

# Package ‘archipelago’

February 10, 2026

**Title** Visualising Variant Set Association Test Results

**Version** 0.1.0

**License** MIT + file LICENSE

**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](https://doi.org/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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**Repository** CRAN

**Date/Publication** 2026-02-10 21:00:02 UTC

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archipelago\_plot      *Archipelago Plot*

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### 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_seg value 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)
```

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variant_pval	<i>Example variant data</i>
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**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

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vsat_pval	<i>Example variant set data</i>
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**Description**

Example variant set-level p-values.

**Usage**

```
vsat_pval
```

**Format**

A data frame with columns:

- set\_ID
- P

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