

Package: PGEhammer (via r-universe)

June 11, 2024

Type Package

Title What the Package Does (Title Case)

Version 0.1.0

Description A series of utility functions that improve the experience of working with other software tools in Plasmodium genomic epidemiology. This includes functions for wrangling data and visualising outputs. Part of the PGEforge set of resources.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

BugReports <https://github.com/mrc-ide/PGEhammer/issues>

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Imports dplyr, rlang, stringr, tibble, tidyr, vcfR

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

RemoteUrl <https://github.com/mrc-ide/PGEhammer>

RemoteRef HEAD

RemoteSha e7c46e38436f3ebb158fc9453276176192cbe88f

Contents

PGEhammer	2
square	2
vcf2long	2

Index	3
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 PGEhammer

PGEhammer

Description

A series of utility functions that improve the experience of working with other software tools in Plasmodium genomic epidemiology. This includes functions for wrangling data and visualising outputs. Part of the **PGEforge** set of resources.

square

Square a vector of values

Description

Simple test function that demonstrates some of the features of this package by squaring an input vector of values.

Usage

```
square(x = 1:5)
```

Arguments

x vector of values.

Examples

```
# Find square of first 100 values
square(1:100)
```

vcf2long

Convert vcf to long format

Description

Convert a vcf into a long format data frame with sample ID, locus, alleles and read counts for each allele.

Usage

```
vcf2long(vcf)
```

Arguments

vcf object of class vcfR

Index

PGEhammer, [2](#)

square, [2](#)

vcf2long, [2](#)