Package 'Rcollectl'

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Title Help use collectl with R in Linux, to measure resource consumption in R processes

Version 1.6.0

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Description Provide functions to obtain instrumentation data on processes in a unix environment. Parse output of a collectl run. Vizualize aspects of system usage over time, with annotation.

Imports utils, ggplot2, lubridate, processx

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URL https://github.com/vjcitn/Rcollectl

BugReports https://support.bioconductor.org/t/Rcollectl

biocViews Software, Infrastructure

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

SystemRequirements collectl

Suggests knitr, BiocStyle, knitcitations, sessioninfo, rmarkdown, testthat, covr

VignetteBuilder knitr

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Contents

`browse_units` *browse a page defining units of collectl reporting*

Description

browse a page defining units of collectl reporting

Usage

```
browse_units(...)
```

Arguments

`...`	passed to browseURL

Value

side effect is running browseURL

Examples

```
if (interactive()) {
browse_units()
}
```

`cl_exists` *check for collectl availability*

Description

check for collectl availability

Usage

```
cl_exists()
```

Value

logical(1)

Examples

```
cl_exists()
```

`cl_parse` *parse a collectl output – could be conditional on discovered call*

Description

parse a collectl output – could be conditional on discovered call

Usage

```
cl_parse(path, tz = "EST", rescale_mem = TRUE)
```

Arguments

`path`	character(1) path to (possibly gzipped) collectl output
`tz`	character(1) POSIXct time zone code, defaults to "EST"
`rescale_mem`	logical(1) if TRUE, divide reported MEM_Used by 1000

Value

a data.frame

Note

A lubridate datetime is added as a column. The test file `demo_1123.tab.gz` is a collectl-generated report for a session ranging over 10 minutes, analyzing RNA-seq data on a multicore machine.

Examples

```
lk = cl_parse(system.file("demotab/demo_1123.tab.gz", package="Rcollectl"))
head(lk)
```

cl_result_path *get full path to collectl report*

Description

get full path to collectl report

Usage

```
cl_result_path(proc)
```

Arguments

proc	an entity inheriting from "Rcollectl_process" S3 class

Value

character(1) path to report

Examples

```
example(cl_start)
```

cl_start *start collectl if possible*

Description

start collectl if possible

Usage

```
cl_start(target = tempfile())
```

Arguments

target	character(1) path; destination of collectl report

Value

instance of `Rcollectl_process` with components `process` (a processx R6 instance) and `target` (a file path where collectl results will be written)

Examples

```
if (cl_exists()) {
  zz = cl_start()
  Sys.sleep(2)
  print(zz)
  Sys.sleep(2)
  print(cl_result_path(zz))
  cl_stop(zz)
  Sys.sleep(2)
  zz$process$is_alive()
}
```

---

cl_stop *stop collectl via processx interrupt*

Description

stop collectl via processx interrupt

Usage

```
cl_stop(proc)
```

Arguments

proc	an entity inheriting from "Rcollectl_process" S3 class

Value

invisibly returns the input

Examples

```
example(cl_start)
```

---

cl_timestamp *Functions to add time stamps to collectl output*

Description

Functions to add time stamps to collectl output

Usage

```
cl_timestamp(proc, step)

cl_timestamp_layer(arg)

cl_timestamp_label(arg, tz = "EST")
```

Arguments

proc	an entity inheriting from "Rcollectl_process" S3 class
step	character(1) name of step within a workflow
arg	proc (an entity inheriting from "Rcollectl_process" S3 class) or path to collectl output
tz	character(1) time zone code

Value

`cl_timestamp()` returns a tab delimited text file

`cl_timestamp_layer()` and `cl_timestamp_label()` return objects that can be combined with ggplot.

Examples

```
id <- cl_start()
Sys.sleep(2)
cl_timestamp(id, "step1")
Sys.sleep(2)
Sys.sleep(2)
cl_timestamp(id, "step2")
Sys.sleep(2)
Sys.sleep(2)
cl_timestamp(id, "step3")
Sys.sleep(2)
cl_stop(id)
path <- cl_result_path(id)
plot_usage(cl_parse(path)) +
  cl_timestamp_layer(path) +
  cl_timestamp_label(path) +
  ggplot2::theme(axis.text.x = ggplot2::element_text(angle = 90, vjust = 0.5, hjust=1))
```

---

plot_usage *elementary display of usage data from collectl*

Description

elementary display of usage data from collectl

Usage

```
plot_usage(x)
```

Arguments

x	output of cl_parse

Value

ggplot with geom_point and facet_grid

Examples

```
lk = cl_parse(system.file("demotab/demo_1123.tab.gz", package="Rcollectl"))
plot_usage(lk)
```

`print.Rcollectl_process` *print method for Rcollectl process*

Description

print method for Rcollectl process

Usage

```
## S3 method for class 'Rcollectl_process'
print(x, ...)
```

Arguments

`x`	an entity inheriting from "Rcollectl_process" S3 class
`...`	not used

Value

invisibly returns the input

Examples

```
example(cl_start)
```

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