

# sprof reference

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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>

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**KeepSource** TRUE

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## R topics documented:

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

---

## Description

Profiling, timing and optimisation utilities

## Details

|          |               |
|----------|---------------|
| Package: | sprof         |
| Type:    | Package       |
| Version: | 0.0-6         |
| Date:    | 2013-08-15    |
| 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 information such as traces of the memory management. |
| 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, 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 empty strings as name. |

**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**

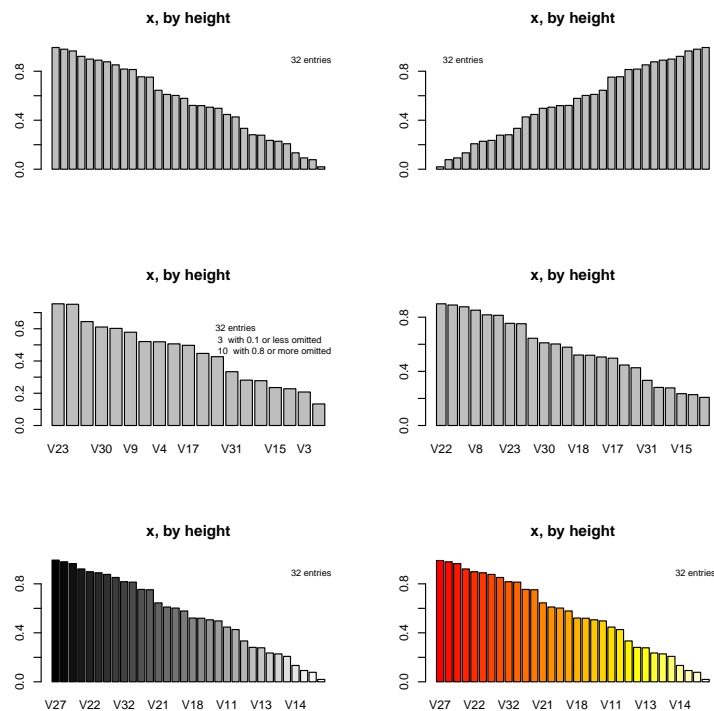
```
barplot_s(height,
sort_by,
decreasing = TRUE,
lowtrim, hightrim, trimlegend = TRUE,
col, coli, colfun,
main, ...)
```

**Arguments**

|            |                                                                                                                                                              |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|
| height     | either a vector or matrix of values describing the bars which make up the plot. See <a href="#">barplot</a> .                                                |
| 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](mailto: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, 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 empty 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, byrow=FALSE, filler = NA)
```

**Arguments**

|        |                                                                   |
|--------|-------------------------------------------------------------------|
| x      | a list of numeric vectors.                                        |
| byrow  | boolean. Arrange list entries as rows. Default is to use columns. |
| filler | a value to be used as a filler                                    |

**Value**

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

**To do**

Arguments should be as as.matrix.

A corresponding list.as.data.frame should be added for mixed types.

Name synchronisation/preservations should be added.

**Note**

This could go to as.matrix().

**Author(s)**

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

**See Also**

[as.matrix.](#)

**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 | <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

- sprofA data structure as returned by [readRprof](#).
- min.freqMinimum frequency of a node to be included.
- icolAn index vector to colour palette, encoding node class. Defaults to `sprof$nodes$icol`.
- colA colour palette.

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.

**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 length 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 | <i>Marginal information for run length from profile</i> |
|----------------|---------------------------------------------------------|

---

## Description

Run length count, by node and run length, 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 nodes with zero count may have been lost in the process, and are added.

## Value

A matrix count[node, run length] with a column giving the number of runs by run length and three additional 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, ...)
```

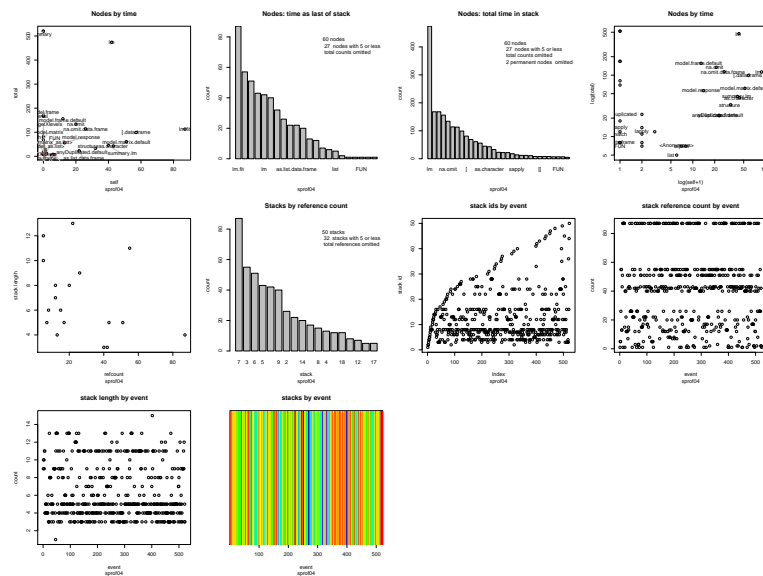
## Arguments

`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.

The `plot.sprof` method for `sprof` objects concatenates three plot functions. Using the plot functions one by one allows better control and will be preferred. [shownodes](#) may be a sufficient summary.

**Author(s)**

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

**References**

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

**See Also**

[shownodes](#)

[summaryRprof](#)

[plot\\_nodes](#) [plot\\_stacks](#) [plot\\_profiles](#)

**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**

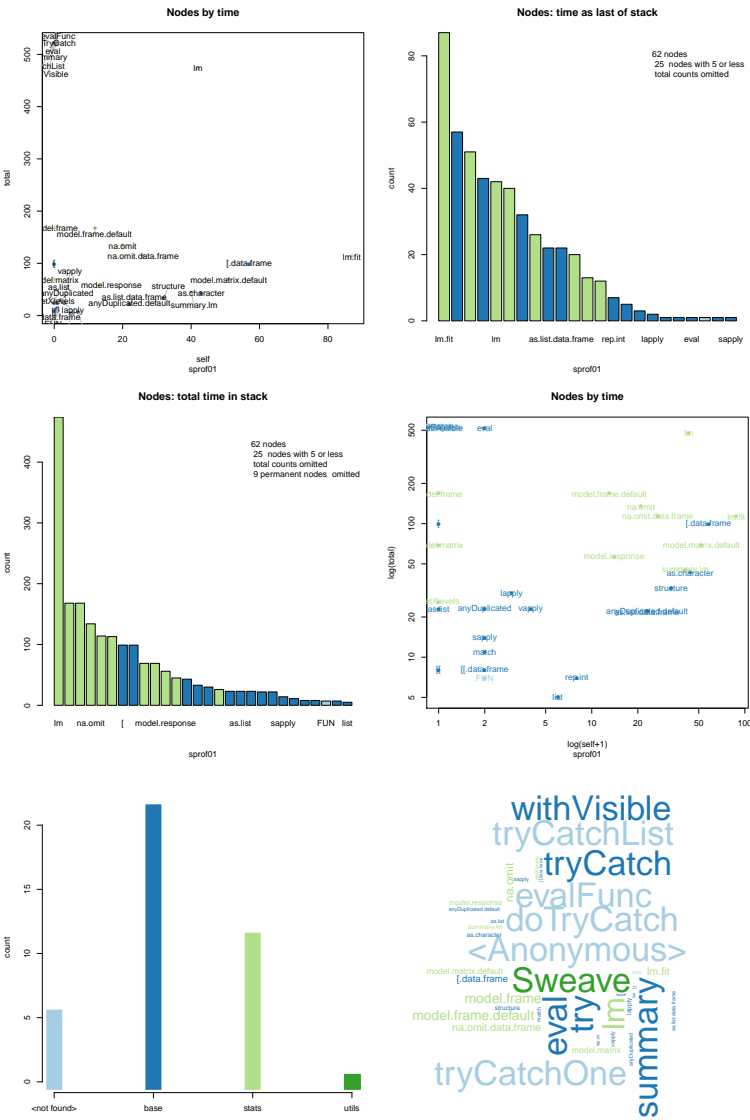
```
plot_nodes(x, which = c(1L, 2L, 3L, 4L), col = NULL,
ask = prod(par("mfcol")) < length(which) && dev.interactive(),
src = NULL, mincount = 5, horiz=FALSE, ...)
```

**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 sproft.

Author(s)

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

**References**

See the vignette of package sprof.

**See Also**

[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**

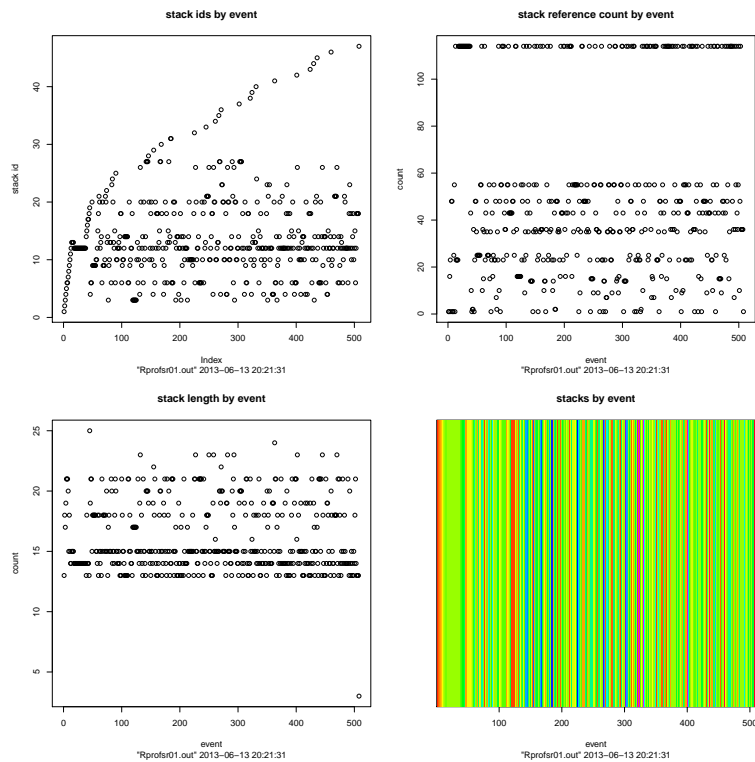
```
plot_profiles(x, which = c(1L, 2L, 3L, 4L), col,
ask = prod(par("mfcol")) < length(which) && dev.interactive(),
src = NULL, ...)
```

**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

[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, ...)
```

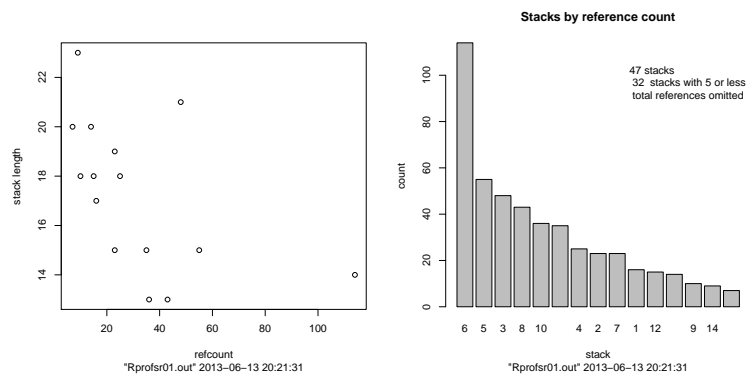
**Arguments**

|          |                                                                   |
|----------|-------------------------------------------------------------------|
| 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**

[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 <a href="#">readRprof</a> . |
| ... | 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 number: time interval between samples, in s. Defaults to 0.02s for consistency with <code>Rprof</code> , but shorter times should be used.       |
| 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.

(This data structure is subject to change.)

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`. "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

|          |                                                                                    |
|----------|------------------------------------------------------------------------------------|
| info     | Summary information.                                                               |
| nodes    | A vector of node names. This may include stray entries from interspersed lines.    |
| stacks   | Stacks, represented as reference list to nodes, and stack frequencies.             |
| profiles | Recorded data, as reference to stacks, and possibly additional data per reference. |

**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 | <i>Index, based on rank.</i> |
|---------|------------------------------|

---

### Description

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

### Usage

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

### Arguments

|                          |                               |
|--------------------------|-------------------------------|
| <code>x</code>           | A vector of data to covert.   |
| <code>maxindex</code>    | Maximum for result            |
| <code>pwr</code>         | See details.                  |
| <code>ties.method</code> | passed to <code>rank</code> . |

### Details

`x` is transformed to a rank scale, using `ties.method`. It is then rescaled to `[0,1]`, and (optionally) a power transformation 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 | <i>Recursive run length encoding.</i> |
|------|---------------------------------------|

---

### 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 data 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

*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)
```

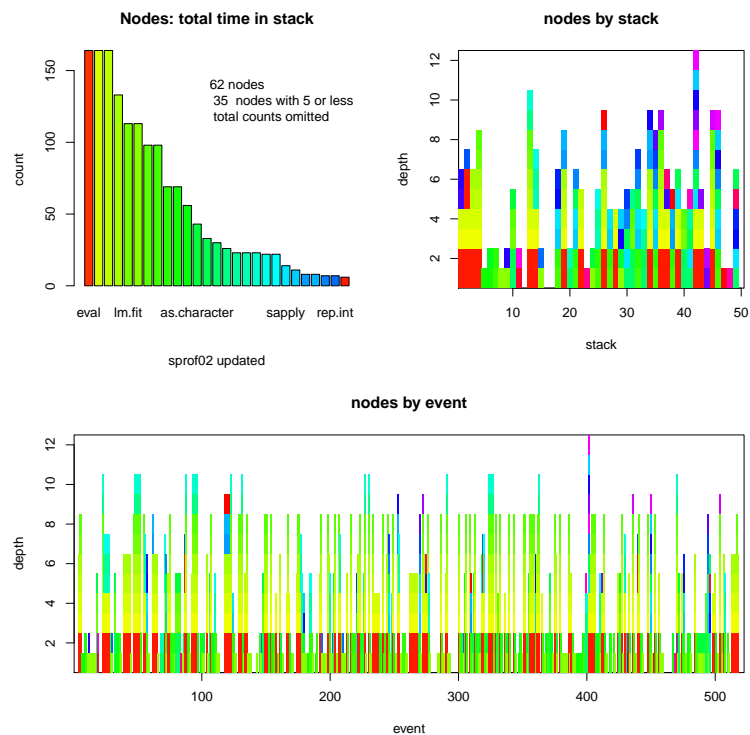
**Arguments**

|       |                                                             |
|-------|-------------------------------------------------------------|
| sprof | A data structure as returned by <a href="#">readRprof</a> . |
| 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 obejct</i> |
|-------------|-------------------------------------------------------|

---

**Description**

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

**Usage**

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

**Arguments**

|       |                                                             |
|-------|-------------------------------------------------------------|
| sprof | A data structure as returned by <a href="#">readRprof</a> . |
| 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 | <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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