

sprof internal

August 3, 2013

Encoding UTF-8

Type Package

Title Profiling, timing and optimization utilitites

Version 0.0-6

Date 2013-08-02

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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:

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| | |
|---------------|--------------------------------------|
| sprof-package | <i>sprof: Analysis of R profiles</i> |
|---------------|--------------------------------------|

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 matrix

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@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

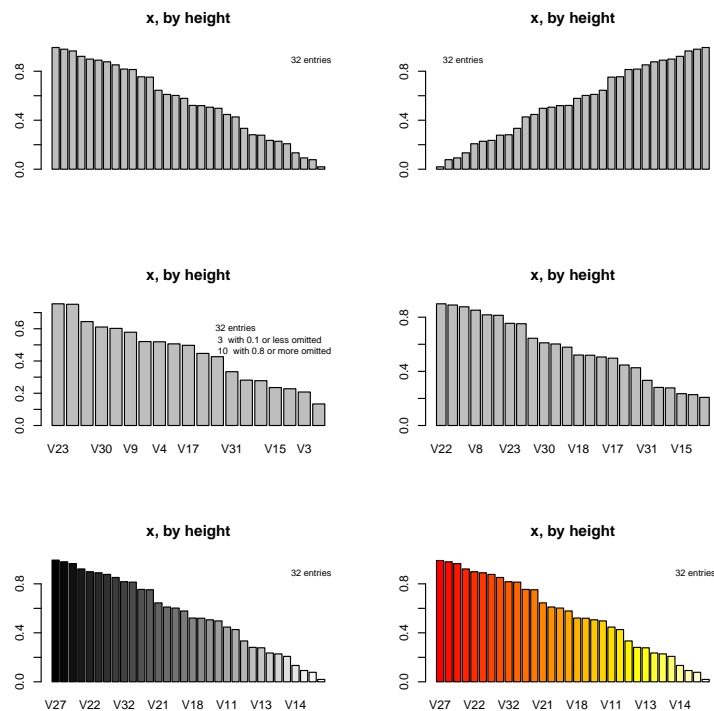
```
barplot_s(height,
sort_by,
decreasing = TRUE,
lowtrim, hightrim, trimlegend = TRUE,
col, coli, colfun,
main, ...)
```

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

rm(x)
```

| | |
|------------|--|
| edgematrix | <i>Expand adjacency information to an edge table</i> |
|------------|--|

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)
```

Arguments

| | |
|--------|--|
| data | an adjacency matrix or a sprof data structure. |
| counts | include a column of counts |
| na.rm | remove lines with a count NA. |

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 from node. |
| count | optional. Frequency of edge. |

Author(s)

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

| | |
|----------------|-------------------------------|
| 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@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 | <i>Find a package that may contain a node</i> |
|-------------|---|

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 | <i>Nodescloud of nodes from profile data</i> |
|------------|--|

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 <code>sprof\$nodes\$icol</code> . |
| col | A colour palette. |

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) )
```

plot.sprof

plot for profiles

Description

plot a plot for the output of class scode.

Usage

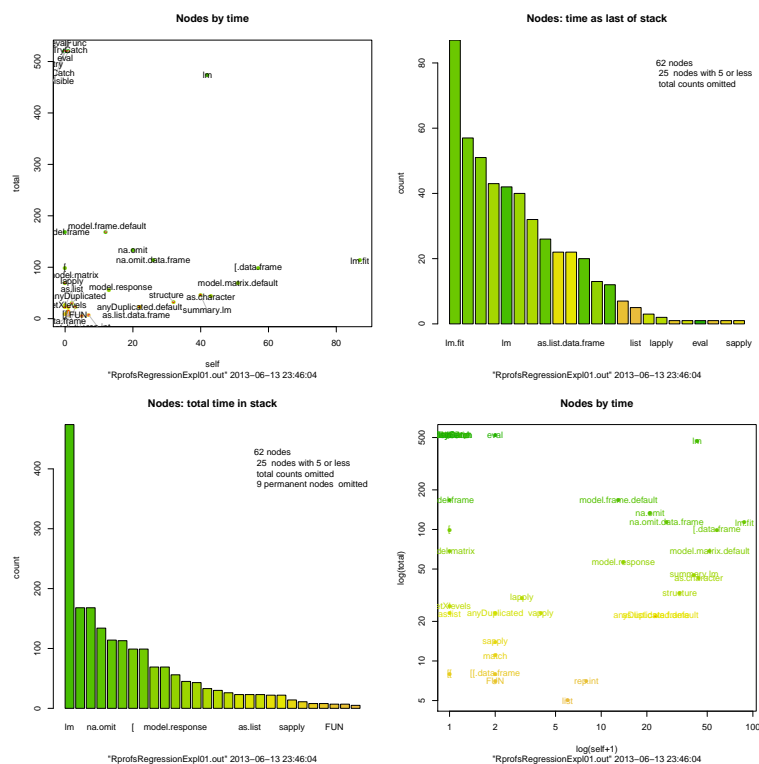
```
## S3 method for class 'sprof'
plot(x, ...)
```

Arguments

| | |
|-----|--|
| x | A data structure as returned by <code>readRprof</code> . |
| ... | 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, ...)

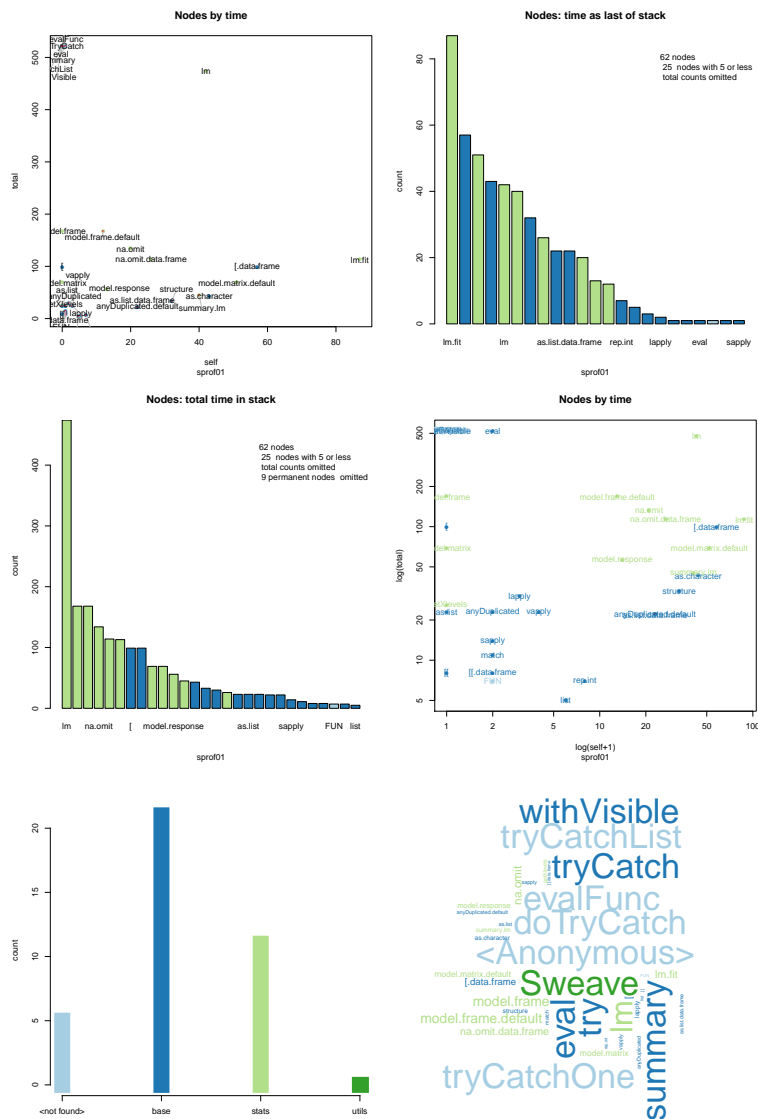
```

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 spraf.

Author(s)

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

References

See the vignette of package spraf.

See Also

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

Examples

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

| | |
|---------------|---|
| plot_profiles | <i>Plot profiling information on profile level.</i> |
|---------------|---|

Description

Various plots of a profile.

Usage

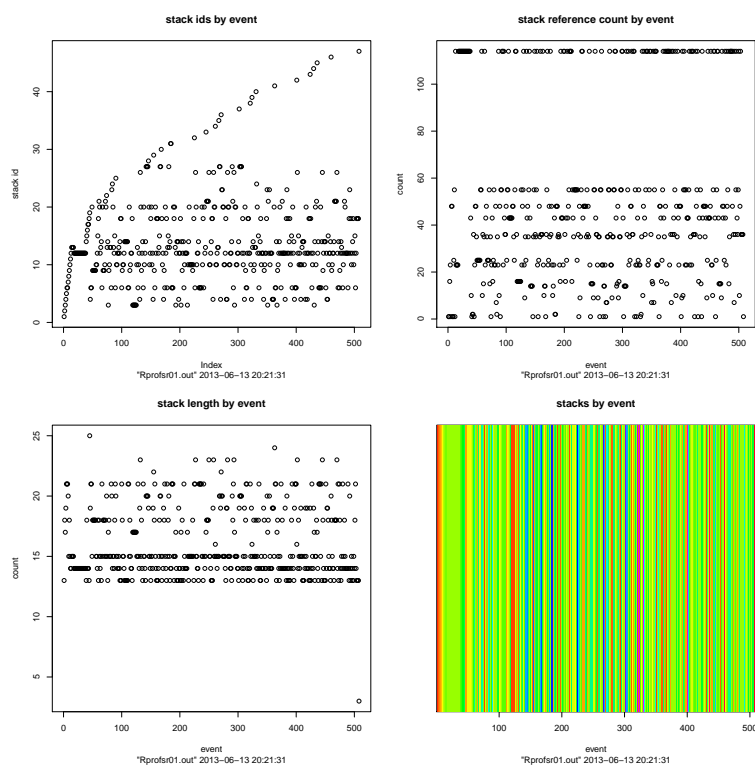
```
plot_profiles(x, which = c(1L, 2L, 3L, 4L), col,
ask = prod(par("mfcol")) < length(which) && dev.interactive(),
src = NULL, ...)
```

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, ...)
```

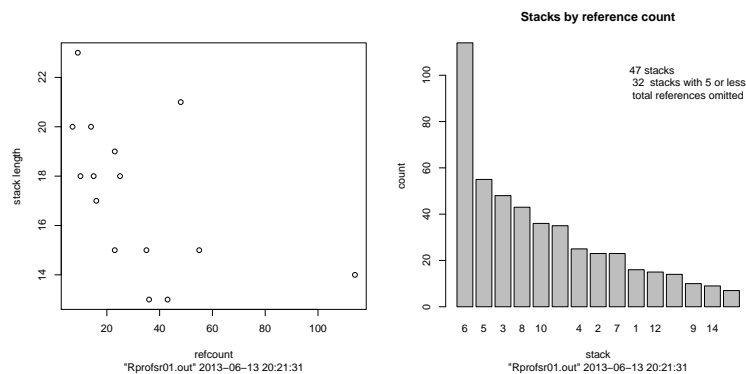
Arguments

| | |
|----------|---|
| 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:



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 | <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.

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 | <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@users.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@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 <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 references to stacks. |
| timesRLE | Vector of sampling intervals, in milliseconds. Run-length encoded. |
| freq | A frequency table summarizing data. |

Author(s)

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

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

str(Rprof_out)

## End(Not run)

```

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 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@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 | <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@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

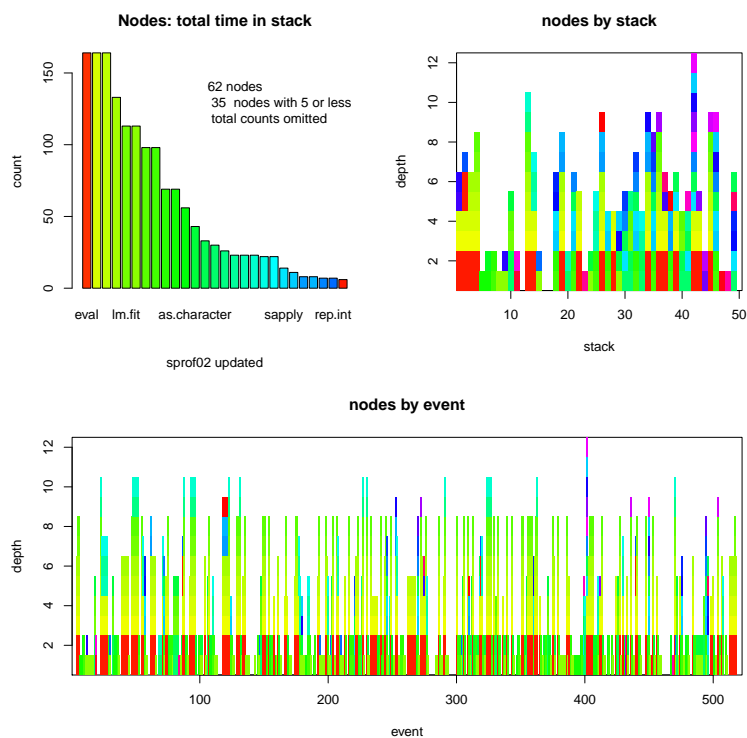
`sprof` A data structure as returned by [readRprof](#).

`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 | <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@users.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@users.r-forge.r-project.org>

Examples

```
data(sprof01lm)
str_prof(sprof01lm)
```

| | |
|---------------|-----------------------------|
| summary.sprof | <i>Summary for profiles</i> |
|---------------|-----------------------------|

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
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@users.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@users.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@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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