Package: geneNR (via r-universe)

March 11, 2025

Title Automated Gene Identification for Post-GWAS Analysis

Version 1.0.1

Description Facilitates the post-Genome Wide Association Studies (GWAS) 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>. 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

Suggests knitr, rmarkdown, devtools

VignetteBuilder knitr

NeedsCompilation no

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Config/pak/sysreqs libicu-dev libxml2-dev libssl-dev libx11-dev zlib1g-dev

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

RemoteUrl https://github.com/cran/geneNR

RemoteRef HEAD

RemoteSha 200d5e33fdedfe5f25ac09f57f6e6d4134e3b955

Contents

`geneSNP` *Identifies Candidate Genes based on identified Single Nucleotide Ploymorphisms (SNPs) from Genome Wide Association Stuides (GWAS) Analysis*

Description

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

Usage

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

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)

Value

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

Examples

```
load(system.file("extdata", "precomputed_sample_results.rda", package = "geneNR"))
message(sample_results)

result <- geneSNP("sample_data_wheat", 10000, 10000, crop = "wheat")
result <- geneSNP("sample_data_rice", 10000, 10000, crop = "rice")
```

`sample_data_rice` *Sample Data*

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_wheat` *Sample Data*

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
```

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