

# Package ‘garfield’

November 22, 2024

**Type** Package

**Title** GWAS Analysis of Regulatory or Functional Information Enrichment with LD correction

**Version** 1.35.0

**Date** 2015-12-14

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**Description** GARFIELD is a non-parametric functional enrichment analysis approach described in the paper GARFIELD: GWAS analysis of regulatory or functional information enrichment with LD correction. Briefly, it is a method that leverages GWAS findings with regulatory or functional annotations (primarily from ENCODE and Roadmap epigenomics data) to find features relevant to a phenotype of interest. It performs greedy pruning of GWAS SNPs ( $LD\ r^2 > 0.1$ ) and then annotates them based on functional information overlap. Next, it quantifies Fold Enrichment (FE) at various GWAS significance cutoffs and assesses them by permutation testing, while matching for minor allele frequency, distance to nearest transcription start site and number of LD proxies ( $r^2 > 0.8$ ).

**biocViews** Software, StatisticalMethod, Annotation, FunctionalPrediction, GenomeAnnotation

**License** GPL-3

**NeedsCompilation** yes

**VignetteBuilder** knitr

**Suggests** knitr

**git\_url** <https://git.bioconductor.org/packages/garfield>

**git\_branch** devel

**git\_last\_commit** ff65122

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-11-22

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|                  |   |
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| garfield-package | <i>GARFIELD - GWAS Analysis of Regulatory or Functional Information Enrichment with LD correction</i> |
|------------------|---|

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## Description

GARFIELD leverages GWAS findings with regulatory or functional annotations to find features relevant to a phenotype of interest. It performs greedy pruning of GWAS SNPs ( $LD\ r^2 > 0.1$ ) and then annotates them based on functional information overlap. Next, it quantifies Fold Enrichment (FE) at various GWAS significance cut-offs and assesses them by permutation testing, while matching for minor allele frequency, distance to nearest transcription start site and number of LD proxies ( $r^2 > 0.8$ ). Finally, it includes visualization tools.

## Details

Package: garfield  
 Type: Package  
 Version: 1.0  
 Date: 2015-12-14  
 License: GPL-3

See `garfield.run` for example analysis usage and `garfield.plot` for plotting examples.

## Author(s)

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## References

Valentina Iotchkova, Graham Ritchie, Matthias Geihs, Sandro Morganella, Josine Min, Klaudia Walter, Nicholas Timpson, UK10K Consortium, Ian Dunham, Ewan Birney and Nicole Soranzo. GARFIELD - GWAS Analysis of Regulatory or Functional Information Enrichment with LD correction. In preparation

## See Also

`garfield.run`, `garfield.plot`

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|               |                                   |
|---------------|-----------------------------------|
| garfield.plot | <i>Garfield plotting function</i> |
|---------------|-----------------------------------|

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## Description

garfield.plot is used for visualization of the enrichment analysis results obtained by the garfield.run permutation step. Internally, it uses garfield.plot.fnx which has been adapted from the 'radial.plot' function from the 'plotrix' package.

## Usage

```
garfield.plot(input_file, num_perm = 100000, output_prefix = "plot",  
              plot_title = "", filter = 10, tr = Inf)
```

## Arguments

|               |   |
|---------------|---|
| input_file    | Input file name as produced by garfield.run permutation step.   |
| num_perm      | Number of permutations used in the garfield.run permutation step.   |
| output_prefix | Figure file prefix. This would create the following files output_prefix.Chromatin_States.pdf, output_prefix.Footprints.pdf, output_prefix.Histone_Modifications.pdf, output_prefix.Peaks.pdf, output_prefix.FAIRE.pdf, output_prefix.Genic.pdf, output_prefix.Hotspots.pdf and output_prefix.TFBS.pdf |
| plot_title    | Optional figure title   |
| filter        | Optional filter for the minimum number of variants at a given threshold. Minimum of 1 should be used, but advisable to set to a larger value (e.g. 10).   |
| tr            | Threshold for denoting significance of an observed enrichment on a $-\log_{10}$ scale. A value of Inf denotes using default threshold of $-\log_{10}(0.05/498)$ .   |

## Details

This function is used for visualization of the enrichment analysis results and produces pdf figures for each class of annotations. Each figure shows the FE values (radial values) at different GWAS thresholds (bottom legend) for each annotation (outer circle and right legend). It further shows the significance at the top 4 GWAS thresholds (if present) as dots on the outer circle, with the most stringent threshold being shown at the inner most side.

## Value

No value is produced, instead output files are generated. See Details and 'output\_prefix' for more information.

## Author(s)

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## References

Valentina Iotchkova, Graham Ritchie, Matthias Geihs, Sandro Morganella, Josine Min, Klaudia Walter, Nicholas Timpson, UK10K Consortium, Ian Dunham, Ewan Birney and Nicole Soranzo. GARFIELD - GWAS Analysis of Regulatory or Functional Information Enrichment with LD correction. In preparation

## See Also

[garfield.run](#), [garfield](#), [garfield.plot.fnx](#)

## Examples

```
garfield.run("tmp", data.dir=system.file("extdata",package = "garfield"),
  trait="trait",run.option = "prep", chrs = c(22),
  exclude = c(895, 975, 976, 977, 978, 979, 98))
```

```
garfield.run("tmp", data.dir=system.file("extdata",package = "garfield"),
  trait="", run.option = "perm", nperm = 1000,
  thresh = c(0.001, 1e-04, 1e-05), pt_thresh = c(1e-04, 1e-05),
  maf.bins = 2, tags.bins = 3, tss.bins = 3, prep.file = "tmp.prep",
  optim_mode = TRUE, minit = 100, thresh_perm = 0.05)
```

```
garfield.plot("tmp.perm", num_perm = 1000, output_prefix = "tmp",
  plot_title = "Sample run", filter = 1, tr = -log10(0.05))
#system("ls -lh tmp.*.pdf")
```

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garfield.plot.fnx      *Internal radial plotting function for the garfield.plot function*

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## Description

This function has been adapted from the 'radial.plot' function from the 'plotrix' package.

## Usage

```
garfield.plot.fnx(lengths, radial.pos = NULL, labels = NA, breaks = NA,
  label.pos = NULL, radlab = FALSE, start = 0, clockwise = FALSE,
  rp.type = "r", label.prop = 1.05, main = "", xlab = "", ylab = "",
  line.col = par("fg"), lty = par("lty"), lwd = par("lwd"),
  mar = c(2, 2, 3, 2), show.grid = TRUE, show.grid.labels = 4,
  show.radial.grid = TRUE, grid.col = "grey", grid.bg = "transparent",
  grid.left = FALSE, grid.unit = NULL, point.symbols = 1,
  point.col = par("fg"), show.centroid = FALSE, radial.lim = NULL,
  radial.labels = NULL, poly.col = NA, add = FALSE, ann.col = 1,
  ann.pch = 15, ann.col.mx = 1, compact = TRUE, ...)
```

**Arguments**

|                  |  |
|------------------|--|
| lengths          | A numeric data vector or matrix. If 'lengths' is a matrix, the rows will be considered separate data vectors.  |
| radial.pos       | A numeric vector or matrix of positions in radians. These are interpreted as beginning at the right (0 radians) and moving counterclockwise. If 'radial.pos' is a matrix, the rows must correspond to rows of 'lengths'. |
| labels           | Character strings to be placed at the outer ends of the lines. If set to NA, will suppress printing of labels, but if missing, the radial positions will be used.  |
| breaks           | A vector of (potentially different) labels to 'labels' according to which to draw radial lines.  |
| label.pos        | The positions of the labels around the plot in radians.  |
| radlab           | Whether to rotate the outer labels to a radial orientation.  |
| start            | Where to place the starting (zero) point. Defaults to the 3 o'clock position.  |
| clockwise        | Whether to interpret positive positions as clockwise from the starting point. The default is counterclockwise.   |
| rp.type          | Whether to draw (r)adial lines, a (p)olygon, (s)ymbols or some combination of these. If 'lengths' is a matrix and rp.type is a vector, each row of 'lengths' can be displayed differently.                               |
| label.prop       | The label position radius as a proportion of the maximum line length.  |
| main             | The title for the plot.  |
| xlab, ylab       | Normally x and y axis labels are suppressed.   |
| line.col         | The color of the radial lines or polygons drawn.   |
| lty              | The line type(s) to be used for polygons or radial lines.  |
| lwd              | The line width(s) to be used for polygons or radial lines.   |
| mar              | Margins for the plot. Allows the user to leave space for legends, long labels, etc.  |
| show.grid        | Logical - whether to draw a circular grid.   |
| show.grid.labels | Whether and where to display labels for the grid - see Details.  |
| show.radial.grid | Whether to draw radial lines to the plot labels.   |
| grid.col         | Color of the circular grid.  |
| grid.bg          | Fill color of above.   |
| grid.left        | Whether to place the radial grid labels on the left side.  |
| grid.unit        | Optional unit description for the grid.  |
| point.symbols    | The symbols for plotting (as in pch).  |
| point.col        | Colors for the symbols.  |
| show.centroid    | Whether to display a centroid.   |
| radial.lim       | The range of the grid circle. Defaults to 'pretty(range(lengths))', but if more than two values are passed, the exact values will be displayed.  |
| radial.labels    | Optional labels for the radial grid. The default is the values of radial.lim.  |

|                         |  |
|-------------------------|--|
| <code>poly.col</code>   | Fill color if polygons are drawn. Use NA for no fill.  |
| <code>add</code>        | Whether to add one or more series to an existing plot.   |
| <code>ann.col</code>    | A vector of colours for symbols to be drawn on the outer circle.   |
| <code>ann.pch</code>    | A pch value for symbols to be drawn on the outer circle.   |
| <code>ann.col.mx</code> | A matrix of colours for dots to be drawn on the outer circle, inside the symbols with 'ann.col' colours. |
| <code>compact</code>    | A flag to specify if labels should be presented in a compact form or not.                                |
| <code>...</code>        | Additional arguments are passed to 'plot'.   |

**Details**

This function is only used internally as part of the [garfield.plot](#) function.

**Value**

No value, but a plot is produced. See Details for further information.

**Author(s)**

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**References**

Valentina Iotchkova, Graham Ritchie, Matthias Geihs, Sandro Morganella, Josine Min, Klaudia Walter, Nicholas Timpson, UK10K Consortium, Ian Dunham, Ewan Birney and Nicole Soranzo. GARFIELD - GWAS Analysis of Regulatory or Functional Information Enrichment with LD correction. In preparation

**See Also**

[garfield.plot](#), [garfield.run](#), [garfield](#)

**Examples**

```
DATA = rbind(rnorm(10,5,0.5),rnorm(10,3.5,0.5),rnorm(10,2,0.5))
garfield.plot.fnx(DATA,ann.col.mx=DATA!=0, ann.col=rep(1:2,each=5),
  ann.pch=15, rp.type="p",line.col=1:3,show.grid=TRUE, show.radial.grid=TRUE,
  labels=paste("label ",c(1:10)," ",sep=""),breaks=(1:10), radlab=TRUE,
  poly.col=1:3)
```

garfield.run

*GARFIELD enrichment analysis function***Description**

garfield.run is used to perform greedy pruning of variants from a genome-wide association study, calculate fold enrichment and test its significance at a given genome-wide significance threshold.

**Usage**

```
garfield.run(out.file, data.dir, trait, run.option = "complete",
  chrs = c(1:22, "X"), exclude = c(895, 975, 976, 977, 978, 979, 98),
  nperm = 100000, thresh = c(0.1, 0.01, 0.001, 1e-04, 1e-05, 1e-06,
  1e-07, 1e-08), pt_thresh = c(1e-05, 1e-06, 1e-07, 1e-08),
  maf.bins = 5, tags.bins = 5, tss.bins = 5, prep.file = "",
  optim_mode = 1, minit = 100, thresh_perm = 1e-04)
```

**Arguments**

|            |   |
|------------|---|
| out.file   | Prefix for output file. Full garfield analysis creates out.file.prep and out.file.perm files from pruning and annotation step and permutation for significance testing step, respectively. These steps can additionally be run separately - for more information see run.option flag.   |
| data.dir   | Path to annotation and p-value files. The directory must contain "annotation", "maftssd", "pval" and "tags" subdirectories with per chromosome files of input data. See details section for further information.  |
| trait      | GWAS phenotype name. This must match a folder name in the data.dir folder. See details for more information.  |
| run.option | an object specifying which part of the analysis to run. Valid options are complete, prep and perm, where prep denotes the preparation step (pruning and annotation of variants), perm denotes the permutation step (calculating fold enrichment and its significance) and complete executes both the preparation and permutation steps. |
| chrs       | A vector of the chromosomes for which to run the enrichment analysis. chrs can have all or subsets of values from c(1:22, 'X').   |
| exclude    | A numeric vector of indices of annotations for which LD tags should not be used for annotation of pruned variants. Value of -1 denotes using LD for annotation for all features.  |
| nperm      | A numeric value of the number of permutations to be performed.  |
| thresh     | A numeric vector of genome-wide significance thresholds to be used for fold enrichment calculation.   |
| pt_thresh  | A numeric vector of genome-wide significance thresholds to be used for calculating the significance of the observed fold enrichment. All values must be contained in the thresh vector.   |

|             |  |
|-------------|--|
| maf.bins    | A numeric value denoting the number of bins for the minor allele frequency matching during permutation testing. Must be greater or equal to 1.   |
| tags.bins   | A numeric value denoting the number of bins for the number of LD tags ( $r^2 \geq 0.8$ ) matching during permutation testing. Must be greater or equal to 1.   |
| tss.bins    | A numeric value denoting the number of bins for the distance to nearest transcription start site matching during permutation testing. Must be greater or equal to 1.   |
| prep.file   | File from pruning stage of algorithm. Only required if using the 'run.option'=perm flag.   |
| optim_mode  | A binary flag denoting whether to run fast version of method (1) or general version (0), where the fast version checks if significance of a given enrichment would still be possible to be obtained after 'minit' number of iterations and terminated permutations if not. |
| minit       | An integer value for the minimum number of permutations to be performed before checking if thresh_perm condition can still be met. Only used if 'optim_mode'=1.  |
| thresh_perm | After 'minit' number of permutations, at each iteration check if EmpPval can still reach 'thresh_perm' value. If not terminate permutations and output obtained results at that stage. Only used if 'optim_mode'=1.  |

## Details

Output files: out.file.prep contains the genomic positions of pruned variants, p-values for association with the trait of interest, number of LD tags ( $r^2 > 0.8$ ), MAF, distance to the nearest TSS and binary representation of annotation information (with LD-tagging  $r^2 > 0.8$ ). out.file.perm contains enrichment analysis results for each annotation, where PThresh is the GWAS p-value threshold used for analysis, FE denotes the fold enrichment statistic (equals -1 if no sufficient data was available for the FE calculation), EmpPval shows the empirical p-value of enrichment (equals -1 if FE is calculated but significance of enrichment analysis is not run at that threshold), NAnnotThresh - the number of variants at the threshold which are annotated with the given feature, NAnnot - the total number of annotated variants, NThresh - the total number of variants at that threshold and N - the total number of pruned variants. The remaining columns show additional information on the annotations used for analysis.

Data directory: data.dir, should point to a location containing "annotation", "maftssd", "pval" and "tags" subdirectories, where (i) the "pval" folder contains subfolders with trait names, which in turn contain per chromosome space separated files with genomic position in the first column and p-value in the second. They should be named chr1, chr2, etc, and be numerically sorted with respect to genomic position; (ii) "annotation" should contain per chromosome space separated files with position in the first column and annotations in stacked binary format in the second. The files should be named chr1, chr2, etc and be sorted numerically according to position. Additionally the directory should contain a link\_file.txt file that links the annotations to relevant information about them; (iii) "maftssd" should contain per chromosome space separated files with position in the first column, minor allele frequency in the second and distance to the nearest TSS in the third. The files should be named chr1, chr2, etc and be sorted numerically according to position; (iv) "tags" should contain two subfolders named r01 and r08, which in turn contain per chromosome space separated files with variant position in the first column and comma separated positions of all variants with  $r^2 > 0.1$  or  $0.8$ , respectively with the variant in the first column. The files should again be named chr1, chr2, etc



and be sorted numerically according to position. For further information on the data.dir structure, please see <http://www.ebi.ac.uk/birney-srv/GARFIELD/documentation/GARFIELD.pdf>

Pre-computed LD (European samples - UK10K sequence data), MAF, TSS distance, p-value files for two example traits (Crohn's Disease from the IBD Consortium and Height from the GIANT consortium) and annotation files for 1005 GENCODE, ENCODE and Roadmap Epigenomics annotations can be downloaded from <http://www.ebi.ac.uk/birney-srv/GARFIELD/package/garfield-data.tar.gz>. Note the data is 5.9Gb in compressed format and needs to be uncompressed prior to analysis (83Gb). Variant genomic position (build 37) is used as an identifier in all data files.

## Value

No value is produced, instead output files are generated. See Details and 'out.file' for more information.

## Author(s)

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## References

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## See Also

[garfield.plot](#), [garfield](#)

## Examples

```
garfield.run("tmp", data.dir=system.file("extdata",package = "garfield"),
  trait="trait",run.option = "prep", chrs = c(22),
  exclude = c(895, 975, 976, 977, 978, 979, 98))

garfield.run("tmp", data.dir=system.file("extdata",package = "garfield"),
  run.option = "perm", nperm = 1000, thresh = c(0.001, 1e-04, 1e-05),
  pt_thresh = c(1e-04, 1e-05), maf.bins = 2, tags.bins = 3, tss.bins = 3,
  prep.file = "tmp.prep", optim_mode = TRUE, minit = 100, thresh_perm = 0.05)

if (file.exists("tmp.perm")){
  perm = read.table("tmp.perm", header=TRUE)
  head(perm)
} else { print("Error: tmp.perm does not exist!") }

##### To get the sample data for enrichment analysis in European samples
##### execute the following - note this can take a long time to run and
##### needs a substantial disk space (see Details)
#
```

```
# download data and decompress
# system("wget http://www.ebi.ac.uk/birney-srv/GARFIELD/package/
# garfield-data.tar.gz")
# system("tar -zxvf garfield-data.tar.gz")
#
# if downloaded in current working directory use the following to execute
# garfield, otherwise please change data.dir location
# garfield.run("cd-meta.output", data.dir="garfield-data", trait="cd-meta",
# run.option = "prep", chrs = c(1:22), exclude = c(895, 975, 976, 977, 978,
# 979, 980))
#
# garfield.run("cd-meta.output", data.dir="garfield-data", run.option = "perm",
# nperm = 100000, thresh = c(0.1,0.01,0.001, 1e-04, 1e-05, 1e-06, 1e-07, 1e-08),
# pt_thresh = c(1e-05, 1e-06, 1e-07, 1e-08), maf.bins = 5, tags.bins = 5,
# tss.bins = 5, prep.file = "cd-meta.output.prep", optim_mode = TRUE,
# minit = 100, thresh_perm = 0.0001)
#
# garfield.plot("cd-meta.output.perm", num_perm = 100000,
# output_prefix = "cd-meta.output", plot_title = "Crohn's Disease",
# filter = 10, tr = -log10(0.05/498))
```

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