

Package ‘mapmixture’

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Title Spatial Visualisation of Admixture on a Projected Map

Version 1.2.0

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 dplyr, ggplot2, ggspatial, grid, purrr, rlang,
rnaturalearthdata, sf, stringr, tidyr

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waiter

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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_border_col = "black",
    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,
    basemap_border = TRUE,
    basemap_border_col = "black",
    basemap_border_lwd = 0.1
  )

```

Arguments

<code>admixture_df</code>	data.frame or tibble containing admixture data (see examples).
<code>coords_df</code>	data.frame or tibble containing coordinates data (see examples).
<code>cluster_cols</code>	character vector of colours the same length as the number of clusters. If NULL, a blue-green palette is used.
<code>cluster_names</code>	character vector of names the same length as the number of clusters. If NULL, the cluster column names are used.
<code>boundary</code>	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.
<code>crs</code>	coordinate reference system. Default is the WGS 84 - World Geodetic System 1984 (EPSG:4326). See <code>?sf::st_crs</code> for details.
<code>basemap</code>	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.
<code>pie_size</code>	vector of numeric values of zero or greater. Can be a single value or a vector the same length as the number of sites.
<code>pie_border</code>	numeric value of zero or greater.
<code>pie_border_col</code>	string denoting colour of pie border.
<code>pie_opacity</code>	numeric value of zero to one.
<code>land_colour</code>	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 <code>ggspatial::annotation_scale()</code> 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.
basemap_border	boolean denoting whether to show basemap polygon borders.
basemap_border_col	string defining colour of basemap polygon borders.
basemap_border_lwd	numeric value defining linewidth of basemap polygon borders.

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.
hvline_type	integer or string defining linetype (1 or "dotted"). Input 0 for no horizontal and vertical lines.
hvline_size	integer defining linewidth.
hvline_colour	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,
  display_site_labels = TRUE,
  site_labels_size = 2,
  site_labels_x = 0,
  site_labels_y = -0.025,
  site_labels_angle = 0,
  site_ticks = TRUE,
  site_ticks_size = -0.01,
  facet_col = NULL,
  facet_row = NULL
)

```

Arguments

<code>admixture_df</code>	data.frame or tibble containing admixture data (see examples).
<code>type</code>	show a traditional STRUCTURE barplot ("structure") or a facet barplot ("facet").
<code>cluster_cols</code>	character vector of colours the same length as the number of clusters. If NULL, a blue-green palette is used.
<code>cluster_names</code>	character vector of names the same length as the number of clusters. If NULL, the cluster column names are used.
<code>legend</code>	add legend at position ("none", "top", "right", "bottom" or "left"). Default is to hide legend.
<code>labels</code>	show labels at the site level or the individual level ("site" or "individual").
<code>flip_axis</code>	flip the axes so that the plot is vertical (TRUE or FALSE). Default is FALSE (horizontal barplot).
<code>ylabel</code>	string for y label.
<code>site_dividers</code>	add dotted lines that divide sites (TRUE or FALSE).
<code>divider_width</code>	width of site divider lines.
<code>divider_col</code>	colour of site divider lines.
<code>divider_type</code>	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.

`display_site_labels` display site labels (TRUE or FALSE).

`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_labels_angle` numeric value for rotating angle of site label.

`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)
```

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