Package 'GenePopStats'

September 16, 2025

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>.

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>

Repository CRAN

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

Contents

GenePopStats *Title GenePopStats: Population Genetics Statistics for Selective Sweep*

Description

Title GenePopStats: Population Genetics Statistics for Selective Sweep

Usage

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

Arguments

vcf_file	Enter the path to VCF File
window_size	Length of the genomic region
step_size	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