

# Package ‘GHRexplore’

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**Title** Exploratory Analysis of Temporal and Spatio-Temporal Health Data

**Version** 0.2.2

**Description** A collection of commonly used visualizations of temporal and spatio-temporal health data including case counts, incidence rates, and covariates. The available plot types include time series, heatmaps, seasonality plots, maps and more. The package supports standard data transformations such as temporal and spatial aggregations, while offering extensive customization options for the resulting figures.

**License** GPL (>= 2)

**URL** <https://gitlab.earth.bsc.es/ghr/ghrexplorer>,  
<https://bsc-es.github.io/GHRtools/docs/GHRexplore/GHRexplore>

**BugReports** <https://gitlab.earth.bsc.es/ghr/ghrexplorer/-/issues>

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**Author** Carles Milà [aut, cre] (ORCID: <<https://orcid.org/0000-0003-0470-0760>>),  
Giovenale Moirano [aut] (ORCID:  
<<https://orcid.org/0000-0001-8748-3321>>),  
Anna B. Kawiecki [aut] (ORCID: <<https://orcid.org/0000-0002-0499-2612>>),  
Rachel Lowe [aut, cph] (ORCID: <<https://orcid.org/0000-0003-3939-7343>>)

**Maintainer** Carles Milà <[carles.milagarcia@bsc.es](mailto:carles.milagarcia@bsc.es)>

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aggregate_cases	<i>Aggregate cases</i>
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## Description

Aggregates a data frame containing disease cases in space and/or time.

## Usage

```
aggregate_cases(
  data = NULL,
  cases = NULL,
  pop = NULL,
  time = NULL,
  area = NULL,
  pt = 1e+05,
  aggregate_space = NULL,
  aggregate_time = NULL
)
```

**Arguments**

data	Data frame containing equally spaced (daily, weekly, monthly) incident cases for one or multiple areas.
cases	Name of the variable that identifies the cases.
pop	Name of the variable that identifies the population.
time	Name of the variable that identifies the temporal dimension. The values must be in date format ("yyyy-mm-dd") representing the day of observation for daily data, the first day of the week for weekly, or the first day of the month for monthly observations.
area	Name of variable that identifies the different locations (e.g., areal units) for which a time series is available.
pt	Scale of the person-time (default 100,000) for incidence rates.
aggregate_space	Name of variable used to define spatial aggregation groups.
aggregate_time	Temporal scale used to perform temporal aggregation. Options are: "week" (ISO 8601), "month", "year".

**Value**

A data frame with the aggregated cases.

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aggregate_cov	<i>Aggregate covariates</i>
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**Description**

Aggregates a data frame containing a covariate of interest in space and/or time.

**Usage**

```
aggregate_cov(
  data = NULL,
  var = NULL,
  time = NULL,
  area = NULL,
  aggregate_space = NULL,
  aggregate_time = NULL,
  aggregate_space_fun = "mean",
  aggregate_time_fun = "mean"
)
```

**Arguments**

data	Data frame containing equally spaced (daily, weekly, monthly) incident cases for one or multiple areas.
var	Name of the variable that identifies the covariate.
time	Name of the variable that identifies the temporal dimension. The values must be in date format ("yyyy-mm-dd") representing the date of observation for daily data, the first day of the week for weekly, or the first day of the month for monthly observations.
area	Name of variable that identifies the different locations (i.e., areal units) for which a time series is available.
aggregate_space	Name of variable used to define spatial aggregation groups.
aggregate_time	Temporal scale used to perform temporal aggregation. Options are: "week" (ISO 8601), "month", "year".
aggregate_space_fun	Character indicating the function to be used in the aggregation over space, default is "mean".
aggregate_time_fun	Character indicating the function to be used in the aggregation over time, default is "mean".

**Value**

A data frame with the aggregated covariate.

---

date_to_epiyw	<i>Convert a date to epiyearweek format</i>
---------------	---

---

**Description**

The conversion is done following the ISO 8601 standard, whereby the first week of the year is the one that contains at least four days of the new year. This coincides with the approach taken by `lubridate::epiweek` and `lubridate::isoweek` but may not coincide with other definitions of epidemiological weeks.

**Usage**

```
date_to_epiyw(date, weekday = "Monday")
```

**Arguments**

date	A vector of type 'Date'.
weekday	The weekday that determines the start of the week. Defaults to 'Monday'.

**Value**

The transformed dates to epiyearweek.

**Examples**

```
# Convert dates in 'dengue_SP' in epiyw
data(dengue_SP)
head(dengue_SP$date)
dengue_SP$epiyw <- date_to_epiyw(as.Date(dengue_SP$date), "Sunday")
head(dengue_SP$epiyw)
```

---

dengue_MS	<i>Dengue cases in Mato Grosso do Sul</i>
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**Description**

Monthly number of notified dengue cases by municipality in the *Mato Grosso do Sul* state of Brazil and a set of spatial and spatio-temporal covariates.

**Usage**

```
data(dengue_MS)
```

**Format**

A data frame with 2,640 rows and 27 columns:

**micro\_code** Unique ID number for each micro region (11 units).

**micro\_name** Name of each micro region.

**micro\_name\_ibge** Name of each micro region in IBGE format.

**meso\_code** Unique ID number for each meso region (4 units).

**meso\_name** Name of each meso region.

**state\_code** Unique ID number for each state (1 unit).

**state\_name** Name of each state.

**region\_code** Unique ID number given to each Brazilian Region. All observations come from the "Southeast Region".

**region\_name** Name of each Brazilian Region. All observations come from the "Southeast Region".

**biome\_code** Biome code.

**biome\_name** Biome name.

**ecozone\_code** Ecozone code.

**ecozone\_name** Ecozone name.

**main\_climate** Most prevalent climate regime in the microregion. Based on Koppen Geiger climate regimes.

- month** Calendar month index, 1 = January, 12 = December.
- year** Year 2000 - 2019.
- time** Time index starting at 1 for January 2000.
- dengue\_cases** Number of notified dengue cases registered in the notifiable diseases system in Brazil (SINAN) in the microregion of reference, at the month of first symptoms.
- population** Estimated population based on projections calculated using the 2000 and 2010 censuses, as well as population counts from 2007 and 2017.
- pop\_density** Population density (number of people per km<sup>2</sup>).
- tmax** Monthly average daily maximum temperature; gridded values (at a 0.5 deg resolution) averaged across each microregion.
- tmin** Monthly average daily minimum temperature; gridded values (at a 0.5 deg resolution) averaged across each microregion.
- pdsi** Self-calibrated Palmer Drought Severity Index for each microregion. It measures how wet or dry a region is relative to usual conditions. Negative values represent periods of drought, positive values represent wetter periods. Calculated by taking the mean value within each microregion.
- urban** Percentage of population living in urban areas (2010 census).
- water\_network** Percentage of population with access to the piped water network according to the 2010 census.
- water\_shortage** Frequency of reported water shortages per microregion between 2000 and 2016.
- date** First day of the month in date format ("%d-%m-%Y").

### Details

In addition to the dengue counts, the dataset contains environmental, socio-economic and meteorological factors. This dataset is a subset of the original containing observations over the entire Brazil.

### Source

[https://github.com/drrachellowe/hydromet\\_dengue](https://github.com/drrachellowe/hydromet_dengue)

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dengue\_SP

*Dengue cases in Sao Paulo*

---

### Description

Data frame containing the weekly number of notified dengue cases in the municipality of *Sao Paulo*, as well as a set of climatic covariates.

### Usage

```
data(dengue_SP)
```

**Format**

A data frame with 678 rows and 8 columns:

- date** First day of the week in date format.
- geocode** Unique ID code for Sao Paulo microregion.
- cases** Number of notified dengue cases.
- year** Year (2010 - 2022).
- temp\_med** Weekly average daily mean temperature.
- precip\_tot** Weekly cumulative precipitation.
- enso** El Niño-Southern Oscillation index.
- pop** Number of inhabitants.

**Source**

<https://info.dengue.mat.br/services/api>

---

epiyw_to_date	<i>Convert a epiyearweek to date format</i>
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---

**Description**

The conversion is done following the ISO 8601 standard, whereby the first week of the year is the one that contains at least four days of the new year. This coincides with the approach taken by `lubridate::epiweek` and `lubridate::isoweek` but may not coincide with other definitions of epidemiological weeks.

**Usage**

```
epiyw_to_date(epiyw, weekday = "Monday")
```

**Arguments**

epiyw	An epiyear-epiweek character vector in 'YYYY-WW' format.
weekday	Starting day of the epiweek. Defaults to Monday.

**Value**

The converted epiyearweeks to dates.

**Examples**

```
epiyw <- c("2025-01", "2025-10", "2025-20", "2025-30")
epiyw_to_date(epiyw)
```

---

GHR_palette	<i>Generate GHR color palettes</i>
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---

### Description

Generates color palettes including custom, ColorBrewer and colorspace palettes.

Creates a visualization of all custom GHR palettes.

### Usage

```
GHR_palette(palette, ncols = 30)
```

```
GHR_palettes()
```

### Arguments

palette	Name of the GHR, RcolorBrewer or colorspace palette. Use "-" before the palette name (e.g., "-Reds") to reverse it. A vector of custom colors is also possible.
ncols	Number of colors to sample.

### Details

See all available options by running `GHR_palettes()`, `RColorBrewer::display.brewer.all()` and `colorspace::hcl_palettes(plot=TRUE)`.

### Value

`GHR_palette()` returns the function that generates the color palette and the attribute 'na\_color'.

`GHR_palettes()` returns a plot with the custom GHR palettes.

### Examples

```
GHR_palette("IDE1", 5)(5)
```

```
GHR_palettes()
```

---

map_MS	<i>Municipality boundaries of Mato Grosso do Sul</i>
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---

**Description**

Administrative boundaries (polygon geometries) of the 11 municipalities in *Mato Grosso do Sul* (Brazil) to be used with the dengue\_MS data set.

**Usage**

```
data(map_MS)
```

**Format**

A simple feature (sf) object including 11 rows and 2 columns:

**code** Unique ID number to each micro region (11 units).

**geometry** Geometries of the sf multipolygon.

---

plot_bivariate	<i>Bivariate plot</i>
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**Description**

Plots a bivariate graph to visually assess associations. It will be a scatterplot if both variables are numeric and grouped boxplots if one of them is categorical.

**Usage**

```
plot_bivariate(  
  data,  
  var,  
  area = NULL,  
  facet = FALSE,  
  free_x_scale = FALSE,  
  free_y_scale = FALSE,  
  title = NULL,  
  var_label = NULL,  
  legend = NULL,  
  palette = NULL,  
  ...  
)
```

**Arguments**

data	Data frame containing equally spaced (daily, weekly, monthly) covariate or disease case observations for one or multiple locations.
var	Character vector of covariate names with length 2 (x, y). One of them can be a factor.
area	Character, the name of the variable that identifies the different areal units or any other grouping of interest. If specified, results are grouped by this variable. Defaults to NULL (no grouping).
facet	If TRUE, plot each grouping in a different facet.
free_x_scale	If TRUE and facet=TRUE, the x-axis scale is free in each facet.
free_y_scale	If TRUE and facet=TRUE, the y-axis scale is free in each facet.
title	Optional title of the plot.
var_label	A 2 character vector with a custom name for the variables.
legend	A character vector with a custom name for the legend.
palette	GHR, RColorBrewer or colorspace palette (e.g. "Purp"). Single R colors in colors() or hex codes can be used when there is no grouping or facets are used. Use "-" before the palette name (e.g., "-Reds") to reverse it. Defaults to a dark green when area is NULL or when facet is TRUE, otherwise defaults to the "IDE2" palette.
...	Additional arguments to be passed to geom_point or geom_boxplot, e.g. alpha=0.5 and size=2.

**Value**

A ggplot2 scatterplot or boxplot graph.

**Examples**

```
# Load data
data("dengue_MS")

# Scatter (two numeric variables) - No grouping
plot_bivariate(dengue_MS,
              var = c("pop_density", "tmin"),
              palette = "#d04a2d")

# Scatter (two numeric variables) - Grouping in the same graph
plot_bivariate(dengue_MS,
              var = c("pop_density", "tmin"),
              var_label = c("Pop. density", "Min temp."),
              area = "micro_code")

# Scatter (two numeric variables) - Grouping in facets
plot_bivariate(dengue_MS,
              var = c("pop_density", "tmin"),
              var_label = c("Pop. density", "Min temp."),
              area = "micro_code", facet = TRUE,
```

```

        free_x_scale = TRUE)

# Boxplots (one numeric, one categorical) - No grouping
plot_bivariate(dengue_MS,
               var = c("pop_density", "biome_name"),
               var_label = c("Pop. density", "Min temp."),
               palette = "royalblue")

# Boxplots (one numeric, one categorical) - Grouping
plot_bivariate(dengue_MS,
               var = c("biome_name", "tmin"),
               area = "meso_code",
               palette = "Accent")

```

---

plot\_combine

*Combine plots*


---

### Description

Combines plots, each representing one variable, into a single plot.

### Usage

```

plot_combine(
  plot_list,
  combine_legend = FALSE,
  combine_xaxis = FALSE,
  ncol = 1,
  align = "v",
  ...,
  ncol_l = 2,
  nrow_l = NULL,
  rel_widths_l = c(3, 1),
  rel_heights_l = c(1, 1),
  ncol_legend = 1
)

```

### Arguments

plot_list	A list of plots to be combined.
combine_legend	Logical. If TRUE, assumes the legend of all plots is the same as the legend of the first plot in plot_list and final plot shows only one instance of the common legend. Default is FALSE.
combine_xaxis	Logical. If TRUE, removes x axis labels from all but the last plot. Default is FALSE.
ncol	(from cowplot) Number of columns in the plot grid. Default is 1.

align	(from cowplot) Specifies how plots should be aligned Options are "none", "hv" (align in both directions), "h", and "v" (default).
...	Additional arguments passed to cowplot::plot_grid.
ncol_l	When combine_legend = TRUE, number of columns in which to align plots and the common legend. Default is 2.
nrow_l	When combine_legend = TRUE, number of rows in which to align plots and the common legend. Default is NULL.
rel_widths_l	When combine_legend = TRUE, vector of widths in which to align plots and the common legend. Default is c(3, 1).
rel_heights_l	When combine_legend = TRUE, vector of heights in which to align plots and the common legend. Default is c(1, 1).
ncol_legend	When combine_legend = TRUE, number of columns the legend should be distributed in. Default is one column.

### Details

This function takes any input from the cowplot::plot\_grid function to customize the organization of the plots.

### Value

A single (cow)plot including the provided multiple plots.

### See Also

[plot\\_compare](#), [plot\\_multiple](#)

### Examples

```
# Load data
data("dengue_MS")

# Multiple time series plot
plots <- plot_multiple(
  plot_function = plot_timeseries,
  data = dengue_MS,
  var = c("tmax", "tmin", "pdsi"),
  type = c("cov", "cov", "cov"),
  aggregate_space = "meso_code",
  pop = "population",
  var_label = c("Max Temp", "Min Temp", "PDSI"),
  time = "date",
  area = "micro_code")

# Combine them with a shared legend
plot_combine(plot_list = plots,
             ncol = 1,
             align = "v",
             combine_legend = TRUE,
```

```
combine_xaxis = TRUE,  
rel_widths_l = c(7,1))
```

---

plot_compare	<i>Compare plots</i>
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---

### Description

Combines multiple plots of several variables in a single graph.

### Usage

```
plot_compare(plot_function, data, var, type, ...)
```

### Arguments

plot_function	Indicates which of the plot types to use. Options are: 'plot_timeseries', 'plot_heatmap', 'plot_seasonality', and 'plot_map'.
data	Data frame containing equally spaced (daily, weekly, monthly) covariate or disease case observations for one or multiple locations.
var	Character vector with the name of the variables to be plotted.
type	Character vector with the same length of var that specifies the types of variable for each element in var. Possible values include 'cov' (covariate, default), 'counts' (case counts), and 'inc' (case incidence). If type='inc', pop is required.
...	Additional arguments for plot_multiple, plot_combine, and the selected plot_function.

### Details

This function takes any input arguments from plot\_combine() and plot\_multiple() to customize the plots and their organization in a grid.

### Value

A single (cow)plot containing plots of several variables.

### See Also

[plot\\_multiple](#), [plot\\_combine](#)

## Examples

```
# Load data
library("sf")
data("dengue_MS")
data("map_MS")

plot_compare(
  plot_function = plot_timeseries,
  data = dengue_MS,
  var = c("dengue_cases", "pdsi"),
  type = c("inc", "cov"),
  pop = "population",
  time = "date",
  area = "micro_code",
  var_label = c("Dengue inc", "PDSI"),
  combine_legend = TRUE,
  ncol_legend = 1,
  ncol = 1,
  align = "h")

# Comparing seasonality plots
plot_compare(
  plot_function = plot_seasonality,
  data = dengue_MS,
  var = c("dengue_cases", "dengue_cases", "pdsi"),
  type = c("counts", "inc", "cov"),
  pop = "population",
  time = "date",
  area = "micro_code",
  aggregate_space = "region_code",
  pt = 100,
  var_label = c("Dengue Cases", "Dengue inc", "Min Temp"),
  ncol_legend = 1,
  combine_legend = TRUE)

# Comparing heatmaps plots
plot_compare(
  plot_function = plot_heatmap,
  data = dengue_MS,
  var = c("dengue_cases", "pdsi"),
  type = c("inc", "cov"),
  pop = "population",
  time = "date",
  area = "micro_code",
  var_label = c("Dengue Cases", "Min Temp"),
  palette = c("Reds", "Blues"),
  ncol_legend = 1,
  combine_xaxis = TRUE)

# Comparing map plots
plot_compare(
  plot_function = plot_map,
```

```

data = dengue_MS,
var = c("dengue_cases", "tmax"),
type = c("inc", "cov"),
pop = "population",
time = "date",
area = "micro_code",
var_label= c("Dengue Incidence", "Max Temperature"),
palette = c("Reds", "Blues"),
map = map_MS,
map_area = "code",
aggregate_time = "all",
ncol_legend = 1,
combine_xaxis =TRUE)

```

---

plot\_correlation      *Correlation plot*

---

## Description

Plots a correlation matrix of a series of variables.

## Usage

```

plot_correlation(
  data,
  var,
  var_label = NULL,
  method = "pearson",
  plot_type = c("circle", "number"),
  scale = 1,
  title = NULL,
  palette = "IDE1",
  print = FALSE
)

```

## Arguments

data	Data frame containing equally spaced (daily, weekly, monthly) covariate or disease case observations for one or multiple locations.
var	Character vector containing variables in data to include in the correlation matrix.
var_label	Optional character vector of the same length as var containing custom names for the variables.
method	Correlation computation method. Options include "pearson" (default), "spearman" or "kendall".
plot_type	Character vector of length 2 indicating the type of plot to use in the lower triangular and diagonal (1st element) and the upper triangular (2nd element). Options include "circle", "number" and "raster".

scale	Circle and number size multiplier, e.g. 1.1 increases the size a 10% while 0.9 decreases it a 10%.
title	Optional title of the plot.
palette	GHR, RColorBrewer or colorspace palette. Use "-" before the palette name (e.g., "-Reds") to reverse it.
print	Logical. If TRUE, print the correlation matrix.

**Value**

A plot of the correlation matrix.

**Examples**

```
# Load data
data("dengue_MS")

# Pearson correlation plot
plot_correlation(dengue_MS,
                 method = "pearson",
                 var = c("dengue_cases", "pop_density",
                        "tmax", "tmin", "pdsi", "urban",
                        "water_network", "water_shortage"),
                 var_label = c("dengue cases", "pop. density",
                              "max temp", "min temp",
                              "drought index", "urbanization",
                              "water network", "water shortage"),
                 title = "Correlation matrix")

# Print spearman correlation plot of type 'raster' and 'number'
# with another palette
plot_correlation(dengue_MS,
                 method = "spearman",
                 var = c("dengue_cases", "pop_density",
                        "tmax", "tmin", "pdsi", "urban",
                        "water_network", "water_shortage"),
                 var_label = c("dengue cases", "pop. density",
                              "max temp", "min temp",
                              "drought index", "urbanization",
                              "water network", "water shortage"),
                 plot_type = c("raster", "number"),
                 palette = "-Blue-Red 3")
```

---

plot\_heatmap

*Heatmap plot*

---

**Description**

Plots temporal heatmaps of covariates, case counts, or incidence rates.

**Usage**

```

plot_heatmap(
  data,
  var,
  time,
  type = "cov",
  pop = NULL,
  pt = 1e+05,
  area = NULL,
  aggregate_space = NULL,
  aggregate_time = "month",
  aggregate_space_fun = "mean",
  aggregate_time_fun = "mean",
  transform = "identity",
  title = NULL,
  var_label = NULL,
  ylab = NULL,
  xlab = NULL,
  palette = NULL,
  centering = NULL
)

```

**Arguments**

<code>data</code>	Data frame containing equally spaced (daily, weekly, monthly) covariate or disease case observations for one or multiple locations.
<code>var</code>	Name of the column identifying the variable to be plotted.
<code>time</code>	Name of the variable that identifies the temporal dimension of the data frame. Its values must be in date format ("yyyy-mm-dd") representing the day of observation for daily data, the first day of the week for weekly, or the first day of the month for monthly observations.
<code>type</code>	Character that specifies the type of variable in <code>var</code> . Possible values include 'cov' (covariate, default), 'counts' (case counts), and 'inc' (case incidence). If <code>type='inc'</code> , <code>pop</code> is required.
<code>pop</code>	Character identifying the variable name for population. Only needed if <code>type='inc'</code> .
<code>pt</code>	Numerical only used for <code>type='inc'</code> . It represents the scale of the person-time (default 100,000) for incidence rates.
<code>area</code>	Name of variable that identifies the different locations (i.e., areal units) for which a time series is available.
<code>aggregate_space</code>	Name of variable used to define spatial aggregation groups.
<code>aggregate_time</code>	Temporal scale used to perform temporal aggregation. Options are: "week" (ISO 8601), "month", "year".
<code>aggregate_space_fun</code>	Character indicating the function to be used in the aggregation over space for <code>type="cov"</code> . Options are "mean" (default), "median", "sum". For case counts and incidence, "sum" is always applied.

aggregate_time_fun	Character indicating the function to be used in the aggregation over time for type="cov". Options are "mean" (default), "median", "sum". For case counts and incidence, "sum" is always applied.
transform	Character, defaults to "identity" (i.e., no transformation). Transforms the color ramp for better visualization. Useful options include "log10p1" $\log_{10}(x+1)$ useful for case counts and incidence with 0s, or any of the in-built ggplot2 options such as "log10" $\log_{10}(x)$ , "log1p" $\log(x+1)$ , and "sqrt" $\sqrt{x}$ (check all possible options using ?scale_y_continuous).
title	Optional title of the plot.
var_label	Character with a custom name for the case or covariate variable.
ylab	Label for the y-axis.
xlab	Label for the x-axis.
palette	GHR, RColorBrewer or colorspace palette. Use "-" before the palette name (e.g., "-Reds") to reverse it.
centering	Numerical or "median", defaults to NULL. If set, it centers the palette on that value.

### Value

A ggplot2 heatmap plot.

### Examples

```
# Load data
data("dengue_MS")

# Covariate heatmap with space aggregation
plot_heatmap(dengue_MS,
  var = "tmin",
  time = "date",
  var_label = "Minimum\ntemp.",
  type = "cov",
  area = "micro_code",
  aggregate_space = "meso_code",
  palette = "Blue-Red")

# Case count heatmap with log scale
plot_heatmap(dengue_MS,
  var = "dengue_cases",
  time = "date",
  type = "counts",
  area = "micro_code",
  palette = "Reds",
  title = "Dengue counts",
  var_label = "Dengue \ncounts",
  transform = "log10p1")

# Case incidence (for 1,000 persons) heatmap with space aggregation
```

```
plot_heatmap(dengue_MS,
             var = "dengue_cases",
             time = "date",
             type = "inc",
             pop = "population",
             pt = 1000,
             area = "micro_code",
             aggregate_space = "meso_code",
             palette = "Purp")
```

---

plot\_map

*Choropleth map*


---

### Description

Plots a choropleth map of covariates, case counts, or incidence rates.

### Usage

```
plot_map(
  data,
  var,
  time,
  type = "cov",
  pop = NULL,
  pt = 1e+05,
  area = NULL,
  map = NULL,
  map_area = NULL,
  by_year = NULL,
  aggregate_time = "year",
  aggregate_time_fun = "mean",
  transform = "identity",
  title = NULL,
  var_label = NULL,
  palette = NULL,
  centering = NULL,
  bins = NULL,
  bins_method = "quantile",
  bins_label = NULL,
  ...
)
```

### Arguments

data	Data frame containing equally spaced (daily, weekly, monthly) covariate or case observations for one or multiple locations.
var	Name of the column identifying the variable to be plotted.

time	Name of the variable that identifies the temporal dimension of the data frame. Its values must be in date format ("yyyy-mm-dd") representing the day of observation for daily data, the first day of the week for weekly, or the first day of the month for monthly observations.
type	Character that specifies the type of variable in var. Possible values include 'cov' (covariate, default), 'counts' (case counts), and 'inc' (case incidence). If type='inc', pop is required.
pop	Character identifying the variable name for population. Only needed if type='inc'.
pt	Scale of the person-time (default 100,000) for incidence rates.
area	Name of variable that identifies the different locations (e.g., areal units) for which a time series is available.
map	Name of the sf object corresponding to the spatial unit specified in 'area'.
map_area	Name of the variable that identifies the different locations (e.g., areal units) in the map object. If not specified, it assumes the same name as in area.
by_year	Deprecated. Use 'aggregate_time' instead.
aggregate_time	Temporal scale for visualization and aggregation. Options include "all" (across all time points) and "year" (default).
aggregate_time_fun	Character indicating the function to be used in the aggregation over time for type="cov". Options are "mean" (default), "median", "sum". For case counts and incidence, "sum" is always applied.
transform	Character, defaults to "identity" (i.e., no transformation). Transforms the color ramp for better visualization. Useful options include "log10p1" $\log_{10}(x+1)$ for case counts and incidence with 0s, or any of the in-built ggplot2 options such as "log10" $\log_{10}(x)$ , "log1p" $\log(x+1)$ , and "sqrt" $\sqrt{x}$ (check all possible options using ?scale_y_continuous).
title	Optional title of the plot.
var_label	Character with a custom name for the case or covariate variable.
palette	GHR, RColorBrewer or colorspace palette. Use "-" before the palette name (e.g., "-Reds") to reverse it.
centering	Numerical or "median", defaults to NULL. If set, it centers the palette on that value.
bins	Number of bins for categorization of numerical variables. Defaults to NULL (no binning).
bins_method	Method to compute the bins, only used when bins is not NULL. Possible values are "quantile" (default) and "equal".
bins_label	Optional labels for the bins. They must have the same length as the number of bins. Defaults to NULL (default interval labels).
...	Additional arguments to be passed to geom_sf. Possible values include colour (e.g., colour="black"), linewidth (e.g., linewidth=0.1), linetype (e.g., linetype=2), and alpha (e.g., alpha=0.8).

**Value**

A ggplot2 choropleth map.

**Examples**

```
# Load data
library("sf")
data("dengue_MS")
data("map_MS")

# Temporal average of a covariate
plot_map(data = dengue_MS,
         var = "tmin",
         time = "date",
         type = "cov",
         area = "micro_code",
         map = map_MS,
         map_area = "code",
         aggregate_time = "all",
         aggregate_time_fun = "mean",
         palette = "Reds",
         var_label = "Min Temp.")

# Categorical covariate
plot_map(data = dengue_MS,
         var = "biome_name",
         time = "date",
         area = "micro_code",
         aggregate_time = "all",
         map = map_MS,
         map_area = "code",
         palette = "Viridis",
         var_label = "Biome")

# Case counts by year (log)
dengue_MS |>
  plot_map(var = "dengue_cases",
          time = "date",
          type = "counts",
          area = "micro_code",
          pop = "population",
          map = map_MS,
          map_area = "code",
          palette = "Reds",
          transform = "log10p1")

# Case incidence by year, binned
plot_map(dengue_MS,
         var = "dengue_cases",
         type = "inc",
         time = "date",
         area = "micro_code",
         pop = "population",
         pt = 1000,
         map = map_MS,
         map_area = "code",
```

```
bins = 5,  
palette = "Viridis")
```

---

plot\_multiple      *Multiple plot*

---

## Description

Produces a list of multiple plots of the same type, each representing one variable.

## Usage

```
plot_multiple(plot_function, ...)
```

## Arguments

`plot_function`    Indicates which of the plot types to use. Options are: 'plot\_timeseries', 'plot\_heatmap', 'plot\_seasonality', and 'plot\_map'.  
`...`             Additional arguments to pass to the plotting function.

## Details

Variable names, types, labels and palette can be customized for each plot, the rest of parameters will be the same for all variables (options depend on the chosen plot type).

## Value

A list of the different generated plots.

## See Also

[plot\\_compare](#), [plot\\_combine](#)

## Examples

```
# Load data  
library("sf")  
data("dengue_MS")  
data("map_MS")  
  
plots <- plot_multiple(  
  plot_function = plot_timeseries,  
  data = dengue_MS,  
  var = c("dengue_cases", "dengue_cases", "tmax"),  
  type = c("counts", "inc", "cov"),  
  pop = "population",  
  var_label = c("Dengue Cases", "Dengue inc", "Max Temp"),  
  palette = c("blue", "red", "darkgreen"),  
  time = "date",
```

```

    area = "micro_code",
    facet = TRUE)

# Acess individual plots
print(plots[[1]])

# Multiple heatmap plots
plots <- plot_multiple(
  plot_function = plot_heatmap,
  data = dengue_MS,
  var = c("dengue_cases", "dengue_cases", "tmax"),
  type = c("counts", "inc", "cov"),
  pop = "population",
  var_label = c("Dengue Cases", "Dengue inc", "Max Temp"),
  palette = c("Blues", "Reds", "BrBG"),
  time = "date",
  area = "micro_code")

# Multiple seasonality plots
plots <- plot_multiple(
  plot_function = plot_seasonality,
  data = dengue_MS,
  var = c("dengue_cases", "dengue_cases", "tmax"),
  type = c("counts", "inc", "cov"),
  pop = "population",
  var_label = c("Dengue Cases", "Dengue inc", "Max Temp"),
  palette = c("Blues", "Reds", "BrBG"),
  time = "date",
  area = "micro_code")

# Multiple map plots
plots <- plot_multiple(
  plot_function = plot_map,
  data = dengue_MS,
  var = c("dengue_cases", "dengue_cases", "tmax"),
  type = c("counts", "inc", "cov"),
  pop = "population",
  var_label = c("Dengue Cases", "Dengue inc", "Max Temp"),
  palette = c("Reds", "Blues", "Viridis"),
  map = map_MS,
  map_area = "code",
  time = "date",
  area = "micro_code")

```

---

plot\_seasonality

*Seasonality plot*


---

### Description

Plots yearly time series of covariates, case counts, or incidence rates to explore seasonality patterns.

**Usage**

```
plot_seasonality(
  data,
  var,
  time,
  type = "cov",
  pop = NULL,
  pt = 1e+05,
  area = NULL,
  aggregate_space = NULL,
  aggregate_time = "month",
  aggregate_space_fun = "mean",
  aggregate_time_fun = "mean",
  transform = "identity",
  title = NULL,
  var_label = NULL,
  ylab = NULL,
  xlab = NULL,
  free_y_scale = FALSE,
  palette = "IDE1"
)
```

**Arguments**

<code>data</code>	Data frame containing equally spaced (daily, weekly, monthly) covariate or disease case observations for one or multiple locations.
<code>var</code>	Name of the column identifying the variable to be plotted.
<code>time</code>	Name of the variable that identifies the temporal dimension of the data frame. Its values must be in date format ("yyyy-mm-dd") representing the day of observation for daily data, the first day of the week for weekly, or the first day of the month for monthly observations.
<code>type</code>	Character that specifies the type of variable in <code>var</code> . Possible values include 'cov' (covariate, default), 'counts' (case counts), and 'inc' (case incidence). If <code>type='inc'</code> , <code>pop</code> is required.
<code>pop</code>	Character identifying the variable name for population. Only needed if <code>type='inc'</code> .
<code>pt</code>	Scale of the person-time (default 100,000) for incidence rates.
<code>area</code>	Name of variable that identifies the different locations (e.g., areal units) for which a time series is available.
<code>aggregate_space</code>	Name of variable used to define spatial aggregation groups.
<code>aggregate_time</code>	Temporal scale used to perform temporal aggregation. Options are: "week" (ISO 8601), "month", "year".
<code>aggregate_space_fun</code>	Character indicating the function to be used in the aggregation over space for <code>type="cov"</code> . Options are "mean" (default), "median", "sum". For case counts and incidence, "sum" is always applied.

aggregate_time_fun	Character indicating the function to be used in the aggregation over time for type="cov". Options are "mean" (default), "median", "sum". For case counts and incidence, "sum" is always applied.
transform	Character, defaults to "identity" (i.e., no transformation). Transforms the y-axis for better visualization. Useful options include "log10p1" $\log_{10}(x+1)$ for case counts and incidence with 0s, or any of the in-built ggplot2 options such as "log10" $\log_{10}(x)$ , "log1p" $\log(x+1)$ , and "sqrt" $\sqrt{x}$ (check all possible options using <code>?scale_y_continuous</code> ).
title	Optional title of the plot.
var_label	Character with a custom name for the case or covariate variable.
ylab	Label for the y-axis.
xlab	Label for the x-axis.
free_y_scale	If TRUE, the y-axis scale is free in each facet.
palette	GHR, RColorBrewer or colorspace palette. Use "-" before the palette name (e.g., "-Reds") to reverse it.

**Value**

A ggplot2 seasonality plot.

**Examples**

```
# Load data
data("dengue_MS")

# Seasonality plot of a covariate with space aggregation
plot_seasonality(dengue_MS,
  var = "tmax",
  time = "date",
  var_label = "Max temp.",
  type = "cov",
  area = "micro_code",
  aggregate_space = "region_code")

# Plot case counts (log scale) with space aggregation
plot_seasonality(dengue_MS,
  var = "dengue_cases",
  time = "date",
  type = "counts",
  area = "micro_code",
  aggregate_space = "meso_code",
  transform = "log10p1",
  var_label = "Monthly Dengue Cases",
  xlab = "Month",
  ylab = "Number of cases",
  free_y_scale = TRUE)

# Seasonality plot of incidence
```

```
plot_seasonality(dengue_MS,
                 var = "dengue_cases",
                 time = "date",
                 type = "inc",
                 pop = "population",
                 area = "micro_code",
                 pt = 1000,
                 title = "Monthly Dengue Incidence",
                 palette = "Reds")
```

---

plot_timeseries	<i>Time series plot</i>
-----------------	-------------------------

---

## Description

Plots time series of covariates, case counts, or incidence rates.

## Usage

```
plot_timeseries(
  data,
  var,
  time,
  type = "cov",
  pop = NULL,
  pt = 1e+05,
  area = NULL,
  aggregate_space = NULL,
  aggregate_time = NULL,
  aggregate_space_fun = "mean",
  aggregate_time_fun = "mean",
  facet = FALSE,
  highlight = NULL,
  transform = "identity",
  title = NULL,
  var_label = NULL,
  legend = NULL,
  ylab = NULL,
  xlab = NULL,
  free_y_scale = FALSE,
  palette = NULL
)
```

## Arguments

data	Data frame containing equally spaced (daily, weekly, monthly) covariate or disease case observations for one or multiple locations.
------	---

var	Name of the column identifying the variable to be plotted.
time	Name of the variable that identifies the temporal dimension of the data frame. Its values must be in date format ("yyyy-mm-dd") representing the day of observation for daily data, the first day of the week for weekly, or the first day of the month for monthly observations.
type	Character that specifies the type of variable in var. Possible values include 'cov' (covariate, default), 'counts' (case counts), and 'inc' (case incidence). If type='inc', pop is required.
pop	Character identifying the variable name for population. Only needed if type='inc'.
pt	Numerical only used for type='inc'. It represents the scale of the person-time (default 100,000) for incidence rates.
area	Name of variable that identifies the different locations (e.g., areal units) for which a time series is available.
aggregate_space	Name of variable used to define spatial aggregation groups.
aggregate_time	Temporal scale used to perform temporal aggregation. Options are: "week" (ISO 8601), "month", "year".
aggregate_space_fun	Character indicating the function to be used in the aggregation over space for type="cov". Options are "mean" (default), "median", "sum". For case counts and incidence, "sum" is always applied.
aggregate_time_fun	Character indicating the function to be used in the aggregation over time for type="cov". Options are "mean" (default), "median", "sum". For case counts and incidence, "sum" is always applied.
facet	If TRUE a separate time series for each space unit is plotted in different facets.
highlight	ID of the area to be highlighted. Using this option will only color the selected spatial unit and set all the rest to grey.
transform	Character, defaults to "identity" (i.e., no transformation). Transforms the y-axis for better visualization. Useful options include "log10p1" $\log_{10}(x+1)$ useful for case counts and incidence with 0s, or any of the in-built ggplot2 options such as "log10" $\log_{10}(x)$ , "log1p" $\log(x+1)$ , and "sqrt" $\sqrt{x}$ (check all possible options using <code>?scale_y_continuous</code> ).
title	Optional title of the plot.
var_label	Character with a custom name for the case or covariate variable.
legend	Character with a custom name for the legend.
ylab	Label for the y-axis.
xlab	Label for the x-axis.
free_y_scale	Logical, default FALSE. Allows different scales in the y_axis when facets are used.
palette	GHR, RColorBrewer or colorspace palette (e.g. "Purp"). Single R colors in colors() or hex codes can be used for single time series or facets. Use "-" before the palette name (e.g., "-Reds") to reverse it. Defaults to a dark green when area is NULL, when facet is TRUE or when highlight is used (i.e. single time series), otherwise defaults to the "IDE2" palette.

**Value**

A ggplot2 time series plot.

**See Also**

[plot\\_timeseries2](#) for dual-axis time series plots.

**Examples**

```
# Load data
data("dengue_MS")

# Plotting a covariate, all areas in a single graph
plot_timeseries(dengue_MS,
                var = "tmin",
                time = "date",
                type = "cov",
                area = "micro_code",
                title = "Minimun Temperature")

# Plotting a covariate with space aggregation and different facets
plot_timeseries(dengue_MS,
                var = "tmin",
                time = "date",
                type = "cov",
                area = "micro_code",
                aggregate_space = "meso_code",
                aggregate_space_fun = "mean",
                facet = TRUE,
                var_label= "Minimum Temperature",
                palette = "violetred")

# Plotting counts, highlight a single area
plot_timeseries(dengue_MS,
                var = "dengue_cases",
                time = "date",
                type = "counts",
                pop = "population",
                area = "micro_code",
                title= "Dengue cases",
                highlight = "50001")

# Plot disease counts (log scale) with temporal and spatial aggregation
plot_timeseries(dengue_MS,
                var = "dengue_cases",
                time = "date",
                type = "counts",
                area = "micro_code",
                aggregate_space = "meso_code",
                aggregate_time = "year",
                title = "Yearly Cases",
                transform = "log10")
```

```
# Plot incidence for 1,000 people with a Brewer palette and log y axis
plot_timeseries(dengue_MS,
                var = "dengue_cases",
                time = "date",
                type = "inc",
                pop = "population",
                area = "micro_code",
                pt = 1000,
                transform = "log10p1")
```

---

plot\_timeseries2      *Time series plot of two variables in two different axes*

---

## Description

Plots dual-axis time series of two covariates, case counts, or incidence rates.

## Usage

```
plot_timeseries2(
  data,
  var,
  time,
  type = c("cov", "cov"),
  pop = NULL,
  pt = 1e+05,
  area = NULL,
  aggregate_space = NULL,
  aggregate_time = NULL,
  aggregate_space_fun = "mean",
  aggregate_time_fun = "mean",
  align = "min",
  title = NULL,
  var_label = NULL,
  legend = "Variable",
  ylab = NULL,
  xlab = NULL,
  free_y_scale = FALSE,
  palette = c("#168c81", "#B98AFB"),
  alpha = 0.9
)
```

## Arguments

**data**                      Data frame containing equally spaced (daily, weekly, monthly) covariate or disease case observations for one or multiple locations.

var	A character vector of length 2 (left axis, right axis) identifying the variables to be plotted.
time	Name of the variable that identifies the temporal dimension of the data frame. Its values must be in date format ("yyyy-mm-dd") representing the day of observation for daily data, the first day of the week for weekly, or the first day of the month for monthly observations.
type	A character vector of length 2 (left axis, right axis) that specifies the types of variable in var. Possible values include 'cov' (covariate, default), 'counts' (case counts), and 'inc' (case incidence). If type='inc', pop is required.
pop	Character identifying the variable name for population. Only needed if type='inc'.
pt	Numerical only used for type='inc'. It represents the scale of the person-time (default 100,000) for incidence rates.
area	Name of variable that identifies the different locations (e.g., areal units) for which a time series is available.
aggregate_space	Name of variable used to define spatial aggregation groups.
aggregate_time	Temporal scale used to perform temporal aggregation. Options are: "week" (ISO 8601), "month", "year".
aggregate_space_fun	Character indicating the function to be used in the aggregation over space for type="cov". Options are "mean" (default), "median", "sum". For case counts and incidence, "sum" is always applied.
aggregate_time_fun	Character indicating the function to be used in the aggregation over time for type="cov". Options are "mean" (default), "median", "sum". For case counts and incidence, "sum" is always applied.
align	Options to align the two plots. Defaults to "min", which forces the minimum of the two variables to be aligned. Other options include "mean" and "median".
title	Optional title of the plot.
var_label	A character vector of length 2 (left axis, right axis) with custom names for the case or covariate variable.
legend	Character with a custom name for the legend.
ylab	A character vector of length 2 (left, right) for the y-axes.
xlab	Label for the x-axis.
free_y_scale	Logical, default FALSE. Allows different scales in the y_axis when facets are used.
palette	A character vector of length 2 (left axis, right axis) indicating the colours (R or hex codes) to use for each of the two variables).
alpha	Numerical between 0 and 1 determining the transparency of the lines.

**Value**

A dual-axis ggplot2 time series plot.

**See Also**

[plot\\_timeseries](#) for single-axis time series plots.

**Examples**

```
# Load data
data("dengue_MS")
data("dengue_SP")

# Plotting two covariates with temporal aggregation, align using the mean
plot_timeseries2(dengue_SP,
                 var = c("temp_med", "precip_tot"),
                 time = "date",
                 align = "mean",
                 aggregate_time = "month")

# Plotting case incidence and a covariate with temporal aggregation
# and customized colours and labels
plot_timeseries2(dengue_SP,
                 var = c("cases", "precip_tot"),
                 type = c("inc", "cov"),
                 var_label = c("Incidence", "Precipitation"),
                 title = "Precipitation and dengue incidence in Sao Paulo",
                 time = "date",
                 pop = "pop",
                 aggregate_time = "month",
                 palette = c("darkgreen", "royalblue"),
                 alpha = 0.8)

# Plotting case incidence and a covariate with spatial aggregation
plot_timeseries2(dengue_MS,
                 var = c("dengue_cases", "pdsi"),
                 type = c("inc", "cov"),
                 pop = "population",
                 time = "date",
                 area = "micro_code",
                 aggregate_space = "meso_code")
```

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