

Package: GenePopStats (via r-universe)

May 17, 2026

Type Package

Title Population Genetics Statistics for Selective Sweep

Version 0.1.0

Imports vcfR

Description Selective Sweep can be calculated by five significant Population Genetics Statistics such as ``Pi'', ``Wattersons_theta'', ``Tajima_D'', ``Kelly_ZnS'' and ``Omega'' Statistics in specified chromosomal region. It has been developed by using the concept of ``Kern'' and ``Schrider'' (2018)<[doi:10.1534/g3.118.200262](https://doi.org/10.1534/g3.118.200262)>.

License GPL-3

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation no

Author Abhik Sarkar [aut, cre], Dwijesh Chandra Mishra [aut], Dipro Sinha [aut], Saikath Das [aut], Krishna Kumar Chaturvedi [aut], Shashi Bhushan Lal [aut], Sanjeev Kumar [aut], Ranjit Kumar Paul [aut], Girish Kumar Jha [aut], Neeraj Budhlakoti [aut], Md Yeasin [aut]

Maintainer Abhik Sarkar <abhik.iasri@gmail.com>

Config/pak/sysreqs libicu-dev

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

Date/Publication 2025-09-16 06:20:02 UTC

RemoteUrl <https://github.com/cran/GenePopStats>

RemoteRef HEAD

RemoteSha 8995ed284e211f9e6b18e7d21e0230a9c56edcf3

Contents

GenePopStats	2
Index	3

GenePopStats

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Description

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Usage

```
GenePopStats(vcf_file, window_size, step_size)
```

Arguments

<code>vcf_file</code>	Enter the path to VCF File
<code>window_size</code>	Length of the genomic region
<code>step_size</code>	Length of slide in the window in forward direction

Value

Results are being obtained as a matrix containing 5 Population Summary Statistics such as "Pi", "Wattersons_theta", "Tajima_D", "Kelly_ZnS" and "Omega" Statistics subdivided into windows as specified chromosomal region

Examples

```
path<-system.file("exdata", "ExampleVCF.vcf", package = "GenePopStats")
GenePopStats(path, 20, 10)
```

Index

GenePopStats, [2](#)