

Package: finemapr (via r-universe)

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Title R wrapper to fine-mappers

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Maintainer Andrey Ziyatdinov <andrey@example.com>

Description R wrapper to fine-mappers.

License GPL (>= 3)

URL <https://github.com/variani/finemapr>

Imports tibble, dplyr, readr, magrittr, ggplot2, ggrepel, cowplot,
data.table, Matrix

Suggests proxysnps, RCurl, gaston, rsnp, testthat, knitr, rmarkdown

Collate 'package.R' 'names.R' 'sumstats.R' 'abf.R' 'cojo.R' 'utils.R'
'read.R' 'datasets.R' 'files.R' 'plots.R' 'finemap.R'
'caviar.R' 'paintor.R' 'classMethods.R'
'classFinemaprPaintor.R' 'classFinemaprFinemap.R'
'classFinemaprCaviar.R' 'finemapr.R' 'ld.R' 'zzz.R'

RoxygenNote 7.1.1

VignetteBuilder knitr

Repository <https://mrcieu.r-universe.dev>

RemoteUrl <https://github.com/remlapmot/finemapr>

RemoteRef suggestions

RemoteSha d99c5ac89d37f06027b783395b45fddfdc6d4aa7

Contents

cojo	2
filename_zscore.FinemaprFinemap	2
filename_zscore.FinemaprPaintor	4
finemapr	5
FinemaprCaviar	6
finemaprPackage	6

plot_zscore.Finemapr	6
proxysnps_ref_ld	8
proxysnps_ref_vcf	8
read_ld	9
read_zscore	9
run_caviar	10
run_finemap	10
run_paintor	11
sumstats_bmi	11

Index	12
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cojo	<i>Run GCTA-COJO.</i>
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Description

<http://gcta.freeforums.net/thread/178/conditional-joint-analysis-using-summary>

Usage

```
cojo(
  tab,
  bed,
  method = c("select", "cond"),
  cmd = "",
  snps_cond = NULL,
  dir_run = "run_cojo",
  tool = getOption("finemapr_cojo"),
  args = ""
)
```

Details

```
tab <- "~/git/hemostat/scc/results/sumstats-cojo/sumstats-1.cojo" bed <- "~/git/hemostat/scc/data/FineMapping/forGCTA_on"
```

filename_zscore.FinemaprFinemap	<i>S3 class FinemaprFinemap.</i>
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Description

S3 class FinemaprFinemap.

Usage

```
## S3 method for class 'FinemaprFinemap'
filename_zscore(x, locus = 1)

## S3 method for class 'FinemaprFinemap'
filename_ld(x, locus = 1)

## S3 method for class 'FinemaprFinemap'
filename_snp(x, locus)

## S3 method for class 'FinemaprFinemap'
filename_config(x, locus)

## S3 method for class 'FinemaprFinemap'
filename_k(x, locus)

## S3 method for class 'FinemaprFinemap'
filename_log(x, locus)

## S3 method for class 'FinemaprFinemap'
filename_master(x)

## S3 method for class 'FinemaprFinemap'
write_files(x, ...)

## S3 method for class 'FinemaprFinemap'
run_tool(x, ...)

## S3 method for class 'FinemaprFinemap'
collect_results(x, ...)

print.FinemaprFinemap(x, ...)

## S3 method for class 'FinemaprFinemap'
plot(
  x,
  grid_nrow = NULL,
  grid_ncol = NULL,
  label_size = getOption("finemapr_label_size"),
  label_size_config = label_size,
  label_size_snp = label_size,
  top_rank = getOption("top_rank"),
  top_rank_config = top_rank,
  top_rank_snp = top_rank,
  lim_prob = getOption("lim_prob"),
  lim_prob_config = lim_prob,
  lim_prob_snp = lim_prob,
  lim_prob_ncausal = lim_prob,
```

```

    ...
  )

## S3 method for class 'FinemaprFinemap'
plot_ncausal(x, locus = 1, lim_prob = c(0, 1), ...)

## S3 method for class 'FinemaprFinemap'
plot_config(
  x,
  locus = 1,
  lim_prob = c(0, 1.5),
  label_size = getOption("finemapr_label_size"),
  top_rank = getOption("top_rank"),
  ...
)

## S3 method for class 'FinemaprFinemap'
plot_snp(
  x,
  locus = 1,
  lim_prob = c(0, 1.5),
  label_size = getOption("finemapr_label_size"),
  top_rank = getOption("top_rank"),
  ...
)

```

```

filename_zscore.FinemaprPainter
      S3 class FinemaprPainter.

```

Description

S3 class FinemaprPainter.

Usage

```

## S3 method for class 'FinemaprPainter'
filename_zscore(x, locus = 1)

## S3 method for class 'FinemaprPainter'
filename_ld(x, locus = 1)

## S3 method for class 'FinemaprPainter'
filename_annot(x, locus = 1)

## S3 method for class 'FinemaprPainter'
filename_master(x)

```

```
## S3 method for class 'FinemaprPainter'
filename_snp(x, locus)

print.FinemaprPainter(x, ...)

## S3 method for class 'FinemaprPainter'
process_annot(x, annots, annotations, ...)

## S3 method for class 'FinemaprPainter'
write_files(x, ...)

## S3 method for class 'FinemaprPainter'
run_tool(x, ...)

## S3 method for class 'FinemaprPainter'
collect_results(x, ...)
```

finemapr

Run FINEMAP.

Description

Run FINEMAP.

Usage

```
finemapr(
  tab,
  ld,
  n,
  annot,
  annotations,
  prop_credible = 0.95,
  method = c("finemap", "paintor"),
  dir_run,
  tool,
  args = "",
  prior_k,
  save_ld = FALSE,
  ret = c("results", "zscore", "ld")
)
```

Examples

```
ex <- example_finemap()
out <- finemapr(list(ex$tab1, ex$tab2), list(ex$ld1, ex$ld2), list(ex$n1, ex$n2), args = "--n-causal-max 1")
out <- finemapr(list(ex$tab1, ex$tab2), list(ex$ld1, ex$ld2), list(ex$n1, ex$n2), method = "paintor", args = "--enu
```

FinemaprCaviar *S3 class FinemaprCaviar.*

Description

S3 class FinemaprCaviar.

Usage

```
print.FinemaprCaviar(x, ...)  
  
## S3 method for class 'FinemaprCaviar'  
plot(x, ...)  
  
## S3 method for class 'FinemaprCaviar'  
plot_snp(  
  x,  
  lim_prob = c(0, 1.5),  
  label_size = getOption("finemapr_label_size"),  
  top_rank = getOption("top_rank"),  
  ...  
)
```

finemaprPackage *Package finemapr.*

Description

R wrapper to fine-mappers.

plot_zscore.Finemapr *S3 class Finemapr.*

Description

S3 class Finemapr.

Usage

```
## S3 method for class 'Finemapr'
plot_zscore(
  x,
  locus = 1,
  label_size = getOption("finemapr_label_size"),
  selected,
  force = 20,
  color_main = "grey75",
  color_selected = "aquamarine4",
  color_credible = "dodgerblue4",
  color_missing = "brown",
  plot_missing = FALSE,
  ...
)

plot_ncausal(x, ...)

print.Finemapr(x, ...)

print.Finemapr(x, ...)

## S3 method for class 'Finemapr'
plot(x, ...)

## S3 method for class 'Finemapr'
plot_snp(
  x,
  lim_prob = c(0, 1.5),
  label_size = getOption("finemapr_label_size"),
  top_rank = getOption("top_rank"),
  ...
)

## S3 method for class 'Finemapr'
extract_credible_set(x, ...)

## S3 method for class 'Finemapr'
process_tab(x, tabs, ...)

## S3 method for class 'Finemapr'
process_ld(x, lds, ...)
```

Note

Colors: <http://www.stat.columbia.edu/~tzheng/files/Rcolor.pdf>

proxysnps_ref_ld	https://github.com/slowkow/proxysnps/blob/master/R/get_vcf.R
------------------	---

Description

https://github.com/slowkow/proxysnps/blob/master/R/get_vcf.R

Usage

```
proxysnps_ref_ld(  
  vcf,  
  tol = 1e-10,  
  measure = c("R.squared", "D.prime"),  
  verbose = 0  
)
```

proxysnps_ref_vcf	https://github.com/slowkow/proxysnps/blob/master/R/get_vcf.R
-------------------	---

Description

https://github.com/slowkow/proxysnps/blob/master/R/get_vcf.R

Usage

```
proxysnps_ref_vcf(  
  chr = 16,  
  start = 53767000,  
  end = 53768000,  
  pop = "EUR",  
  snps = NULL,  
  verbose = 0  
)
```

read_ld	<i>Read LD matrix from a file.</i>
---------	------------------------------------

Description

Read LD matrix from a file.

Usage

```
read_ld(file_ld, snps)
```

Examples

```
f1 <- system.file("extdata/region1.ld", package = "finemapr")  
ld <- read_ld(f1)
```

read_zscore	<i>Read z-scores from a file.</i>
-------------	-----------------------------------

Description

Read z-scores from a file.

Usage

```
read_zscore(file_zscore)
```

Examples

```
f1 <- system.file("extdata/region1.z", package = "finemapr")  
ztab <- read_zscore(f1)
```

`run_caviar`*Run CAVIAR.*

Description

Output file ('*_post'): column #1 is the variant name; column #2 is the posterior prob. that the variant is causal (<https://github.com/fhormoz/caviar/issues/1#issuecomment-286521771>); column #3 is the amount that this variant contributes to 95

Usage

```
run_caviar(  
  tab,  
  ld,  
  dir_run = "run_caviar",  
  tool = getOption("finemapr_caviar"),  
  args = ""  
)
```

Examples

```
ex <- example_finemap()  
out <- run_caviar(ex$tab1, ex$ld1, args = "-c 2")  
out <- run_caviar(ex$tab1, ex$ld1, args = "-c 0")
```

`run_finemap`*Run FINEMAP.*

Description

Run FINEMAP.

Usage

```
run_finemap(  
  tab,  
  ld,  
  n,  
  dir_run = "run_finemap",  
  tool = getOption("finemapr_finemap"),  
  args = ""  
)
```

Examples

```
ex <- example_finemap()
out <- run_finemap(ex$tab1, ex$ld1, ex$n1, args = "--n-causal-max 3")
out <- run_finemap(ex$tab1, ex$ld1, ex$n1, args = "--n-causal-max 1")
```

run_paintor

*Run Paintor.***Description**

Run Paintor.

Usage

```
run_paintor(
  tab,
  ld,
  n,
  annot,
  annotations,
  dir_run = "run_paintor",
  tool = getOption("finemapr_paintor"),
  args = ""
)
```

Examples

```
ex <- example_finemap()
out <- run_paintor(ex$tab1, ex$ld1)
```

sumstats_bmi

https://data.broadinstitute.org/alkesgroup/sumstats_formatted/readme.txt
<https://github.com/bulik/ldsc/wiki/Partitioned-Heritability>

Description

https://data.broadinstitute.org/alkesgroup/sumstats_formatted/readme.txt <https://github.com/bulik/ldsc/wiki/Partitioned-Heritability>

Usage

```
sumstats_bmi()
```

Index

cojo, 2
collect_results.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
collect_results.FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4
extract_credible_set.Finemapr
 (plot_zscore.Finemapr), 6
filename_annot.FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4
filename_config.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
filename_k.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
filename_ld.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
filename_ld.FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4
filename_log.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
filename_master.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
filename_master.FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4
filename_snp.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
filename_snp.FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4
filename_zscore.FinemaprFinemap, 2
filename_zscore.FinemaprPainter, 4
Finemapr (plot_zscore.Finemapr), 6
finemapr, 5
FinemaprCaviar, 6
FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
finemaprPackage, 6
FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4
plot.Finemapr (plot_zscore.Finemapr), 6
plot.FinemaprCaviar (FinemaprCaviar), 6
plot.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
plot_config.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
plot_ncausal (plot_zscore.Finemapr), 6
plot_ncausal.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
plot_snp.Finemapr
 (plot_zscore.Finemapr), 6
plot_snp.FinemaprCaviar
 (FinemaprCaviar), 6
plot_snp.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2
plot_zscore.Finemapr, 6
print.Finemapr (plot_zscore.Finemapr), 6
print.FinemaprCaviar (FinemaprCaviar), 6
print.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2

print.FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4

process_annot.FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4

process_ld.Finemapr
 (plot_zscore.Finemapr), 6

process_tab.Finemapr
 (plot_zscore.Finemapr), 6

proxysnps_ref_ld, 8

proxysnps_ref_vcf, 8

read_ld, 9

read_zscore, 9

run_caviar, 10

run_finemap, 10

run_painter, 11

run_tool.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2

run_tool.FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4

sumstats_bmi, 11

write_files.FinemaprFinemap
 (filename_zscore.FinemaprFinemap),
 2

write_files.FinemaprPainter
 (filename_zscore.FinemaprPainter),
 4