

Package ‘microhaplot’

October 3, 2019

Type Package

Title Microhaplotype Constructor and Visualizer

Version 1.0.1

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

Depends R (>= 3.1.2)

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 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Thomas Ng [aut, cre]

Maintainer Thomas Ng <tngthomasng@gmail.com>

Repository CRAN

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mvShinyHaplot	<i>Transfer a copy of microhaplot app.</i>
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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())
```

prepHaplotFiles	<i>Extracts haplotype from alignment reads.</i>
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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 haPLOTtype. 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 haPLOTtype 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.")}
```

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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