

Package ‘mboxr’

February 24, 2019

Title Converting an Mbox File into a Tibble

Version 0.1.4

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Description Importing and converting an mbox file into a tibble object.

SystemRequirements Anaconda (<https://www.anaconda.com/download/>)

License GPL-3

VignetteBuilder knitr

URL <https://github.com/jooyoungseo/mboxr>

BugReports <https://github.com/jooyoungseo/mboxr/issues>

Encoding UTF-8

LazyData true

Imports reticulate, tibble, magrittr, purrr, dplyr, lubridate

RoxygenNote 6.1.1.9000

Suggests knitr, rmarkdown, testthat, covr

NeedsCompilation no

Repository CRAN

Date/Publication 2019-02-24 20:10:03 UTC

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merge_mbox_all *Merging all mbox files in current directory into one tibble.*

Description

Use this function for merging all mbox files into one tibble object.

Usage

```
merge_mbox_all(path = ".", out = NULL)
```

Arguments

path	A character vector of full path names; the default corresponds to the working directory, <code>getwd</code> . Tilde expansion (see <code>path.expand</code>) is performed. Missing values will be ignored.
out	Output Rda file if you want to save. The default is NULL, which is not saving the output as a file.

Details

merge_mbox_all
See example below.

Value

One tibble object for all the merged mbox files in your current directory will be returned.

Author(s)

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References

<https://en.wikipedia.org/wiki/Mbox>
<https://docs.python.org/3/library/mailbox.html>
<https://www.anaconda.com/download/>

Examples

```
# Changing working directory to temp for the demonstration purpose only.  
setwd(tempdir())  
library(mboxr)  
test_path <- system.file("extdata", package = "mboxr")  
# Save your own Rda file as an output if you need it:
```

```
data <- merge_mbox_all(path = test_path, out = "output.Rda")
# Now you can use the imported file as a tibble.
str(data)
```

read_mbox	<i>Converting an mbox file into a tibble data_frame.</i>
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Description

Use this function for importing and converting an mbox file into a tibble object.

Usage

```
read_mbox(file = NULL, out = NULL)
```

Arguments

file	Input mbox file.
out	Output Rda file if you want to save. The default is NULL, which is not saving the output as a file.

Details

read_mbox

See example below.

Value

Tibble object for the input mbox file will be returned.

Author(s)

JooYoung Seo, <jooyoung@psu.edu>

Soyoung Choi, <sxc940@psu.edu>

References

<https://en.wikipedia.org/wiki/Mbox>

<https://docs.python.org/3/library/mailbox.html>

<https://www.anaconda.com/download/>

Examples

```
# Changing working directory to temp for the demonstration purpose only.
setwd(tempdir())
library(mboxr)
# Feeding an mbox file through read_mbox function:
test <- system.file("extdata", "test1.mbox", package = "mboxr")
data <- read_mbox(test, out = "output.Rda")
# Now you can use the imported file as a tibble.
str(data)
```

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