

# Package ‘ggmugs’

May 7, 2024

**Type** Package

**Title** Visualization of Multiple Genome-Wide Association Study Summary Statistics

**Version** 0.6.0

**Description** A 'grammar of graphics' approach for visualizing summary statistics from multiple Genome-wide Association Studies (GWAS). It offers geneticists, bioinformaticians, and researchers a powerful yet flexible tool for illustrating complex genetic associations using data from various GWAS datasets. The visualizations can be extensively customized, facilitating detailed comparative analysis across different genetic studies. Reference: Uffelmann, E. et al. (2021) <[doi:10.1038/s43586-021-00056-9](https://doi.org/10.1038/s43586-021-00056-9)>.

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**Encoding** UTF-8

**Suggests** spelling, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Imports** data.table, dplyr, ggplot2, purrr, tibble, tidyr

**Language** en-US

**RoxygenNote** 7.3.1

**NeedsCompilation** no

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## R topics documented:

ggmugs . . . . . 2

**Index** . . . . . 4

## Description

This function processes and combines summary statistics from multiple genetic studies and creates a visualization for all studies. The genetic loci are colored based on three significance thresholds to facilitate the visualization of highly significant genomic regions.

## Usage

```
ggmugs(  
  study_name = c("sumstat1", "sumstat2", "sumstat3", "sumstat4", "sumstat5"),  
  summary_stat = c("data/sumstat1.txt", "data/sumstat2.txt", "data/sumstat3.txt",  
    "data/sumstat4.txt", "data/sumstat5.txt"),  
  p1 = 0.001,  
  p2 = 5e-05,  
  p3 = 1e-08,  
  color1 = "#FFFFFF0",  
  color2 = "#FFC300",  
  color3 = "#FF5733"  
)
```

## Arguments

study_name	A character vector of names for the studies.
summary_stat	A character vector of file paths where each path points to the summary statistics data file for the corresponding study. Files should be in a tabular format readable by 'fread' from the 'data.table' package. The files should contain 3 fields: 'chr' (Chromosome), 'pos' (chromosome position), and 'p' (association p-value). The positions of multiple GWAS summary statistics should have consistent genome builds.
p1	The first significance level threshold for p-values (default is 1e-3).
p2	The second, more stringent significance level threshold for p-values (default is 5e-5).
p3	The most stringent significance level threshold for p-values (default is 1e-8).
color1	The color for points below the first significance level (default is "#FFFFFF0").
color2	The color for points between the first and second significance levels (default is "#FFC300").
color3	The color for points above the second significance level (default is "#FF5733").

## Value

A 'ggplot' object representing the visualization with the specified data.

**Examples**

```
### NOT RUN
# ggmugs(
#   study_name = c("study1", "study2", "study3", "study4", "study5"),
#   summary_stat = c("https://raw.githubusercontent.com/Broccolito/ggmugs_data/main/sumstat1.txt",
#                    "https://raw.githubusercontent.com/Broccolito/ggmugs_data/main/sumstat2.txt",
#                    "https://raw.githubusercontent.com/Broccolito/ggmugs_data/main/sumstat3.txt",
#                    "https://raw.githubusercontent.com/Broccolito/ggmugs_data/main/sumstat4.txt",
#                    "https://raw.githubusercontent.com/Broccolito/ggmugs_data/main/sumstat5.txt"),
#   p1 = 1e-4,
#   p2 = 1e-6,
#   p3 = 1e-8,
#   color1 = "#FFFFE0",
#   color2 = "#FFC300",
#   color3 = "#FF5733"
# )
```

# Index

ggmugs, [2](#)