

sprof internal

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Type Package

Title Profiling, timing and optimization utilitites

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Description Support utilities for profiling and dynamic code analysis.

License GPL-2 | GPL-3

Suggests wordcloud, timeit

URL <http://sintro.r-forge.r-project.org>

ByteCompile FALSE

KeepSource TRUE

BuildVignettes FALSE

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sprof-package

sprof: Analysis of R profiles

Description

Profiling, timing and optimization utilitites

Details

Package: sprof
 Type: Package
 Version: 0.0-5
 Date: 2013-07-23
 License: GPL-2 | GPL-3

[readRprof\(\)](#) reads a profile file from [Rprof\(\)](#) or other profilers and returns a composite structure of class sprof. The basic components of sprof are (conceptually) four data frames

info	general information and summaries
nodes	node specific information
stacks	node specific information. Stacks are random snapshots from the program execution, possibly including side in
profiles	collected records of a profile, encoded as references to stacks

To create a profile on the fly, use [sampleRprof](#).

To import profile information written by [Rprof](#) or other profilers, use [readRprof](#).

For sprof, the usual access functions are supported.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

Examples

```
## Not run:
data(sprof01lm)
str(sprof01lm)
plot(sprof01lm)
```

```
## End(Not run)
```

adjacency	<i>sprof to adjacency matix</i>
-----------	---------------------------------

Description

convert node information from a sprof structure to adjacency matrix.

Usage

```
adjacency(sprof, keep.names = TRUE, rmzero=TRUE)
```

Arguments

sprof	a sprof structure.
keep.names	boolean. Copy node names as row- and column names.
rmzero	boolean. Remove nodes with no edges.

Value

a correspondence matrix

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

References

See the vignette of package sprof.

Examples

```
data(sprof01lm)
adjacency(sprof01lm)
```

barplot_s	<i>Sorted Bar Plots</i>
-----------	-------------------------

Description

Creates a sorted bar plot with vertical or horizontal bars.

Usage

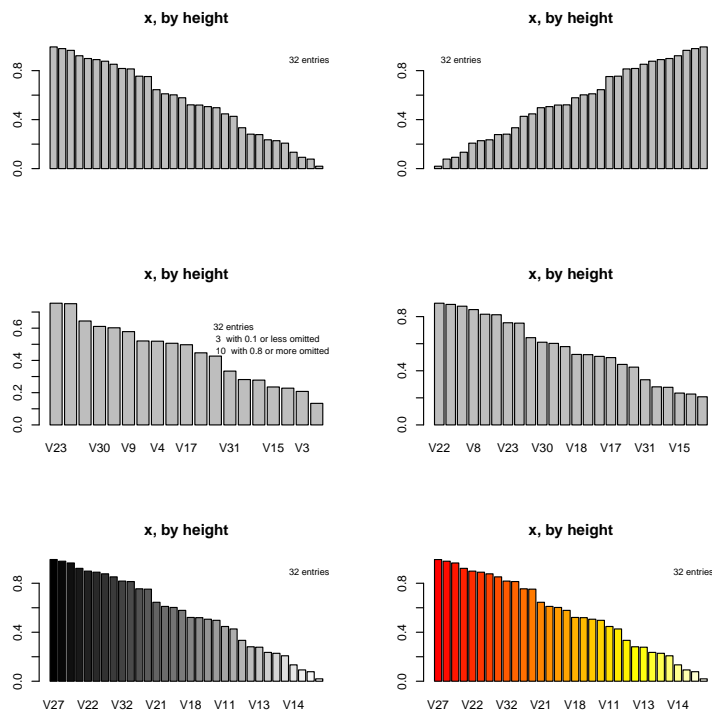
```
barplot_s(height,
sort_by, decreasing = TRUE,
lowtrim, hightrim, trimlegend = TRUE,
col, coli, colfun,
main, ...)
```

Arguments

height	either a vector or matrix of values describing the bars which make up the plot. See barplot .
sort_by	a variable to sort by. Defaults to height.
decreasing	boolean. Sorting direction.
lowtrim	A optional lower trim value. Observations with sort_by values up to lowtrim are discarded.
hightrim	A optional upper trim value. Observations with sort_by values from lowtrim are discarded.
trimlegend	Boolean. Show a legend about trimmed values.
col	a vector of colors for the bars or bar components. By default, grey is used if height is a vector, and a gamma-corrected grey palette if height is a matrix.
coli	An index into the col table, based on original sorting.
colfun	A function to generate a col palette. grey is rescaled to 1..n.
main	overall title for the plot
...	Passed to barplot

Details

To come. Plots are from this collection:



Value

Invisible: A data frame with components

x	height
perm	the permutation applied
coli	the colour index applied
col	optional: the colours selected

Note

Part of this could go to the R base function [barplot](#).

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

See Also

[barplot](#)

Examples

```
x <- runif(10)
barplot_s(x)
rm(x)
```

list.as.matrix	<i>Convert list to matrix</i>
----------------	-------------------------------

Description

Convert list to matrix. List entries go to matrix columns, filled for equal length.

Usage

```
list.as.matrix(x, filler = NA)
```

Arguments

x	a list of numeric vectors.
filler	a value to be used as a filler

Value

A matrix with the values from x, filled to matrix shape.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

```
x <- list(x1=c(1,2,3),x2=3, x3=4:8)
list.as.matrix(x)
list.as.matrix(x,filler=0)
```

nodescloud	<i>Nodescloud of nodes from rprofile data</i>
------------	-----------------------------------------------

Show the nodes from a profile, with class encoded as colour and frequency encoded as size.

```
nodescloud(sprof, min.freq = 3, col)
```

sprof	A data structure as returned by readRprof .
min.freq	Minimum frequency to be included.
col	A colour palette.

Note: these figures may be outdated. Please run the examples.
Plots are from this collection:



Value

Used for the side effect of showing the plots.

Note

See the vignette of package sprof.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

Examples

```
## Not run:
data(sprof01lm)
nodescloud(sprof01lm)

## End(Not run)
```

plot.sprof	<i>plot for profiles</i>
------------	--------------------------

Description

plot a plot for the output of class scode.

Usage

```
## S3 method for class 'sprof'
plot(x, ...)
```

Arguments

x	A data structure as returned by readRprof .
...	further arguments passed to or from other methods.

Value

subject to change

Note

See the vignette for in-context explanations.
Displays of the graph structure are given in the vignette.

References

<http://sintro.r-forge.r-project.org/>

See Also

[summaryRprof](#)
[plot_profiles](#)
[plot_nodes](#) [plot_stacks](#)

Examples

```
data(sprof01lm)

oldpar <- par(mfrow=c(2,2))
plot_nodes(sprof01lm)
par(oldpar)

oldpar <- par(mfrow=c(2,2))
plot_stacks(sprof01lm)
par(oldpar)

oldpar <- par(mfrow=c(2,2))
plot_profiles(sprof01lm)
par(oldpar)
```

plot_nodes	<i>Plot profiling information on node level.</i>
------------	--------------------------------------------------

Description

Various plots of a profile.

Usage

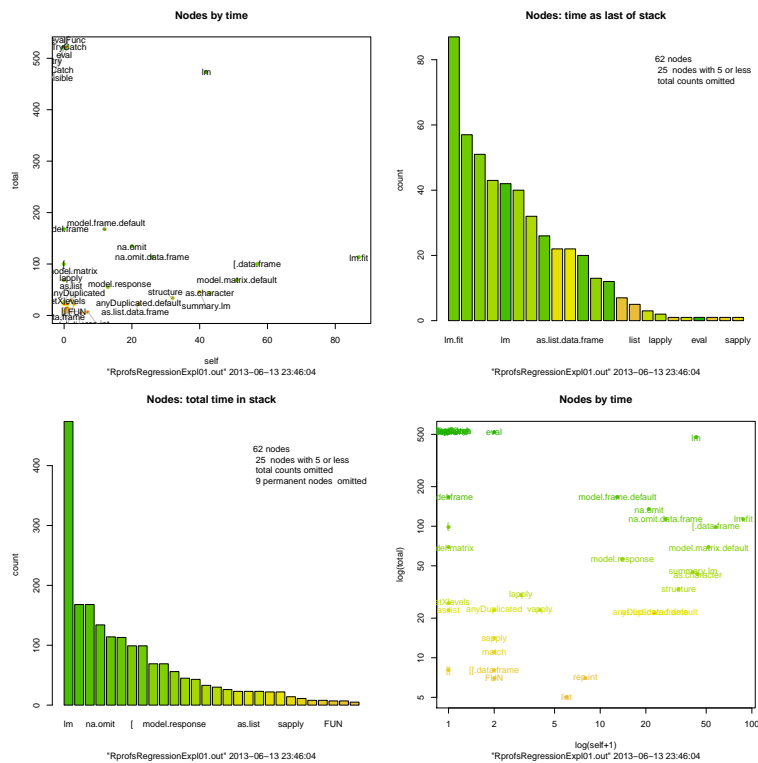
```
plot_nodes(x, which = c(1L, 2L, 3L, 4L), col = NULL,
ask = prod(par("mfcol")) < length(which) && dev.interactive(),
src = NULL, mincount = 5, ...)
```

Arguments

x	preferably a sprof object. Other data structures may be extended
which	Selector of plots to show.
col	Colour table
ask	boolean. Ask for a new page?
src	String to be used as source identifier.
mincount	minimum total frequency count for node to be shown in barcharts.
...	passed.

Details

Plots are from this collection:

**Value**

To come.

Note

See the vignette of package sprofr.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

References

See the vignette of package `sprof`.

See Also

See Also as [plot.sprof](#), ~~~

Examples

```
data(sprof01lm)
oldpar <- par(mfrow=c(2,2))
plot_nodes(sprof01lm)
par(oldpar)
```

plot_profiles

Plot profiling information on profile level.

Description

Various plots of a profile.

Usage

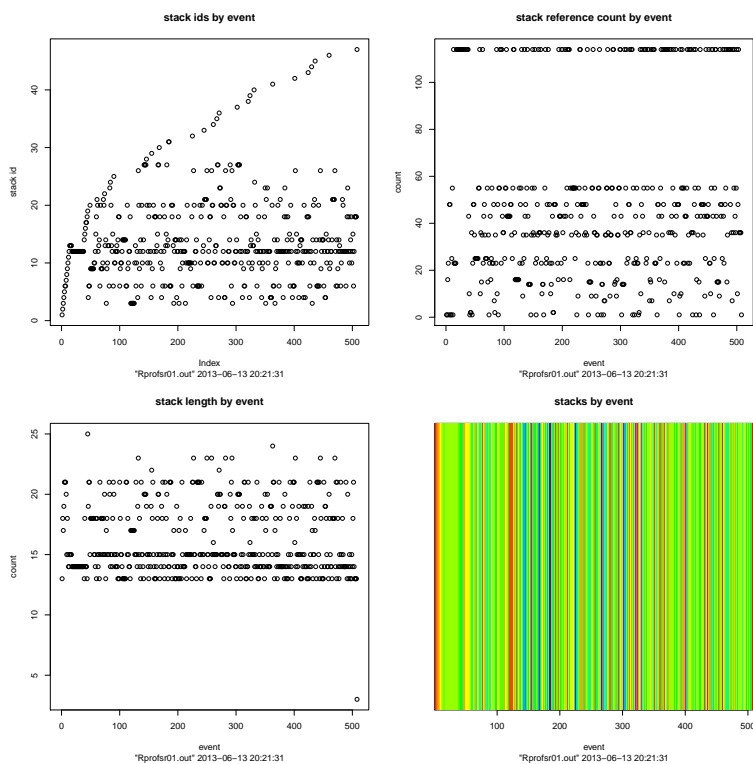
```
plot_profiles(x, which = c(1L, 2L, 3L, 4L), col,
ask = prod(par("mfcol")) < length(which) && dev.interactive(),
src = NULL, ...)
```

Arguments

x	preferably a sprof object. Other data structures may be extended
which	Selector of plots to show.
col	Colour table
ask	boolean. Ask for a new page?
src	String to be used as source identifier.
...	passed.

Details

Plots are from this collection:



Note

See the vignette of package sprof.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

References

See the vignette of package sprof.

See Also

See Also as [plot.sprof](#), ~~~

Examples

```
data(sprof01lm)
oldpar <- par(mfrow=c(2,2))
plot_profiles(sprof01lm)
par(oldpar)
```

plot_stacks

Plot profiling information on stack level.

Description

Various plots of a profile.

Usage

```
plot_stacks(x, which = c(1L, 2L), ask = prod(par("mfcol")) < length(which) && dev.interactive(), src = NULL)
```

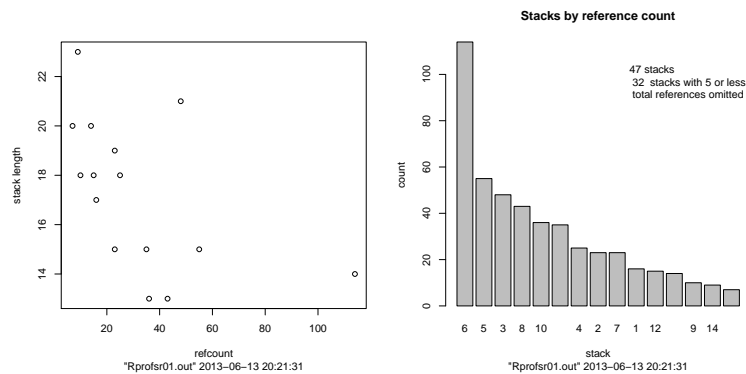
Arguments

x	preferably a sprof object. Other data structures may be extended
which	Selector of plots to show.
ask	boolean. Ask for a new page?
src	String to be used as source identifier.
mincount	minimum total frequency count for stack to be shown in barcharts.
...	passed.

Details

Note: these figures may be ourdated. Please run the examples.

Plots are from this collection:



Value

To come.

Note

See the vignette of package sprof.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

References

See the vignette of package sprof.

See Also

See Also as [plot.sprof](#), ~~~

Examples

```
data(sprof01lm)
oldpar <- par(mfrow=c(2,2))
plot_stacks(sprof01lm)
par(oldpar)
```

print.sprof	<i>print for profiles</i>
-------------	---------------------------

Description

Print a print for the output of class scode.

Usage

```
## S3 method for class 'sprof'  
print(x, ...)
```

Arguments

x	A data structure as returned by readRprof .
...	further arguments passed to or from other methods.

Value

None.

References

<http://sintro.r-forge.r-project.org/>

See Also

[summaryRprof](#) [plot.sprof](#)

Examples

```
data(sprof01lm)  
print(sprof01lm)
```

print_profiles	<i>Print profile information</i>
----------------	----------------------------------

Description

Print profile information.

Usage

```
print_profiles(x)
```

Arguments

x	a sprof data structure.
---	-------------------------

Value

none

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

Examples

```
data(sprof01lm)
print_profiles(sprof01lm)
```

profiles_matrix	<i>Extract a node incidence matrix from profile information.</i>
-----------------	------------------------------------------------------------------

Description

Extract a node incidence matrix from profile information.

Usage

```
profiles_matrix(x)
```

Arguments

x an sprof data structure.

Value

an incidence matrix, NA filled.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

Examples

```
data(sprof01lm)
smat <- profiles_matrix(sprof01lm)
image(smat)
```

readRprof

Read Rprof Output files and Stack Logs

Description

Read a log of stack entries, such as the output of the [Rprof](#) function, and generate a more accessible representation.

Usage

```
readRprof(filename = "Rprof.out", chunksize = 5000,
interval = 0.02,
head = c("auto", "none", "Rprofmem"),
id = NULL)
```

Arguments

filename	Name of a file produced by <code>Rprof()</code> .
chunksize	Number of lines to read at a time.
interval	Real: time interval between samples, in s.
head	<code>c("auto", "none", "Rprofmem")</code> to interpret control information as provided by <code>Rprof</code> or <code>Rprofmem</code> . See details.
id	An optional identification string. Defaults to filename and date.

Details

This function reads a log file of stacks, one stack snapshot per line, stack entries separated by space.

As profiling output file could be very large, it is read in blocks of `chunksize` lines. Increasing `chunksize` will make the function run faster if sufficient memory is available.

The input format is controlled by the `head` argument. Format "auto" tries to detect control lines as interspersed by `Rprof`. These lines are not included in the output.

"none" ignores all control information and includes these lines as strange stacks.

"Rprofmem" isolates headers as provided by `Rprofmem`. new page entries are encoded as malloc requests with length 0.

Value

This data structure is subject to change.

Temporarily: A list with components

firstline	A verbatim copy of the first line of the input file. Typically this contains timing or formatting information.
nodes	A vector of node names. This may include stray entries from interspersed lines.
stacks	A vector of unique stacks found in input, stored as verbatim copies.
stacksrenc	A list of unique stacks in top down order (top first), encoded as vectors or references to stacks.
data	A vector encoding the data file as referenes to stacks.

timesRLE	Vector of sampling intervals, in milliseconds. Run-length encoded.
freq	A frequency table summarizing data.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>, based on the code of [summaryRprof](#)

References

<http://sintro.r-forge.r-project.org/>

See Also

[summaryRprof](#)

[summaryRprof](#)

[flatProfile](#) in library(proftools).

{parse_rprof} in library(profr).

The chapter on “Tidying and profiling R code” in “Writing R Extensions” (see the ‘doc/manual’ subdirectory of the R source tree).

[Rprof](#) is a sampling profiler.

[tracemem](#) traces copying of an object via the C function duplicate.

[Rprofmem](#) is a non-sampling memory-use profiler.

<http://developer.r-project.org/memory-profiling.html>

Examples

```
## Not run:
## Rprof() is not available on all platforms
profintrval <- 0.001
simruns <- 100

n <- 10000
x <- runif(n)
y0 <- 2 + 3 * x

sinknull <- textConnection(NULL, "w"); sink(sinknull)
Rprof(tmp <- tempfile(), interval = profintrval)
for (i in 1:simruns) {y <- y0 + rnorm(n); xxx<- summary(lm(y~x))}
Rprof()

Rprof_out <- readRprof(tmp)

unlink(tmp)
sink(); close(sinknull)

str(Rprof_out)

## End(Not run)
```

rrle	<i>Recursive run length encoding.</i>
------	---------------------------------------

Description

Encode a matrix as run-length, top down. Encoding respects previous runs, e.g line 2 encodes rns in each run of line 1.

Usage

```
rrle(x)
```

Arguments

x a matrix.

Value

list of run length encoded lines

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

See Also

[rrleb](#), [~~~](#)

Examples

```
x <- matrix(c(
  1,1,1,2,2,
  3,3,4,4,4,
  5,5,6,6,7,
  8,9,9,0,0
),nrow=4, ncol =5, byrow=TRUE)
xrrle <- rrle(x)
xrrle

t(sapply(xrrle, inverse.rle))
```

rrleb	<i>Recursive run length encoding bottom up.</i>
-------	-------------------------------------------------

Description

Encode a matrix as run-length, bottom up. Encoding respects previous runs, e.g line n-1 encodes runs in each run of line n.

May be removed.

Usage

```
rrleb(x)
```

Arguments

x a matrix.

Value

list of run length encoded lines

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

See Also

[rle](#), [~~~](#)

Examples

```
x <- matrix(c(
  3,3,4,4,4,
  5,5,6,6,7,
  8,9,9,0,0,
  1,1,1,2,2
),nrow=4, ncol =5, byrow=TRUE)
xrrleb <- rrleb(x)
xrrleb

t(sapply(xrrleb, inverse.rle))
```

sampleRprof	<i>Get a sample profile</i>
-------------	-----------------------------

Description

Get a sample profile and return it as a sprof data structure.

Usage

```
sampleRprof(expr, runs = NULL, gcFirst = TRUE, interval = 0.001, ...)
```

Arguments

expr	an expression to be profiled.
runs	nr of runs to profile.
gcFirst	boolean. Profile GC.
interval	Real: time interval between samples, in s.
...	additional parameters, passed to Rprof

Value

A list of type sprof

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

References

<http://sintro.r-forge.r-project.org/>

Examples

```
res_lm <- sampleRprof(for (i in 1:1000) yy<- lm(runif(1000)~rnorm(1000)), runs=100)
```

shownodes	<i>Show node information from a profile</i>
-----------	---------------------------------------------

Description

Plot node information from a profile in various plots.

Usage

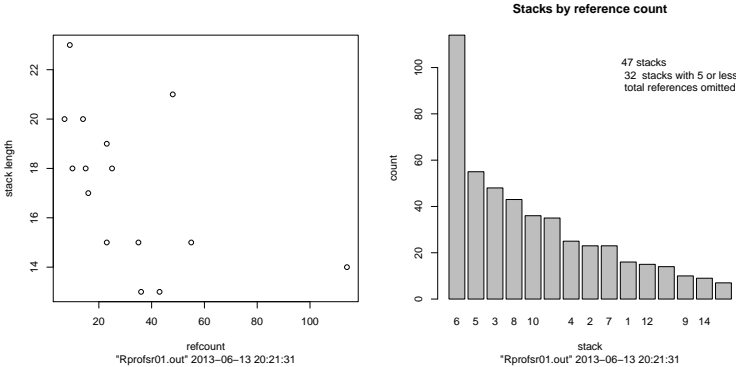
```
shownodes(sprof, col)
```

Arguments

sprof	A data structure as returned by readRprof .
col	A colour palette for the plots.

Details

Note: these figures may be ourdated. Please run the examples.
Plots are from this collection:



Value

Used for the side effect of showing the plots.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

Examples

```
## Not run:
data(sprof01lm)
shownodes(sprof01lm)

## End(Not run)
```

sprof01lm	<i>sprof sample data</i>
-----------	--------------------------

Description

An example data set for the functions in package sprof.

Usage

```
data(sprof01lm)
```

Format

The format is: A List of 4 \$ info : 'data.frame': 1 obs. of 8 variables: \$ nodes : 'data.frame': 62 obs. of 5 variables: \$ stacks : 'data.frame': 50 obs. of 7 variables: \$ profiles: List of 4

References

See the vignette of package sprof.

Examples

```
data(sprof01lm)
str(sprof01lm)
plot(sprof01lm)
```

stackstoadj	<i>Stacks to adjacency matrix</i>
-------------	-----------------------------------

Description

convert stack information to adjacency matrix

Usage

```
stackstoadj(xstacks, xfreq, maxnode)
```

Arguments

xstacks	list of stack ids
xfreq	vector of frequencies or weights
maxnode	maximum of nodes (maybe higher then in stacks)

Value

the adjacency matrix

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

Examples

```
#
```

str_prof	<i>str for sprof objects</i>
----------	------------------------------

Description

str for sprof objects

Usage

```
str_prof(x)
```

Arguments

x	an sprof object
---	-----------------

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

Examples

```
data(sprof01lm)
str__prof(sprof01lm)
```

summary.sprof

Summary for profiles

Description

Print a summary for the output of class scode.

Usage

```
## S3 method for class 'sprof'
summary(object, ...)
```

Arguments

object	A data structure as returned by readRprof .
...	further arguments passed to or from other methods.

Value

None.

References

<http://sintro.r-forge.r-project.org/>

See Also

[summaryRprof](#)

Examples

```
## Not run:
## Rprof() is not available on all platforms
profininterval <- 0.001
simruns <- 100

n <- 10000
x <- runif(n)
y0 <- 2 + 3 * x

sinknull <- textConnection(NULL, "w"); sink(sinknull)
Rprof(tmp <- tempfile(), interval = profinterval)
for (i in 1:simruns) {y <- y0 + rnorm(n); xxx<- summary(lm(y~x))}
Rprof()
```

```

Rprof_out <- readProf(tmp)

unlink(tmp)
sink(); close(sinknull)

summary(Rprof_out)

## End(Not run)

```

summary_terminals	<i>Tabulate leaf nodes</i>
-------------------	----------------------------

Description

Tabulate leaf nodes

Usage

```
summary_terminals(x)
```

Arguments

x an sprof data structure.

Value

A table of frequencies, bystack.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

Examples

```

data(sprof01lm)
summary_terminals(sprof01lm)

```

updateRprof	<i>Update statistics and tables in a sprof object</i>
-------------	-------------------------------------------------------

Description

Synchronize information from profiles and stack tables, and update statistics.

Usage

```
updateRprof(sprof)
```

Arguments

sprof A data structure as returned by [readRprof](#).

Value

An updated sprof data structure.

Note

See the vignette of package sprof.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

writeRprof	<i>Write profile data</i>
------------	---------------------------

Description

Write a profile data file from a sprof data structure.

Usage

```
writeRprof(sprof, filename = "Rprof.Out")
```

Arguments

sprof a data structure from package sprof
 filename The file to be used for exporting the profiling results.

Details

writeRprof only writes the stack entries for the profile.

This can be used to export information after preprocessing with sprof to some package designed for Rprof output.

Value

An invisible list with the profile entries, headers removed.

Note

See the vignette for in-context explanations.

Displays of the graph structure are given in the vignette.

Author(s)

Günther Sawitzki <gsawitzki@r-forge.r-project.org>

References

<http://sintro.r-forge.r-project.org/>

Examples

```
## Not run:  
data(sprof01lm)  
writeRprof(sprof01lm)  
  
## End(Not run)
```

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