

Package ‘mapmixture’

April 29, 2024

Title Spatial Visualisation of Admixture on a Projected Map

Version 1.1.2

Description Visualise admixture as pie charts on a projected map, admixture as traditional structure barplots or facet barplots, and scatter plots from genotype principal components analysis. A 'shiny' app allows users to create admixture maps interactively. Jenkins TL (2024) <[doi:10.1111/1755-0998.13943](https://doi.org/10.1111/1755-0998.13943)>.

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.3.1

URL <https://github.com/Tom-Jenkins/mapmixture>

BugReports <https://github.com/Tom-Jenkins/mapmixture/issues>

Imports bslib (>= 0.5.0), colourpicker, dplyr, ggplot2, ggspatial, grid, htmltools, purrr, rlang, rnaturalearthdata, sf, shiny, shinyFeedback, shinyjs, shinyWidgets, stringr, tidyr, waiter

Suggests shinytest2, terra, testthat (>= 3.2.0)

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Depends R (>= 4.1.0)

NeedsCompilation no

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R topics documented:

launch_mapmixture	2
mapmixture	2
scatter_plot	5
structure_plot	7

Index	10
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launch_mapmixture *Launch Shiny App*

Description

Wrapper function used to start mapmixture interactive app.

App tested with the following package versions:

shiny v1.8.0, shinyFeedback v0.4.0, shinyjs v2.1.0, shinyWidgets 0.8.4, bslib 0.7.0, colourpicker 1.3.0, htmltools v0.5.8.1, waiter 0.2.5.

Usage

```
launch_mapmixture(...)
```

Arguments

... additional arguments passed to shiny::runApp().

Value

No return value.

Examples

```
if (interactive()){
  launch_mapmixture(launch.browser = TRUE)
}
```

mapmixture *Plot Pie Charts on Map*

Description

Plot admixture proportions as pie charts on a projected map. In data sets where there are multiple individuals per site, the function will calculate the mean average admixture proportion for each site.

Usage

```
mapmixture(
  admixture_df,
  coords_df,
  cluster_cols = NULL,
  cluster_names = NULL,
  boundary = NULL,
  crs = 4326,
```

```

    basemap = NULL,
    pie_size = 1,
    pie_border = 0.2,
    pie_opacity = 1,
    land_colour = "#d9d9d9",
    sea_colour = "#deebf7",
    expand = FALSE,
    arrow = TRUE,
    arrow_size = 1,
    arrow_position = "t1",
    scalebar = TRUE,
    scalebar_size = 1,
    scalebar_position = "t1",
    plot_title = "",
    plot_title_size = 12,
    axis_title_size = 10,
    axis_text_size = 8
  )

```

Arguments

admixture_df	data.frame or tibble containing admixture data (see examples).
coords_df	data.frame or tibble containing coordinates data (see examples).
cluster_cols	character vector of colours the same length as the number of clusters. If NULL, a blue-green palette is used.
cluster_names	character vector of names the same length as the number of clusters. If NULL, the cluster column names are used.
boundary	named numeric vector defining the map bounding. e.g. <code>c(xmin=-15, xmax=15, ymin=30, ymax=50)</code> . If NULL, a default bounding box is calculated.
crs	coordinate reference system. Default is the WGS 84 - World Geodetic System 1984 (EPSG:4326). See <code>?sf::st_crs</code> for details.
basemap	SpatRaster or sf object to use as the basemap. A SpatRaster object can be created from a file using the <code>terra::rast()</code> function. A sf object can be created from a file using the <code>sf::st_read()</code> function. If NULL, world country boundaries are used.
pie_size	numeric value of zero or greater.
pie_border	numeric value of zero or greater.
pie_opacity	numeric value of zero to one.
land_colour	string defining the colour of land.
sea_colour	string defining the colour of sea.
expand	expand axes (TRUE or FALSE).
arrow	show arrow (TRUE or FALSE). Added using the <code>ggspatial::annotation_north_arrow()</code> function.
arrow_size	numeric value of zero or greater.

arrow_position string defining the position of the arrow ("tl", "tr", "bl", "br").
scalebar show scalebar (TRUE or FALSE). Added using the `ggspatial::annotation_scale()` function.
scalebar_size numeric value of zero or greater.
scalebar_position string defining the position of the scalebar ("tl", "tr", "bl", "br").
plot_title string defining the main title of the plot.
plot_title_size numeric value of zero or greater.
axis_title_size numeric value of zero or greater.
axis_text_size numeric value of zero or greater.

Value

A ggplot object.

Examples

```

# Admixture Format 1
file <- system.file("extdata", "admixture1.csv", package = "mapmixture")
admixture1 <- read.csv(file)

# Admixture Format 2
file <- system.file("extdata", "admixture2.csv", package = "mapmixture")
admixture2 <- read.csv(file)

# Admixture Format 3
file <- system.file("extdata", "admixture3.csv", package = "mapmixture")
admixture3 <- read.csv(file)

# Coordinates Format
file <- system.file("extdata", "coordinates.csv", package = "mapmixture")
coordinates <- read.csv(file)

# Plot using default parameters
mapmixture(admixture1, coordinates)

# Plot using the ETRS89-extended / LAEA Europe coordinate reference system
mapmixture(admixture1, coordinates, crs = 3035)

# Plot using custom parameters
mapmixture(
  admixture_df = admixture1,
  coords_df = coordinates,
  cluster_cols = c("#f1a340", "#998ec3"),
  cluster_names = c("Group 1", "Group 2"),
  crs = "+proj=merc +a=6378137 +b=6378137 +lat_ts=0 +lon_0=0 +x_0=0 +y_0=0 +units=m",
  boundary = c(xmin=-15, xmax=16, ymin=40, ymax=62),
  pie_size = 1.5,

```

```
pie_border = 0.2,  
pie_opacity = 1,  
land_colour = "#d9d9d9",  
sea_colour = "#deebf7",  
expand = FALSE,  
arrow = TRUE,  
arrow_size = 1,  
arrow_position = "t1",  
scalebar = TRUE,  
scalebar_size = 1,  
scalebar_position = "t1",  
plot_title = "Mapmixture Figure",  
plot_title_size = 15,  
axis_title_size = 12,  
axis_text_size = 10  
)
```

scatter_plot

PCA or DAPC Scatter Plot

Description

Plot a scatter plot of PCA or DAPC results.

Usage

```
scatter_plot(  
  dataframe,  
  group_ids,  
  other_group = NULL,  
  type = "points",  
  ...,  
  labels = NULL,  
  axes = c(1, 2),  
  colours = NULL,  
  centroids = TRUE,  
  segments = TRUE,  
  point_size = 3,  
  point_type = 21,  
  centroid_size = 3,  
  hvline_type = "dotted",  
  hvline_size = 0.5,  
  hvline_colour = "black",  
  xlab = "Axis",  
  ylab = "Axis",  
  percent = NULL,  
  plot_title = ""  
)
```

Arguments

dataframe	data.frame or tibble containing results from a PCA or DAPC (see examples).
group_ids	character vector of IDs representing the group each row belongs to. This is used to colour the scatter plot and (optionally) add centroids and segments. E.g. a vector of site names, a vector of biological categories such as male or female, etc.
other_group	secondary character vector of IDs defining how to colour the scatter plot. E.g. a vector of country names (see examples). If NULL, scatter plot is coloured by group_ids.
type	string defining whether to show points ("points"), labels ("labels"), or text ("text").
...	additional arguments passed to ggplot2::geom_point when type = "points", or to ggplot2::geom_label when type = "labels", or to ggplot2::geom_text when type = "text".
labels	character vector of IDs defining labels when type = "label" or type = "text". If NULL, row names are used (integers from 1:nrow(dataframe)).
axes	integer vector of length two defining which axes to plot.
colours	character vector of colours the same length as the number of groups defined in group_ids or other_group.
centroids	add centroids to plot (TRUE or FALSE).
segments	add segments to plot (TRUE or FALSE).
point_size	numeric value for point size.
point_type	numeric value for point type (shape).
centroid_size	numeric value for centroid label size.
hvltype	integer or string defining linetype (1 or "dotted"). Input 0 for no horizontal and vertical lines.
hvlsize	integer defining linewidth.
hvlcolour	string defining line colour.
xlab	string defining x axis label.
ylab	string defining y axis label.
percent	numeric vector the same length as ncol(dataframe) defining the percentage of variance explained by each axis.
plot_title	string defining the main title of the plot.

Value

A ggplot object.

Examples

```

# Results from a Principal Components Analysis
file <- system.file("extdata", "pca_results.csv", package = "mapmixture")
pca_results <- read.csv(file)

# Define parameters
ind_names <- row.names(pca_results)
site_names <- rep(c("Pop1", "Pop2", "Pop3", "Pop4", "Pop5", "Pop6"), each = 100)
region_names <- rep(c("Region1", "Region2"), each = 300)
percent <- c(5.6, 4.5, 3.2, 2.0, 0.52)

# Scatter plot
scatter_plot(pca_results, site_names)

# Scatter plot with axes 1 and 3 and percent on axis labels
scatter_plot(pca_results, site_names, axes = c(1,3), percent = percent)

# Scatter plot with no centroids and segments
scatter_plot(pca_results, site_names, axes = c(1,2), percent = percent,
             centroids = FALSE, segments = FALSE)

# Scatter plot with custom colours and coloured by other_group
scatter_plot(pca_results, site_names, other_group = region_names,
             percent = percent, colours = c("#f1a340", "#998ec3"))

# Scatter plot with individual labels
scatter_plot(pca_results, site_names, type = "labels",
             labels = rownames(pca_results))

# Scatter plot with individual text
scatter_plot(pca_results, site_names, type = "text",
             labels = rownames(pca_results))

```

structure_plot

STRUCTURE Barplot

Description

Plot a traditional STRUCTURE barplot or a facet barplot from individual admixture proportions.

Usage

```

structure_plot(
  admixture_df,
  type = "structure",
  cluster_cols = NULL,
  cluster_names = NULL,
  legend = "none",
  labels = "site",

```

```

flip_axis = FALSE,
ylabel = "Proportion",
site_dividers = TRUE,
divider_width = 1,
divider_col = "white",
divider_type = "dashed",
site_order = NULL,
site_labels_size = 2,
site_labels_x = 0,
site_labels_y = -0.025,
site_ticks = TRUE,
site_ticks_size = -0.01,
facet_col = NULL,
facet_row = NULL
)

```

Arguments

admixture_df	data.frame or tibble containing admixture data (see examples).
type	show a traditional STRUCTURE barplot ("structure") or a facet barplot ("facet").
cluster_cols	character vector of colours the same length as the number of clusters. If NULL, a blue-green palette is used.
cluster_names	character vector of names the same length as the number of clusters. If NULL, the cluster column names are used.
legend	add legend at position ("none", "top", "right", "bottom" or "left"). Default is to hide legend.
labels	show labels at the site level or the individual level ("site" or "individual").
flip_axis	flip the axes so that the plot is vertical (TRUE or FALSE). Default is FALSE (horizontal barplot).
ylabel	string for y label.
site_dividers	add dotted lines that divide sites (TRUE or FALSE).
divider_width	width of site divider lines.
divider_col	colour of site divider lines.
divider_type	linetype of site divider line.
site_order	character vector of site labels used to customise the order of sites. If NULL, sites are ordered alphabetically.
site_labels_size	numeric value for site label size.
site_labels_x	numeric value for site label horizontal position.
site_labels_y	numeric value for site label vertical position.
site_ticks	show ticks when labels = "site".
site_ticks_size	numeric value for site tick size.
facet_col	number of columns to display for facet barplot.
facet_row	number of rows to display for facet barplot.

Value

A ggplot object.

Examples

```
# Admixture Format 1
file <- system.file("extdata", "admixture1.csv", package = "mapmixture")
admixture1 <- read.csv(file)

structure_plot(admixture1, type = "structure")
structure_plot(admixture1, type = "facet", facet_col = 5)
```

Index

launch_mapmixture, [2](#)

mapmixture, [2](#)

scatter_plot, [5](#)

structure_plot, [7](#)