, length.out = 10)
```

imp_corr_mat	<i>Import 'Raven' batch correlator output</i>
--------------	---

Description

imp_corr_mat imports the output of 'Raven' batch correlator.

Usage

```
imp_corr_mat(file, path = NULL)
```

Arguments

file	A character string with the name of the output '.txt' file generated by Raven.
path	A character string indicating the path of the directory in which to look for the text files. If not provided (default) the function searches into the current working directory.

Details

The function imports the output of a batch correlation routine in Raven. Both the correlation and lag matrices contained in the output '.txt' file are read and both waveform and spectrogram (cross-correlation) correlations can be imported.

Value

A list with 2 matrices. The first one contains the correlation coefficients and the second one the time lags of the peak correlations.

Author(s)

Marcelo Araya-Salas (<araya-salas@cornell.edu>)

See Also

[imp_raven](#); [exp_raven](#)

Examples

```
## Not run:
# Load data
library(warbleR)
data(list = c("Phae.long1", "Phae.long2", "Phae.long3", "Phae.long4", "selec.table"))

writeWave(Phae.long1, "Phae.long1.wav", extensible = FALSE) #save sound files
writeWave(Phae.long2, "Phae.long2.wav", extensible = FALSE)
writeWave(Phae.long3, "Phae.long3.wav", extensible = FALSE)
writeWave(Phae.long4, "Phae.long4.wav", extensible = FALSE)

#create new folder to put cuts
dir.create("cuts")

# cut files
cut_sels(X = selec.table, mar = 0.05, path = tempdir(), dest.path = file.path(tempdir(), "cuts"))

#Now run 'Raven' batch correlator un the cuts and save the output in the same folder

# Import output (change the name of the file if you used a different one)
xcorr.rav <- imp_corr_mat(file = "BatchCorrOutput.txt",
path = file.path(tempdir(), "cuts"))

# check results

## correlation matrix
xcorr.rav[[1]]

## time lag matrix
xcorr.rav[[2]]

## End(Not run)
```

imp_raven	<i>Import 'Raven' selections</i>
-----------	----------------------------------

Description

imp_raven imports 'Raven' selection files simultaneously from many files. Files must be in '.txt' format.

Usage

```
imp_raven(path = NULL, sound.file.col = NULL, all.data = FALSE, recursive = FALSE,
name.from.file = FALSE, ext.case = NULL, freq.cols = TRUE, waveform = FALSE,
parallel = 1, pb = TRUE, unread = FALSE, rm_dup = FALSE)
```

Arguments

path	A character string indicating the path of the directory in which to look for the 'Raven' selection (text) files. If not provided (default) the function searches into the current working directory.
sound.file.col	A character string with the name of the column containing the sound files in the selection text files. Default is NULL. If provided, the output data frame will contained all columns needed for subsequent analysis in the acoustic analysis package warbleR . Duplicated rows, as when "waveform" and "spectrogram" information are included for the same selection, will be removed. All selection files must contain "Selection", "Begin.Time" and "End.Time" columns.
all.data	Logical. If TRUE all columns in the selection files are returned, keeping the name columns as in the 'Raven' files. Default is FALSE. Columns absent in some selection files will be filled with NA's.
recursive	Logical. If TRUE the listing recurse into sub-directories.
name.from.file	Logical. If TRUE the sound file names are extracted from the selection text file name. It assumes that selections files contained the suffix "Table.1.selections.txt" or "selections.txt". Note that by default it will assume that the extension file name is ".wav". This can be control using the argumet 'ext.wav'. Default is FALSE). Ignored if sound.file.col' is provided and/or all.data is TRUE).
ext.case	Character string of length 1 to specify whether sound file extensions are in upper or lower case. This should match the extension of the of the .wav files from which the selection were made. It must be either 'upper' or 'lower'. Only needed when 'name.from.file' is TRUE. Ignored if 'sound.file.col' is provided and/or all.data is TRUE.
freq.cols	Logical. If TRUE 'Low Freq' and 'High Freq' columns are also imported. Ignored if all.data is TRUE.
waveform	Logical to control if waveform view data should be included (this data is typically duplicated in spectrogram view data). Default is FALSE (not to include it).

<code>parallel</code>	Numeric. Controls whether parallel computing is applied. It specifies the number of cores to be used. Default is 1 (i.e. no parallel computing).
<code>pb</code>	Logical argument to control progress bar. Default is TRUE. Note that progress bar is only used when <code>parallel = 1</code> .
<code>unread</code>	Logical. If TRUE a list (instead of a data frame). The first element of the list contains the selections\ whole the second one is a character vector with the names of sound files that could not be read. Default is FALSE.
<code>rm_dup</code>	Logical. If TRUE duplicated rows are removed. Usefull when selection files have been duplicated. Default is FALSE.

Details

The function import 'Raven' selection data from many files simultaneously. Files must be in '.txt' format. Selection files including data from multiple recordings can also be imported.

Value

A single data frame with information of the selection files. If `unread = TRUE` the function returns a list of length 2 with the selection data frame and a vector with the names of files that could not be read (see 'unread' argument). If 'all.data' argument is set to FALSE the data frame contains the following columns: `selec`, `start`, `end`, and `selec.file`. If `sound.file.col` is provided the data frame will also contain a 'sound.files' column. In addition, all rows with duplicated data are removed. This is useful when both spectrogram and waveform views are included in the 'Raven' selection files. If `all.data` is set to TRUE then all columns in the 'Raven' selection files are returned.

Author(s)

Marcelo Araya-Salas (<araya-salas@cornell.edu>)

See Also

[imp_syrinx](#)

Examples

```
#load data
data(selection_files)

#save 'Raven' selection tables in the temporary directory
out <- lapply(1:2, function(x)
writeLines(selection_files[[x]], con = names(selection_files)[x]))

#providing the name of the column with the sound file names
rvn.dat <- imp_raven(sound.file.col = "Begin.File", all.data = FALSE)

# View(rvn.dat)
```

imp_syrinx	<i>Import 'Syrinx' selections</i>
------------	-----------------------------------

Description

imp_syrinx imports 'Syrinx' selection data from many files simultaneously. All files must have the same columns.

Usage

```
imp_syrinx(path = NULL, all.data = FALSE, recursive = FALSE,  
exclude = FALSE, hz.to.khz = TRUE)
```

Arguments

path	A character string indicating the path of the directory in which to look for the text files. If not provided (default) the function searches into the current working directory. Default is NULL.
all.data	Logical. If TRUE all columns in text files are returned. Default is FALSE. Note that all files should contain exactly the same columns in the same order.
recursive	Logical. If TRUE the listing recurse into sub-directories.
exclude	Logical. Controls whether files that cannot be read are ignored (TRUE). Default is FALSE.
hz.to.khz	Logical. Controls if frequency variables should be converted from Hz (the unit used by Syrinx) to kHz (the unit used by warbleR and other bioacoustic analysis packages in R). Default if TRUE. Ignored if all.data is TRUE.

Value

A single data frame with information of the selection files. If all.data argument is set to FALSE the data frame contains the following columns: selec, start, end, and selec.file. If sound.file.col is provided the data frame will also contain a 'sound.files' column. If all.data is set to TRUE then all columns in selection files are returned.

Author(s)

Marcelo Araya-Salas (<araya-salas@cornell.edu>)

See Also

[imp_raven](#)

Examples

```
## Not run:
#load data
data(selection_files)

#save 'Raven' selection tables in the temporary directory
writeLines(selection_files[[7]], con = names(selection_files)[7])

syr.dat <- imp_syrinx(all.data = FALSE)

# View(syr.dat)

#getting all the data
syr.dat <- imp_syrinx(all.data = TRUE)

# View(syr.dat)

## End(Not run)
```

match_wav_case

Fix the extension case of sound files

Description

match_wav_case fixes the extension case of sound files in a selection table.

Usage

```
match_wav_case(X, path = NULL, output = "data.frame", verbose = TRUE)
```

Arguments

X	Data frame containing columns for sound file (sound.files), selection (selec), start and end time of signals ('start' and 'end') and low and high frequency ('bottom.freq' and 'top.freq', optional). See example data 'selec.table' in the warbleR package.
path	A character string indicating the path of the directory in which to look for sound files. If not provided (default) the function searches into the current working directory.
output	Character string. Controls whether a complete data frame ('data.frame') or only the sound file names ("names") are returned. Default is 'data.frame'.
verbose	Logical to control if messages are printed (TRUE, default).

Details

The function returns the data from the input data frame with extension file names in the 'sound.files' column matching those of the sound files (in case there was) any mismatch. The function needs the path to the sound files to compare extension names.

Value

The same data as in the input data frame but with the case of the extension file names in the 'sound.files' column matching those of the sound files themselves.

Author(s)

Marcelo Araya-Salas (<araya-salas@cornell.edu>)

See Also

[sort_colms](#); [relabel_colms](#)

Examples

```
library(warbleR)
data(list = c("Phae.long1", "Phae.long2", "Phae.long3", "Phae.long4",
"selec.table"))

writeWave(Phae.long1, "Phae.long1.wav", extensible = FALSE) #save sound files
writeWave(Phae.long2, "Phae.long2.wav", extensible = FALSE)
writeWave(Phae.long3, "Phae.long3.wav", extensible = FALSE)
writeWave(Phae.long4, "Phae.long4.wav", extensible = FALSE)

# change one extension
selec.table$sound.files <- as.character(selec.table$sound.files)
selec.table$sound.files[1] <- gsub("\\.wav$", ".WAV", selec.table$sound.files[1])

# fixed extension an return data frame
match_wav_case(X = selec.table)

# fixed extension an return sound file names
match_wav_case(X = selec.table, output = "names")
```

raven_batch_detec	<i>Run 'Raven' batch detector</i>
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Description

raven_batch_detec Runs 'Raven' batch detector on multiple sound files sequentially

Usage

```
raven_batch_detec(raven.path = NULL, sound.files, path = NULL,
detector = "Amplitude detector",
relabel_colms = TRUE, pb = TRUE)
```

Arguments

raven.path	A character string indicating the path of the directory in which to look for the 'Raven' executable file (where 'Raven' was installed).
sound.files	character vector indicating the files that will be analyzed. In OSX (mac) only one file at the time can be run (use loops instead!). If NULL (default) then 'Raven' will be run without opening any file.
path	A character string indicating the path of the directory in which to look for the sound files. If not provided (default) the function searches into the current working directory. Default is NULL.
detector	Character string specifying the type of detector to be called. There are 3 options available in Raven: 'Amplitude detector' (default), 'Band Limited Energy Detector' and 'Band Limited Entropy Detector'. Detector parameters must be set in 'Raven' before running the function.
relabel_colms	Logical. If TRUE (default) columns are labeled to match the selection table format from the acoustic analysis package warbleR
pb	Logical argument to control progress bar. Default is TRUE.

Details

The function runs 'Raven' sound analysis software (Cornell Lab of Ornithology), detector on multiple sound files sequentially. 'Raven' Pro must be installed. Note that batch detection in 'Raven' can also take sound files in 'mp3', 'flac' and 'aif' format.

Value

A data frame with the selections produced during the detection. See [imp_raven](#) for more details on how selections are imported.

Author(s)

Marcelo Araya-Salas (<araya-salas@cornell.edu>)

See Also

[imp_raven](#); [imp_syrinx](#); [run_raven](#)

Examples

```
## Not run:

# here replace with the path where 'Raven' is install in your computer
raven.path <- "PATH_TO_RAVEN_DIRECTORY_HERE"

# Run detector on raven example sound files

# single sound file
detec.res <- raven_batch_detec(raven.path = raven.path,
  sound.files = "BlackCappedVireo.aif", path = file.path(raven.path, "Examples"))
```

```
# on raven examples 2 files
detec.res <- raven_batch_detec(raven.path = raven.path,
  sound.files = c("BlackCappedVireo.aif", "CanyonWren.wav"),
  path = file.path(raven.path, "Examples"))

# using 'Band Limited Energy Detector'
detec.res <- raven_batch_detec(raven.path = raven.path,
  sound.files = c("BlackCappedVireo.aif", "CanyonWren.wav"),
  path = file.path(raven.path, "Examples"), detector = "Band Limited Energy Detector")

## End(Not run)
```

relabel_colms	<i>Relabel columns to match the selection table format</i>
---------------	--

Description

relabel_colms relabels columns to match the selection table format (as in the R package [warbleR](#))

Usage

```
relabel_colms(X, extra.cols.name = NULL, extra.cols.new.name = NULL,
  khz.to.hz = FALSE, hz.to.khz = FALSE, waveform = FALSE)
```

Arguments

X	Data frame imported from Raven.
extra.cols.name	Character vector with the names of additional columns to be relabeled. Default is NULL. 'extra.cols.new.name' must be also provided.
extra.cols.new.name	Character vector with the new names for the additional columns to be relabeled. Default is NULL. 'extra.cols.name' must be also provided.
khz.to.hz	Logical. Controls if frequency variables ('top.freq' and 'bottom.freq') should be converted from kHz (the unit used by other bioacoustic analysis R packages like warbleR) to Hz (the unit used by Raven). Default is TRUE.
hz.to.khz	Logical. Controls if frequency variables ('top.freq' and 'bottom.freq') should be converted from Hz (the unit used by other bioacoustic analysis R packages like Raven) to kHz (the unit used by warbleR). Default is FALSE. Ignored if 'kHz.to.hz' is provided.
waveform	Logical to control if 'waveform' related data should be included (this data is typically duplicated in 'spectrogram' data). Default is FALSE (not to include it).

Details

This function relabels columns to match the selection table format to match then ones used by other bioacoustic analysis R packages like [warbleR](#).

Value

The function returns the input data frame with new column names for time and frequency 'coordinates' and sound files and selections.

Author(s)

Marcelo Araya-Salas (<araya-salas@cornell.edu>)

See Also

[imp_raven](#); [exp_raven](#)

Examples

```
# Load data
data(selection_files)

#save 'Raven' selection tables in the temporary directory
writeLines(selection_files[[5]], con = names(selection_files)[5])

## import data to R
rvn.dat <- imp_raven(all.data = TRUE)

names(rvn.dat)

# Select data for a single sound file
rvn.dat2 <- relabel_colms(rvn.dat)

names(rvn.dat2)

# plus 1 additional column
rvn.dat2 <- relabel_colms(rvn.dat, extra.cols.name = "selec.file", "Raven selection file")

names(rvn.dat2)

# plus 2 additional column
rvn.dat2 <- relabel_colms(rvn.dat, extra.cols.name = c("selec.file", "View"),
c("Raven selection file", "Raven view"))

names(rvn.dat2)
```

Raven

Raven: Exchange data and open sound files in 'Raven' from R

Description

Raven is a package designed to facilitate the exchange of data between R and 'Raven' sound analysis software (Cornell Lab of Ornithology)

Details

License: GPL (≥ 2)

@section Functions:

`extract_ts`: Extract time series parameters from data imported from Raven

`exp_raven`: Export R selection tables into 'Raven' selection file format

`imp_corr_mat`: Import 'Raven' batch correlator output

`imp_raven`: Importing 'Raven' selections

`imp_syrinx`: Importing 'Syrinx' selections

`relabel_colms`: Relabel columns to match the selection table format

`run_raven`: Open sound files in Raven

Author(s)

Marcelo Araya-Salas

Maintainer: Marcelo Araya-Salas (<araya-salas@cornell.edu>)

run_raven

Open sound files in 'Raven' sound analysis software

Description

run_raven opens several sound files in 'Raven' sound analysis software

Usage

```
run_raven(raven.path = NULL, sound.files = NULL, path = NULL, at.the.time = 10,
import = FALSE, redo = FALSE, view.preset = NULL, pb = TRUE, ...)
```

Arguments

raven.path	A character string indicating the path of the directory in which to look for the 'Raven' executable file (where 'Raven' was installed).
sound.files	character vector indicating the files that will be analyzed. If NULL (default) then 'Raven' will be run without opening any file.
path	A character string indicating the path of the directory in which to look for the sound files. If not provided (default) the function searches into the current working directory. Default is NULL.
at.the.time	Numeric vector of length 1 controlling how many files will be open in 'Raven' at the same time. Note that opening too many files at once could make 'Raven' run out of memory. You need to close 'Raven' every time the batch of files is analyzed, so the next batch is opened. Default is 10. Not available in OSX (mac).
import	Logical. Controls if the selection tables generated should be returned as a data frame into the R environment. This only works if the selections are saved in the "Selections" folder in the 'Raven' directory. This argument calls the imp_raven internally. Additional arguments can be passed to imp_raven to control the way the data is imported.
redo	Logical. Controls whether only the subset of files with no 'Raven' selections (.txt file) in the 'Raven' 'selections' folder are analyzed (if FALSE). Useful when resuming the analysis. Default is FALSE.
view.preset	Character string defining the 'Raven' view preset to be used. It should match exactly the name of the present in the 'Raven' folder 'Presets/Sound Window'. If not provided the default view preset is used.
pb	Logical argument to control progress bar. Default is TRUE.
...	Additional arguments to be passed to imp_raven for customizing how selections are imported (ignored if import = FALSE).

Details

The function runs 'Raven' sound analysis software (Cornell Lab of Ornithology), opening many files simultaneously. 'Raven' will still run if no sound files are provided (i.e. `sound.files = NULL`). At the end of the analysis the data can be automatically imported back into R using the 'import' argument. 'Raven' Pro must be installed. Note that 'Raven' can also take sound files in 'mp3', 'flac' and 'aif' format.

Value

If `import = TRUE` a data frame with the selections produced during the analysis will be return as an data frame. See [imp_raven](#) for more details on how selections are imported.

Author(s)

Marcelo Araya-Salas (<araya-salas@cornell.edu>)

See Also

`imp_raven; imp_syrinx; run_raven`

Examples

```
## Not run:
# First set temporary folder
setwd(tempdir())

# save sound files
library(warbleR)
data(list = c("Phae.long1", "Phae.long2", "Phae.long3", "Phae.long4"))
writeWave(Phae.long1, "Phae.long1.wav", extensible = FALSE)
writeWave(Phae.long2, "Phae.long2.wav", extensible = FALSE)

# here replace with the path where 'Raven' is install in your computer
raven.path <- "PATH_TO_RAVEN_DIRECTORY_HERE"

# run function
run_raven(raven.path = raven.path, sound.files = c("Phae.long1.wav", "Phae.long2.wav"),
  at.the.time = 2, import = T, name.from.file = T, ext.case = "upper",
  all.data = TRUE, path = tempdir())

#getting all the data
rav.dat<-run_raven(all.data = TRUE, raven.path = raven.path)
# View(rav.dat)

writeWave(Phae.long3, "Phae.long3.wav", extensible = FALSE)
writeWave(Phae.long4, "Phae.long4.wav", extensible = FALSE)

# run function on all the wav files in the working directory 3 at the time
run_raven(raven.path = raven.path, sound.files = list.files(pattern = "\\wav$",
  ignore.case = TRUE, path = tempdir()), at.the.time = 3, import = FALSE,
  path = tempdir())

## End(Not run)
```

selection_files

A list of 'Raven' selection tables.

Description

List of 'Raven' and 'Syrinx' selection tables containing *Phaethornis longirostris* (Long-billed Hermit) songs from the example sound files included in the [warbleR](#) package (times 1 to 5), a 'Raven' correlation matrix (item 6) and one selection from cane-brake wrens (item 7; no sound file available).

Usage

```
data(selection_files)
```

Format

List of 7 selection tables. The first 5 items are 'Raven' selection tables of Long billed hermit songs. The 5th table contains a multiple sound file selection table. The 6th item is a 'Raven' correlation matrix and the last one a table in 'Syrinx' format.

Source

Marcelo Araya-Salas

sort_colms	<i>Sort columns in a more intuitive order</i>
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Description

sort_colms sorts selection table columns in a more intuitive order.

Usage

```
sort_colms(X)
```

Arguments

X Data frame containing columns for sound file (sound.files), selection (selec), start and end time of signals ('start' and 'end') and low and high frequency ('bottom.freq' and 'top.freq', optional). See example data 'selec.table' in the [warbleR](#) package.

Details

The function returns the data from the input data frame with the most relevant information for acoustic analysis located in the first columns. The priority order for column names is: "sound.files", "channel", "selec", "start", "end", "top.freq", and "bottom.freq".

Value

The same data as in the input data frame but with the most relevant information for acoustic analysis located in the first columns.

Author(s)

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See Also

[match_wav_case](#); [relabel_colms](#)

Examples

```
library(warbleR)
data("selec.table")

# mess column order
selec.table <- selec.table[, sample(1:ncol(selec.table))]

#check names
names(selec.table)

selec.table <- sort_colms(X = selec.table)

#check names again
names(selec.table)
```

Index

*Topic **datasets**

selection_files, [17](#)

approx, [4](#)

as.ts, [4](#)

dfDTW, [4](#)

exp_raven, [2](#), [4](#), [6](#), [14](#), [15](#)

extract_ts, [4](#), [15](#)

imp_corr_mat, [5](#), [15](#)

imp_raven, [3](#), [4](#), [6](#), [7](#), [9](#), [12](#), [14–17](#)

imp_syrinx, [3](#), [8](#), [9](#), [12](#), [15](#), [17](#)

match_wav_case, [10](#), [18](#)

raven_batch_detec, [11](#)

relabel_colms, [11](#), [13](#), [15](#), [18](#)

Raven, [15](#)

Raven-package (Raven), [15](#)

run_raven, [12](#), [15](#), [15](#), [17](#)

selection_files, [17](#)

sort_colms, [11](#), [18](#)

warbleR, [2](#), [3](#), [7](#), [10](#), [12–14](#), [17](#), [18](#)