# Package: geneNR (via r-universe)

March 10, 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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**Repository** CRAN

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

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

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### 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")
```

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## `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
```

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## `sample_data_wheat` *Sample Data*

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### 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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