Package: microhaplot (via r-universe)

August 20, 2024

Type Package

Title Microhaplotype Constructor and Visualizer

Version 1.0.2

Description A downstream bioinformatics tool to construct and assist
curation of microhaplotypes from short read sequences.

Depends R (>= 3.5.0)

Encoding UTF-8

License GPL-3

LazyData TRUE

Imports DT (>= 0.1), dplyr (>= 0.4.3), ggplot2 (>= 2.1.0), grid (>=
3.1.2), gtools (>= 3.5.0), magrittr (>= 1.5), scales (>=
0.4.0), shiny (>= 0.13.2), shinyBS (>= 0.61), tidyr (>= 0.4.1),
shinyWidgets (>= 0.4.3), ggiraph (>= 0.6.0)

URL https://github.com/ngthomas/microhaplot

BugReports https://github.com/ngthomas/microhaplot/issues

RoxygenNote 7.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

Repository https://ngthomas.r-universe.dev

RemoteUrl https://github.com/ngthomas/microhaplot

RemoteRef HEAD

RemoteSha 42c9ed924e61b90f970286e28211cba03c609e07

Contents

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mvShinyHaplot   *Transfer a copy of microhaplot app.*

Description

Moves shiny microhaplot app to a different directory

Usage

```
mvShinyHaplot(path)
```

Arguments

path   string. directory path. Required

Value

a logical value of whether `file.copy` is successfully transferred Shiny app to its new directory

Examples

```
mvShinyHaplot(tempdir())
```

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prepHaplotFiles   *Extracts haplotype from alignment reads.*

Description

The function `microhaplot` extracts haplotype from sequence alignment files through perl script `hapture` and returns a summary table of the read depth and read quality associate with haplotype.

Usage

```
prepHaplotFiles(
  run.label,
  sam.path,
  label.path,
  vcf.path,
  out.path = tempdir(),
  add.filter = FALSE,
  app.path = tempdir(),
  n.jobs = 1
)
```

Arguments

`run.label`	character vector. Run label to be used to display in haPLOType. Required
`sam.path`	string. Directory path folder containing all sequence alignment files (SAM). Required
`label.path`	string. Label file path. This customized label file is a tab-separate file that contains entries of SAM file name, individual ID, and group label. Required
`vcf.path`	string. VCF file path. Required
`out.path`	string. Optional. If not specified, the intermediate files are created under TEMPDIR, with the assumption that directory is granted for written permission.
`add.filter`	boolean. Optional. If true, this removes any haplotype with unknown and deletion alignment characters i.e. "*" and "_", removes any locus with large number of haplotypes (# > 40) , and remove any locus with fewer than half of the total individuals.
`app.path`	string. Path to shiny haPLOType app. Optional. If not specified, the path is default to TEMPDIR.
`n.jobs`	positive integer. Number of SAM files to be parallel processed. Optional. This multithread is only available for non Window OS. Recommend two times the number of processors/core.

Value

This function returns a dataframe of 9 columns i.e group, id, locus, haplotype, depth, sum of Phred score, max of Phred score, allele balance and haplotype rank from highest to lowest read depth. This dataframe will also be saved in `out.path`.

Examples

```
run.label <- "sebastes"

sam.path <- tempdir()
untar(system.file("extdata",
                  "sebastes_sam.tar.gz",
                  package="microhaplot"),
      exdir = sam.path)


label.path <- file.path(sam.path, "label.txt")
vcf.path <- file.path(sam.path, "sebastes.vcf")

mvShinyHaplot(tempdir())
app.path <- file.path(tempdir(), "microhaplot")

# retrieve system Perl version number
perl.version <- as.numeric(system('perl -e "print $];"', intern=TRUE))

if (perl.version >= 5.014) {
haplo.read.tbl <- prepHaplotFiles(run.label = run.label,
                          sam.path = sam.path,
```

```
                              out.path = tempdir(),
                              label.path = label.path,
                              vcf.path = vcf.path,
                              app.path = app.path)
   }else {
   message("Perl version is outdated. Must >= 5.014.")}
```

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runShinyHaplot   *Run shiny microhaplot*

Description

Run shiny microhaplot app

Usage

```
runShinyHaplot(
  path = system.file("shiny", "microhaplot", package = "microhaplot")
)
```

Arguments

path   Path to shiny microhaplot app. Optional. If not specified, the path is default to
                local app path.

Value

Runs shiny microhaplot application via shiny::runApp which typically doesn't return; interrupt R
to stop the application (usually by pressing Ctrl+C or Esc).

Examples

```
if(interactive()){
runShinyHaplot()
}
```

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