

# Package ‘proftools’

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## Description

Tools for examining and displaying output from the Rprof R profiling tool.

## Details

**proftools** provides a set of tools for summarizing and displaying time profile output produced by R's [Rprof](#).

The starting point for a profiling analysis using **proftools** is to profile code using [Rprof](#) and then use [readProfileData](#) to read in the profile data into a suitable format for further processing. An alternative is to use the [profileExpr](#) function to handle profiling and reading in one step. The function [filterProfileData](#) can be used to narrow the profile data to particular regions of interest.

The summary functions [funSummary](#) and [callSummary](#) produce summaries at the function and call level. [pathSummary](#) produces a summary for each unique call stack, or path; and [hotPaths](#) identifies and produces path data ordered to show the hottest paths first.

If source information is recorded when profiling then [srcSummary](#) to show profiling by source lines, and [annotateSource](#) produces an annotated version of the source files.

The [plot](#) method for profile data objects can produce call graphs, tree maps, flame graphs, and time graphs; the type argument chooses the particular visualization to produce. These graphs can also be produced by the functions [plotProfileCallGraph](#), [calleeTreeMap](#), and [flameGraph](#).

The function [writeCallgrindFile](#) writes a file for use by the codekcachegrind program available on some operating systems.

[flatProfile](#)

## Examples

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
funSummary(pd)
callSummary(pd)
pathSummary(pd)
hotPaths(pd)
plot(pd)
plot(filterProfileData(pd, focus = "glm", self.pct=1, total.pct=10))
```

---

annotateSource	<i>Annotate Source Files</i>
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---

## Description

Annotates source files with profile information.

## Usage

```
annotateSource(pd, value = c("pct", "time", "hits"), GC = TRUE,
               sep = ": ", show = TRUE, ...)
```

## Arguments

pd	profile data as returned by readProfileData.
value	character; show result as percentage, time, or hits.
GC	logical; include GC information or not.
sep	character; separator between profile info and source lines.
show	logical; if true, show files with file.show.
...	additional arguments for file.show.

## Details

For lines that appear in the stack trace the percent time and, optionally, GC time are shown before each line.

## Value

A list of character vectors of the annotated file lines.

## Author(s)

Luke Tierney

## See Also

[Rprof](#), [summaryRprof](#), [flatProfile](#), [filterProfileData](#), [readProfileData](#), [srcSummary](#)

## Examples

```
## This defines the function rw()
source(system.file("samples", "rw.R", package="proftools"))

## Execute the function and collect profile data
Rprof(tmp <- tempfile(), gc.profiling = TRUE, line.profiling = TRUE)
w <- rw(200000)
Rprof(NULL)
```

```
pd <- readProfileData(tmp)
unlink(tmp)

## Annotate the sources
annotateSource(pd)
```

---

callTreeGraphs                      *Call Tree Graphs*

---

## Description

Produce a flame graph or a callee tree map for the call tree in a profile stack trace.

## Usage

```
flameGraph(pd, svgfile, order = c("hot", "alpha", "time"),
           colormap = NULL, srclines = FALSE, cex = 0.75,
           main = "Call Graph", tooltip = FALSE)

calleeTreeMap(pd, srclines = FALSE, cex = 0.75, colormap = NULL,
              main = "Callee Tree Map", squarify = FALSE, border = NULL)

## S3 method for class 'proftools_calleeTreeMap'
identify(x, n = 1, print = FALSE, ...)

## S3 method for class 'proftools_flameGraph'
identify(x, n = 1, print = FALSE,
        outline = FALSE, ...)
```

## Arguments

pd	profile data as returned by readProfileData.
svgfile	character; name for SVG output file.
order	character; see details below.
colormap	a function or NULL; see details below.
srclines	logical; include source information, if available, or not.
cex	numeric character expansion value.
main	character; plot title.
tooltip	logical; whether SVG should show details in tooltips.
border	character or NULL; border color for rectangles.
squarify	logical; whether the squarified tiling algorithm should be used.
x	flameGraph or calleeTreeMap object to use.
n	integer; number of items to identify.
print	logical; whether to print result on each click.
outline	logical; whether to outline rectangles corresponding to identified call.
...	Further arguments for the identify methods; currently ignored.

## Details

`calleeTreeMap` shows a tree map of the calls in a stack trace's call tree. The tiling algorithm used depends on the `squarify` argument. If `squarify` is `TRUE` then the *squarified* algorithm is used; otherwise, the longer side is partitioned.

`flameGraph` produces a *flame graph* of the call tree. The vertical positions of rectangles represent call depth on the stack. The widths of the rectangles represent the amount of time spent in a call at a particular call or set of calls at a particular depth. The `order` argument determines the ordering of call rectangles at a particular level within a call at the lower level. The "alpha" ordering orders the calls alphabetically; "hot" uses the hot path ordering with the call with the largest amount of time first. The "time" ordering preserves the original time ordering within the stack trace file.

Default colors are based on the rainbow palette. Alternative colors can be specified by a `colormap` function. This function is called with three argument vectors, with one element for each rectangle. The arguments are the function name, call depth, and number of hits.

The results returned by `flameGraph` and `calleeTreeMap` can be passed to `identify`. The `identify` method for `calleeTreeMap` returns a list of the call stacks for the identified rectangles. The `identify` method for `flameGraph` returns a character vector of the labels of the identified rectangles.

## Value

Objects that can be used with `identify`.

## Author(s)

Luke Tierney

## See Also

[Rprof](#), [summaryRprof](#), [flatProfile](#), [filterProfileData](#), [readProfileData](#), [plotProfileCallGraph](#), [profileCallGraph2Dot](#), [hotPaths](#)

## Examples

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
flameGraph(pd)
calleeTreeMap(pd)
```

---

filterProfileData      *Filter Profile Data*

---

## Description

Allow profile data to be filtered on several criteria.

## Usage

```
filterProfileData(pd, ..., normalize = FALSE, regex = FALSE)
```

**Arguments**

<code>pd</code>	profile data as returned by <code>readProfileData</code> .
<code>...</code>	filter specifications in <code>filter = value</code> form as described below.
<code>normalize</code>	logical; if true the total hit count is set to the total number of hits in the reduced profile data; otherwise the original value is retained.
<code>regex</code>	logical; if true the specifications in <code>select</code> , and <code>omit</code> , and <code>focus</code> filters are treated as regular expressions; otherwise exact matches are required.

**Details**

This function can be used to make plots and summaries more readable or relevant by removing functions that are not of direct interest or have low hit counts.

Filters are specified in `filter = value` form with `value` typically specifying a filter level or argument. Possible filters and their argument values are:

`select` character vector specifying names of functions; call stacks not containing functions matching any of these names are dropped.

`omit` character vector specifying names of functions; call stacks containing functions matching any of these names are dropped.

`focus` character vector specifying names of functions; call stacks not containing functions matching any of these names are dropped, and functions at the bottom of the stack not matching the focus specification are dropped.

`skip` integer; the number of elements to trim from the bottom of the stacks.

`maxdepth` integer; stacks are truncated to have at most `maxdepth` elements.

`self.pct` numeric; functions at the bottom of the stacks with self percentages below this value are removed.

`total.pct` numeric; functions at the top of the stacks with total percentages below this value are removed.

`interval` integer vector of length 2 specifying first and last sample to use.

`merge.pct` numeric; functions at the top of the stacks are removed and stack traces merged until each retained trace accounts for at least this percentage of run time.

**Value**

A reduced profile data structure.

**Author(s)**

Luke Tierney

**See Also**

[Rprof](#), [summaryRprof](#), [flatProfile](#), [readProfileData](#), [plotProfileCallGraph](#), [profileCallGraph2Dot](#)

## Examples

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
plotProfileCallGraph(pd)
plotProfileCallGraph(filterProfileData(pd, self.pct = 1))
plotProfileCallGraph(filterProfileData(pd, self.pct = 1, total.pct = 10))
plotProfileCallGraph(filterProfileData(pd, select = "glm", self.pct=1,
                                       total.pct=10))
```

---

flatProfile

*Flat Profile for Rprof Profile Data*

---

## Description

Computes a flat profile reflecting time spent in functions themselves (self) and functions plus callees (total).

## Usage

```
flatProfile(pd, byTotal = TRUE, GC = TRUE)
```

## Arguments

pd	profile data as returned by readProfileData.
byTotal	logical; sort by total time if true, self time if not.
GC	logical; include GC information or not.

## Details

If byTotal is true then the result is analogous to the by.total component of the result returned by summaryRprof. Otherwise, the result is analogous to the by.self component returned by summaryRprof but with an additional cumulative self times column. The result returned when byTotal is not true is analogous to the flat profile produced by gprof.

## Value

A matrix with one row per function recorded in the profile data.

## Author(s)

Luke Tierney

## References

User manual for gprof, the GNU profiler.

**See Also**

[Rprof](#), [summaryRprof](#), [readProfileData](#), [plotProfileCallGraph](#), [printProfileCallGraph](#), [profileCallGraph2Dot](#)

**Examples**

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
flatProfile(pd)
flatProfile(pd, FALSE)
```

---

hotPaths

*Hot Paths in Profile Data*


---

**Description**

Computes and displays hot paths in profiling data.

**Usage**

```
hotPaths(pd, value = c("pct", "time", "hits"), self = TRUE,
         srclines = TRUE, GC = FALSE, maxdepth = 10,
         self.pct = 0, total.pct = 0, short = ". ", nlines = NA)
```

**Arguments**

pd	profile data as returned by readProfileData.
value	character; show result as percentage, time, or hits.
self	logical; include self time for each stack in the result.
srclines	logical; include source information, if available, or not.
GC	logical; include GC information or not.
maxdepth	integer; stacks are truncated to have at most maxdepth elements.
self.pct	numeric; stacks with self percent values below this level are dropped.
total.pct	numeric; stacks with total percent values below this level are dropped.
short	character; abbreviation to be used for functions lower on the stack.
nlines	integer; number of lines to show. The lines shown are the ones with the highest total percentage.

**Details**

The hot path ordering sorts stacks in the profile data first by the frequency with which the bottom functions on the stack are called, with highest frequency first, then within each bottom function by the frequency of the bottom two, and so on. Examining the result of hotPaths starting with low values of maxdepth and then moving to higher levels is a useful way to explore where the computational effort is concentrated.



**Value**

A data frame designed to produce a useful printed result.

**Author(s)**

Luke Tierney

**See Also**

[Rprof](#), [summaryRprof](#), [flatProfile](#), [filterProfileData](#), [readProfileData](#), [plotProfileCallGraph](#), [profileCallGraph2Dot](#)

**Examples**

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
hotPaths(pd)
hotPaths(pd, maxdepth = 8)
```

---

plot.proftools\_profData

*Plot Profile Data*

---

**Description**

Plot method for objects of class "proftools\_profData".

**Usage**

```
## S3 method for class 'proftools_profData'
plot(x, type = c("call", "tree", "flame", "time"),
     ...)
```

**Arguments**

x	an object of class "proftools_profData".
type	the type of plot to be drawn; default is a call graph.
...	additional arguments for specific plot types.

**Details**

Depending on the type argument the profile data plot method calls `link{plotProfileCallGraph}`, `calleeTreeMap`, or `flameGraph` with `order = "hot"` or `order = "time"`.

**See Also**

[plotProfileCallGraph](#), [calleeTreeMap](#), [flameGraph](#)

**Examples**

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
plot(pd)
plot(pd, style = plain.style)
plot(pd, type = "call")
plot(pd, type = "flame")
```

---

plotProfileCallGraph *Plot Call Graph for Rprof Profile Data*

---

**Description**

Uses the graph and Rgraphviz packages to plot a call graph for profile data produced by Rprof.

**Usage**

```
plotProfileCallGraph(pd, layout = "dot",
  score = c("none", "total", "self"),
  transfer = function(x) x, nodeColorMap = NULL,
  edgeColorMap = NULL, mergeCycles = FALSE,
  edgesColored = FALSE, rankDir = c("TB", "LR"),
  nodeDetails = FALSE, edgeDetails = FALSE,
  nodeSizeScore = c("none", "total", "self"),
  edgeSizeScore = c("none", "total"),
  shape = "ellipse", style, GC = TRUE,
  maxnodes = NA, total.pct = 0, ...)
```

**Arguments**

pd	profile data as returned by readProfileData.
layout	The layout method to use: One of "dot", "neato", and "twopi".
score	character string specifying whether to use total time or self time for coloring nodes/edges; no color used if missing.
transfer	function; maps score values in unit interval to unit interval
nodeColorMap, edgeColorMap	character vectors of color specifications as produced by rainbow; transfer of score is mapped to color
mergeCycles	logical; whether to merge each cycle of recursion into a single node
edgesColored	logical; whether to color edges
rankDir	The direction that the plot is laid out in, one of either "TB" for Top-to-Bottom or "LR" for Left-to-Right. The default value is "LR". This argument is only useful for dot layouts.
nodeDetails, edgeDetails	logical; whether count information should be shown.

nodeSizeScore	character; value to encode in the size of the nodes.
edgeSizeScore	character; value to encode in the width of the edges.
shape	character; node shape.
style	named list of values for arguments score through layout to use if not explicitly supplied.
...	additional arguments for the graphNEL plot method.
GC	logical; include GC information or not.
maxnodes	integer; maximal number of nodes to use; nodes with lower total hit counts are dropped.
total.pct	numeric; if positive, nodes with hit percentages below this level are dropped.

### Details

Color is used to encode the fraction of total or self time spent in each function or call. The scores used correspond to the values in the printed representation produced by `printProfileCallGraph`. For now, see the `gprof` manual for further details. The color encoding for a score  $s$  and a color map  $m$  is `m[ceiling(length(m) * transfer(s))]`

A style can be specified to set options to a set of `cvalues` that work well together.

### Value

Used for side effect.

### Note

Because of lazy evaluation, nested calls like `f(g(x))` appear in the profile graph as `f` or one of its callees calling `g`.

### Author(s)

Luke Tierney

### References

User manual for `gprof`, the GNU profiler.

Graphviz: <http://www.research.att.com/sw/tools/graphviz/>

### See Also

[Rprof](#), [summaryRprof](#), [readProfileData](#), [flatProfile](#), [profileCallGraph2Dot](#) [printProfileCallGraph](#)  
[plain.style](#) [google.style](#)

### Examples

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
plotProfileCallGraph(pd)
plotProfileCallGraph(pd, score = "none")
plotProfileCallGraph(pd, style = plain.style, score = "total")
```

---

printProfileCallGraph *Print Call Graph for Rprof Profile Data*

---

**Description**

Prints a representation of the call graph for profile data produced by Rprof. Output can be directed to a connection or a file.

**Usage**

```
printProfileCallGraph(pd, file = stdout(), percent = TRUE, GC = TRUE,  
                      maxnodes = NA, total.pct = 0)
```

**Arguments**

pd	profile data as returned by readProfileData.
file	a connection or the name of the file where the profile graph will be written.
percent	logical; if true use percent of total time; otherwise use time in seconds
GC	logical; include GC information or not.
maxnodes	integer; maximal number of nodes to use; nodes with lower total hit counts are dropped.
total.pct	numeric; if positive, nodes with hit percentages below this level are dropped.

**Details**

printProfileCallGraph produces a printed representation of the call graph for profile data produced by Rprof. The representation is analogous to the call graph produced by gprof with a few minor changes. Eventually more complete documentation of the format will be provided here; for now, reading the gprof manual section on the call graph should help understanding this output. The output is similar enough to gprof output for the cgprof script to be able to produce a visual representation of the call graph via Graphviz.

**Value**

Used for side effect.

**Note**

Because of lazy evaluation, nested calls like  $f(g(x))$  appear in the profile graph as  $f$  or one of its callees calling  $g$ .

**Author(s)**

Luke Tierney

**References**

User manual for gprof, the GNU profiler.

cgprof: <http://mvertes.free.fr/>

Graphviz: <http://www.research.att.com/sw/tools/graphviz/>

**See Also**

[Rprof](#), [summaryRprof](#), [flatProfile](#), [readProfileData](#), [plotProfileCallGraph](#), [profileCallGraph2Dot](#)

**Examples**

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
printProfileCallGraph(pd)
## Not run:
## If you have graphviz and cgprof installed on a UNIX-like system
## then in R do:

pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
printProfileCallGraph(pd, "foo.graph")

## and then in a shell do (to use the interactive dotty):

cgprof -TX foo.graph

## or (to create a postscript version and view with gv):

cgprof -Tps foo.graph > foo.ps
gv foo.ps

## End(Not run)
```

---

profileCallGraph2Dot    *Write Call Graph for Rprof Profile Data to Graphviz Dot File*

---

**Description**

Prints a Graphviz .dot file representation of the call graph for profile data produced by Rprof.

**Usage**

```
profileCallGraph2Dot(pd, score = c("none", "total", "self"),
  transfer = function(x) x, nodeColorMap = NULL,
  edgeColorMap = NULL, filename = "Rprof.dot",
  landscape = FALSE, mergeCycles = FALSE,
  edgesColored = FALSE,
  rankDir = c("TB", "LR"),
  nodeDetails = FALSE, edgeDetails = FALSE,
  nodeSizeScore = c("none", "total", "self"),
```

```

edgeSizeScore = c("none", "total"),
center = FALSE, size, shape = "ellipse",
layout = "dot", style, GC = TRUE,
maxnodes = NA, total.pct = 0)

```

## Arguments

pd	profile data as returned by readProfileData.
score	character string specifying whether to use total time or self time for coloring nodes/edges; no color used if missing.
transfer	function; maps score values in unit interval to unit interval
nodeColorMap, edgeColorMap	character vectors of color specifications as produced by rainbow; transfer of score is mapped to color
filename	name of .dot file
landscape	logical; whether to add the rotate=90 option to the .dot file
mergeCycles	logical; whether to merge each cycle of recursion into a single node
edgesColored	logical; whether to color edges
rankDir	character; value to use for the rankdir= option to specify the direction that the plot is laid out using the dot layout; must be either "TB" for Top-to-Bottom or "LR" for Left-to-Right. The default value is "LR".
nodeDetails, edgeDetails	logical; whether count information should be shown.
nodeSizeScore	character; value to encode in the size of the nodes.
edgeSizeScore	character; value to encode in the width of the edges.
center	logical; whether to add the center=1 option to the .dot file.
size	character; string to add as size= option in the .dot file.
shape	character; node shape.
layout	character; layout method to use.
style	named list of values for arguments score through layout to use if not explicitly supplied.
GC	logical; include GC information or not.
maxnodes	integer; maximal number of nodes to use; nodes with lower total hit counts are dropped.
total.pct	numeric; if positive, nodes with hit percentages below this level are dropped.

## Details

Writes the call graph as a Graphviz .dot file. Color is used to encode the fraction total or self time spent in each function or call. The scores used correspond to the values in the printed representation produced by printProfileCallGraph. For now, see the gprof manual for further details. The color encoding for a score  $s$  and a color map  $m$  is  $\text{ceiling}(\text{length}(m) * \text{transfer}(s))$

A style can be specified to set options to a set of cvalues that work well together.

**Value**

Used for side effect.

**Note**

Because of lazy evaluation, nested calls like  $f(g(x))$  appear in the profile graph as  $f$  or one of its callees calling  $g$ .

**Author(s)**

Luke Tierney

**References**

User manual for gprof, the GNU profiler.

Graphviz: <http://www.research.att.com/sw/tools/graphviz/>

**See Also**

[Rprof](#), [summaryRprof](#), [readProfileData](#), [flatProfile](#), [plotProfileCallGraph](#), [printProfileCallGraph](#)  
[plain.style](#) [google.style](#)

**Examples**

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
tmp <- tempfile()
profileCallGraph2Dot(pd, filename = tmp)
file.show(tmp)
unlink(tmp)

## Not run:
## If you have graphviz installed on a UNIX-like system
## then in R do:

tmp.dot <- tempfile()
tmp.pdf <- tempfile()

profileCallGraph2Dot(pd, filename = tmp.dot)
system(sprintf("dot -Tpdf -o
browseURL(sprintf("file://

profileCallGraph2Dot(pd, filename = tmp.dot)
system(sprintf("dot -Tpdf -o
browseURL(sprintf("file://

unlink(tmp.dot)
unlink(tmp.pdf)

## End(Not run)
```

---

profileExpr	<i>Read Rprof Profile Data</i>
-------------	--------------------------------

---

**Description**

Return profile data collected while evaluating an expression.

**Usage**

```
profileExpr(expr, GC = TRUE, srclines = TRUE)
```

**Arguments**

expr	Valid R expression to be profiled.
srclines	logical; include source information, if available, or not.
GC	logical; include GC information or not.

**Details**

profileExpr uses [Rprof](#) to profile execution of expr and returns the profile data read in using [readProfileData](#). By default GC and source information are included in the profile data.

**Value**

R representation of Rprof data.

**Author(s)**

Luke Tierney

**See Also**

[Rprof](#), [funSummary](#), [srcSummary](#), [plotProfileCallGraph](#),

**Examples**

```
## This defines the function rw()
source(system.file("samples", "rw.R", package="proftools"))

## Execute the function and collect profile data
pd <- profileExpr(rw(200000))

## Examine the profile data
funSummary(pd)
callSummary(pd)
hotPaths(pd)
srcSummary(pd)
plotProfileCallGraph(pd)
```



---

readProfileData	<i>Read Rprof Profile Data</i>
-----------------	--------------------------------

---

**Description**

Reads in Rprof profile data for further processing.

**Usage**

```
readProfileData(filename = "Rprof.out")
```

**Arguments**

filename      Name of a file produced by Rprof()

**Details**

readProfileData reads the data in the file produced by Rprof into a data structure for processing by other functions. The details of the structure are subject to change.

**Value**

R representation of Rprof data,

**Author(s)**

Luke Tierney

**See Also**

[Rprof](#), [summaryRprof](#), [flatProfile](#), [plotProfileCallGraph](#), [printProfileCallGraph](#), [profileCallGraph2Dot](#)

**Examples**

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
flatProfile(pd)
flatProfile(pd, FALSE)
```

---

 styles
 

---

*Style Specifications for Call Graphs*


---

**Description**

Styles providing coordinated settings of display parameters for the call graph display functions `plotProfileCallGraph` and `profileCallGraph2Dot`.

**Usage**

```
plain.style
google.style
```

**Details**

The `plain.style` style corresponds to the default parameter settings in the display functions. It can be used as the basis for creating a new custom style.

The `google.style` style is based on the display style used in the `pprof` tool from the Google Performance Tools suite.

**Value**

A list containing the following components:

<code>layout</code>	The layout method to use: One of "dot", "neato", and "twopi".
<code>score</code>	character string specifying whether to use total time or self time for coloring nodes/edges; no color used if missing.
<code>transfer</code>	function; maps score values in unit interval to unit interval
<code>nodeColorMap, edgeColorMap</code>	character vectors of color specifications as produced by <code>rainbow</code> ; transfer of score is mapped to color
<code>mergeCycles</code>	logical; whether to merge each cycle of recursion into a single node
<code>edgesColored</code>	logical; whether to color edges
<code>rankDir</code>	The direction that the plot is laid out in, one of either "TB" for Top-to-Bottom or "LR" for Left-to-Right. The default value is "LR". This argument is only useful for dot layouts.
<code>nodeDetails, edgeDetails</code>	logical; whether count information should be shown.
<code>nodeSizeScore</code>	character; value to encode in the size of the nodes.
<code>edgeSizeScore</code>	character; value to encode in the width of the edges.
<code>shape</code>	character; node shape.
<code>maxnodes</code>	integer; maximal number of nodes to use; nodes with lower total hit counts are dropped.
<code>total.pct</code>	numeric; if positive, nodes with hit percentages below this level are dropped.

**Author(s)**

Luke Tierney

**References**

<http://google-perftools.googlecode.com/svn/trunk/doc/cpuprofile.html>.

**See Also**

[Rprof](#), [flatProfile](#), [summaryRprof](#), [readProfileData](#), [plotProfileCallGraph](#), [printProfileCallGraph](#), [profileCallGraph2Dot](#)

**Examples**

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
plotProfileCallGraph(pd, style = plain.style)
plotProfileCallGraph(pd, style = google.style)
```

---

summaries

*Basic Profile Data Summaries*

---

**Description**

Functions to summarize profile data.

**Usage**

```
funSummary(pd, byTotal = TRUE, value = c("pct", "time", "hits"),
           srclines = TRUE, GC = TRUE, self.pct = 0, total.pct = 0)
callSummary(pd, byTotal = TRUE, value = c("pct", "time", "hits"),
            srclines = TRUE, GC = TRUE, self.pct = 0, total.pct = 0)
pathSummary(pd, value = c("pct", "time", "hits"),
            srclines = FALSE, GC = TRUE, total.pct = 0, ...)
srcSummary(pd, byTotal = TRUE, value = c("pct", "time", "hits"),
           GC = TRUE, total.pct = 0, source = TRUE, width = getOption("width"))
```

**Arguments**

pd	profile data as returned by readProfileData.
byTotal	logical; sort by total or by self time.
value	character; show result as percentage, time, or hits.
srclines	logical; include source information, if available, or not.
GC	logical; include GC information or not.
self.pct	numeric; functions at the bottom of the stacks with self percentages below this value are removed.

<code>total.pct</code>	numeric; functions at the top of the stacks with total percentages below this value are removed.
<code>source</code>	logical; if true, include source lines if available.
<code>width</code>	maximal line length to use; source lines are abbreviated to fit if necessary.
<code>...</code>	arguments to control path formatting; not useful at this time.

### Details

`funSummary` returns a summary of the time spent in each function, or each call site if source information is available and requested. It is similar to `flatProfile`.

`callSummary` provides a breakdown by calls, again with an option of distinguishing call and callee sites if source information is available.

`pathSummary` returns a summary of time spent in each unique call path contained in the profile data.

For profile data containing source information `srcSummary` returns a summary of time spent in each file line recorded in the profile data.

### Value

A data frame of summary information.

### Author(s)

Luke Tierney

### See Also

[Rprof](#), [flatProfile](#), [summaryRprof](#), [readProfileData](#), [plotProfileCallGraph](#), [printProfileCallGraph](#), [profileCallGraph2Dot](#)

### Examples

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
funSummary(pd)
callSummary(pd)
pathSummary(pd)
```

---

utils

*Profile Data Utilities*

---

### Description

Utility functions for developing new profile data analysis tools.

### Usage

```
profileDataCycles(pd, GC)
```

**Arguments**

pd	profile data as returned by readProfileData.
GC	logical; include GC information or not.

**Details**

These functions are experimental and subject to change.

**Author(s)**

Luke Tierney

---

writeCallgrindFile	<i>Write Out Profile Data in Callgrind Format</i>
--------------------	---

---

**Description**

Writes the profile data in callgrind format suitable for use with kcacheGrind or qcacheGrind.

**Usage**

```
writeCallgrindFile(pd, file = "Rprof.cg", GC = TRUE, dropSource = TRUE)
```

**Arguments**

pd	profile data as returned by readProfileData.
file	a connection or the name of the file where the callgrind output will be written.
GC	logical; if true include GC information.
dropSource	logical; if true drop initial stack entried from a source call and add a top level marker.

**Details**

The callgrind format is used by Valgrind's callgrind tool. The KDE tool kcacheGrind can be used to display the file; kcacheGrind displays the summary statistics, a call graph, and annotated source code if source information is available. kcacheGrind is available in Linux and Windows; on Mac OSX qcacheGrind is available.

**Value**

Used for side effect.

**Author(s)**

Luke Tierney

**See Also**

[Rprof](#), [summaryRprof](#), [flatProfile](#), [readProfileData](#), [plotProfileCallGraph](#), [profileCallGraph2Dot](#)

**Examples**

```
pd <- readProfileData(system.file("samples", "glmEx.out", package="proftools"))
tmp <- tempfile()
writeCallgrindFile(pd, file = tmp)
file.show(tmp)
unlink(tmp)
## Not run:
## If you have kcachegrind installed on a UNIX-like system then do:
tmp <- tempfile()
writeCallgrindFile(pd, file = tmp)
system(sprintf("kcachegrind
unlink(tmp)

## End(Not run)
```

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