R PROFILING AND OPTIMISATION

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Pending changes

- Control information may be included as special stack in raw format.
- A list of profiles may become default. Only one profiling interval value per profile.
- Nodes may implemented as `factor`.

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Profiling facilities in R

R provides the basic instruments for profiling, both for time based samplers as for event based instrumentation. However this source of information seems to be rarely used.

Maybe the supporting tools are not adequate. The summaries provided by R reduce the information beyond necessity. Additional packages are available, but these are not sufficiently action oriented.

With package *sprof* we want to give a data representation that keeps the full profile information. Tools to answer common questions are provided. The data structure should make it easy to extend the tools as required.

The package is currently distributed at r-forge as part of the *sintro* material.

To install this package directly within R, type
`install.packages("sprof",repos="http://r-forge.r-project.org")`

To install the recent package from source directly within R, type
`install.packages("sprof",repos="http://r-forge.r-project.org",type="source")`

LaTeX Layout Tools and Utilities

Print parameters used here:

Input
```
options(width = 72)
options(digits = 6)
```

We want immediate warnings, if necesary. Set to level 2 to handle warnings as error.

Input
```
message("switching  options(warn=1) -- immediate warning on")
options(warn=1)
```

For larger tabels and data frames, we use a cludge to avoid long outputs.

Input
```
xcutdata.frame <- function(df,  cut, margin){
#! keep3, to add: margin top - random center - margin bottom
        if (!is.data.frame(df)) return(df)
        nrow <- nrow(df)
        # cut a range if it is not empty. Quiet noop else. Does not cut single lines.
         cutrng <- function(cutfrom,cutto){
                 if (cutfrom<cutto){
                df[cutfrom,] <- NA
                if (!is.null(rownames(df))) rownames(df)[cutfrom] <- "< cut >"
                if (!is.null(df$name)) df$name[cutfrom] <- ""

                cutfrom <- cutfrom+1
```

```
                df[-(cutfrom:cutto),]
                }#if
        }
        if (!missing(cut))  {df <- cutrng(cut[1],cut[2]); return(df)}
        if (!missing(margin))  {
                if (length(margin)==1) margin <-  c(margin,margin)
        cut <- c(margin[1]+1,nrow-margin[2])
        df <-cutrng(cut[1],cut[2]);
        return(df)}
#        if (!missing(keep3))  { cut <- c(keep3[1]+1, keep3[1]+1,
#                nrow-keep3[3]-1,nrow-keep3[3]-1)
#        if (cut[3]-cut[4] > keep3[2]+2){delta<-(cut[3]-cut[2]) div 2; cut[3]<-0
#        browser()
#        } else df <- cutrng(cut[1],cut[4])
#        cutrng(cut[1],cut[4]) return(df)}
}
```

We use the R function *xtable()* for output and LaTeX *longtable*. A convenient wrapper to use this in out *Sweave* source is:

Input

```
library(xtable)
prxt <- function (x, digits=3,          caption=NULL,
        label=NULL, ...)  {
        margin <- 10
        if (nrow(x)> 2*margin+3) x <-xcutdata.frame(x, margin=margin)
        print(
                xtable(x, digits=digits, caption=caption, label=label, ...),
                floating=FALSE, tabular.environment="longtable", NA.string="\\vdots")
        }
```

This is to be used with `<<print = FALSE, results = tex, label=tab:prxxxx>>=`

1. Profiling

The basic information provided by all profilers in is a protocol of sampled stacks. For each recorded event, the protocol has one record, such as a line with a text string showing the sampled stack.

We use profiles to provide hints on the dynamic behaviour of programs. Most often, this is used to improve or even optimise programs. Sometimes, it is even used to understand some algorithm.

Profiles represent the program flow, which is considered to be laid out by the control structure of a program. The control structure is represented by the control graph, and this leads to the common approach to (re)construct the control graph, map the profile to this graph, and used graph based methods for further analysis. The prime example for this strategy is the GNU profiler *gprof* (see `http://sourceware.org/binutils/docs/gprof/`) which is used as master plan for many common profilers.

It is only half of the truth that the control graph can serve as a base for the profiled stacks. In R, we have some peculiarities.

lazy evaluation: Arguments to functions can passed as promises. These are only evaluated when needed, which may be at a later time, and may then lead to insertions in the stack. So we may have information resulting from the data flow, interspersed with the control flow.

memory management: Allocation of memory, and garbage collection, may interfere and leave their traces in the stack. While allocation is closely related to the visible control flow, garbage collection is a collective effect largely out of control of the code to execute.

primitives: Internal functions may escape the usual stack conventions and execute without leaving any identifiable trace on the stack.

control structures: In R, many control structures are implemented as function. Most notably, the *apply()* family appear as function calls and lead to cliques in the graph representation that do not correspond to relevnat structures. Since these functions are well know, they can have a special treatment.

So while the stack follows an overall well known dynamics, in R there are exceptions from regularity. The general approach, by *summaryRprof()* and others, is to reduce the profile to node information, or two consider single transitions.

We take a different approach. We take the stacks, as recorded in the profiles as our basic information unit. From this, we ask: what are the actions we need to answer our questions? Representation in graphs may come later, if they can help.

If the stacks would come from the control flow only, we could make use of the sequential nature of stacks. But since we have to live with the R specific interferences, we stay with the raw stacks.

Input

```
options(error = recover)
library(sprof)
```

In this presentation, we will use a small list of examples Since *Rprof* is not implemented on all systems, and since the profiles tend to get very large, we use some prepared examples that are frozen in this vignette and not included in the distribution, but all the code to generate the examples is provided.

1.1. **Simple regression example.**

Input

```
n <- 10000
x <- runif(n)
err <- rnorm(n)
y <- 2+ 3 * x + err
reg0data <- data.frame(x=x, y=y, err=err)
rm(x,y,err)
```

We will use this example to illustrate the basics. Of course the immediate questions are the variance between varying samples, and the influence of the sample size n. We keep everything fixed, so the only issue for now is the computational performance under strict iid conditions.

Still we have parameters to choose. We can determine the profiling granularity by setting the timing interval, and we can use repeated measurements to increase precision below the timing interval.

The timing interval should depend on the clock speed. Using for example 1ms amounts to some 1000 steps on a current CPU, per kernel.

If we use repeated samples, the usual rules of statistics applies. So taking 100 runs and taking the mean reduces the standard deviation by a factor 1/10.

Input

```
profinterval <- 0.001
simruns <- 100
Rprof(filename="RprofsRegressionExpl.out", interval = profinterval)
for (i in 1:simruns) xxx<- summary(lm(y~x, data=reg0data))
Rprof(NULL)
```

We now have the profile data in a file *RprofsRegressionExpl.out*. For this vignette, we use a frozen version *RprofsRegressionExpl01.out*.

1.1.1. *R basic.* The basic R invites us to get a summary.

Input

```
sumRprofRegressionExpl <- summaryRprof("RprofsRegressionExpl01.out")
str(sumRprofRegressionExpl, vec.len=3)
```

Output

```
List of 4
 $ by.self        :'data.frame':        41 obs. of  4 variables:
  ..$ self.time : num [1:41] 0.087 0.057 0.051 0.043 0.042 0.04 0.032 0.026 ...
  ..$ self.pct  : num [1:41] 16.67 10.92 9.77 8.24 ...
  ..$ total.time: num [1:41] 0.113 0.099 0.069 0.043 0.474 0.045 0.033 0.114 ...
  ..$ total.pct : num [1:41] 21.65 18.97 13.22 8.24 ...
 $ by.total       :'data.frame':        62 obs. of  4 variables:
  ..$ total.time: num [1:62] 0.522 0.522 0.521 0.521 0.521 0.521 0.521 0.521 ...
  ..$ total.pct : num [1:62] 100 100 99.8 99.8 ...
  ..$ self.time : num [1:62] 0.006 0 0.001 0 0 0 0 0 ...
  ..$ self.pct  : num [1:62] 1.15 0 0.19 0 0 0 0 0 ...
 $ sample.interval: num 0.001
 $ sampling.time  : num 0.522
```

The summary reduces the information contained in the profile to marginal statistics per node. This is provided in two data frames giving the same information, only in different order.

The file contains several spurious recordings: nodes that have been recorded only few times. It is worth noting these, but then they better be discarded. We use a

time limit of 4ms, which given our sampling interval of 1ms means we require more than four observations.

Input

```
prxt(sumRprofRegressionExpl$by.self,
        caption="summaryRprof result: by.self as final stack entry, all records",
        label="tab:prSRREbs")
```

	self.time	self.pct	total.time	total.pct
”lm.fit”	0.087	16.670	0.113	21.650
”[.data.frame”	0.057	10.920	0.099	18.970
”model.matrix.default”	0.051	9.770	0.069	13.220
”as.character”	0.043	8.240	0.043	8.240
”lm”	0.042	8.050	0.474	90.800
”summary.lm”	0.040	7.660	0.045	8.620
”structure”	0.032	6.130	0.033	6.320
”na.omit.data.frame”	0.026	4.980	0.114	21.840
”anyDuplicated.default”	0.022	4.210	0.022	4.210
”as.list.data.frame”	0.022	4.210	0.022	4.210
< cut >	⋮	⋮	⋮	⋮
”FUN”	0.001	0.190	0.007	1.340
”%in%”	0.001	0.190	0.004	0.770
”deparse”	0.001	0.190	0.002	0.380
”$”	0.001	0.190	0.001	0.190
”as.list.default”	0.001	0.190	0.001	0.190
”as.name”	0.001	0.190	0.001	0.190
”coef”	0.001	0.190	0.001	0.190
”file”	0.001	0.190	0.001	0.190
”NCOL”	0.001	0.190	0.001	0.190
”terms.formula”	0.001	0.190	0.001	0.190

Table 1: summaryRprof result: by.self as final stack entry, all records

Input

```
prxt(sumRprofRegressionExpl$by.total[sumRprofRegressionExpl$by.total$total.time>0.004,],
        caption="summaryRprof result: by.total, total time > 0.004s",
        label="tab:prSRREbt")
```

	total.time	total.pct	self.time	self.pct
”<Anonymous>”	0.522	100.000	0.006	1.150
”Sweave”	0.522	100.000	0.000	0.000
”eval”	0.521	99.810	0.001	0.190
”doTryCatch”	0.521	99.810	0.000	0.000
”evalFunc”	0.521	99.810	0.000	0.000
”try”	0.521	99.810	0.000	0.000
”tryCatch”	0.521	99.810	0.000	0.000
”tryCatchList”	0.521	99.810	0.000	0.000
”tryCatchOne”	0.521	99.810	0.000	0.000

"withVisible"	0.521	99.810	0.000	0.000
< cut >	⋮	⋮	⋮	⋮
"as.list"	0.023	4.410	0.000	0.000
"anyDuplicated.default"	0.022	4.210	0.022	4.210
"as.list.data.frame"	0.022	4.210	0.022	4.210
"sapply"	0.014	2.680	0.001	0.190
"match"	0.011	2.110	0.001	0.190
"[[.data.frame"	0.008	1.530	0.001	0.190
"[["	0.008	1.530	0.000	0.000
"rep.int"	0.007	1.340	0.007	1.340
"FUN"	0.007	1.340	0.001	0.190
"list"	0.005	0.960	0.005	0.960

Table 2: summaryRprof result: by.total, total time > 0.004s

1.1.2. *Package sprof.* In contrast, in our implementation we take a two step approach. First we read in the profile file to an internal representation.

Input
```
sprof01lm <- readRprof("RprofsRegressionExpl01.out")
sprof01 <- sprof01lm
```

We keep this example and use the copy `sprof01` of it extensively for illustration.

Input
```
save(sprof01lm, file="sprof01lm.RData")
```

To run the vignette with a different profile, replace ircodesprof01 by your example. You still have ircodesprof01lm for reference.

Package `sprof` provides a function `sampleRprof()` to take a sample and create a profile on the fly, as in

Input
```
sprof01temp <- sampleRprof(runif(10000), runs=100)
```

The basic data structure consists of four data frames. The ircodeinfo section collects global infromation from the input file, such as an identification strings and various global matrix. The `nodes` section inititally gives the same information marginal information as `summaryRprof`. The `stacks` section puts the node information into their calling context as found in the input profile file. The `profiles` section gives the temporal context. It is implemented as a list, but conceptually it is a data frame. Implementing it as a list allows run length encoding of variables, which unfortunately is not allowed by R in data frames.

Input
```
str(sprof01, max.level=2, vec.len=3,nchar.max=40)
```

Output
```
List of 4
 $ info    :'data.frame':        1 obs. of  8 variables:
  ..$ id       : Factor w/ 1 level "\"RprofsRegressionExpl01.out\" 2013-06-"| __truncated__: 1
  ..$ date     : POSIXct[1:1], format: "2013-07-09 23:03:29"
  ..$ nrnodes  : int 62
  ..$ nrstacks : int 50
  ..$ nrrecords: int 522
  ..$ firstline: Factor w/ 1 level "sample.interval=1000": 1
  ..$ ctllines : Factor w/ 1 level "sample.interval=1000": 1
  ..$ ctllinenr: num 1
 $ nodes   :'data.frame':        62 obs. of  5 variables:
  ..$ name      : Factor w/ 62 levels "!","..getNamespace",..: 1 2 3 4 5 6 7 8 ...
  ..$ self.time : num [1:62] 2 0 2 0 0 57 0 1 ...
  ..$ self.pct  : num [1:62] 0.38 0 0.38 0 ...
  ..$ total.time: num [1:62] 2 1 4 26 99 99 8 8 ...
  ..$ total.pct : num [1:62] 0.03 0.01 0.05 0.34 1.29 1.29 0.1 0.1 ...
 $ stacks  :'data.frame':        50 obs. of  7 variables:
  ..$ nodes         :List of 50
  ..$ shortname     : Factor w/ 50 levels "S<A>eFttCtCLtCOdTCwVeesleem.m..n.n...[["| __truncated__,..: 1
```

```
 ..$ refcount      : num [1:50] 1 5 26 55 13 43 51 87 ...
 ..$ stacklength   : int [1:50] 19 20 19 21 14 15 15 14 ...
 ..$ stackheadnodes: int [1:50] 52 52 52 52 52 52 52 52 ...
 ..$ stackleafnodes: int [1:50] 27 28 41 6 39 14 38 30 ...
 ..$ stackssrc     : Factor w/ 50 levels "! [.data.frame [ na.omit.data.frame na."| __truncated__,..: 2
$ profiles:List of 4
 ..$ data    : int [1:522] 1 2 2 3 4 4 5 5 ...
 ..$ mem     : NULL
 ..$ malloc  : NULL
 ..$ timesRLE:List of 2
 .. ..- attr(*, "class")= chr "rle"
- attr(*, "class")= chr [1:2] "sprof" "list"
```

The nodes do not come in a specific order. Access via a permutation vector is preferred. Thisallows different views onthe same data set. For example, table 3 uses a permutation by total time, and a selection (compare to table 2 on page 7).

Input

```
nodes <- sprof01$nodes[order(sprof01$nodes$total.time, decreasing=TRUE),]
prxt(nodes[nodes$total.time>4,],
caption="splot result: by.total, total time > 0.004s",
       label="tab:prspbt")
```

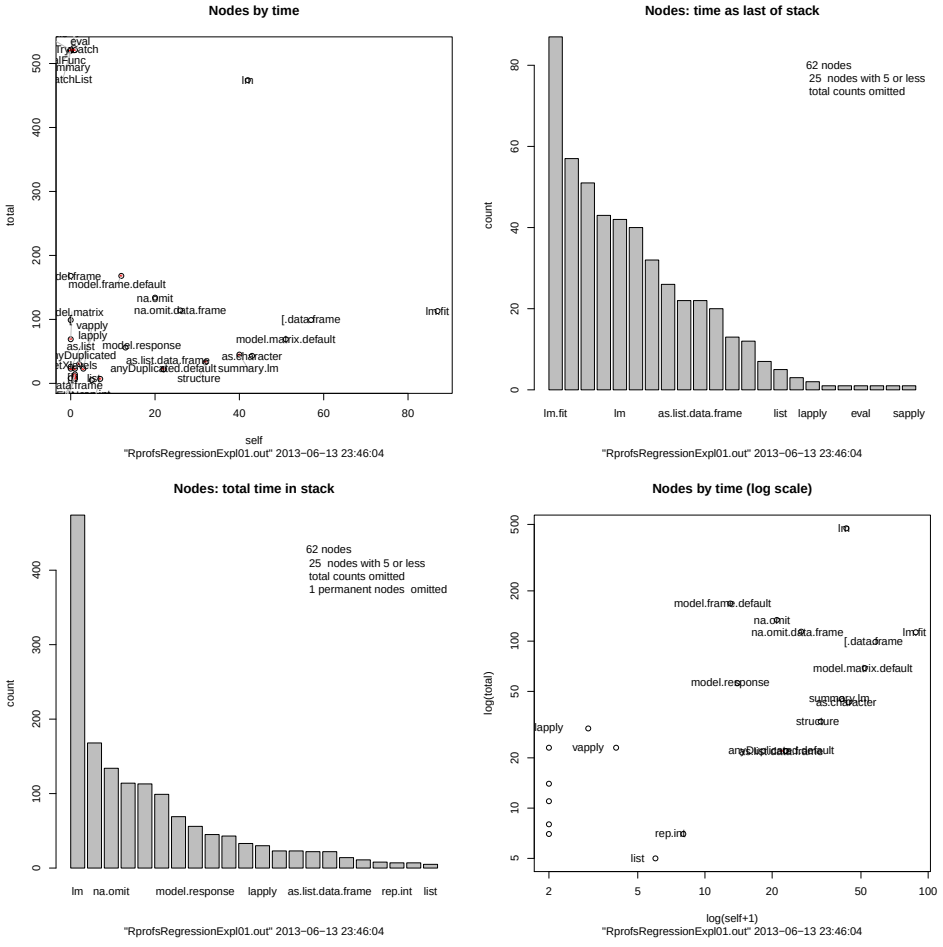
	name	self.time	self.pct	total.time	total.pct
10	<Anonymous>	6.000	1.150	522.000	6.790
52	Sweave	0.000	0.000	522.000	6.790
21	doTryCatch	0.000	0.000	521.000	6.780
22	eval	1.000	0.190	521.000	6.780
23	evalFunc	0.000	0.000	521.000	6.780
55	try	0.000	0.000	521.000	6.780
56	tryCatch	0.000	0.000	521.000	6.780
57	tryCatchList	0.000	0.000	521.000	6.780
58	tryCatchOne	0.000	0.000	521.000	6.780
62	withVisible	0.000	0.000	521.000	6.780
< cut >	\vdots	⋮	⋮	⋮	⋮
61	vapply	3.000	0.570	23.000	0.300
13	anyDuplicated.default	22.000	4.210	22.000	0.290
16	as.list.data.frame	22.000	4.210	22.000	0.290
47	sapply	1.000	0.190	14.000	0.180
31	match	1.000	0.190	11.000	0.140
7	[[	0.000	0.000	8.000	0.100
8	[[.data.frame	1.000	0.190	8.000	0.100
25	FUN	1.000	0.190	7.000	0.090
46	rep.int	7.000	1.340	7.000	0.090
28	list	5.000	0.960	5.000	0.070

Table 3: splot result: by.total, total time > 0.004s

Common rearrangements as by total time and by self time are supplied by the display functions. Plot, for example, currently gives a choice of four displays for nodes.

Input

```
oldpar <- par(mfrow=c(2,2))
plot_nodes(sprof01)
par(oldpar)
```



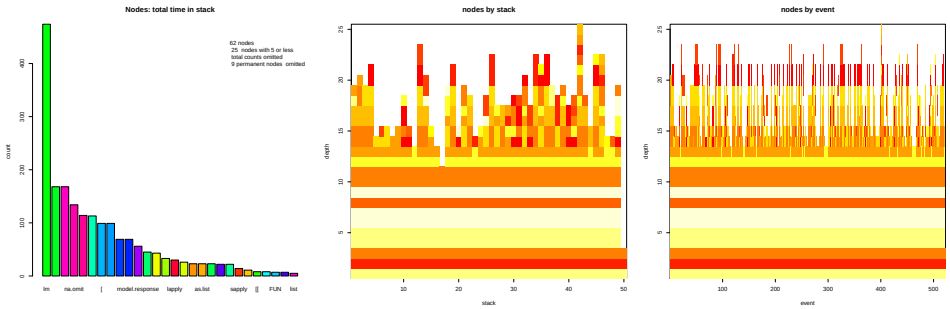
2. A better grip on profile information

The basic information provided by all profilers in R is a protocol of sampled stacks. The conventional approach is to break the information down to nodes and edges. The stacks provide more information than this. One way to access it is to use linking to pass information. To illustrate this, we encode the number the nodes by an arbitrary order and encode this by colour. Of course this is a poor information, and we use rainbow colours, which is about the poorest of all colour encodings. Just for demonstration.

This is what we get for free on our three levels: node, stack, and profile.

Input

```
oldpar <- par(mfrow=c(1,3))
#colp <- rainbow(sprof01$info$nrnodes)

#plot_nodes # 3
xnodes <- sprof01$nodes
src <- sprof01$info$src
mincount <- 5
        nrnodes <- dim(xnodes)[1]
         totaltime <- sum(xnodes$self.time)
colp <- rainbow(nrnodes)
colp <- colp[order(xnodes$total.time,decreasing=TRUE)]
 xnodes$colp <- colp
        xnodes <- xnodes[xnodes$total.time < totaltime,]
        #browser()
        if (mincount>0) xnodes <- xnodes[xnodes$total.time>=mincount,]
        trimmed <- nrnodes-dim(xnodes)[1]
        legnd <-function(trimmed=0, fulltime=0){
                ltext <- paste(nrnodes,"nodes\n")
                if (trimmed>0) ltext <- paste(ltext,trimmed," nodes with",mincount,"or less\n total co
                if (fulltime>0) ltext  <- paste(ltext,fulltime,"permanent nodes  omitted\n")
                legend("topright", legend=ltext, bty="n")
}
totaltime <- sum(xnodes$self.time)
                        fulltime <- dim(xnodes)[1]
                         xnodes <- xnodes[xnodes$total.time < totaltime,]
                         fulltime <- fulltime - dim(xnodes)[1]
                        ordertotal<- order(xnodes$total.time,decreasing=TRUE);
                        barplot(xnodes[ordertotal,]$total.time,
                        main="Nodes: total time in stack",
                        names.arg = xnodes[ordertotal,]$name, sub=src, ylab="count",
                        col=xnodes$colp);
                        legnd(trimmed=trimmed, fulltime=fulltime)
stacks_nodes <- list.as.matrix(sprof01$stacks$nodes)
#<<fig=TRUE, label=sREimgstacks>>=
image(x=1:ncol(stacks_nodes),y=1:nrow(stacks_nodes),
t(stacks_nodes),xlab="stack", ylab="depth", main="nodes by stack")
profile_nodes <- profiles_matrix(sprof01)
#<<fig=TRUE, label=sREimgprofiles>>=
image(x=1:ncol(profile_nodes),y=1:nrow(profile_nodes),
t(profile_nodes),xlab="event", ylab="depth", main="nodes by event")
par(oldpar)
```



The obvious message is that if seen by level, there are different structures. Profiling usually takes place in a framework. So at the base of the stacks, we find entries that are (almost) resistent. Then in general we have some few steps where the algorithm splits, and then we have the finer details. This can be identified on the stack level.

Not so often, but a frequent phenomenon is to have some "burn in" or "fade out". To identify this, we need to look at the profile level.

At a closer look, we may find stack patterns (maybe marked by specific nodes) that indicate administrative intervention and rather should be handled as aseparators between distinct profiles than as part of the general dynamics.

Stable framework effect can be detected automatically. "burn in" or "fade out' may need a closer look, and special stacks need and individual inspection on low frequency stacks.

Before starting additional inspection, the data better be trimmed. At this point, it is a decision whether to adapt the timing information, or keept the original information. Since this decision does affect the structural information, it is not critical. But analysis is easier if unused nodes are eliminated.

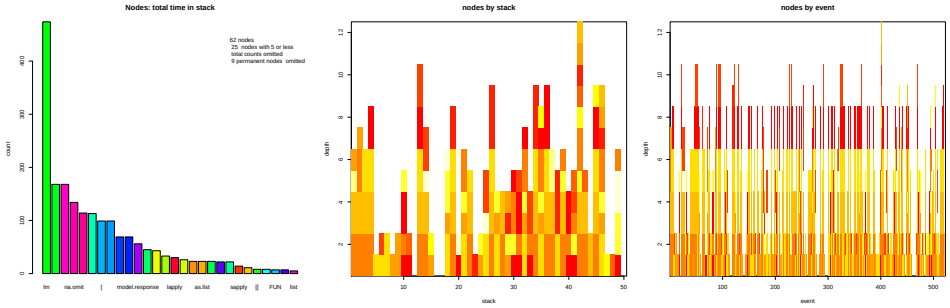
Input

```
sprof02 <- sprof01
basetrim <- 13
sprof02$stacks$nodes <- sapply(sprof02$stacks$nodes, function (x){if (length(x)> basetrim) x[-(1:baset
#sprof02$stacks$nodes <- sprof02$stacks$nodes[[!is.null(sprof02$stacks$nodes)]]
```

Input

```
oldpar <- par(mfrow=c(1,3))
#colp <- rainbow(sprof02$info$nrnodes)

#plot_nodes # 3
xnodes <- sprof02$nodes
src <- sprof02$info$src
mincount <- 5
        nrnodes <- dim(xnodes)[1]
         totaltime <- sum(xnodes$self.time)
colp <- rainbow(nrnodes)
colp <- colp[order(xnodes$total.time,decreasing=TRUE)]
 xnodes$colp <- colp
        xnodes <- xnodes[xnodes$total.time < totaltime,]
        #browser()
```

```
        if (mincount>0) xnodes <- xnodes[xnodes$total.time>=mincount,]
        trimmed <- nrnodes-dim(xnodes)[1]
        legnd <-function(trimmed=0, fulltime=0){
                ltext <- paste(nrnodes,"nodes\n")
                if (trimmed>0) ltext <- paste(ltext,trimmed," nodes with",mincount,"or less\n total co
                if (fulltime>0) ltext  <- paste(ltext,fulltime,"permanent nodes  omitted\n")
                legend("topright", legend=ltext, bty="n")
}
totaltime <- sum(xnodes$self.time)
                        fulltime <- dim(xnodes)[1]
                         xnodes <- xnodes[xnodes$total.time < totaltime,]
                         fulltime <- fulltime - dim(xnodes)[1]
                        ordertotal<- order(xnodes$total.time,decreasing=TRUE);
                        barplot(xnodes[ordertotal,]$total.time,
                        main="Nodes: total time in stack",
                        names.arg = xnodes[ordertotal,]$name, sub=src, ylab="count",
                        col=xnodes$colp);
                        legnd(trimmed=trimmed, fulltime=fulltime)
stacks_nodes <- list.as.matrix(sprof02$stacks$nodes)
#<<fig=TRUE, label=sREimgstacks>>=
image(x=1:ncol(stacks_nodes),y=1:nrow(stacks_nodes),
t(stacks_nodes),xlab="stack", ylab="depth", main="nodes by stack")
profile_nodes <- profiles_matrix(sprof02)
#<<fig=TRUE, label=sREimgprofiles>>=
image(x=1:ncol(profile_nodes),y=1:nrow(profile_nodes),
t(profile_nodes),xlab="event", ylab="depth", main="nodes by event")
par(oldpar)
```



For a visual inspection, runs of the same node and level in the profile are easily perceived. For an analytical inspection, we have to reconstruct the runs from the data. In stacks, runs are organized hierarchically. On the root level, runs are just ordinary runs. On the next levels, runs have to be defined given (within) the previous runs. So we need a recursive version of `rle`, applied to the profile information. This gives a detailed information about the presence time of each node, by stack level.

Input

```
profile_nodes_rle<- rrle(profile_nodes)
profile_nodes_rlet <- lapply(profile_nodes_rle, function(x) table(x,dnn=c("count","node")) )
invisible(lapply(profile_nodes_rlet, function(x) print.table(x,zero.print = ".") ))
```

Output

```
     node
count  2  4 11 19 22 30 32 37 39 43
    1  1 17  1  1 40 46  2 55 35  1
    2  .  1  .  . 17 18  .  4  3  .
    3  .  1  .  .  6  3  .  2  3  .
    4  .  1  .  .  4  1  .  .  .  .
    5  .  .  .  .  2  1  .  .  .  .
    6  .  .  .  .  6  1  .  .  1  .
    7  .  .  .  .  2  1  .  .  .  .
     node
count 14 18 22 26 27 33 38 46 47 49 61
    1 34  1 40 16  1  2 55  7  3 10  .
    2  3  . 17  .  .  .  4  .  .  1  .
    3  1  .  6  .  .  .  2  .  .  .  1
    4  .  .  4  1  .  .  .  .  .  .  .
    5  .  .  2  .  .  .  .  .  .  .  .
    6  .  .  6  .  .  .  .  .  .  1  .
    7  .  .  2  .  .  .  .  .  .  .  .
     node
count  5  7  9 15 26 31 35 48 61
    1 14  1  1  2  2  9 40  1  6
    2  .  .  .  .  .  . 17  .  1
    3  .  .  .  .  .  .  6  .  .
    4  1  .  .  .  .  .  4  .  .
    5  .  .  .  .  .  .  2  .  .
    6  .  .  .  .  .  .  6  .  .
    7  .  .  .  .  .  .  2  .  .
     node
count  6  8 15 16 25 31 36 47 59
    1 14  1  7  2  1  1 40  9  1
    2  .  .  1  .  .  . 17  .  .
    3  .  .  .  .  .  .  6  .  .
    4  1  .  .  .  .  .  4  .  .
    5  .  .  .  .  .  .  2  .  .
    6  .  .  .  .  .  .  6  .  .
    7  .  .  .  .  .  .  2  .  .
     node
count  3 10 12 16 17 20 22 26 40 47 48 49 53 60 61
    1  1  1  1  6  1  1  3  5 46  2  3 11  2  1  7
    2  .  .  .  1  .  .  1  . 10  .  .  .  .  .  .
    3  .  .  .  .  .  .  .  .  5  .  .  .  .  .  .
    4  .  .  .  .  .  .  .  .  4  .  .  1  .  .  .
    5  .  .  .  .  .  .  .  .  1  .  .  .  .  .  1
    6  .  .  .  .  .  .  .  .  3  .  .  .  .  .  .
    7  .  .  .  .  .  .  .  .  2  .  .  .  .  .  .
     node
count 15 22 25 26 27 41 54 59
    1  7  3  5  3  1 43  1  3
    2  .  1  .  .  .  7  .  .
    3  .  .  .  .  .  4  .  .
    4  .  .  .  .  .  5  .  .
    5  1  .  .  .  .  .  .  .
    6  .  .  .  .  .  3  .  .
```

```
    7  .  .  .  .  .  1  .  .
     node
count  3  5  7  9 16 25 28
    1  3 46  2  1  7  1  3
    2  .  4  .  .  .  .  1
    3  .  3  .  .  .  .  .
    4  .  3  .  .  .  .  .
    5  .  .  1  .  1  .  .
    6  .  1  .  .  .  .  .
     node
count  6  8 31 44 45
    1 46  2  1  1  2
    2  4  .  .  .  .
    3  3  .  .  .  .
    4  3  .  .  .  .
    5  .  1  .  .  .
    6  1  .  .  .  .
     node
count 1 9 10 12 20 34 42
    1 2 1  .  9  1  1  2
    4 . .  .  2  .  .  .
    5 . .  1  1  .  .  .
     node
count 9 13
    1 1  9
    4 .  2
    5 .  1
     node
count 31
    1  1
     node
count 34
    1  1
```

ToDo: add current level

ToDo: generate a coplot representation

ToDo: add time per call information

2.1. **The details.** For each recorded event, the protocol records one line with a text string showing the sampled stack (in reverse order: most recent first). The stack lines may be preceded by header lines with event specific information. The protocol may be interspersed with control information, such as information about the timing interval used.

We know that the structural information, static information as well as dynamic information, can be represented with the help of a graph. For a static analysis, the graph representation may be the first choice. For a dynamic analysis, the stack information is our first information. A stack is a connected path in the program graph. If we start with nodes and edges, we loose information which is readily available in record of stacks.

As we know that we are working with stacks, we know that they have their peculiarities. Stacks tend to grow and shrink. Subsequent events will have extensions and shrinkages of stacks (if the recording is on a fine scale), or stack sharing common stumps (if the recording is on a coarser scale).

There have always been interrupts, and these show up in profiles. In R, this is related problem (GC)

The graph is a second instance that is (re)constructed from the stack recording.

Here is the way we represent the profile information:

The profile log file is sanitised:

- Control lines are extracted and recorded in a separate list.
- Head parts, if present, ere extracted and recorded in a matrix that is kept line-aligned with the remainder
- Line content is standardised, for example by removing stray quotation marks etc.

After this, the sanitised lines are encoded as a vector of stacks, and references to this.

If necessary, these steps are done by chunks to reduce memory load.

From the vector of stacks, a vector of nodes (or rather node names) is derived.

The stacks are now encoded by references to the nodes table. For convenience, we keep the (sanitised) textual representation of the stacks.

So far, texts are in reverse order. For each stack, we record the trailing leaf, and then we reverse order. The top of stack is now on first position.

Several statistics can be accumulated easily as a side effect.

Conceptually, the data structure consist of three tables (the implementation may differ, and is subject to change).

The profiles table is the representation of the input file. Control lines are are collected in a special table. With the control lines removed, the rest is a table, one row per input line. The body of the line, the stack, is encoded as a reference to a stacks table (obligatory) and header information (optional).

The stacks table contains the collected stacks, each stack encoded as a list of references to the node table. This is obligatory. This list is kept in reverse order (root at position 1). A source line representing the stack information may be kept (optional).

The nodes table keeps the names at the nodes.

3. XXX

Input

```
# xtable cannot handle posix
str(sprof01$info,
        caption="splot node info",
        label="tab:prSREinfo0")
```

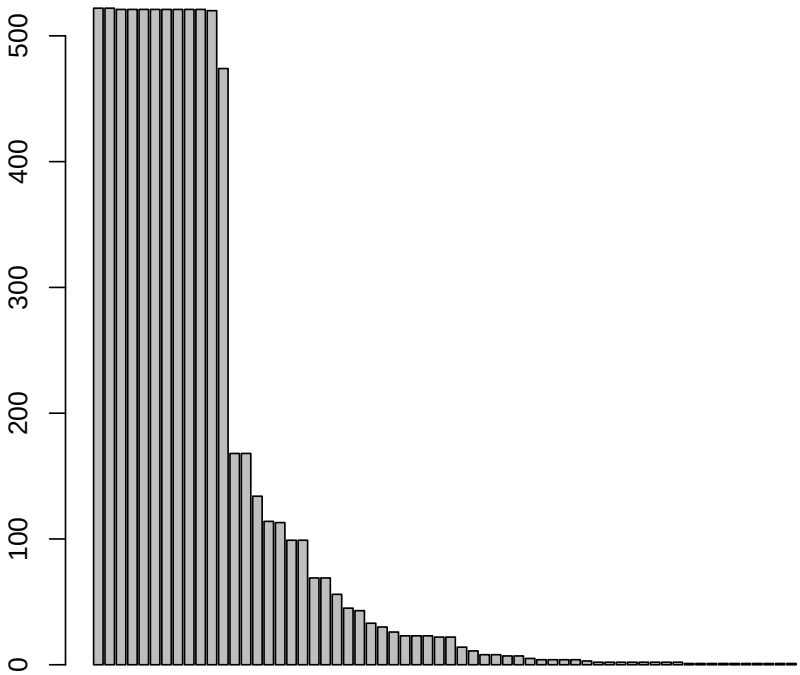
Output

```
'data.frame':        1 obs. of  8 variables:
 $ id       : Factor w/ 1 level "\"RprofsRegressionExpl01.out\" 2013-06-13 23:46:04": 1
 $ date     : POSIXct, format: "2013-07-09 23:03:29"
 $ nrnodes  : int 62
 $ nrstacks : int 50
 $ nrrecords: int 522
 $ firstline: Factor w/ 1 level "sample.interval=1000": 1
 $ ctllines : Factor w/ 1 level "sample.interval=1000": 1
 $ ctllinenr: num 1
```

As a convention, we do not re-arrange items for ad-hoc choices, but use a permutation vector instead.

Input

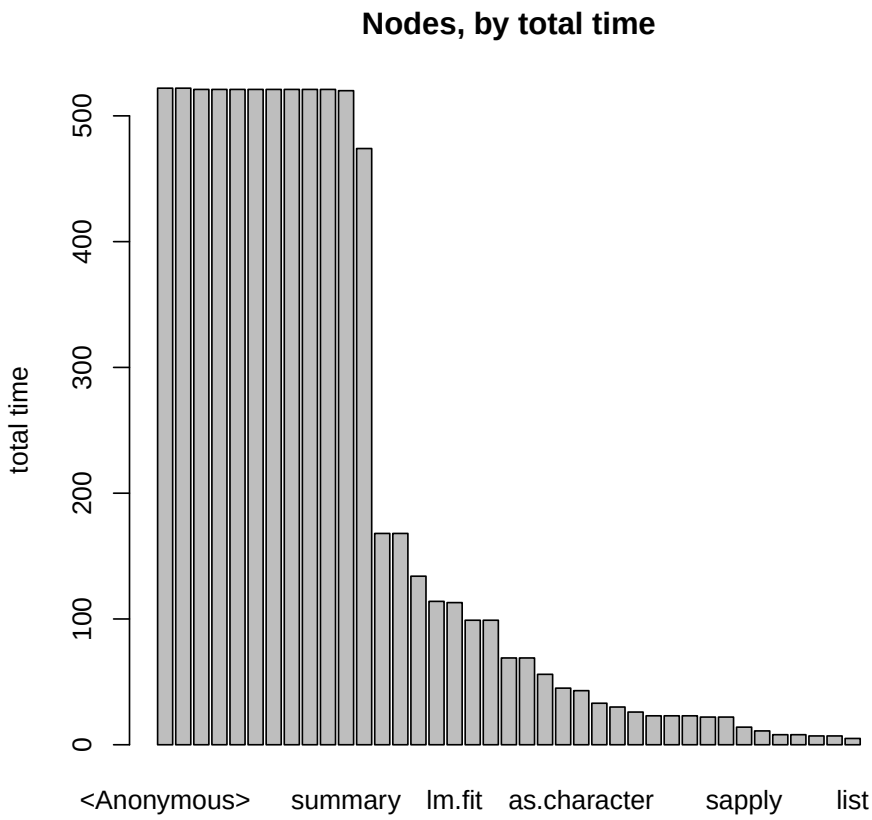
```
rownames(sprof01$nodes) <- sprof01$nodes$names
nodesperm <- order(sprof01$nodes$total.time,decreasing=TRUE)
barplot(sprof01$nodes$total.time[nodesperm])
```



Selections are recorded as selection vectors, with reference to the original order. This needs some caution to align them with the order choices.

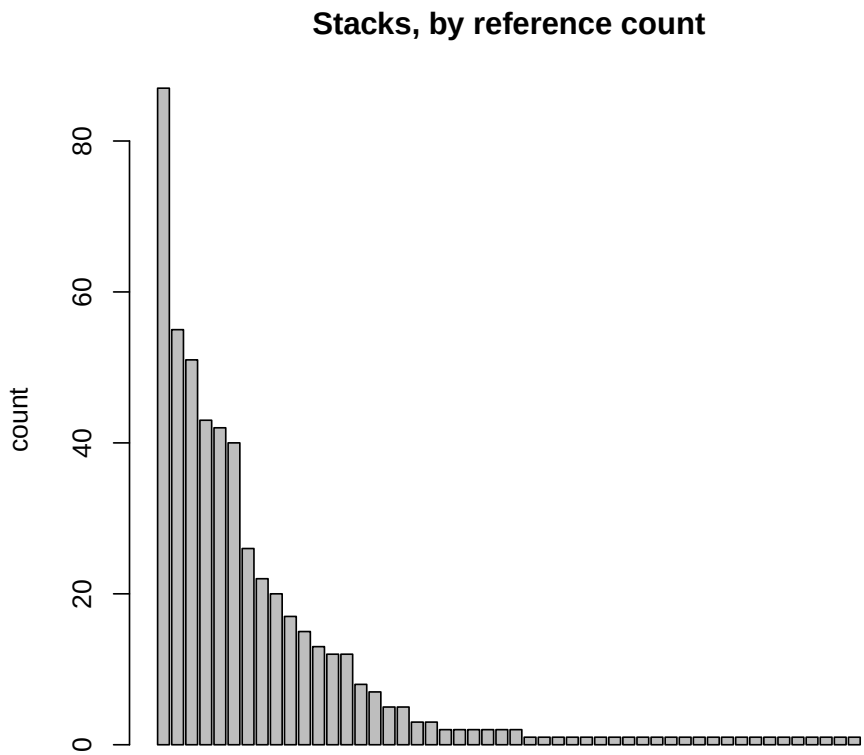
Input

```
nodesnrobsok <- sprof01$nodes$total.time > 4
sp <- sprof01$nodes$total.time[nodesperm][nodesnrobsok[nodesperm]]
names(sp) <- sprof01$nodes$name[nodesperm][nodesnrobsok[nodesperm]]
barplot(sp,
 main="Nodes, by total time", ylab="total time")
```



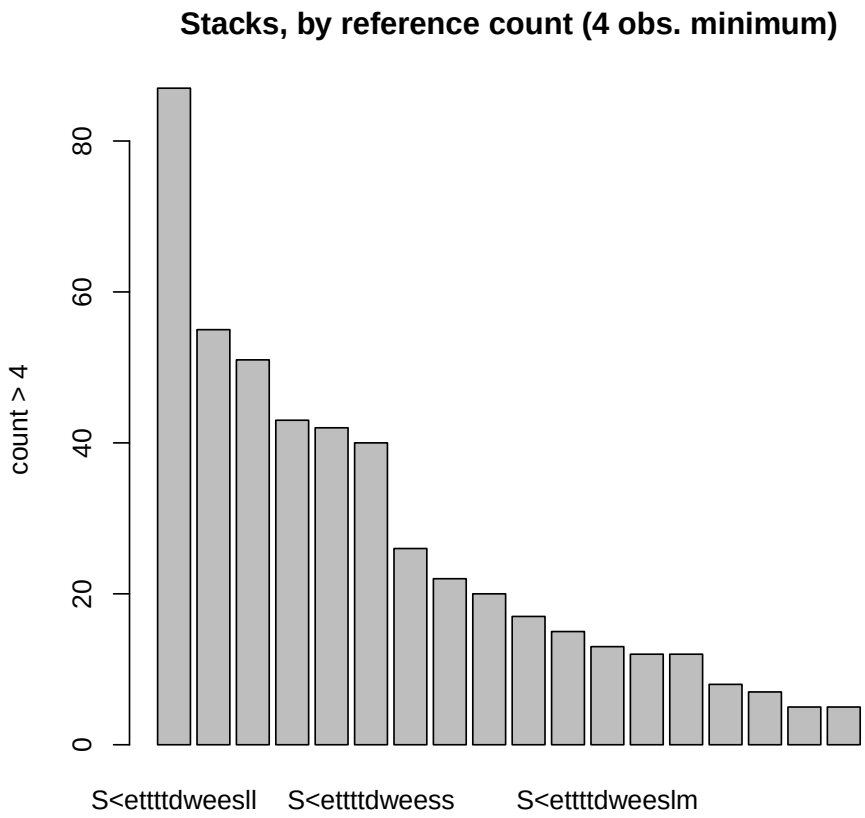
Input

```
#rownames(sprof01$nodes) <- sprof01$nodes$names
stacksperm <- order(sprof01$stacks$refcount,decreasing=TRUE)
barplot(sprof01$stacks$refcount[stacksperm],main="Stacks, by reference count", ylab="count")
```



Input

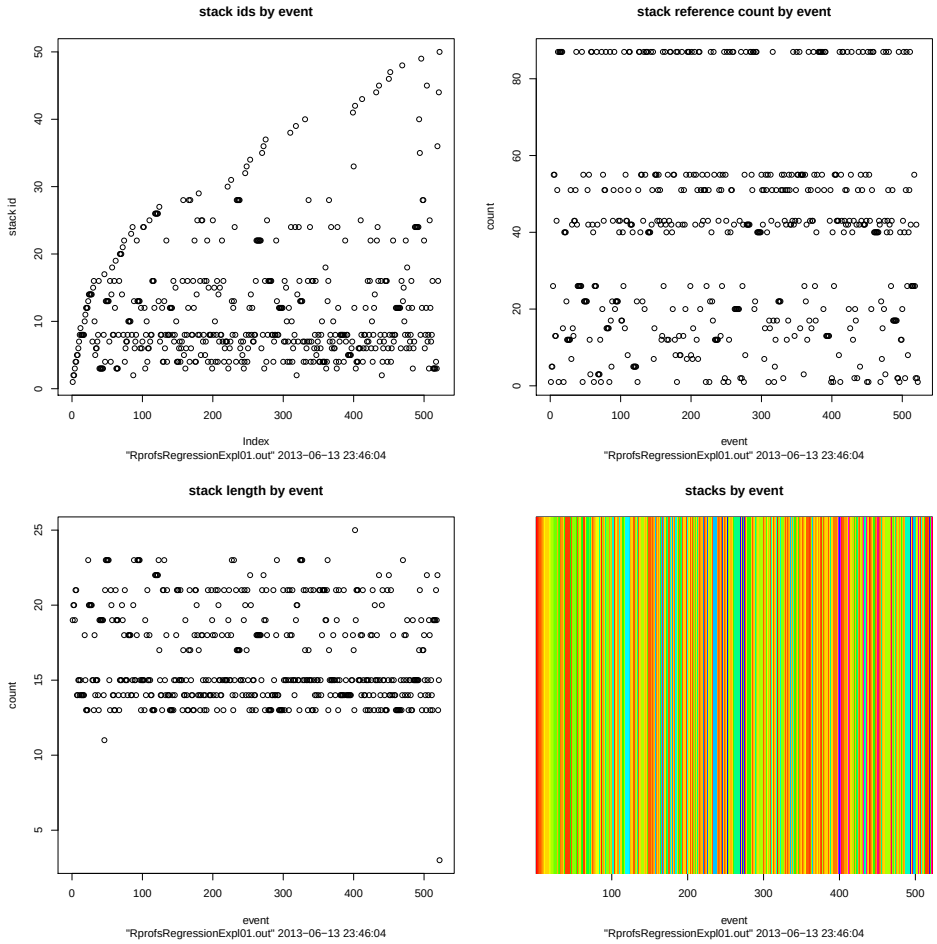
```
stacksnrobsok <- sprof01$stacks$refcount > 4
sp4 <- sprof01$stacks$refcount[stacksperm][stacksnrobsok[stacksperm]]
names(sp4) <- sprof01$stacks$shortname[stacksperm][stacksnrobsok[stacksperm]]
barplot(sp4,
 main="Stacks, by reference count (4 obs. minimum)", ylab="count > 4")
```



On the first look, information on the profile level is not informative. Profile records are just recordings of some step, taken at regular intervals. We get a minimal information, if we encode the stacks in colour.

Input

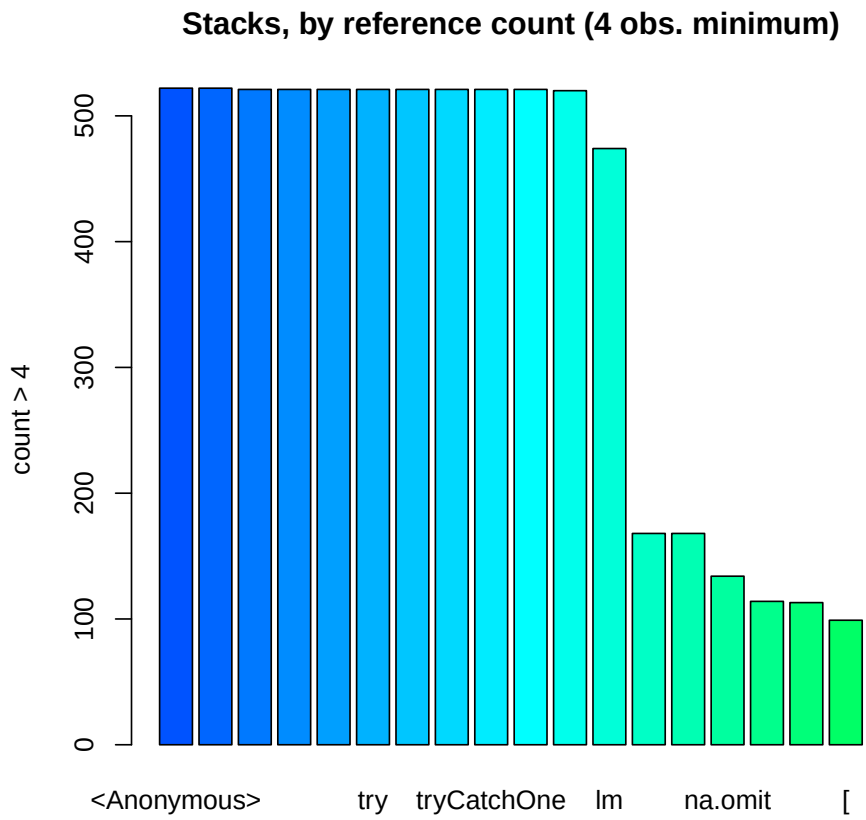
```
oldpar<-par(mfrow=c(2,2))
plot_profiles(sprof01)
par(oldpar)
```



We now do a step down analysis. Aggregating the information from the profiling events, we have the frequency of stack references. On the stack level, we encode the frequency in colour, and linking propagates this to the profile level.

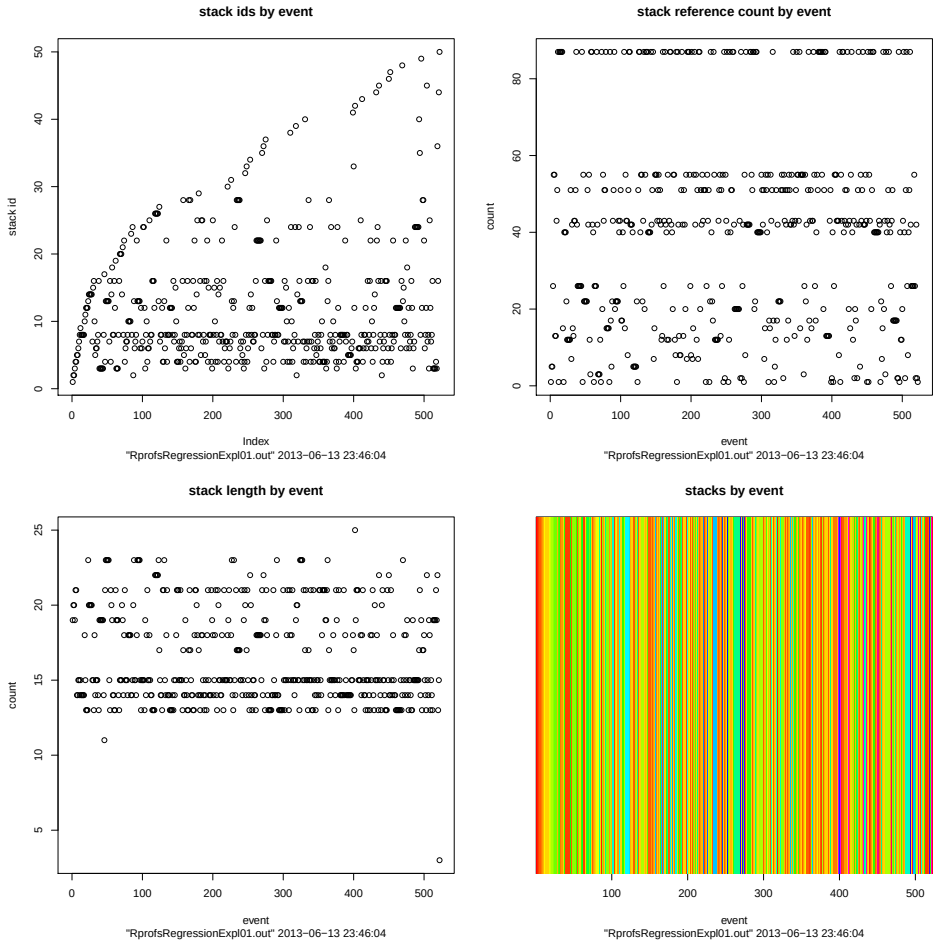
Input

```
stackfreqscore <- rank(sprof01$stacks$refcount,ties.method="random")
stackfreqscore4<- stackfreqscore[stacksperm][stacksnrobsok[stacksperm]]
barplot(sp[stacksnrobsok[stacksperm]], main="Stacks, by reference count (4 obs. minimum)", ylab="count
col=rainbow(80)[stackfreqscore4])
```



Input

```
oldpar<- par(mfrow=c(2,2))
plot_profiles(sprof01)
par(oldpar)
```


stack ids by event
stack id
Index
"RprofsRegressionExpl01.out" 2013−06−13 23:46:04
stack reference count by event
count
event
"RprofsRegressionExpl01.out" 2013−06−13 23:46:04
stack length by event
count
event
"RprofsRegressionExpl01.out" 2013−06−13 23:46:04
stacks by event
event
"RprofsRegressionExpl01.out" 2013−06−13 23:46:04

Input

```
prxt(sprof01$nodes,
        caption="nodes",
        label="tab:prSREnodes")
```

	name	self.time	self.pct	total.time	total.pct
1	!	2.000	0.380	2.000	0.030
2	..getNamespace	0.000	0.000	1.000	0.010
3	.deparseOpts	2.000	0.380	4.000	0.050
4	.getXlevels	0.000	0.000	26.000	0.340
5	[	0.000	0.000	99.000	1.290
6	[.data.frame	57.000	10.920	99.000	1.290
7	[[	0.000	0.000	8.000	0.100
8	[[.data.frame	1.000	0.190	8.000	0.100
9	%in%	1.000	0.190	4.000	0.050
10	<Anonymous>	6.000	1.150	522.000	6.790
< cut >	\vdots	⋮	⋮	⋮	⋮
53	terms	0.000	0.000	2.000	0.030
54	terms.formula	1.000	0.190	1.000	0.010
55	try	0.000	0.000	521.000	6.780
56	tryCatch	0.000	0.000	521.000	6.780
57	tryCatchList	0.000	0.000	521.000	6.780
58	tryCatchOne	0.000	0.000	521.000	6.780
59	unique	3.000	0.570	4.000	0.050
60	unlist	0.000	0.000	1.000	0.010
61	vapply	3.000	0.570	23.000	0.300
62	withVisible	0.000	0.000	521.000	6.780

Table 4: nodes

Input

```
str(sprof01$stacks, max.level=1)
```

Output

```
'data.frame':        50 obs. of  7 variables:
 $ nodes         :List of 50
 $ shortname     : Factor w/ 50 levels "S<A>eFttCtCLtCOdTCwVeesleem.m..n.n...[[.",..: 27 17 19 1 35 36 3
 $ refcount      : num  1 5 26 55 13 43 51 87 1 15 ...
 $ stacklength   : int  19 20 19 21 14 15 15 14 15 18 ...
 $ stackheadnodes: int  52 52 52 52 52 52 52 52 52 52 ...
 $ stackleafnodes: int  27 28 41 6 39 14 38 30 27 49 ...
 $ stackssrc     : Factor w/ 50 levels "! [.data.frame [ na.omit.data.frame na.omit model.frame.default
```

Input

Input

```
str(sprof01$profiles, max.level=1)
```

Output

```
List of 4
 $ data    : int [1:522] 1 2 2 3 4 4 5 5 6 7 ...
 $ mem     : NULL
 $ malloc  : NULL
 $ timesRLE:List of 2
  ..- attr(*, "class")= chr "rle"
```

Input

A summary is provided on request.

Input

```
sumsprof01 <- summary.sprof(sprof01)
str(sumsprof01, max.level=2)
```

Output

```
List of 4
 $ info    :'data.frame':        1 obs. of  8 variables:
  ..$ id       : Factor w/ 1 level "\"RprofsRegressionExpl01.out\" 2013-06-13 23:46:04": 1
  ..$ date     : POSIXct[1:1], format: "2013-07-09 23:03:29"
  ..$ nrnodes  : int 62
  ..$ nrstacks : int 50
  ..$ nrrecords: int 522
  ..$ firstline: Factor w/ 1 level "sample.interval=1000": 1
  ..$ ctllines : Factor w/ 1 level "sample.interval=1000": 1
  ..$ ctllinenr: num 1
 $ nodes   :'data.frame':        62 obs. of  5 variables:
  ..$ name      : Factor w/ 62 levels "!","..getNamespace",..: 1 2 3 4 5 6 7 8 9 10 ...
  ..$ self.time : num [1:62] 2 0 2 0 0 57 0 1 1 6 ...
  ..$ self.pct  : num [1:62] 0.38 0 0.38 0 0 ...
  ..$ total.time: num [1:62] 2 1 4 26 99 99 8 8 4 522 ...
  ..$ total.pct : num [1:62] 0.03 0.01 0.05 0.34 1.29 1.29 0.1 0.1 0.05 6.79 ...
 $ stacks  :'data.frame':        50 obs. of  7 variables:
```

```
  ..$ nodes         :List of 50
  ..$ shortname     : Factor w/ 50 levels "S<A>eFttCtCLtCOdTCwVeesleem.m..n.n...[[.",..: 27 17 19 1 35 3
  ..$ refcount      : num [1:50] 1 5 26 55 13 43 51 87 1 15 ...
  ..$ stacklength   : int [1:50] 19 20 19 21 14 15 15 14 15 18 ...
  ..$ stackheadnodes: int [1:50] 52 52 52 52 52 52 52 52 52 52 ...
  ..$ stackleafnodes: int [1:50] 27 28 41 6 39 14 38 30 27 49 ...
  ..$ stackssrc     : Factor w/ 50 levels "! [.data.frame [ na.omit.data.frame na.omit model.frame.defau
 $ profiles:List of 4
  ..$ data    : int [1:522] 1 2 2 3 4 4 5 5 6 7 ...
  ..$ mem     : NULL
  ..$ malloc  : NULL
  ..$ timesRLE:List of 2
  .. ..- attr(*, "class")= chr "rle"
 - attr(*, "class")= chr [1:2] "sprof" "list"
```

The classical approach hides the work that has been done. Actually it breaks down the data to record items. This figure is not reported anywhere. In our case, it can be reconstructed. The profile data have 8456 words in 524 lines.

In our approach, we break down the information. Two lines of control information are split off. We have 522 lines of profile with 50 unique stacks, referencing 62 nodes. Instead of reducing it to a summary, we keep the full information. Information is always kept on its original level.

On the profiles level, we know the sample interval length, and the id of the stack recorded. On the stack level, for each stack we have a reference count, with the sample interval lengths used as weights. This reference count is added up for each node in the stack to give the node timings.

Cheap statistics are collected as the come by. For example, from the stacks table it is cheap to identify root and leaf nodes, and this mark is propagated to the nodes table.

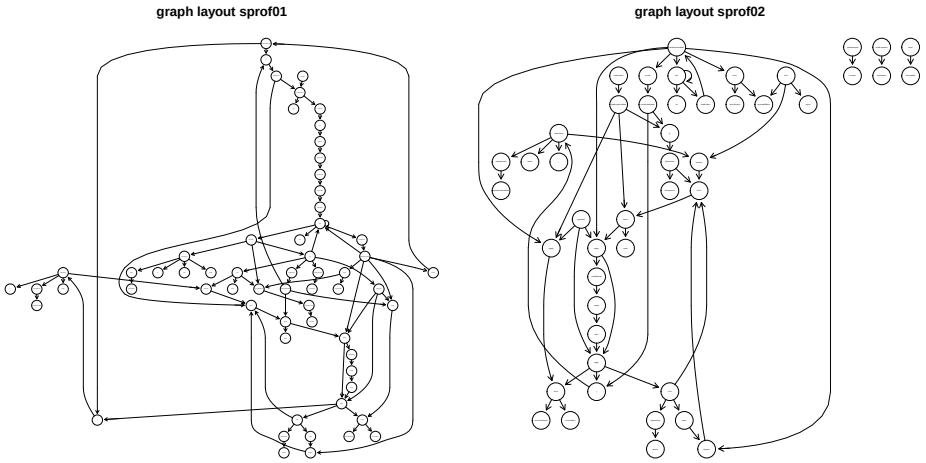
4. Surgery

Looking at nodes gives you a pointwise horizon. Looking at edges gives you a one step horizon. The stacks give a wider horizon, typically a step size of 10 or more. The stacks we get from R have peculiarities, and we can handle with this broader perspective. These are not relevant if we look pointwise, but may become dominating if we try to get a global picture. We take a look ahead (details to come in section 7 on page 48 and nave a preview how our example is represented as a graph. Left is the original graph es recovered from the edge information, right the graph after we have cut off the scaffold effects.

4.1. **graph Package.**

Input

```
oldpar <- par(mfrow=c(1,2))
library(graph)
plot(as(adjacency(sprof01),"graphNEL"),  main="graph layout sprof01", cex.main=2)
plot(as(adjacency(sprof02),"graphNEL"),  main="graph layout sprof02", cex.main=2)
par(oldpar)
```



R ist function based, and control structures in general are implemented as functions. In a graph representation, they appear as nodes, concentrating and seeding to unrelated paths. We can detect these on the stack level and replace them by surrogates, introducing new nodes.

ToDo: implement

Input

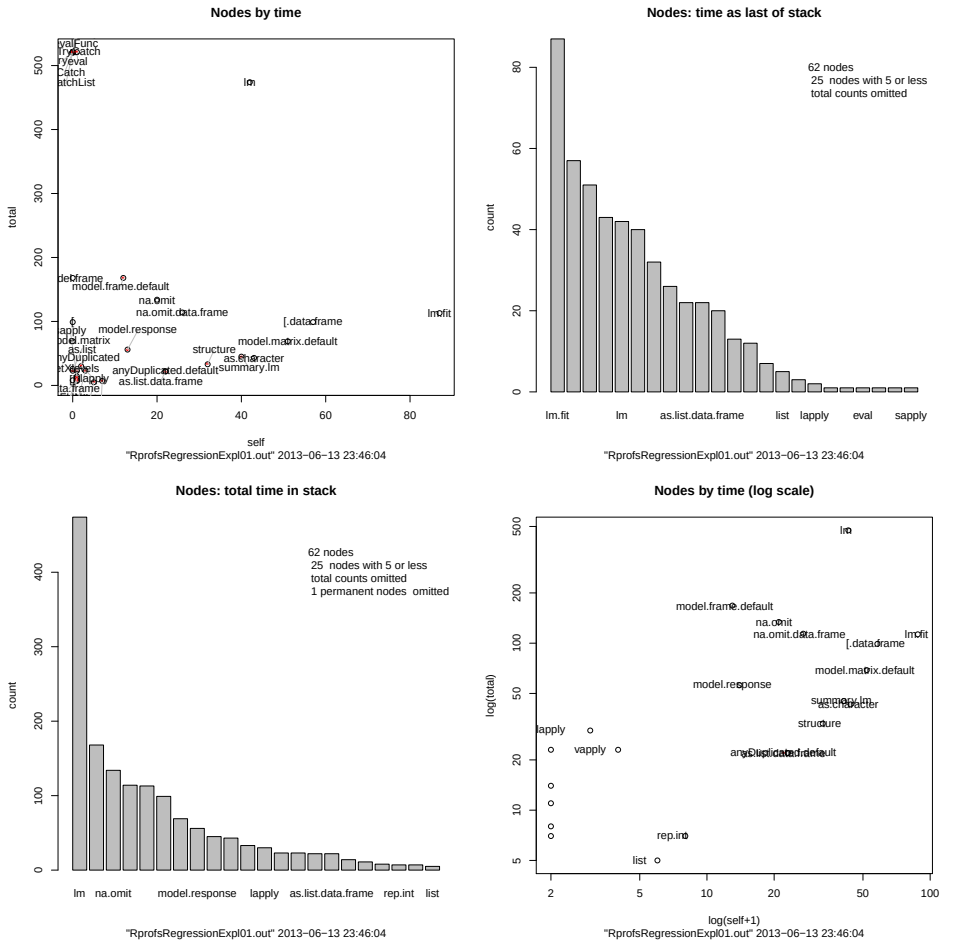
```
newchopnode <- function(nodenames, chop) {
tmpname <- paste("<",as.character(nodenames[chop]),">")
# chec for existing.
# add if necessary
tmpname
}
chopstack <- function(x , chop, replacement)
{
# is chop in x`
# y: cut x.
# merge x <- head + replacement + tiail
return(x)
}
```

5. YYY

5.0.1. *Plot.* Looking at lists of numbers is not too informative. We get a first impression by plotting the data.

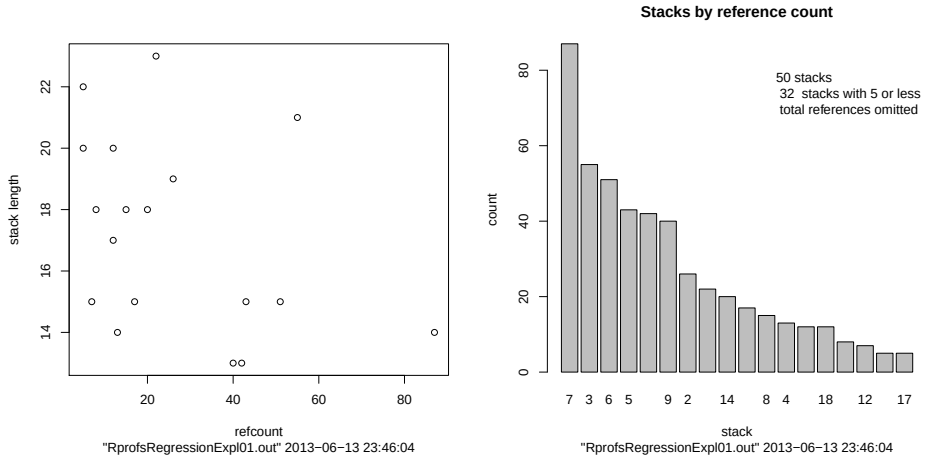
Input

```
#plot_nodes(sprof01, col=nodescol[nodescore])
oldpar <- par(mfrow=c(2,2))
plot_nodes(sprof01)
par(oldpar)
```



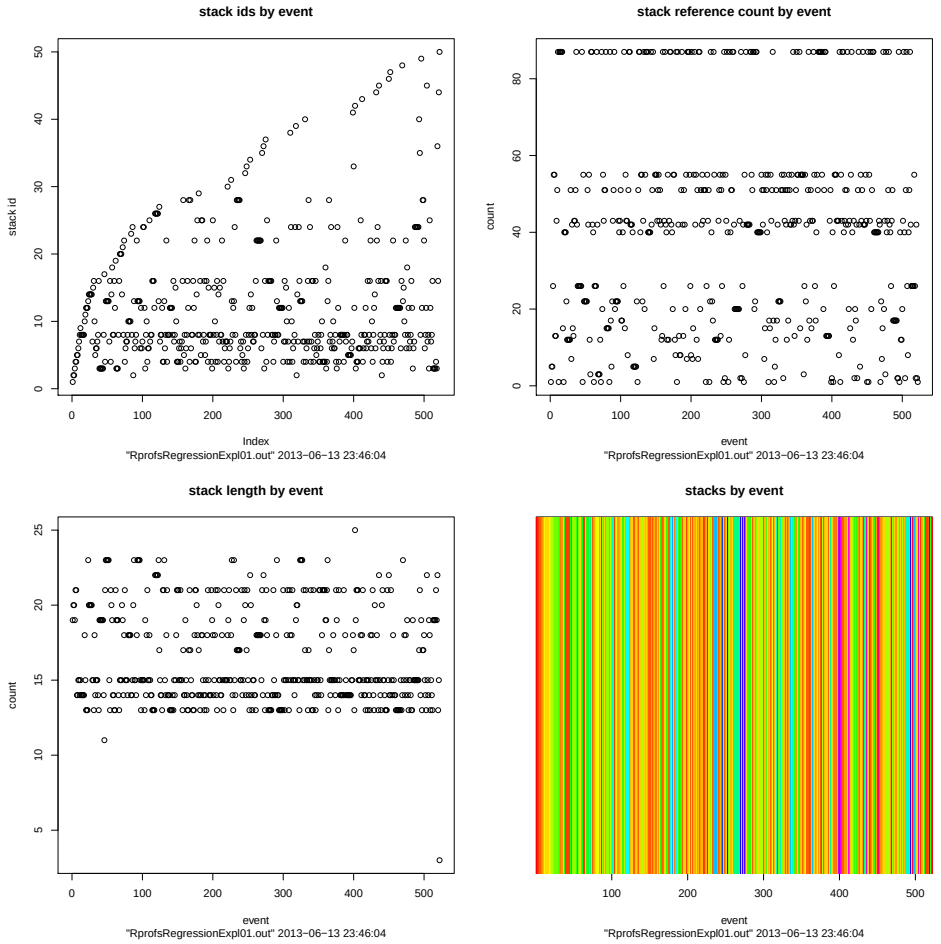
Input

```
oldpar <- par(mfrow=c(1,2))
plot_stacks(sprof01)
par(oldpar)
```



Input

```
oldpar <-par(mfrow=c(2,2))
plot_profiles(sprof01)
par(oldpar)
```



The *plot()* method for *sprof* objects concatenates these three functions.

5.1. **analysis.**

Input

```
profile_nodes_rrle <- rrle(profile_nodes)
str(profile_nodes_rrle)
```

Output

```
List of 12
 $ :List of 2
  ..$ lengths: int [1:361] 6 3 1 7 1 1 1 1 1 6 ...
  ..$ values : int [1:361] 22 39 37 30 4 2 NA NA NA 22 ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:407] 6 1 1 1 1 1 1 1 1 1 ...
  ..$ values : int [1:407] 22 NA NA 14 38 NA 27 NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:427] 6 1 1 1 1 1 1 1 1 1 ...
```

```
  ..$ values : int [1:427] 35 NA NA NA NA NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:427] 6 1 1 1 1 1 1 1 1 ...
  ..$ values : int [1:427] 36 NA NA NA NA NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:450] 1 2 3 1 1 1 1 1 1 1 ...
  ..$ values : int [1:450] 53 22 40 NA NA NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:466] 1 2 3 1 1 1 1 1 1 1 ...
  ..$ values : int [1:466] 27 22 41 NA NA NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:489] 1 2 1 2 1 1 1 1 1 1 ...
  ..$ values : int [1:489] NA 28 NA 5 NA NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:494] 1 1 1 1 2 1 1 1 1 1 ...
  ..$ values : int [1:494] NA NA NA NA 6 NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:508] 1 1 1 1 1 1 1 1 1 1 ...
  ..$ values : int [1:508] NA NA NA NA NA NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:512] 1 1 1 1 1 1 1 1 1 1 ...
  ..$ values : int [1:512] NA NA NA NA NA NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:522] 1 1 1 1 1 1 1 1 1 1 ...
  ..$ values : int [1:522] NA NA NA NA NA NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
 $ :List of 2
  ..$ lengths: int [1:522] 1 1 1 1 1 1 1 1 1 1 ...
  ..$ values : int [1:522] NA NA NA NA NA NA NA NA NA NA ...
  ..- attr(*, "class")= chr "rle"
```

5.2. **trimming.**

Input

```
trimstacks <- function(sprof, level){
lapply(sprof$stacks$nodes, function(x) {x[-(1:level)]})
}
```

Input

```
sprof01Tr <- trimstacks(sprof01, 11)
#profile_nodesTr <- profiles_matrix(sprof01Tr)
#image(x=1:ncol(profile_nodesTr),y=1:nrow(profile_nodesTr), t(profile_nodesTr),xlab="event", ylab="dep
```

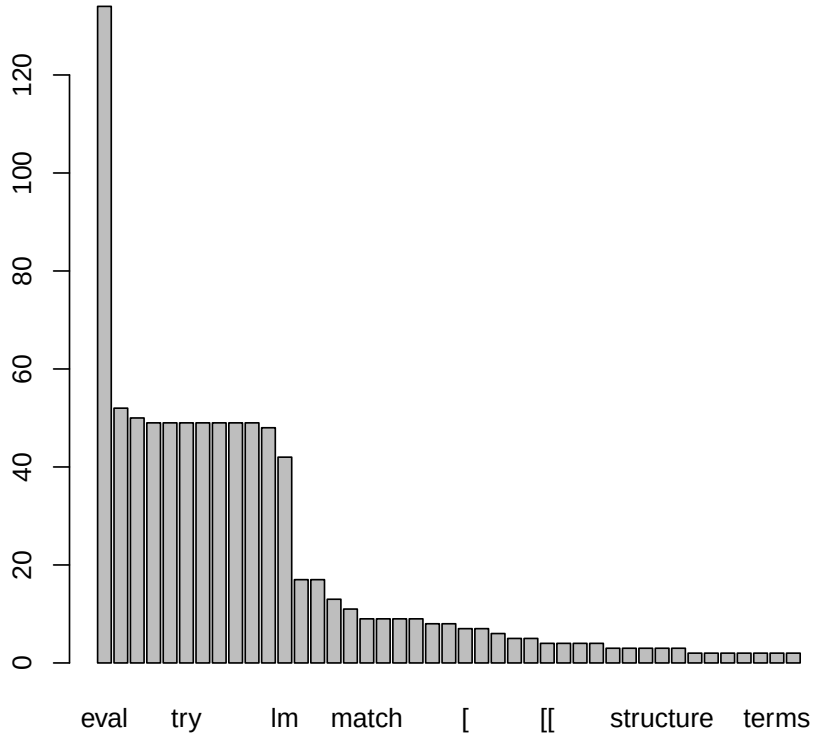
Input

```
nodefreq <- rep(0,length(sprof01$nodes$name))
for (i in (1:length(sprof01$stacks$nodes))){
        nodefreq <- nodefreq +
                table( factor(sprof01$stacks$nodes[[i]],
                        levels <- 1:length(sprof01$nodes$name),
                        ordered=FALSE))
        }
names(nodefreq) <- sprof01$nodes$name
```

Top frequent nodes.

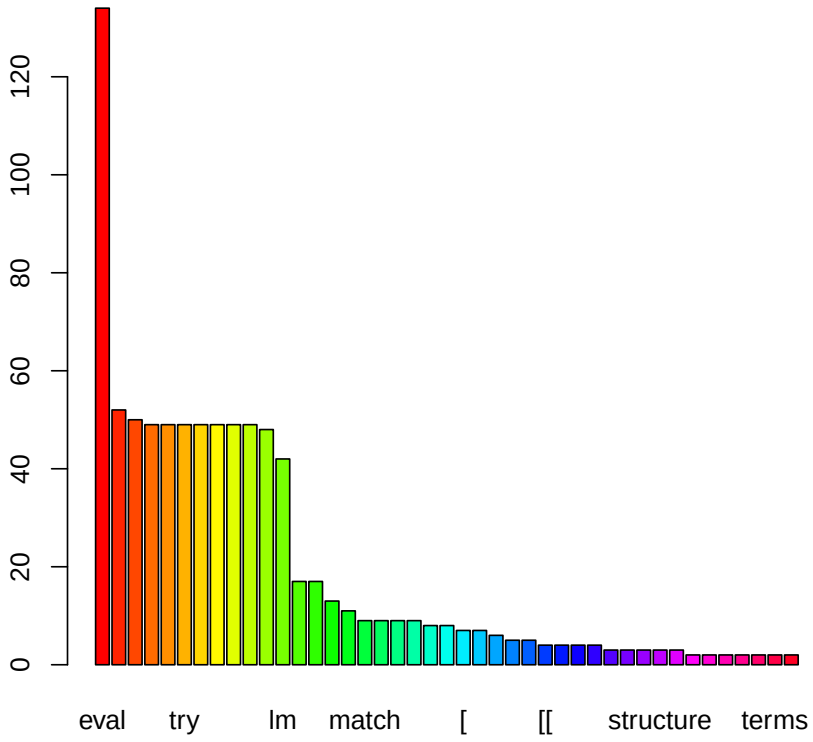
Input

```
ndf <- nodefreq[nodefreq>1]
ondf <- order(ndf,decreasing=TRUE)
barplot(ndf[ondf])
```



Input

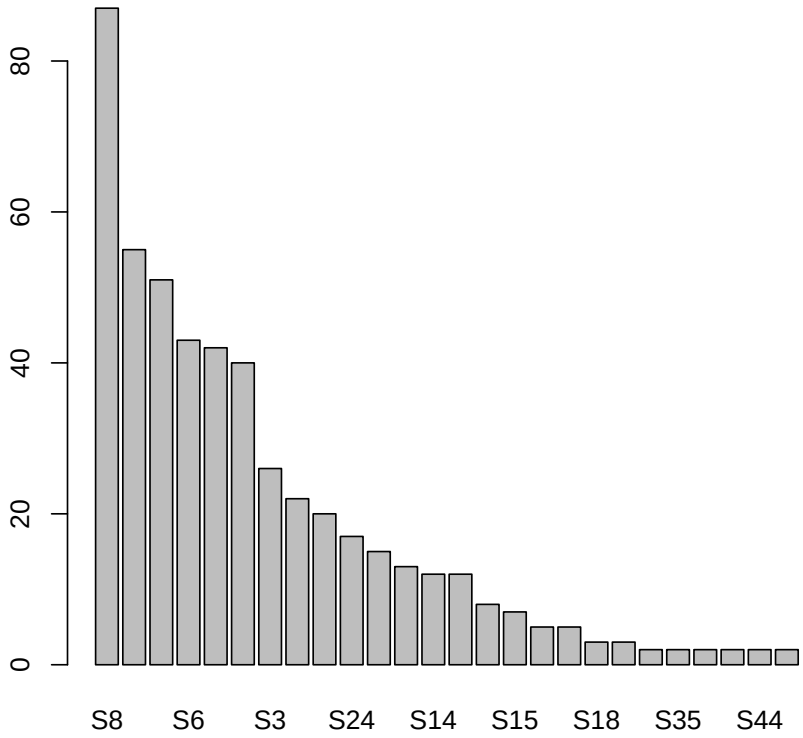
```
barplot(ndf[ondf], col=rainbow(length(ondf)))
```



Top frequent stacks.

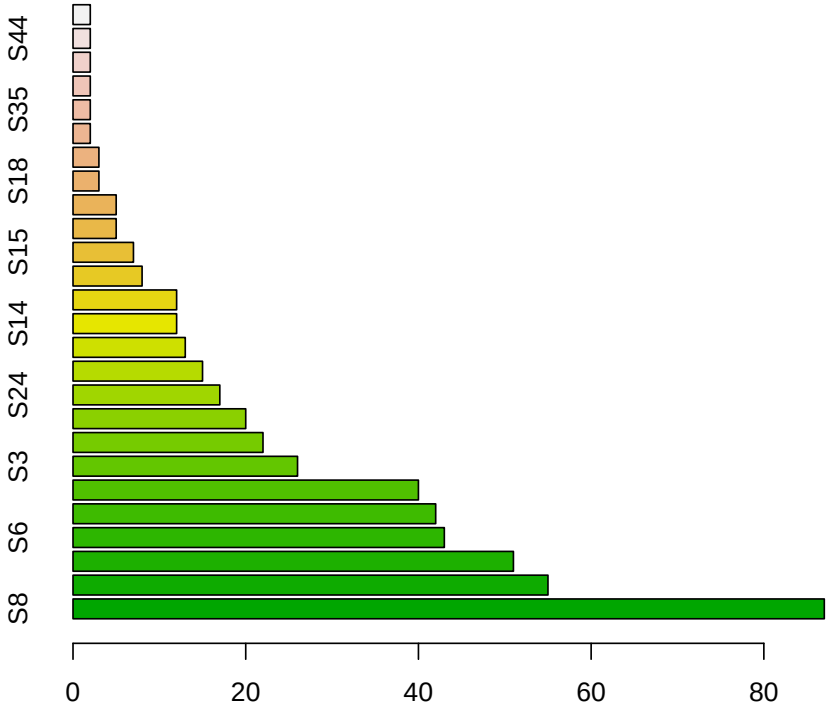
Input

```
x <- sprof01
xsrc <- as.matrix(x$stacks$refcount)
rownames(xsrc) <- rownames(xsrc, do.NULL=FALSE, prefix="S")
#stf <- x$stacks$refcount[x$stacks$refcount>1]
#names(stf) <-  x$stacks$shortname[x$stacks$refcount>1]
stf <- xsrc[xsrc>1]
names(stf) <- rownames(xsrc)[xsrc>1]
ostf <- order(stf,decreasing=TRUE)
barplot(stf[ostf])
```



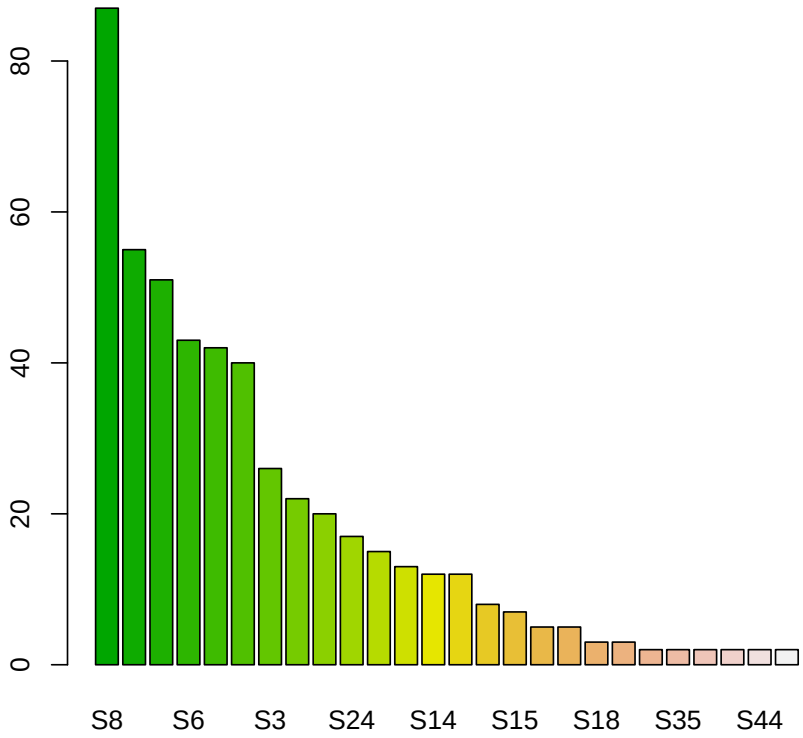
Input

```
barplot(stf[ostf], col=terrain.colors(length(ostf)), horiz=TRUE)
```



Input

```
barplot(stf[ostf], col=terrain.colors(length(ostf)))
```



There is no statistics on profiles. Profiling are our elementary data. However we can link to our derived data to get a more informative display. For example, going one step back we can encode stacks and use these colour codes in the display of a profile.

Or going two steps back, we can encode nodes in colour, giving coloured stacks, and use these in the display of profile data.

6. Standard output

Input

```
sprof <- sprof01
```

6.1. **Summary.**

Input

```
summary_nodes(sprof)
```

Output

	shortname	root	leaf	self.time	self.pct	total.time
!	!	-	LEAF	2	Inf	0
..getNamespace	..gN	-	-	0	NaN	0
.deparseOpts	.dpO	-	LEAF	2	Inf	0
.getXlevels	.gtX	-	-	0	NaN	0
[	[	-	-	0	NaN	0
[.data.frame	[.d.	-	LEAF	57	Inf	0
[[	[[	-	-	0	NaN	0
[[.data.frame	[[..	-	LEAF	1	Inf	0
%in%	%in%	-	LEAF	1	Inf	0
<Anonymous>	<An>	-	LEAF	6	Inf	0
$	$	-	LEAF	1	Inf	0
anyDuplicated	anyD	-	LEAF	1	Inf	0
anyDuplicated.default	anD.	-	LEAF	22	Inf	0
as.character	as.c	-	LEAF	43	Inf	0
as.list	as.l	-	-	0	NaN	0
as.list.data.frame	a...	-	LEAF	22	Inf	0
as.list.default	as..	-	LEAF	1	Inf	0
as.name	as.n	-	LEAF	1	Inf	0
coef	coef	-	LEAF	1	Inf	0
deparse	dprs	-	LEAF	1	Inf	0
doTryCatch	dTrC	-	-	0	NaN	0
eval	eval	-	LEAF	1	Inf	0
evalFunc	evlF	-	-	0	NaN	0
file	file	-	LEAF	1	Inf	0
FUN	FUN	-	LEAF	1	Inf	0
lapply	lppl	-	LEAF	2	Inf	0
lazyLoadDBfetch	lLDB	-	LEAF	2	Inf	0
list	list	-	LEAF	5	Inf	0
lm	lm	-	LEAF	42	Inf	0
lm.fit	lm.f	-	LEAF	87	Inf	0
match	mtch	-	LEAF	1	Inf	0
mean	mean	-	-	0	NaN	0
mean.default	mn.d	-	LEAF	2	Inf	0
mode	mode	-	LEAF	2	Inf	0
model.frame	mdl.f	-	-	0	NaN	0
model.frame.default	mdl.f.	-	LEAF	12	Inf	0
model.matrix	mdl.m	-	-	0	NaN	0
model.matrix.default	mdl.m.	-	LEAF	51	Inf	0
model.response	mdl.r	-	LEAF	13	Inf	0
na.omit	n.mt	-	LEAF	20	Inf	0
na.omit.data.frame	n...	-	LEAF	26	Inf	0
names	nams	-	LEAF	2	Inf	0
NCOL	NCOL	-	LEAF	1	Inf	0
paste	past	-	-	0	NaN	0
pmatch	pmtc	-	LEAF	2	Inf	0
rep.int	rp.n	-	LEAF	7	Inf	0
sapply	sppl	-	LEAF	1	Inf	0
simplify2array	smp2	-	-	0	NaN	0
structure	strc	-	LEAF	32	Inf	0
summary	smmr	-	-	0	NaN	0
summary.lm	smm.	-	LEAF	40	Inf	0

```
Sweave                    Swev ROOT    -         0      NaN          0
terms                     trms    -    -         0      NaN          0
terms.formula             trm.    - LEAF         1      Inf          0
try                        try    -    -         0      NaN          0
tryCatch                  tryC    -    -         0      NaN          0
tryCatchList              trCL    -    -         0      NaN          0
tryCatchOne               trCO    -    -         0      NaN          0
unique                    uniq    - LEAF         3      Inf          0
unlist                    unls    -    -         0      NaN          0
vapply                    vppl    - LEAF         3      Inf          0
withVisible               wthV    -    -         0      NaN          0
                       total.pct
!                            NaN
..getNamespace               NaN
.deparseOpts                 NaN
.getXlevels                  NaN
[                            NaN
[.data.frame                 NaN
[[                           NaN
[[.data.frame                NaN
%in%                         NaN
<Anonymous>                  NaN
$                            NaN
anyDuplicated                NaN
anyDuplicated.default        NaN
as.character                 NaN
as.list                      NaN
as.list.data.frame           NaN
as.list.default              NaN
as.name                      NaN
coef                         NaN
deparse                      NaN
doTryCatch                   NaN
eval                         NaN
evalFunc                     NaN
file                         NaN
FUN                          NaN
lapply                       NaN
lazyLoadDBfetch              NaN
list                         NaN
lm                           NaN
lm.fit                       NaN
match                        NaN
mean                         NaN
mean.default                 NaN
mode                         NaN
model.frame                  NaN
model.frame.default          NaN
model.matrix                 NaN
model.matrix.default         NaN
model.response               NaN
na.omit                      NaN
na.omit.data.frame           NaN
```

```
names                   NaN
NCOL                    NaN
paste                   NaN
pmatch                  NaN
rep.int                 NaN
sapply                  NaN
simplify2array          NaN
structure               NaN
summary                 NaN
summary.lm              NaN
Sweave                  NaN
terms                   NaN
terms.formula           NaN
try                     NaN
tryCatch                NaN
tryCatchList            NaN
tryCatchOne             NaN
unique                  NaN
unlist                  NaN
vapply                  NaN
withVisible             NaN
```

Input

```
summary_stacks(sprof)
```

Output

```
   len refcount root leafs
1   19        1   52    27
2   20        5   52    28
3   19       26   52    41
4   21       55   52     6
5   14       13   52    39
6   15       43   52    14
7   15       51   52    38
8   14       87   52    30
9   15        1   52    27
10  18       15   52    49
11  15        1   52    18
12  13       40   52    51
13  23       22   52    13
14  20       12   52    16
15  15        7   52    46
16  13       42   52    29
17  11        1   52    22
18  19        3   52    59
19  21        1   52     8
20  15        3   52    61
21  19        1   52    25
22  18       20   52    40
23  14        1   52    11
24  15       17   52    49
25  18        8   52    16
26  22        5   52    10
```

```
27  17        1   52    47
28  17       12   52    36
29  17        1   52    31
30  18        1   52     3
31  18        1   52    12
32  20        1   52     3
33  17        2   52    16
34  22        1   52     9
35  21        2   52    45
36  22        2   52     1
37  19        1   52    54
38  18        1   52    10
39  19        1   52    26
40  17        2   52     6
41  18        1   52    17
42  25        1   52    34
43  18        1   52    20
44  15        2   52    33
45  22        2   52    42
46  22        1   52    34
47  14        1   52    43
48  14        1   52    19
49  19        1   52    26
50   3        1   52    24
```

Input

```
summary_profiles(sprof)
```

Output

```
$id
[1] "Profile Summary Tue Jul  9 23:03:38 2013"

$len
[1] 522

$uniquestacks
[1] 50

$nr_runs
[1] 396
```

The *summary()* method for *sprof* objects concatenates these three functions.

6.2. **Print.**

Input

```
print_nodes(sprof)
```

Output

```
                    shortname root leaf self.time self.pct total.time
!                           !    - LEAF         2      Inf          0
..getNamespace             ..gN    -    -         0      NaN          0
.deparseOpts               .dpO    - LEAF         2      Inf          0
```

.getXlevels	.gtX	-	-	0	NaN	0
[	[	-	-	0	NaN	0
[.data.frame	[.d.	-	LEAF	57	Inf	0
[[	[[	-	-	0	NaN	0
[[.data.frame	[[..	-	LEAF	1	Inf	0
%in%	%in%	-	LEAF	1	Inf	0
<Anonymous>	<An>	-	LEAF	6	Inf	0
$	$	-	LEAF	1	Inf	0
anyDuplicated	anyD	-	LEAF	1	Inf	0
anyDuplicated.default	anD.	-	LEAF	22	Inf	0
as.character	as.c	-	LEAF	43	Inf	0
as.list	as.l	-	-	0	NaN	0
as.list.data.frame	a...	-	LEAF	22	Inf	0
as.list.default	as..	-	LEAF	1	Inf	0
as.name	as.n	-	LEAF	1	Inf	0
coef	coef	-	LEAF	1	Inf	0
deparse	dprs	-	LEAF	1	Inf	0
doTryCatch	dTrC	-	-	0	NaN	0
eval	eval	-	LEAF	1	Inf	0
evalFunc	evlF	-	-	0	NaN	0
file	file	-	LEAF	1	Inf	0
FUN	FUN	-	LEAF	1	Inf	0
lapply	lppl	-	LEAF	2	Inf	0
lazyLoadDBfetch	lLDB	-	LEAF	2	Inf	0
list	list	-	LEAF	5	Inf	0
lm	lm	-	LEAF	42	Inf	0
lm.fit	lm.f	-	LEAF	87	Inf	0
match	mtch	-	LEAF	1	Inf	0
mean	mean	-	-	0	NaN	0
mean.default	mn.d	-	LEAF	2	Inf	0
mode	mode	-	LEAF	2	Inf	0
model.frame	mdl.f	-	-	0	NaN	0
model.frame.default	mdl.f.	-	LEAF	12	Inf	0
model.matrix	mdl.m	-	-	0	NaN	0
model.matrix.default	mdl.m.	-	LEAF	51	Inf	0
model.response	mdl.r	-	LEAF	13	Inf	0
na.omit	n.mt	-	LEAF	20	Inf	0
na.omit.data.frame	n...	-	LEAF	26	Inf	0
names	nams	-	LEAF	2	Inf	0
NCOL	NCOL	-	LEAF	1	Inf	0
paste	past	-	-	0	NaN	0
pmatch	pmtc	-	LEAF	2	Inf	0
rep.int	rp.n	-	LEAF	7	Inf	0
sapply	sppl	-	LEAF	1	Inf	0
simplify2array	smp2	-	-	0	NaN	0
structure	strc	-	LEAF	32	Inf	0
summary	smmr	-	-	0	NaN	0
summary.lm	smm.	-	LEAF	40	Inf	0
Sweave	Swev	ROOT	-	0	NaN	0
terms	trms	-	-	0	NaN	0
terms.formula	trm.	-	LEAF	1	Inf	0
try	try	-	-	0	NaN	0
tryCatch	tryC	-	-	0	NaN	0

tryCatchList	trCL	-	-	0	NaN	0
tryCatchOne	trCO	-	-	0	NaN	0
unique	uniq	-	LEAF	3	Inf	0
unlist	unls	-	-	0	NaN	0
vapply	vppl	-	LEAF	3	Inf	0
withVisible	wthV	-	-	0	NaN	0

	total.pct
!	NaN
..getNamespace	NaN
.deparseOpts	NaN
.getXlevels	NaN
[	NaN
[.data.frame	NaN
[[	NaN
[[.data.frame	NaN
%in%	NaN
<Anonymous>	NaN
$	NaN
anyDuplicated	NaN
anyDuplicated.default	NaN
as.character	NaN
as.list	NaN
as.list.data.frame	NaN
as.list.default	NaN
as.name	NaN
coef	NaN
deparse	NaN
doTryCatch	NaN
eval	NaN
evalFunc	NaN
file	NaN
FUN	NaN
lapply	NaN
lazyLoadDBfetch	NaN
list	NaN
lm	NaN
lm.fit	NaN
match	NaN
mean	NaN
mean.default	NaN
mode	NaN
model.frame	NaN
model.frame.default	NaN
model.matrix	NaN
model.matrix.default	NaN
model.response	NaN
na.omit	NaN
na.omit.data.frame	NaN
names	NaN
NCOL	NaN
paste	NaN
pmatch	NaN
rep.int	NaN

```
sapply                  NaN
simplify2array          NaN
structure               NaN
summary                 NaN
summary.lm              NaN
Sweave                  NaN
terms                   NaN
terms.formula           NaN
try                     NaN
tryCatch                NaN
tryCatchList            NaN
tryCatchOne             NaN
unique                  NaN
unlist                  NaN
vapply                  NaN
withVisible             NaN
```

Input

```
print_stacks(sprof)
```

Output

```
   len refcount root leafs
1   19        1   52    27
2   20        5   52    28
3   19       26   52    41
4   21       55   52     6
5   14       13   52    39
6   15       43   52    14
7   15       51   52    38
8   14       87   52    30
9   15        1   52    27
10  18       15   52    49
11  15        1   52    18
12  13       40   52    51
13  23       22   52    13
14  20       12   52    16
15  15        7   52    46
16  13       42   52    29
17  11        1   52    22
18  19        3   52    59
19  21        1   52     8
20  15        3   52    61
21  19        1   52    25
22  18       20   52    40
23  14        1   52    11
24  15       17   52    49
25  18        8   52    16
26  22        5   52    10
27  17        1   52    47
28  17       12   52    36
29  17        1   52    31
30  18        1   52     3
31  18        1   52    12
```

```
32  20        1   52    3
33  17        2   52   16
34  22        1   52    9
35  21        2   52   45
36  22        2   52    1
37  19        1   52   54
38  18        1   52   10
39  19        1   52   26
40  17        2   52    6
41  18        1   52   17
42  25        1   52   34
43  18        1   52   20
44  15        2   52   33
45  22        2   52   42
46  22        1   52   34
47  14        1   52   43
48  14        1   52   19
49  19        1   52   26
50   3        1   52   24
```

Input

```
print_profiles(sprof)
```

Output

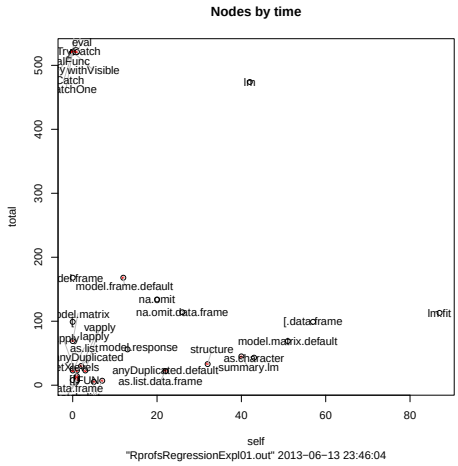
```
$id
[1] "Profile Summary Tue Jul  9 23:03:39 2013"

$len
[1] 522

$uniquestacks
[1] 50

$nr_runs
[1] 396
```

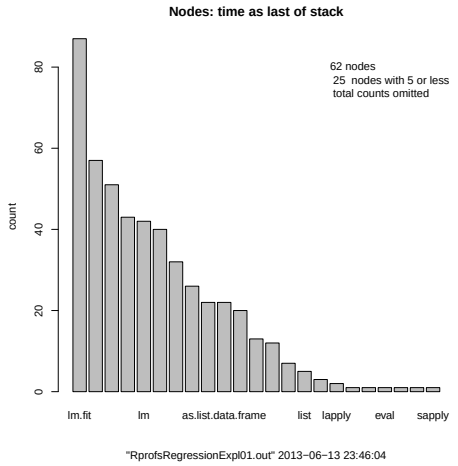
The *print()* method for *sprof* objects concatenates these three functions.

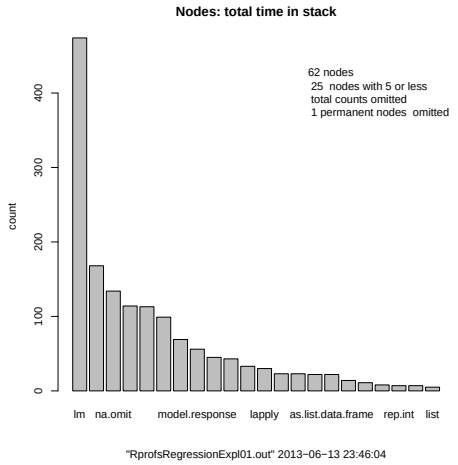
6.3. **Plot.**

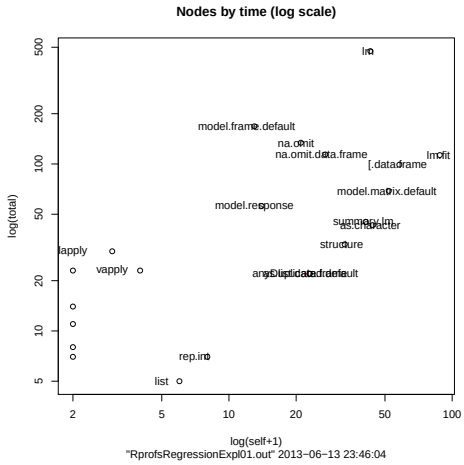
Input

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



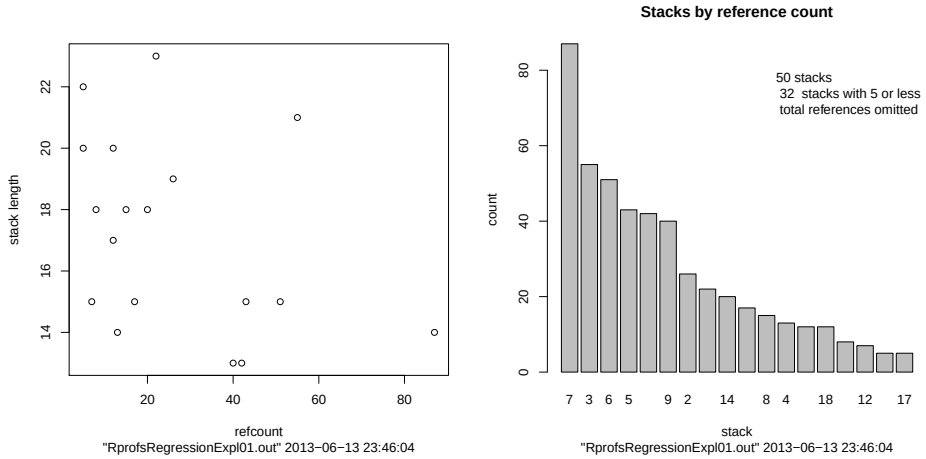






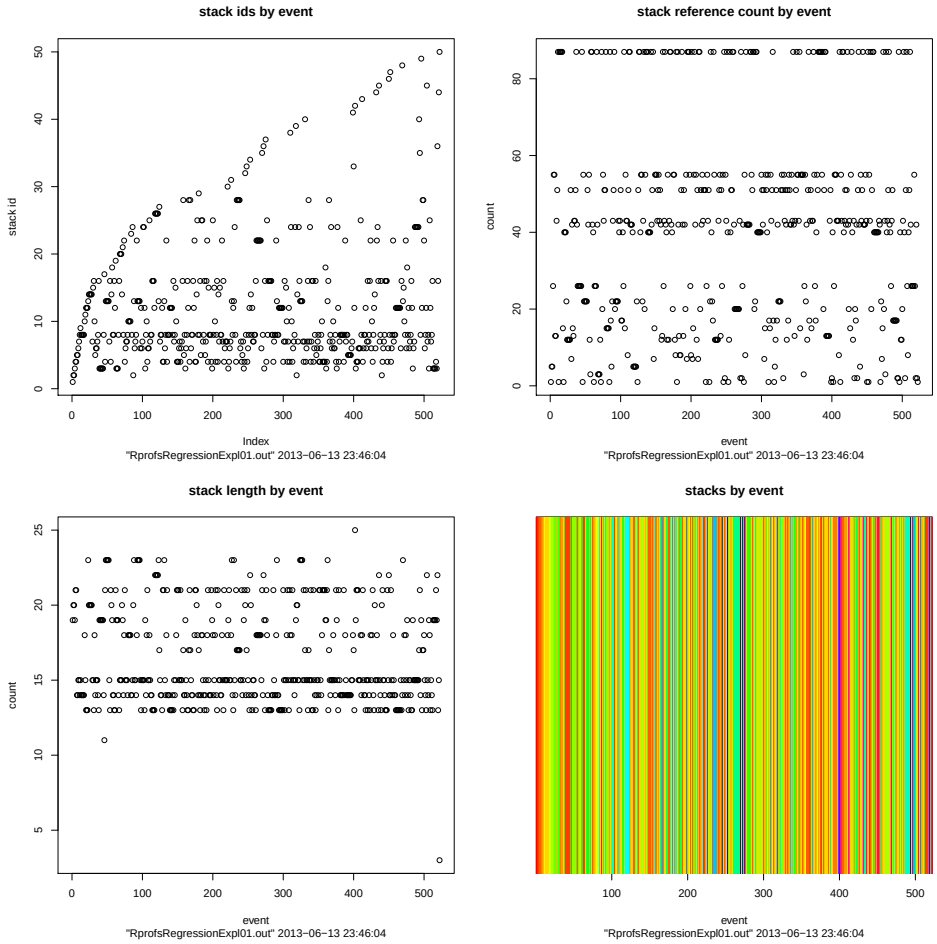
Input

```
oldpar<- par(mfrow=c(1,2))
plot_stacks(sprof)
par(oldpar)
```



Input

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



The *plot()* method for *sprof* objects concatenates these three functions.

7. Graph

In this section, we use the recent version of our example, *sprof02* for demonstration. You con re-run it, using your *sprof* data by modifying this instruction:

Input

```
sprof <- sprof02
```

To interface *sprof* to a graph handling package, *until()* can extract the adjacency matrix from the profile.

Input

```
sprofadj <- adjacency(sprof)
```

This is a format any graph package can handle.

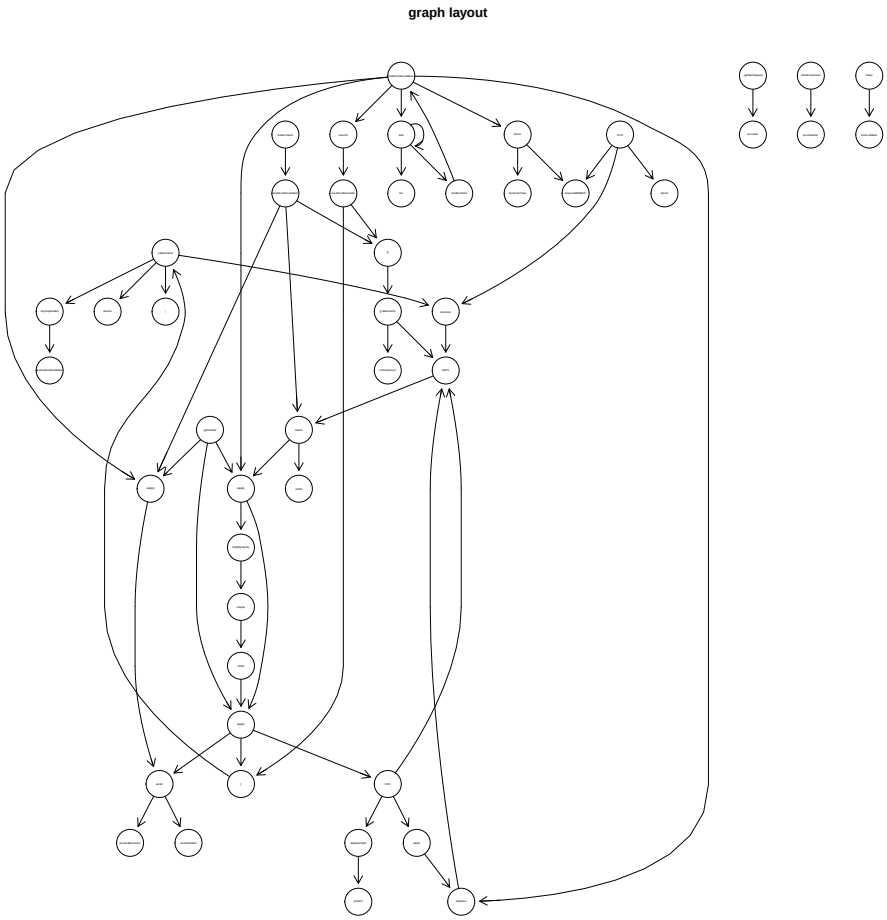
7.1. **graph Package.**

Input

```
library(graph)
sprofadjNEL <- as(sprofadj,"graphNEL")
```

Input

```
plot(sprofadjNEL,  main="graph layout", cex.main=2)
#detach("package:graph")
```



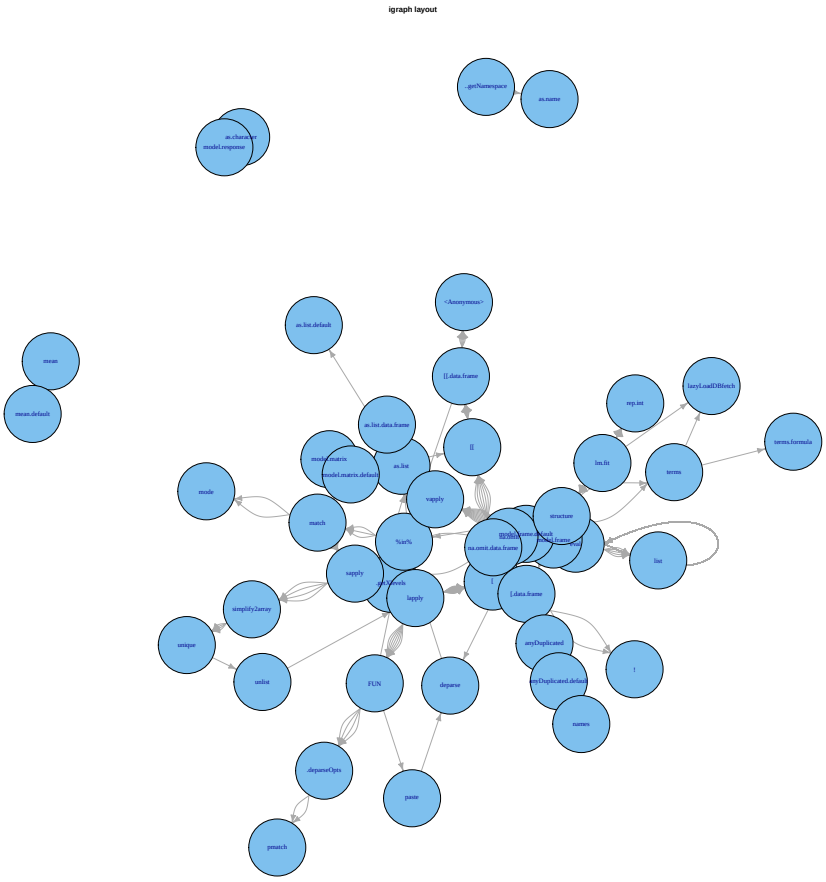
7.1.1. *igraph Package.*

Input

```
library(igraph)
sprofig <- graph.adjacency(sprofadj)
```

Input

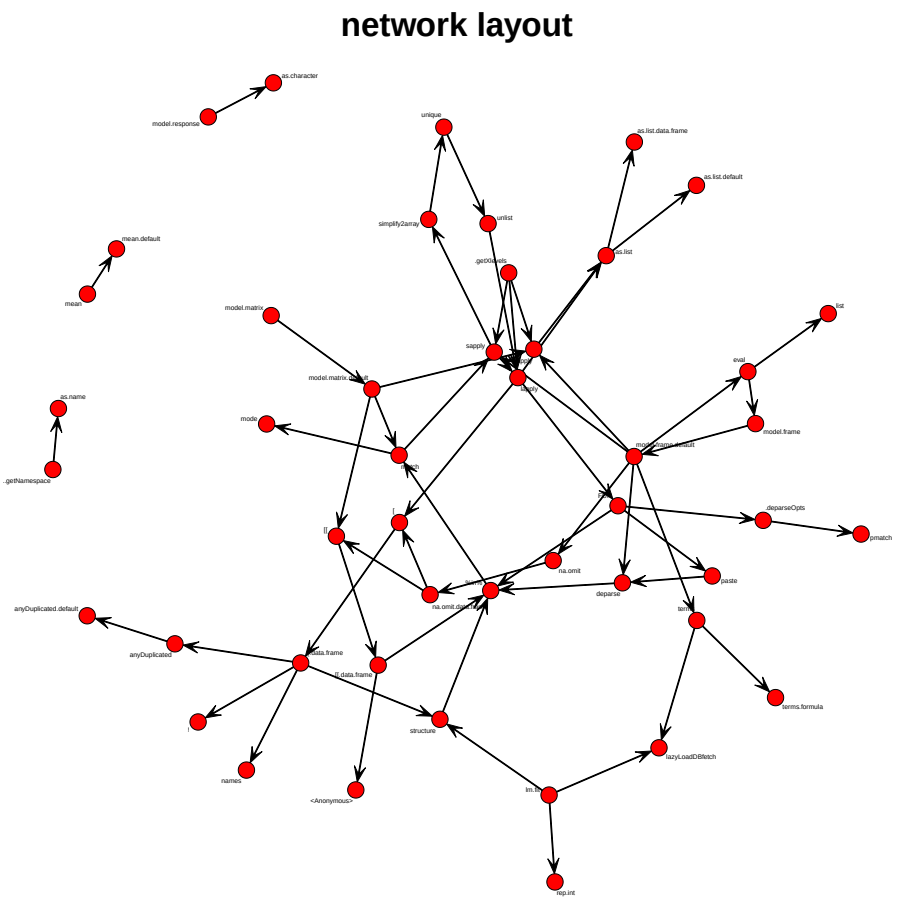
```
#plot(sprofig, main="igraph layout", cex.main=5)
plot(sprofig, main="igraph layout")
detach("package:igraph")
```



7.1.2. *network Package.*

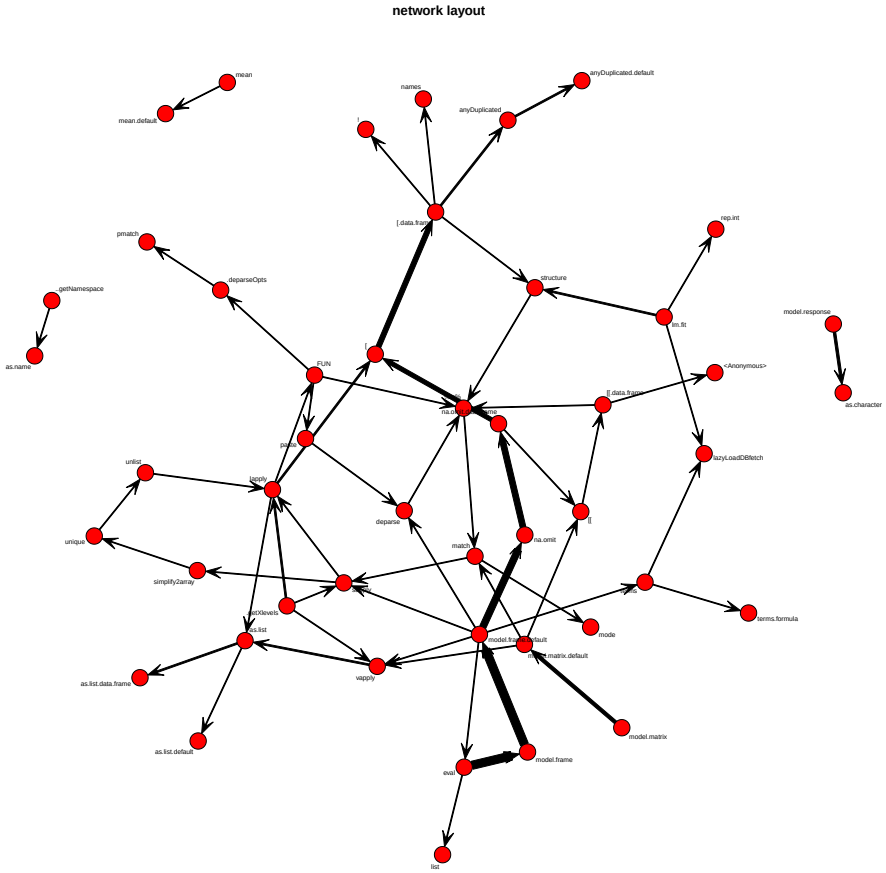
Input

```
library(network)
nwsprofadj <- as.network(sprofadj) # names is not imported
network.vertex.names(nwsprofadj) <- rownames(sprofadj) # not honoured by plot
plot(nwsprofadj, label=rownames(sprofadj), main="network layout", cex.main=5)
```



Input

```
edge.lwd <- trunc(sprofadj/max(sprofadj)*10)+1
plot(nwsprofadj, label=rownames(sprofadj), main="network layout", cex.main=2, edge.lwd=edge.lwd)
detach("package:network")
```


network layout
mean
mean.default
names
anyDuplicated
anyDuplicated.default
[.data.frame
rep.int
pmatch
structure
parseOpts
getNamespace
as.name
FUN
as.fit
model.response
<Anonymous>
as.character
lazyLoadDBfetch
unlist
lapply
deparse
unique
match
na.omit
simplify2array
terms.formula
mode
as.list
vapply
as.list.data.frame
as.list.default
model.matrix
model.frame
eval
list

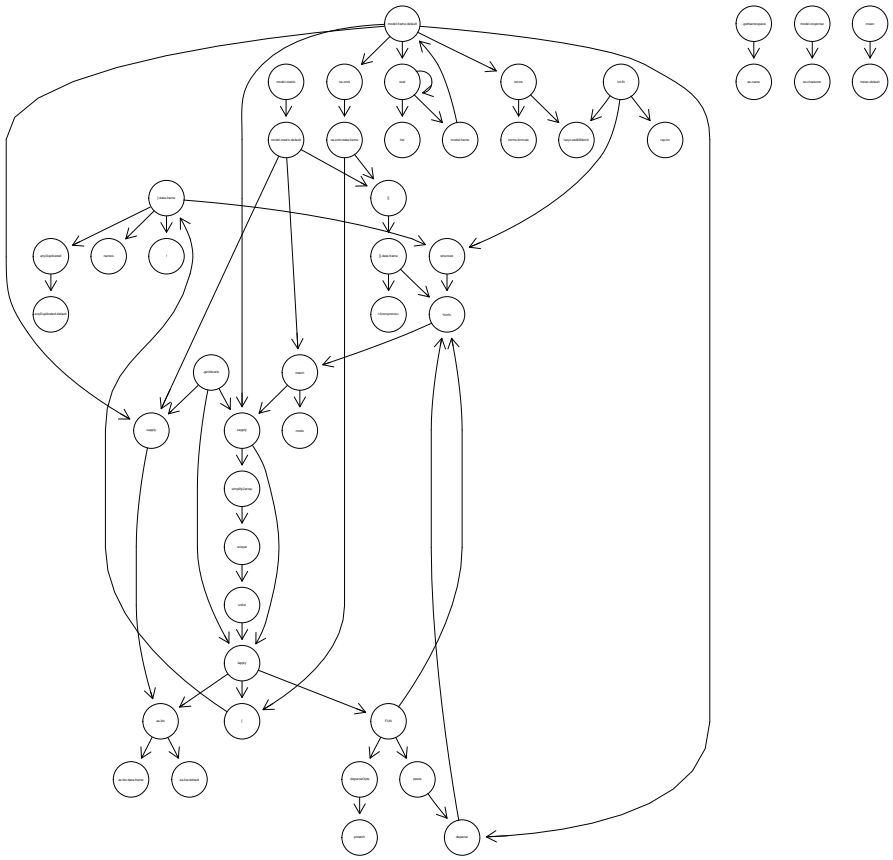
7.1.3. *Rgraphviz Package.*

Input

```
library(Rgraphviz)
sprofadjRag <- agopen(sprofadjNEL, name="Rprof Example")
```

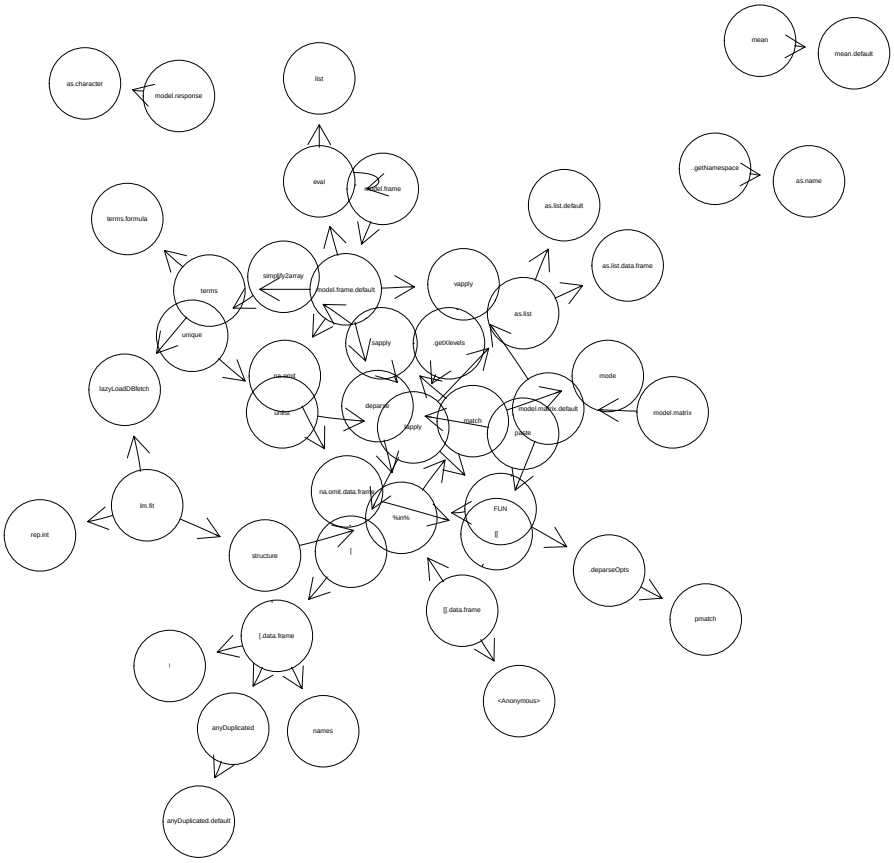
Input

```
plot(sprofadjRag, main="Graphviz dot layout", cex.main=5)
```



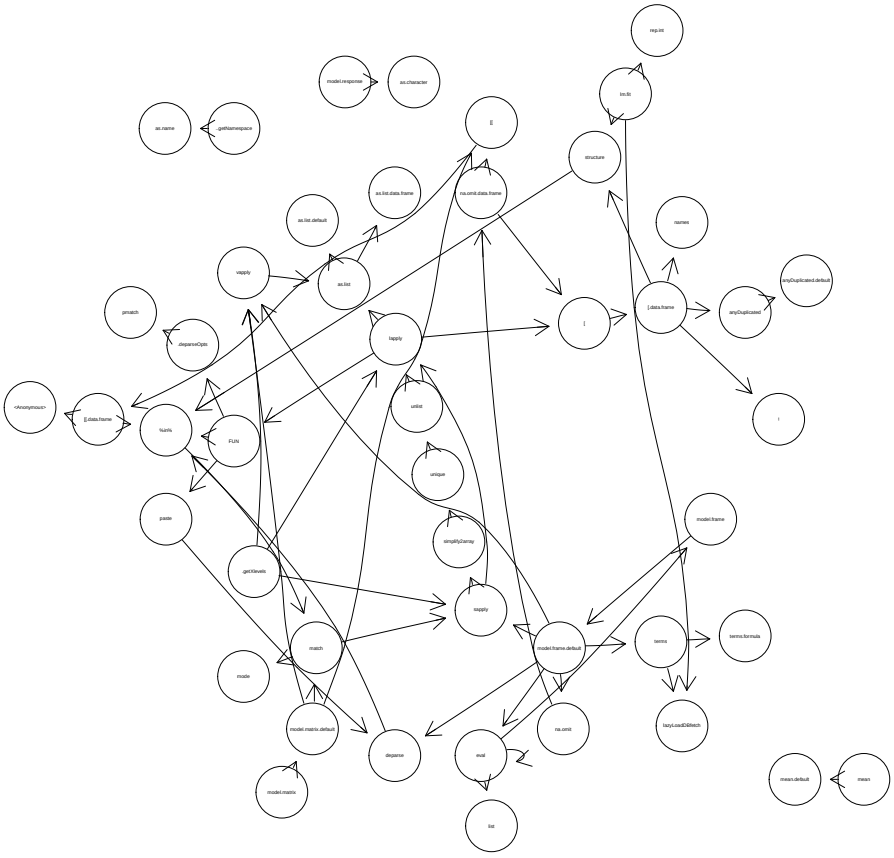
Input

```
plot(sprofadjRag,"neato", main="Graphviz neto layout", cex.main=5)
```



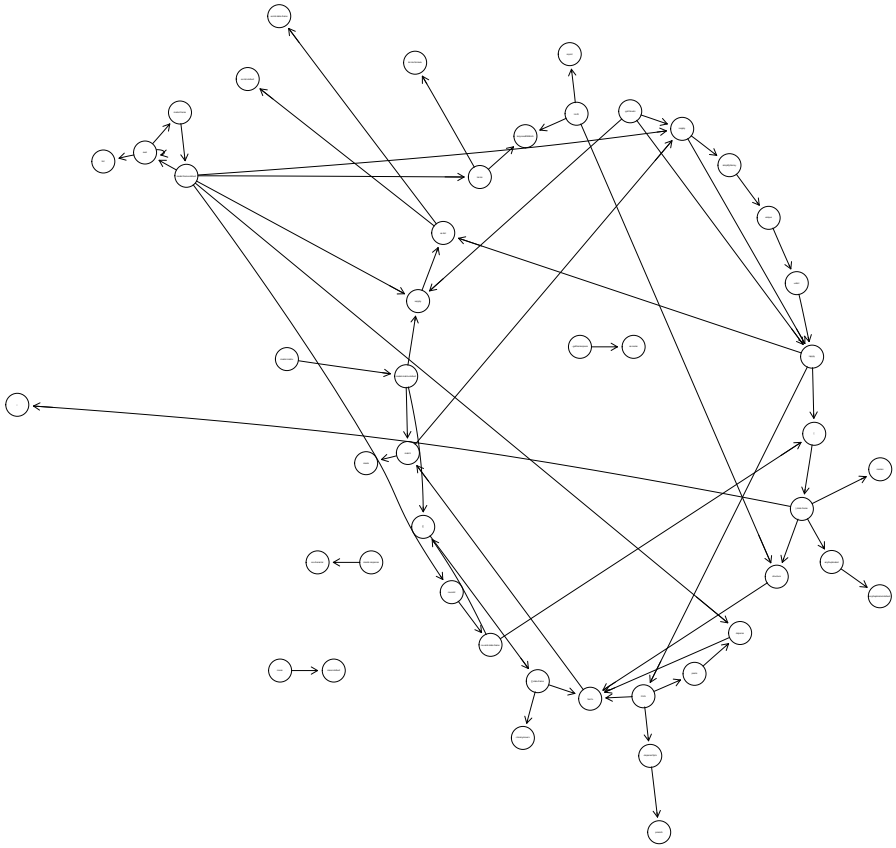
Input

```
plot(sprofadjRag,"twopi", main="Graphviz twopi layout", cex.main=5)
```



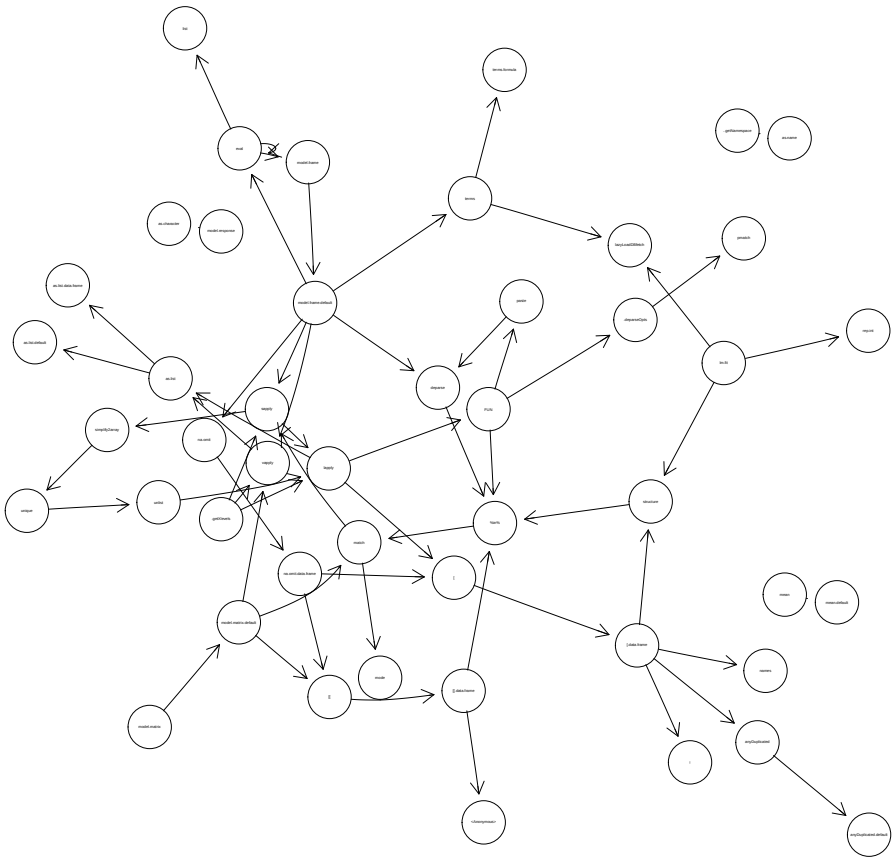
Input

```
plot(sprofadjRag,"circo", main="Graphviz circo layout", cex.main=5)
```



Input

```
plot(sprofadjRag,"fdp", main="Graphviz fdp layout", cex.main=5)
```



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R session info:

- R version 3.0.1 (2013-05-16), `x86_64-apple-darwin10.8.0`
- Locale: `en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8`
- Base packages: base, datasets, graphics, grDevices, grid, methods, stats, utils
- Other packages: graph 1.38.2, RColorBrewer 1.0-5, Rcpp 0.10.3, Rgraphviz 2.4.0, sprof 0.0-5, wordcloud 2.4, xtable 1.7-1
- Loaded via a namespace (and not attached): BiocGenerics 0.6.0, igraph 0.6.5-2, network 1.7.2, parallel 3.0.1, slam 0.1-28, stats4 3.0.1, tools 3.0.1

svn repository info:

```
$HeadURL: svnssh://gsawitzki@svn.r-forge.r-project.org/svnroot/sintro/pkg/sprof/vignettes/sprofiling.Rnw +
$Source: /u/math/j40/cvsroot/lectures/src/insider/profile/Rnw/profile.Rnw,v $
$Id: sprofiling.Rnw 163 2013-07-09 07:29:03Z gsawitzki $
$Revision: 163 $
$Date: 2013-07-09 09:29:03 0200(Tue, 09Jul2013)+
$name:  $
$Author: gsawitzki $
```

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