

Package ‘geneNR’

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Title Automated Gene Identification for Post-GWAS and QTL Analysis

Version 3.0.0

Description Facilitates the post-Genome Wide Association Studies (GWAS) and Quantitative Trait Loci (QTL) analysis of identifying candidate genes within user-defined search window, based on the identified Single Nucleotide Polymorphisms (SNPs) as given by Mazumder AK (2024) <[doi:10.1038/s41598-024-66903-3](https://doi.org/10.1038/s41598-024-66903-3)>. It supports candidate gene analysis for wheat and rice. Just import your GWAS result as explained in the sample_data file and the function does all the manual search and retrieve candidate genes for you, while exporting the results into ready-to-use output.

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Encoding UTF-8

RoxygenNote 7.3.2

Depends R (>= 3.5)

LazyData TRUE

Imports readr, stringr, utils, httr, rvest, xml2, writexl, vcfR,
ggplot2, ggrepel

Suggests knitr, rmarkdown, devtools

VignetteBuilder knitr

NeedsCompilation no

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geneQTL	<i>Identifies Candidate Genes based on identified Quantitative Trait Loci (QTL) analysis</i>
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Description

Identifies Candidate Genes based on identified Quantitative Trait Loci (QTL) analysis

Usage

```
geneQTL(data_file, crop = "wheat", genome_source = "online", gff3_file = NULL)
```

Arguments

data_file	The input data in .csv format. (sample_data_wheat_qtl or sample_data_rice_qtl for demo purpose)
crop	Either "wheat" or "rice". (by default it will be wheat)
genome_source	Character specifying either "online" (default Ensembl lookup) or "local" (uses a local GFF3 file).
gff3_file	Path to a local custom .gff3 file. Only utilized if genome_source = "local".

Value

A data frame containing traits, QTL, gene_id, gene_size, and gene_type.

Examples

```
load(system.file("extdata", "precomputed_sample_results_qtl.rda", package = "geneNR"))
message(sample_results)
## Not run:
result <- geneQTL("sample_data_wheat_qtl", crop="wheat")
# Local mapping workflow:
# gff_path <- system.file("extdata", "sample_crop.gff3", package = "geneNR")
# result <- geneQTL("sample_data_wheat_qtl", genome_source="local", gff3_file=gff_path)

## End(Not run)
```

geneSNP	<i>Identifies Candidate Genes based on identified Single Nucleotide Polymorphisms (SNPs) from Genome Wide Association Studies (GWAS) Analysis</i>
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Description

Identifies Candidate Genes based on identified Single Nucleotide Polymorphisms (SNPs) from Genome Wide Association Studies (GWAS) Analysis

Usage

```
geneSNP(
  data_file,
  upstream = 1e+06,
  downstream = 1e+06,
  crop = "wheat",
  genome_source = "online",
  gff3_file = NULL
)
```

Arguments

data_file	The input data in .csv format. (sample_data_wheat or sample_data_rice for demo purpose)
upstream	The search window upstream of the current position of the SNP. (default: 1000000)
downstream	The search window downstream of the current position of the SNP. (default: 1000000)
crop	Either "wheat" or "rice". (default: wheat)
genome_source	Character specifying either "online" (default Ensembl lookup) or "local" (uses a local GFF3 file).
gff3_file	Path to a local custom .gff3 file. Only utilized if genome_source = "local".

Value

A data frame containing traits, SNP, search_window, gene_size, gene_id, and gene_type.

Examples

```
load(system.file("extdata", "precomputed_sample_results.rda", package = "geneNR"))
message(sample_results)
## Not run:
result <- geneSNP("sample_data_wheat", 10000, 10000, crop = "wheat")
result <- geneSNP("sample_data_rice", 10000, 10000, crop = "rice")
# Local mapping workflow:
# gff_path <- system.file("extdata", "sample_crop.gff3", package = "geneNR")
# result <- geneSNP("sample_data_wheat", 500000, 500000, genome_source="local", gff3_file=gff_path)

## End(Not run)
```

geneSNPcustom	<i>Identifies Candidate Genes based on identified Single Nucleotide Polymorphisms (SNPs) from Genome Wide Association Studies (GWAS) Analysis</i>
---------------	---

Description

Identifies Candidate Genes based on identified Single Nucleotide Polymorphisms (SNPs) from Genome Wide Association Studies (GWAS) Analysis

Usage

```
geneSNPcustom(
  data_file,
  crop = "wheat",
  genome_source = "online",
  gff3_file = NULL
)
```

Arguments

data_file	The input data in .csv format. (sample_data_wheat_custom for demo purpose)
crop	Either "wheat" or "rice". (default: wheat)
genome_source	Character specifying either "online" (default Ensembl lookup) or "local" (uses a local GFF3 file).
gff3_file	Path to a local custom .gff3 file. Only utilized if genome_source = "local".

Value

A data frame containing traits, SNP, search_window, gene_size, gene_id, and gene_type.

Examples

```
load(system.file("extdata", "precomputed_sample_results_custom.rda", package = "geneNR"))
message(sample_results)
## Not run:
result <- geneSNPcustom("sample_data_wheat_custom", crop = "wheat")

## End(Not run)
```

import_hmp	<i>Imports Hapmap genotypic data file</i>
------------	---

Description

Imports Hapmap genotypic data file

Usage

```
import_hmp(file_path, header = TRUE, sep = "\t", stringsAsFactors = FALSE)
```

Arguments

file_path	Provide the actual path of Hapmap genotypic data file
header	by default it will be True
sep	by default it will be tab separated
stringsAsFactors	by default it will be False

Value

Hampmap genotypic data

Examples

```
demo_SNP <- system.file("extdata", "demo_SNP.hmp.txt", package = "geneNR")
hapmap_data <- import_hmp(demo_SNP)
head(hapmap_data)
```

import_vcf	<i>Imports VCF (Variant Call Format) data file</i>
------------	--

Description

Imports VCF (Variant Call Format) data file

Usage

```
import_vcf(file_path)
```

Arguments

file_path Provide the actual path of the VCF file

Value

A vcfR object containing the imported data

Examples

```
demo_SNP <- system.file("extdata", "demo_SNP.vcf", package = "geneNR")
vcf_data <- import_vcf(demo_SNP)
vcf_data
```

plot_SNP	<i>Plot SNP Distribution on Chromosome Map</i>
----------	--

Description

Plots SNP positions across chromosomes with centromere markers using given chromosome details and SNP data.

Usage

```
plot_SNP(
  chromosome_details,
  data,
  chromosome_color = "steelblue",
  title = "Chromosome map with SNPs",
  label_color = "black",
  image_width = 10,
  image_height = 10
)
```

Arguments

chromosome_details	A data frame containing chromosome details with columns Chr, start and stop
data	A data frame containing SNP data with columns Chr, Pos, and SNP.
chromosome_color	Color of the chromosome bars (default: "skyblue").
title	Title of the chromosome plot depicting the identified SNPs
label_color	Color of the SNP labels (default: "black").
image_width	width of the chromosome plot
image_height	height of the chromosome plot

Value

A ggplot object for the SNP distribution plot.

Examples

```
chromosome_details <- read.csv(system.file("extdata", "chromosome_details.csv", package = "geneNR"))
data <- read.csv(system.file("extdata", "identified_SNP.csv", package = "geneNR"))
chromosome_plot <- plot_SNP(chromosome_details = chromosome_details, data = data,
  chromosome_color = "steelblue", title = "Chromosome map with SNPs", label_color = "black",
  image_width = 15, image_height = 10)
print(chromosome_plot)
```

plot_summariseSNP	<i>Plot SNP Distribution Across Chromosomes</i>
-------------------	---

Description

Creates a bar chart representing the distribution of SNPs across chromosomes. Allows customization of bar color, label size, and label color. Saves the plot to a user-specified directory or a temporary directory.

Usage

```
plot_summariseSNP(
  snp_distribution,
  file_name = "snp_bar_chart.jpeg",
  output_dir = tempdir(),
  bar_color = "lightblue",
  label_size = 3,
  label_color = "black"
)
```

Arguments

- snp_distribution A data frame with columns Chr and SNP_Count.
- file_name The name of the file to save the plot (default: "snp_bar_chart.jpeg").
- output_dir The directory to save the file (default: tempdir()).
- bar_color The color of the bars (default: "lightblue").
- label_size The size of the text labels on the bars (default: 3).
- label_color The color of the text labels on the bars (default: "black").

Value

A ggplot object for the created bar chart.

Examples

```
demo_SNP <- system.file("extdata", "demo_SNP.hmp.txt", package = "geneNR")
data <- import_hmp(demo_SNP)
snp_distribution <- summariseSNP(data)
plot <- plot_summariseSNP(snp_distribution, bar_color = "skyblue",
label_size = 3, label_color = "red")
print(plot)
```

sample_data_rice	<i>Sample Data</i>
------------------	--------------------

Description

A dataset containing sample data related to genetic markers and associated traits.

Usage

```
sample_data_rice
```

Format

- A data frame with columns:
- SNP** SNP identifier, character.
 - Chr** Chromosome location, character.
 - Pos** Position on the chromosome, numeric.
 - traits** Associated traits, character.

Source

Basha FTM, Sar P, Bhowmick PK, Mahato A, Bisht DS, Iquebal MA, Chakraborty K, Banerjee A, Verma BC, Bhaduri D, Kumar J, Ngangkham U, Saha S, Priyamedha, Mandal NP, Roy S. Genome-wide association study identified QTLs and genes underlying early seedling vigour in aus rice (*Oryza sativa* L.). Mol Genet Genomics. 2024 Dec 3;299(1):112. doi: 10.1007/s00438-024-02204-8. PMID: 39625651.

Examples

```
data(sample_data_rice)    #lazy loading
```

```
sample_data_rice_qtl    Sample Data
```

Description

A dataset containing sample data related to genetic markers and associated traits.

Usage

```
sample_data_rice_qtl
```

Format

A data frame with columns:

traits Associated traits, character.

Chr Chromosome location, character.

start Position on the chromosome where QTL starts, numeric.

stop Position on the chromosome where QTL stops, numeric.

Source

Generated for demonstration purposes

Examples

```
data(sample_data_rice_qtl)    #lazy loading
```

sample_data_wheat	<i>Sample Data</i>
-------------------	--------------------

Description

A dataset containing sample data related to genetic markers and associated traits.

Usage

sample_data_wheat

Format

A data frame with columns:

- SNP** SNP identifier, character.
- Chr** Chromosome location, character.
- Pos** Position on the chromosome, numeric.
- traits** Associated traits, character.

Source

Generated for demonstration purposes

Examples

```
data(sample_data_wheat)    #lazy loading
```

sample_data_wheat_custom	<i>Sample Data</i>
--------------------------	--------------------

Description

A dataset containing sample data related to genetic markers and associated traits.

Usage

sample_data_wheat_custom

Format

A data frame with columns:

traits Associated traits, character.

SNP SNP identifier, character.

Chr Chromosome location, character.

start Position on the chromosome where search window starts, numeric.

stop Position on the chromosome where search window stops, numeric.

Source

Generated for demonstration purposes

Examples

```
data(sample_data_wheat_custom)    #lazy loading
```

sample_data_wheat_qtl *Sample Data*

Description

A dataset containing sample data related to genetic markers and associated traits.

Usage

```
sample_data_wheat_qtl
```

Format

A data frame with columns:

traits Associated traits, character.

Chr Chromosome location, character.

start Position on the chromosome where QTL starts, numeric.

stop Position on the chromosome where QTL stops, numeric.

Source

Generated for demonstration purposes

Examples

```
data(sample_data_wheat_qtl)    #lazy loading
```

`summariseSNP`*Distribution of SNPs Across Chromosomes*

Description

Distribution of SNPs Across Chromosomes

Usage

```
summariseSNP(data)
```

Arguments

`data` A data frame containing a column named Chr

Value

A data frame with chromosome names and the count of SNPs for each chromosome

Examples

```
demo_SNP <- system.file("extdata", "demo_SNP.hmp.txt", package = "geneNR")
data <- import_hmp(demo_SNP)
snp_distribution <- summariseSNP(data)
print(snp_distribution)
```

`summariseSNP_vcf`*Distribution of SNPs Across Chromosomes from VCF*

Description

Distribution of SNPs Across Chromosomes from VCF

Usage

```
summariseSNP_vcf(vcf_data)
```

Arguments

`vcf_data` A vcfR object containing VCF data.

Value

A data frame with chromosome names and the count of SNPs for each chromosome.

Examples

```
demo_SNP <- system.file("extdata", "demo_SNP.vcf", package = "geneNR")
vcf_data <- import_vcf(demo_SNP)
snp_distribution <- summariseSNP_vcf(vcf_data)
print(snp_distribution)
```

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