

RRootDetection - Provides simple visualization and parsing functions for RootDetection's database data

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1 Introduction

The R-package *RRootDetection* is a collection of basic visualization and parsing functions for **RootDetection**'s database data. Its primary purpose is the data access of root system architecture (RSA) traits measured with **RootDetection** <http://www.labutils.de> and the simple visualization of this data in barplots, boxplots or histograms. The **RootDetection** data is accessed via the R-package *RSQLite* and can then easily statistically analysed with the R core functions or other R-packages.

2 Short Background

3 Data connection with *RRootDetection*

3.1 Prdefined list for storing connection details

RD.state: This predefined list is used to store mandatory connection details, which can be set by the **RD.load()** function. The first list value stores the path of the database file. The second list value is the 'SQLite Connection' class used to connect to the database file.

```
#####
#Short example
#
library(RRootDetection)
file <- system.file("extdata/example.db", package = "RRootDetection")
```

```

#Setting Connection to database file
RD.load(file)

#Show connection details
RD.state

```

For related topics see also:

```

%current function
help("RD.state")
%additional functions set by \seealso
help("RD.load")
help("dbConnect")

```

3.2 Connection to a RootDetection database

`RD.load`: Establish a connection to a database file generated with `RootDetection`. Saves the connection parameters in the `RD.state` variable. The path needs to include the database file.

```

#####
#Short example
#
library(RRootDetection)
file <- system.file("extdata/example.db", package = "RRootDetection")

#Setting Connection to database file
RD.load(file)

#To print connection details
RD.state

```

For related topics see also:

```

%current function
help("RD.list.directories")
%additional functions set by \seealso
help("RD.list.images")
help("RD.list.roots")

```

After a connection to a `RootDetection` database is set one can continue to browse the included RSA trait data.

4 Data access with *RRootDetection*

4.1 Execute an SQL statement on the connected Root-Detection database

`RD.select`: Uses the `dbGetQuery` function [package:DBI] to submit and execute an SQL statement on the connected RootDetection database. The query and the connection from `RD.state[[2]]` is passed to the `dbGetQuery` function [package:DBI]. For details please see `dbGetQuery` function [package:DBI].

```
#####
#Short example
#
library(RRootDetection)
file <- system.file("extdata/example.db", package = "RRootDetection")

#Setting Connection to database file
RD.load(file)

#To print connection details
RD.state

tmp_query = "select * from images"
#tmp_connection = RD.state[[2]]

#To perfom query as SQL statement on the RootDetection database
#
#Equals: dbGetQuery(tmp_connection,tmp_query)[1,]
#
RD.select(tmp_query)[1,]
```

For related topics see also:

```
%current function
help("RD.select")
%additional functions set by \seealso
help("dbGetQuery")
help("dbConnect")
help("RD.load")
help("RD.list.directories")
help("RD.list.images")
help("RD.list.roots")
help("RD.list.label")
```

4.2 Extract path of directories stored in a RootDetection database file

`RD.list.directories`: Returns the path of directories (folders) which were analyzed with RootDetection and stored in a RootDetection database file. Uses SQLite select: "select distinct dirname from images" to extract directories from RootDetection database file.

```
#####
#Short example
#
library(RRootDetection)
file <- system.file("extdata/example.db", package = "RRootDetection")
#Setting Connection to database file
RD.load(file)

#Extract directories from database file
#Equals: RD.select("select distinct dirname from images")
RD.list.directories()

#Select one directory for further analysis
RD.list.directories()[1]
```

For related topics see also:

```
%current function
help("RD.load")
%additional functions set by \seealso
help("dbConnect")
```

4.3

4.4

4.5

5 Data parsing with *RRootDetection*

5.1

5.2

6 Data visualization with *RRootDetection*

6.1 Barplot of mean root length values

`RD.plot.bar`: This function produces barplots from root length values from a matrix generated with the `RD.list.roots()` function as input. It plots the mean root length values for the groups in that matrix plus the standard error of the mean or the standard deviation ('error.bars'). The mean values can be sorted to get an overview of the maximal and minimal mean root length values ('sort'). All the data used for plotting the barplots can also be returned as a summary ('return.summary'). Optional the root length values can be processed with the `remove.sd()` function to remove outliers within certain thresholds ('remove.outliers'). If roots were measured with RootDetection on one picture in different image regions they can be combined so that all roots on one image are handled as one group ('by.image'). It is also possible to combine roots which share the same label definition ('by.label').

```
> #####
> #Short example
> #
> library(RRootDetection)
> file <- system.file("extdata/example.db", package="RRootDetection")
> #Setting Connection to database file
> RD.load(file)
> #Select one directory for further analysis
> tmp_dir <- RD.list.directories()[1]
> #Extract root data from the specified directory using default settings for
> #
> #For the RD.list.roots() options please see 'help("RD.list.roots")'
> #tmp_root_directory <- RD.list.roots(directory=tmp_dir, image = NULL, num =
```

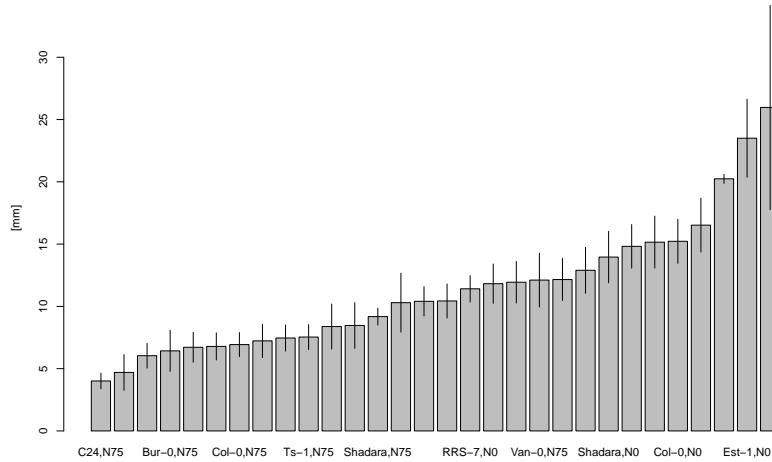


Figure 1: BARPLOT1.

```

>   #
>   tmp_root_directory <- RD.list.roots(directory=tmp_dir)
>   #Plot a barplot from the tmp_root_directory matrix using default settings
>   RD.plot.bar(tmp_root_directory)

#####
#Short example
#
library(RRootDetection)
file <- system.file("extdata/example.db", package="RRootDetection")
#Setting Connection to database file
RD.load(file)

#Select one directory for further analysis
tmp_dir <- RD.list.directories()[1]

#Extract root data from the specified directory using default settings for the
#
#For the RD.list.roots() options please see 'help("RD.list.roots")'
#tmp_root_directory <- RD.list.roots(directory=tmp_dir, image = NULL, num = NUL
#
#tmp_root_directory <- RD.list.roots(directory=tmp_dir)

```

```

#Plot a barplot from the tmp_root_directory matrix using default settings for -
RD.plot.bar(tmp_root_directory)

#####
#Plot a barplot from the tmp_root_directory matrix using custom settings for t
#
#RD.plot.bar(tmp_root_directory, scale = TRUE, by.image = FALSE, by.label = FA

#plot pixel lengths (scale = FALSE)
RD.plot.bar(tmp_root_directory, scale = FALSE)

#####
#standard deviation (error.bars = "sd")
RD.plot.bar(tmp_root_directory, error.bars = "sd")

#####
#ggroup by label (by.label = TRUE)
RD.plot.bar(tmp_root_directory, by.label = TRUE)

#####
#plot the data unsorted (sort = FALSE)
RD.plot.bar(tmp_root_directory, sort = FALSE)

#####
#return the mean root length data as a summary (return.summary = TRUE)
RD.plot.bar(tmp_root_directory, return.summary = TRUE)

#####
#remove outliers from the data (remove.outliers = TRUE) using the standard set
RD.plot.bar(tmp_root_directory, remove.outliers = TRUE)

#####
#remove outliers from the data with custom settings (remove.outliers = TRUE, so
RD.plot.bar(tmp_root_directory, remove.outliers = TRUE, sd.factor = 3, thresho

#####
#define other plot functions like the plot title
RD.plot.bar(tmp_root_directory, main = "plot title")

#####

```

```

#Optional one can use first the 'return.summary = TRUE' option and then plot the
#
tmp_root_directory.summary <- RD.plot.bar(tmp_root_directory, return.summary = TRUE)
barplot(unlist(tmp_root_directory.summary[, "mean"]))
barplot.pos <- barplot(unlist(tmp_root_directory.summary[, 1]), plot = FALSE)
barplot.mean <- unlist(tmp_root_directory.summary[, "mean"])
barplot.sd <- unlist(tmp_root_directory.summary[, "sd"])
barplot.n <- unlist(tmp_root_directory.summary[, "n"])
barplot.sem <- barplot.sd/sqrt(barplot.n)
arrows(barplot.pos, barplot.mean-barplot.sd, barplot.pos, barplot.mean+barplot.sd)
arrows(barplot.pos, barplot.mean-barplot.sem, barplot.pos, barplot.mean+barplot.sem)

#####
#To output barplots as jpeg, png, pdf or postscript please use the standard R functions
#
output_file <- "tmp.pdf"
pdf(file = output_file)
RD.plot.bar(tmp_root_directory)
dev.off()

```

For related topics see also:

```

%current function
help("RD.plot.bar")
%additional functions set by \seealso
help("RD.list.roots")
help("extract.len")
help("remove.sd")
help("barplot")
help("png")
help("jpeg")
help("pdf")
help("postscript")

```

References