sprof internal

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Type Package

Title Profiling, timing and optimization utilitites

Version 0.0-6

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Author Günther Sawitzki

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Description Support utilities for profiling and dynamic code analysis.

License GPL-2 | GPL-3

Suggests wordcloud, timeit, RColorBrewer

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

ByteCompile FALSE

KeepSource TRUE

BuildVignettes FALSE

R topics documented:

sprof-package *sprof: Analysis of R profiles*

Description

Profiling, timing and optimization utilitites

Details

Package:	sprof
Type:	Package
Version:	0.0-6
Date:	2013-08-02
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.

Note

Version 0.0-6 is a clean-up version. Recommendations/requests for the interface definition are requested at this point.

Author(s)

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

Examples

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

## End(Not run)
```

---

adjacency *sprof to adjacency matix*

Description

convert node information from a sprof structure to adjacancy matrix.

Usage

```
adjacency(sprof, keep.names = TRUE, rmzero=TRUE,  no.name="<nn>")
```

Arguments

sprof	a sprof structure.
keep.names	boolean. Copy node names as row- and column names.
rmzero	boolean. Remove nodes with no edges.
no.name	If not null: replacement for empy strings as name.

Value

a correspondency matrix

Author(s)

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

References

See the vignette of package sprof.

Examples

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

barplot_s *Sorted Bar Plots*

Description

Creates a sorted bar plot with vertical or horizontal bars.

Usage

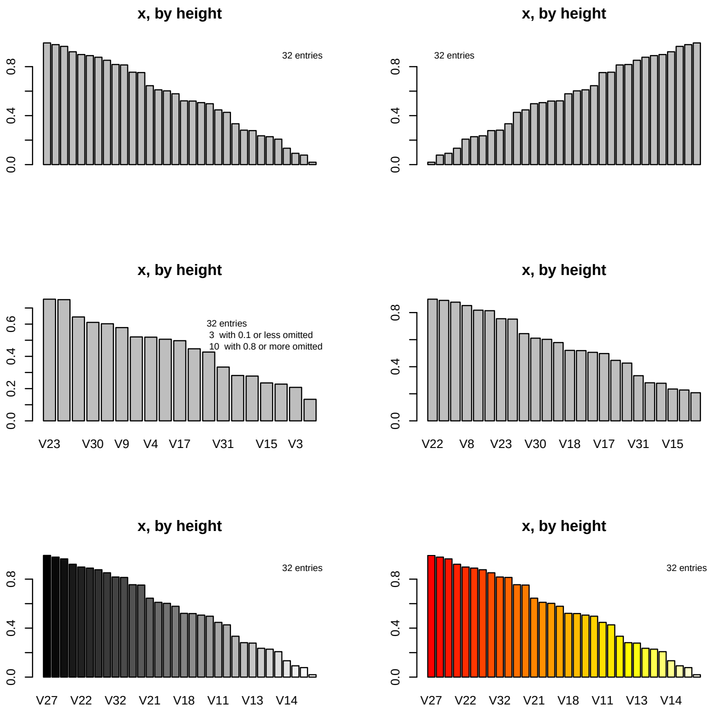
```
barplot_s(height,
sort_by,
decreasing = TRUE,
lowtrim, hightrim, trimlegend = TRUE,
col, coli, colfun,
main, ...)
```

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@users.r-forge.r-project.org>

See Also

barplot

Examples

```
x <- runif(100)

barplot_s(x)

x <- rnorm(100)
```

```
barplot_s(x, colfun=heat.colors, lowtrim=-1)

rm(x)
```

---

edgematrix *Expand adjacency information to an edge table*

Description

Expand adjacency information from an adjacency matrix or a sprof data structure to an edge table

Usage

```
edgematrix(data, counts = TRUE, na.rm = TRUE,  no.name="<nn>")
```

Arguments

data	an adjacency matrix or a sprof data structure.
counts	include a column of counts
na.rm	remove lines with a count NA.
no.name	If not null: replacement for empy strings as name.

Details

The adjacency matrix is flattened. Lines with a count zero are eliminated.

Value

A data frame.

from	Name of from node.
to	Name of to node.
count	optional. Frequencies of edges.

Author(s)

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

list.as.matrix *Convert list to matrix*

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@users.r-forge.r-project.org>

Examples

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

nodepackage *Find a package that may contain a node*

Description

getAnywhere() is used to look up x, and the package or namespace information is used to give a source package.

Usage

```
nodepackage(x)
```

Arguments

x	a character string or name, or a vector.

Details

There is no indication whether the information is from a namespace or from a package information.

No indication is given if multiple hits are encountered.

The information is based on the run time environment of this function. This may be different from the environment the object is taken from.

See the help information for getAnywhere() for more warnings.

Value

a character string or a vector of strings with the package names.

Author(s)

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

See Also

getAnywhere()

Examples

```
nodepackage("getAnywhere")
```

nodescloud *Nodescloud of nodes from profile data*

Description

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

Usage

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

Arguments

sprof	A data structure as returned by readRprof.
min.freq	Minimum frequency to be included.
icol	An index vector to colour palette. Defaults to sprof$nodes$icol.
col	A colour palette.

Details

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

Plots are from this collection:

tryCatchOne
tryCatch
try
doTryCatch
<Anonymous>
summary
lm
evalFunc
eval
Sweave
withVisible
tryCatchList
model.matrix.default
.getXlevels
[[.data.frame
anyDuplicated
rep.int
summary.lm
[
list
FUN
lm.fit
as.list.data.frame
sapply
as.list
as.character
match
na.omit
vapply
[[
lapply
na.omit.data.frame
[.data.frame
structure
model.frame
model.matrix
anyDuplicated.default
model.frame.default
model.response

Value

Used for the side effect of showing the plots.

Note

See the vignette of package sprof.

Author(s)

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

Examples

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

## End(Not run)
```

nodesprofile *Run length matrix*

Description

Extracts run length information from a sprof data structure with profiling information.

Usage

```
nodesprofile(sprof)
```

Arguments

sprof	a sprof data structure with profiling information.

Details

Run lenght counts by node, level and run length.

Value

counts[node, level, run length] .

Note

This expands a sparse matrix to full. Avoid to use it.

Author(s)

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

Examples

```
data(sprof01lm)
  str(nodesprofile(sprof01lm) )
```

nodesrunlength *Marginal information for run length from profile*

Description

Run length count, by node and run lenght, from profile.

Usage

```
nodesrunlength(sprof, clean=TRUE)
```

Arguments

sprof	a sprof data structure with profiling information.
clean	boolean.

Details

If clean=TRUE, zero results are removed and the nodes are sorted by average time.

If clean=TRUE, zero results and sorting are preserved. Trailing zero count nodes may have been lost in the process, and are added.

Value

A matrix count[node, run length] with additonal columns

nr_runs	sum of counts over all run lengths.
total_time	sum of count*run length
avg_time	total_time / count

Author(s)

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

Examples

```
data(sprof01lm)
  nodesrunlength(sprof01lm)
```

---

plot.sprof *plot for profiles*

Description

plot a plot for the output of class scode.

Usage

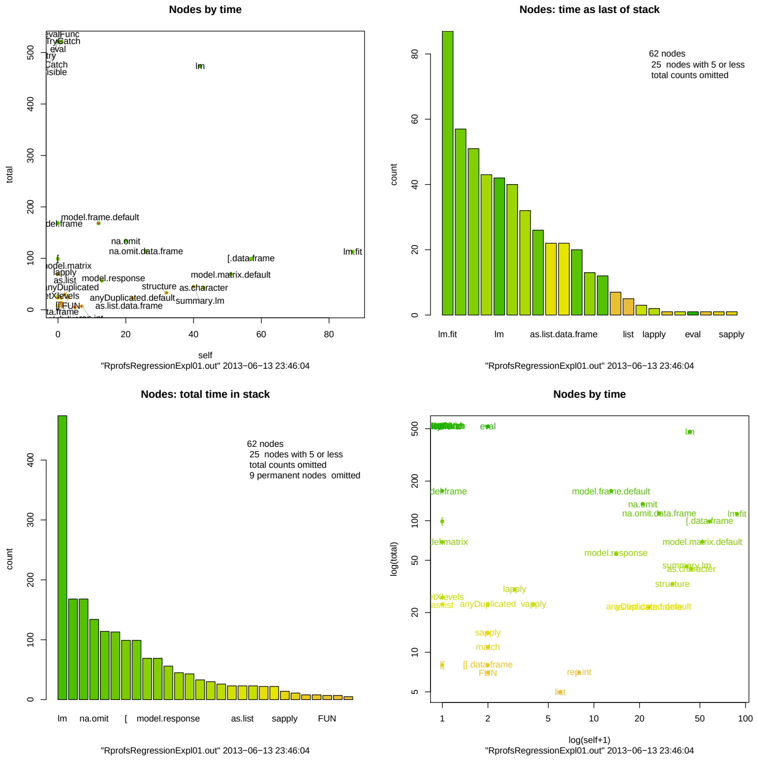
```
## S3 method for class 'sprof'
plot(x, ...)
```

Arguments

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

Details

These displays may be outdated. Please run the examples. Plots are from this collection:



Value

subject to change

Note

See the vignette for in-context explanations.

Displays of the graph structure are given in the vignette.

Author(s)

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

References

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

See Also

summaryRprof

plot_profiles

plot_nodes plot_stacks

Examples

```
data(sprof01lm)

oldpar <- par(mfrow=c(3,4))
plot.sprof(sprof01lm)
par(oldpar)
```

---

plot_nodes *Plot profiling information on node level.*

Description

Various plots of a profile.

Usage

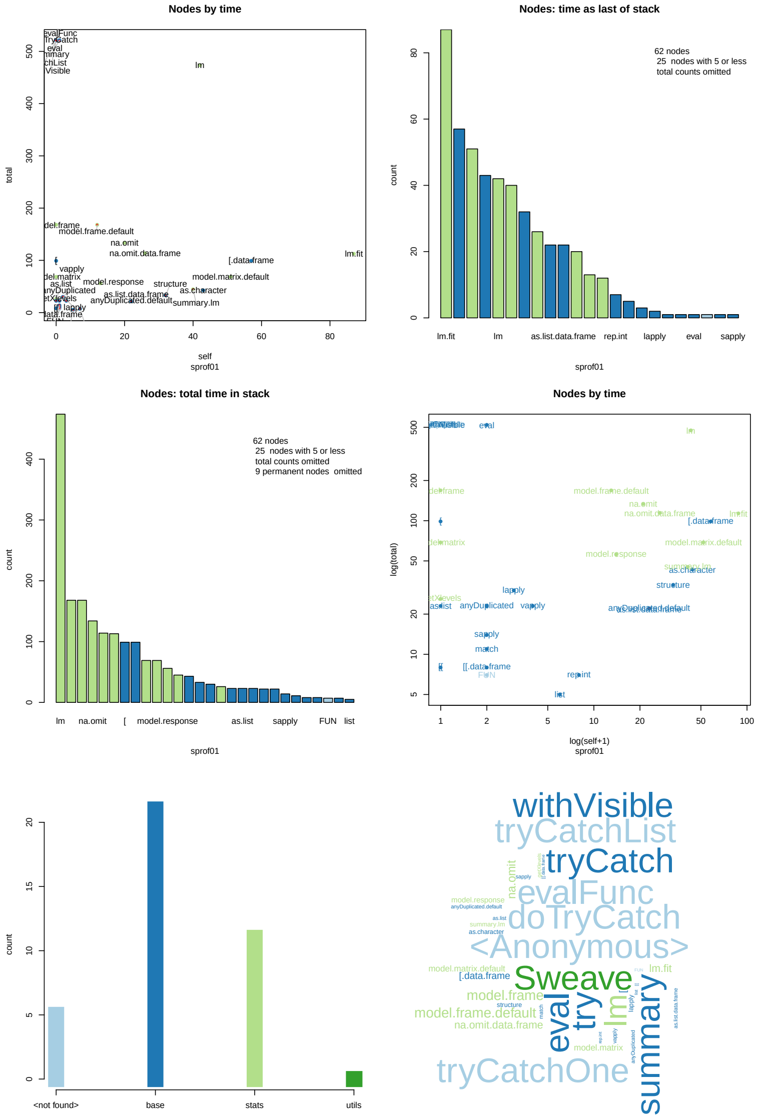
```
plot_nodes(x, which = c(1L, 2L, 3L, 4L), col = NULL,
ask = prod(par("mfcol")) < length(which) && dev.interactive(),
src = NULL, mincount = 5, horiz=FALSE, ...)
```

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.
horiz	draw horizontal bar plots.
...	passed.

Details

These displays may be outdated. Please run the examples. Plots are from this collection:



Value

To come.

Note

See the vignette of package sprof.

Author(s)

Günther Sawitzki <gsawitzki@users.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

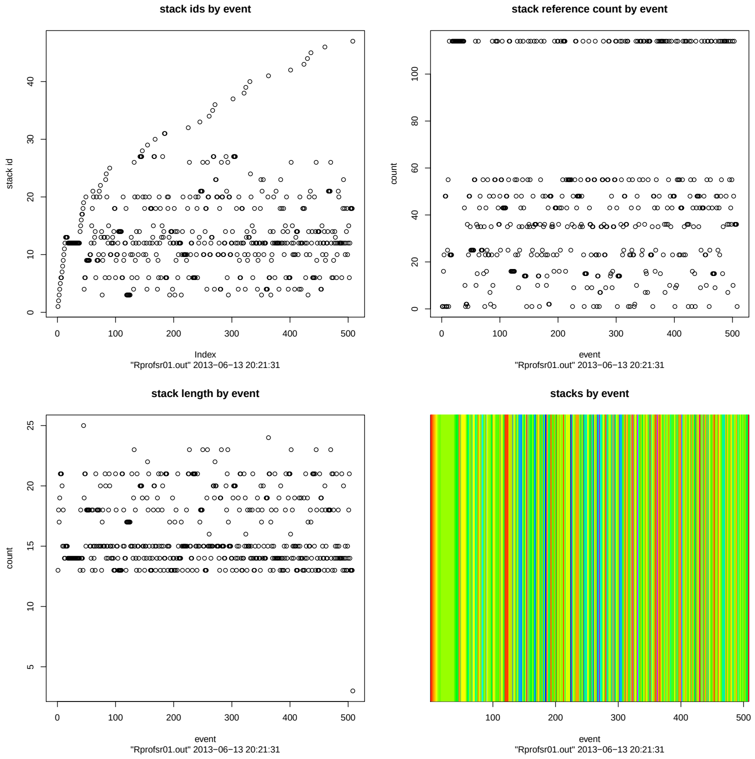
```
plot_profiles(x, which = c(1L, 2L, 3L, 4L), col,
ask = prod(par("mfcol")) < length(which) && dev.interactive(),
src = NULL, ...)
```

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@users.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, mincount = 5, horiz = FALSE, ...)
```

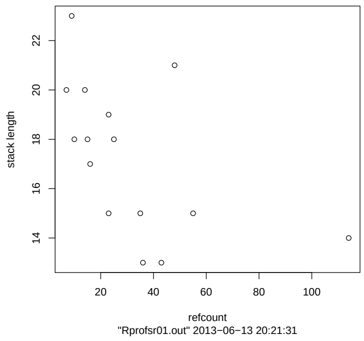
Arguments

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.
horiz	draw horizontal bar plots.
...	passed.

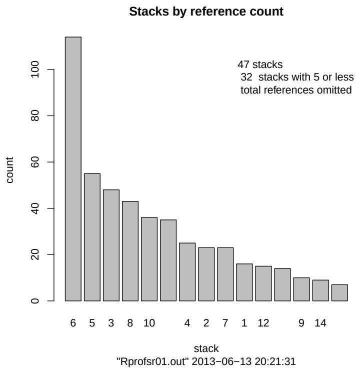
Details

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

Plots are from this collection:



"Rprofsr01.out" 2013−06−13 20:21:31



"Rprofsr01.out" 2013−06−13 20:21:31

Value

To come.

Note

See the vignette of package sprof.

Author(s)

Günther Sawitzki <gsawitzki@users.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 *print for profiles*

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.

Author(s)

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

References

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

See Also

summaryRprof plot.sprof

Examples

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

---

print_profiles *Print profile information*

Description

Print profile information.

Usage

```
print_profiles(x)
```

Arguments

x	a sprof data structure.

Value

none

Author(s)

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

Examples

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

---

profiles_matrix *Extract a node incidence matrix from profile information.*

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@users.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 Rprof().
chunksize	Number of lines to read at a time.
interval	Real: time interval between samples, in s.
head	c("auto", "none", "Rprofmem") to interpret control information as provided by Rprof or Rprofmem. 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" igores 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 interperspersed 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 miliseconds. Run-length encoded.
freq	A frequency table summarizing data.

Author(s)

Günther Sawitzki <gsawitzki@users.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
profinterval <- 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 <- readRprof(tmp)

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

str(Rprof_out)

## End(Not run)
```

---

rkindex *Index, based on rank.*

Description

Convert x to an index in $1...maxindex$

Usage

```
rkindex(x, maxindex = length(x), pwr = 1, ties.method = "random")
```

Arguments

x	A vector of data to covert.
maxindex	Maximum for result
pwr	See details.
ties.method	passed to rank.

Details

x is transformed to a rank scale, using ties.method. It is then rescaled to $[0,1]$, and (optionally) a power transfromation is applied. In visualisation terms, this is a gamma correction. The result is rescaled to 1 ... maxindex.

Value

A vector of rescaled values.

Author(s)

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

rrle *Recursive run length encoding.*

Description

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

Usage

```
rrle(x, collapseNA =FALSE)
```

Arguments

x	a matrix.
collapseNA	boolean. Collapse runs of NA.

Details

By default, different NA data are not considered equal. collapseNA collapses runs of NA in the result. For recursion however they are treated as singular data, not as runs. This may need discussion.

Value

list of run length encoded lines

Note

This could go to rle in package base.

The date structure used for rle would be better represented as a data.frame.

Run length and other compressions might be implemented in data.frames by default.

Author(s)

Günther Sawitzki <gsawitzki@users.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 *Recursive run length encoding bottom up.*

Description

Encode a matrix as run-length, bottom up. Encoding respects previous runs, e.g line n-1 encodes rns 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@users.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 *Get a sample profile*

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@users.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 *Show node information from a profile*

Description

Plot node information from a profile in various plots.

Usage

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

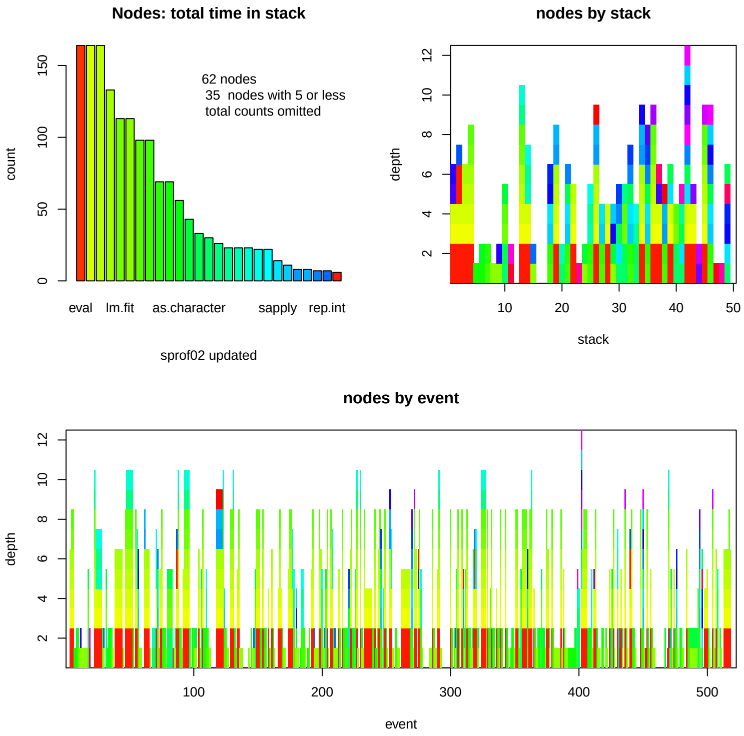
Arguments

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

Details

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

Plots are from this collection:



Value

Used for the side effect of showing the plots.

Author(s)

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

Examples

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

## End(Not run)
```

---

sprof01lm *sprof sample data*

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

Author(s)

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

References

See the vignette of package sprof.

Examples

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

---

stackstoadj *Stacks to adjacency matrix*

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@users.r-forge.r-project.org>

Examples

```
#
```

str_prof *str for sprof objects*

Description

str for sprof objects

Usage

```
str_prof(x)
```

Arguments

x	an sprof object

Author(s)

Günther Sawitzki <gsawitzki@users.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.

Author(s)

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

References

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

See Also

summaryRprof

Examples

```
## Not run:
## Rprof() is not available on all platforms
profinterval <- 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 *Tabulate leaf nodes*

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@users.r-forge.r-project.org>

Examples

```
data(sprof01lm)
summary_terminals(sprof01lm)
```

updateRprof *Update statistics and tables in a* sprof *obejct*

Description

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

Usage

```
updateRprof(sprof, id)
```

Arguments

sprof	A data structure as returned by readRprof.
id	optional. A replacement for the info$id string .

Value

An updated sprof data structure.

Note

See the vignette of package sprof.

Author(s)

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

writeRprof *Write profile data*

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 invisble 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@users.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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