Package: archipelago (via r-universe)

May 11, 2026

Title Visualising Variant Set Association Test Results

Version 0.1.0

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Language en-GB

Description Provides a graphical method for joint visualisation of Variant Set Association Test (VSAT) results and individual variant association statistics. The Archipelago method assigns genomic coordinates to variant set statistics, allowing simultaneous display of variant-level and set-level signals in a unified plot. This supports interpretation of both collective and individual variant contributions in genetic association studies using variant aggregation approaches. For more see Lawless et al. (2026) <doi:10.1002/gepi.70025>.

Encoding UTF-8

Imports ggplot2, dplyr

RoxygenNote 7.3.3

VignetteBuilder knitr

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

Depends R (>= 4.1.0)

LazyData true

NeedsCompilation no

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RemoteUrl https://github.com/cran/archipelago

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Contents

`archipelago_plot` *Archipelago Plot*

Description

Plot p-values from variant and variant-set tests.

Arguments

`df1`	A dataframe of variant-set data.
`df2`	A dataframe of variant data.
`plot_title`	Title for the plot.
`add_title`	Logical; add title if TRUE.
`plot_subtitle`	Subtitle for the plot.
`add_subtitle`	Logical; add subtitle if TRUE.
`chr_ticks`	Logical; show chromosome ticks if TRUE.
`show_legend`	Logical; display the legend if TRUE.
`color_theme`	Name of the colour theme.
`custom_colors`	Vector of custom colours.
`color_labels`	Labels for the colour groups.
`crit_val`	Critical p-value threshold.
`point_size`	Size of the points.
`point_size_large`	Size of the large points of interest such as VSAT.
`fig_width`	Width of the archipelago plot.
`fig_height`	Height of the archipelago plot.
`raw_fig_width`	Width of the raw plot.
`raw_fig_height`	Height of the raw plot.
`output_path`	File path for the plot.
`output_raw`	File path for the raw plot.
`file_type`	Use .png, .jpg, or .pdf. Defaults to png. pdf is slow and large for many SNPs.
`alpha_point`	Use the alpha_point value to set point transparency.
`alpha_seg`	Use the alpha_segvalue to set line segment transparency.

`better_space`	Use better_space = TRUE to make sure that x-axis chr do not squash.
`legend_position`	Default right, allows bottom top left right.
`annotate_thresholds`	Logical; if TRUE, annotate plot with VSAT and single-variant p-value thresholds.

Value

A ggplot object.

Examples

```
data("vsat_pval")
data("variant_pval")
archipelago_plot(vsat_pval, variant_pval)
```

`variant_pval` *Example variant data*

Description

Example variant-level p-values from a genome-wide association study.

Usage

```
variant_pval
```

Format

A data frame with columns:

- set_ID
- BP
- P
- CHR
- SNP

`vsat_pval` *Example variant set data*

Description

Example variant set-level p-values.

Usage

```
vsat_pval
```

Format

A data frame with columns:

- set_ID
- P

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