

# Package ‘GenePopStats’

May 7, 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

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GenePopStats

*Title GenePopStats: Population Genetics Statistics for Selective Sweep*

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### **Description**

Title GenePopStats: Population Genetics Statistics for Selective Sweep

### **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)
```

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