Package ‘deeptime’

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Title Plotting Tools for Anyone Working in Deep Time

Version 2.2.0

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Description Extends the functionality of other plotting packages (notably 'ggplot2') to help facilitate the plotting of data over long time intervals, including, but not limited to, geological, evolutionary, and ecological data. The primary goal of 'deeptime' is to enable users to add highly customizable timescales to their visualizations. Other functions are also included to assist with other areas of deep time visualization.

URL `https://williamgearty.com/deeptime/`,
`https://github.com/willgearty/deeptime`

BugReports `https://github.com/willgearty/deeptime/issues`

Depends R (>= 3.5)

License GPL (>= 3)

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`coord_geo` *Transformed coordinate system with geological timescale*

Description

`coord_geo` behaves similarly to `ggplot2::coord_trans()` in that it occurs after statistical transformation and will affect the visual appearance of geoms. The main difference is that it also adds a geological timescale to the specified side(s) of the plot.

Usage

```
coord_geo(
  pos = "bottom",
  dat = "periods",
  xlim = NULL,
  ylim = NULL,
  xtrans = identity_trans(),
  ytrans = identity_trans(),
  clip = "on",
  expand = FALSE,
  fill = NULL,
  alpha = 1,
  height = unit(2, "line"),
  bord = c("left", "right", "top", "bottom"),
  lwd = 0.25,
  color = "black",
  lab = TRUE,
  lab_color = NULL,
  rot = 0,
  family = "sans",
  fontface = "plain",
  size = 5,
  skip = c("Quaternary", "Holocene", "Late Pleistocene"),
  abbrv = TRUE,
  neg = FALSE,
  center_end_labels = FALSE,
  dat_is_discrete = FALSE,
  fittext_args = list()
)
```

Arguments

`pos`	Which side to add the scale to (left, right, top, or bottom). First letter may also be used.
`dat`	Either A) a string indicating a built-in dataframe with interval data from the ICS ("periods", "epochs", "stages", "eons", or "eras"), B) a string indicating a timescale from macrostrat (see list here: `https://macrostrat.org/api/defs/timescales?all`), or C) a custom data.frame of time interval boundaries (see Details).
`xlim, ylim`	Limits for the x and y axes.
`xtrans, ytrans`	Transformers for the x and y axes. For more information see `ggplot2::coord_trans()`.
`clip`	Should drawing be clipped to the extent of the plot panel? A setting of `"on"` (the default) means yes, and a setting of `"off"` means no. In most cases, the default of `"on"` should not be changed, as setting `clip = "off"` can cause unexpected results. It allows drawing of data points anywhere on the plot, including in the plot margins. If limits are set via `xlim` and `ylim` and some data points fall

	outside those limits, then those data points may show up in places such as the axes, the legend, the plot title, or the plot margins.
`expand`	If `FALSE`, the default, limits are taken exactly from the data or `xlim`/`ylim`. If `TRUE`, adds a small expansion factor to the limits to ensure that data and axes don't overlap.
`fill`	The fill color of the boxes. The default is to use the `color` column included in `dat`. If a custom dataset is provided with `dat` without a `color` column and without fill, a greyscale will be used. Custom fill colors can be provided with this option (overriding the `color` column) and will be recycled if/as necessary.
`alpha`	The transparency of the fill colors.
`height`	The height (or width if `pos` is `left` or `right`) of the scale.
`bord`	A vector specifying on which sides of the scale to add borders (same options as `pos`).
`lwd`	Line width.
`color`	The outline color of the interval boxes.
`lab`	Whether to include labels.
`lab_color`	The color of the labels. The default is to use the `lab_color` column included in `dat`. If a custom dataset is provided with `dat` without a `lab_color` column and without fill, all labels will be black. Custom label colors can be provided with this option (overriding the `lab_color` column) and will be recycled if/as necessary.
`rot`	The amount of counter-clockwise rotation to add to the labels (in degrees).
`family`	The font family to use for the labels. There are only three fonts that are guaranteed to work everywhere: "sans" (the default), "serif", or "mono".
`fontface`	The font face to use for the labels. The standard options are "plain" (default), "bold", "italic", and "bold.italic".
`size`	Label size. Either a number as you would specify in `ggplot2::geom_text()` or `"auto"` to use `ggfittext::geom_fit_text()`.
`skip`	A vector of interval names indicating which intervals should not be labeled. If `abbrv` is `TRUE`, this can also include interval abbreviations.
`abbrv`	If including labels, should the labels be abbreviated? If `TRUE`, the `abbr` column will be used for the labels. If `FALSE`, the `name` column will be used for the labels. If `"auto"`, the `abbreviate()` function will be used to abbreviate the values in the `name` column. Note that the built-in data and data retrieved via `get_scale_data()` already have built-in abbreviations. However, using the `"auto"` option here will create new unique abbreviations based on only the intervals that are being plotted. In many cases, this may result in abbreviations that are shorter in length because there are fewer similar interval names to abbreviate.
`neg`	Set this to `TRUE` if your x-axis is using negative values.
`center_end_labels`	Should labels be centered within the visible range of intervals at the ends of the axis?

`dat_is_discrete`	Are the ages in `dat` already converted for a discrete scale?
`fittext_args`	A list of named arguments to provide to `ggfittext::geom_fit_text()`. Only used if `size` is set to `"auto"`.

Details

Transforming the side with the scale is not currently implemented. If a custom data.frame is provided (with `dat`), it should consist of at least 3 columns of data. See `data(periods)` for an example.

- The `name` column lists the names of each time interval. These will be used as labels if no abbreviations are provided.
- The `max_age` column lists the oldest boundary of each time interval.
- The `min_age` column lists the youngest boundary of each time interval.
- The `abbr` column is optional and lists abbreviations that may be used as labels.
- The `color` column is also optional and lists a color for the background for each time interval.
- The `lab_color` column is also optional and lists a color for the label for each time interval.

If the axis of the time scale is discrete, `max_age` and `min_age` will automatically be converted to the discrete scale. In this case, the categories of the discrete axis should match the values in the `name` column. If the ages within `dat` are already discretized, you can set `dat_is_discrete` to `TRUE` to prevent this automatic conversion. This can be useful for adding a time scale where categories and time intervals are not 1:1.

`pos` may also be a `list` of sides (including duplicates) if multiple time scales should be added to the plot. In this case, `dat`, `fill`, `alpha`, `height`, `bord`, `lwd`, `color`, `lab`, `lab_color`, `rot`, `family`, `fontface`, `size`, `skip`, `abbrv`, `neg`, `center_end_labels`, and `dat_is_discrete` can also be `list`s. If these `list`s are not as long as `pos`, the elements will be recycled. If individual values (or vectors) are used for these parameters, they will be applied to all time scales (and recycled as necessary).

Examples

```
library(ggplot2)
# single scale on bottom
ggplot() +
  geom_point(aes(y = runif(1000, 0, 8), x = runif(1000, 0, 1000))) +
  scale_x_reverse() +
  coord_geo(xlim = c(1000, 0), ylim = c(0, 8)) +
  theme_classic()

# stack multiple scales
ggplot() +
  geom_point(aes(y = runif(1000, 0, 8), x = runif(1000, 0, 100))) +
  scale_x_reverse() +
  coord_geo(
    xlim = c(100, 0), ylim = c(0, 8), pos = as.list(rep("bottom", 3)),
    dat = list("stages", "epochs", "periods"),
    height = list(unit(4, "lines"), unit(4, "lines"), unit(2, "line")),
    rot = list(90, 90, 0), size = list(2.5, 2.5, 5), abbrv = FALSE
```

```
) +
theme_classic()
```

`coord_geo_polar` *Polar coordinate system with geological timescale*

Description

[Deprecated]

`coord_geo_polar` behaves similarly to `ggplot2::coord_polar()` in that it occurs after statistical transformation and will affect the visual appearance of geoms. The main difference is that it also adds a geological timescale to the background of the plot.

Usage

```
coord_geo_polar(
  dat = "periods",
  theta = "y",
  start = -pi/2,
  direction = -1,
  clip = "on",
  fill = NULL,
  alpha = 1,
  lwd = 0.25,
  color = "grey80",
  lty = "solid",
  lab = FALSE,
  abbrv = TRUE,
  skip = c("Quaternary", "Holocene", "Late Pleistocene"),
  neg = TRUE,
  prop = 1,
  textpath_args = list()
)
```

Arguments

`dat`	Either A) a string indicating a built-in dataframe with interval data from the ICS ("periods", "epochs", "stages", "eons", or "eras"), B) a string indicating a timescale from macrostrat (see list here: `https://macrostrat.org/api/defs/timescales?all`), or C) a custom data.frame of time interval boundaries (see Details).
`theta`	variable to map angle to (x or y)
`start`	Offset of starting point from 12 o'clock in radians. Offset is applied clockwise or anticlockwise depending on value of `direction`.
`direction`	1, clockwise; -1, anticlockwise

`clip`	Should drawing be clipped to the extent of the plot panel? A setting of `"on"` (the default) means yes, and a setting of `"off"` means no. For details, please see `coord_cartesian()`.
`fill`	The fill color of the background. The default is to use the `color` column included in `dat`. If a custom dataset is provided with `dat` without a `color` column and without fill, a greyscale will be used. Custom fill colors can be provided with this option (overriding the `color` column) and will be recycled if/as necessary.
`alpha`	The transparency of the fill colors.
`lwd`	Line width for lines between intervals. Set to `NULL` to remove lines.
`color`	The color of the lines between intervals.
`lty`	Line type for lines between intervals.
`lab`	Whether to include labels. Requires the `geomtextpath` package.
`abbrv`	If including labels, whether to use abbreviations instead of full interval names.
`skip`	A vector of interval names indicating which intervals should not be labeled. If `abbrv` is `TRUE`, this can also include interval abbreviations.
`neg`	Set this to true if your theta-axis is using negative values. This is usually true if you are using `ggtree`.
`prop`	This is the rotational proportion of the background that the scale takes up.
`textpath_args`	A list of named arguments to provide to `geomtextpath::geom_textpath()`. Only used if `lab` is set to `TRUE`. Useful arguments include `color` (font color), `family` (font family), `fontface`, `hjust` (radial adjustment), and `size` (font size).

Details

If a custom data.frame is provided (with `dat`), it should consist of at least 2 columns of data. See `data(periods)` for an example.

- The `max_age` column lists the oldest boundary of each time interval.
- The `min_age` column lists the youngest boundary of each time interval.
- The `abbr` column is optional and lists abbreviations that may be used as labels.
- The `color` column is optional and lists a color for the background for each time interval.

`dat` may also be a list of values and/or dataframes if multiple time scales should be added to the background. Scales will be added sequentially starting at `start` and going in the specified `direction`. By default the scales will all be equal in circular/rotational proportion, but this can be overridden with `prop`. If `dat` is a list, `fill`, `alpha`, `lwd`, `color`, `lty`, `lab`, `abbrv`, `skip`, `neg`, `prop`, and `textpath_args` can also be lists (N.B. `textpath_args` would be a list of lists). If these lists are not as long as `dat`, the elements will be recycled. If individual values (or vectors) are used for these parameters, they will be applied to all time scales (and recycled as necessary).

If the sum of the `prop` values is greater than 1, the proportions will be scaled such that they sum to 1. However, the `prop` values may sum to less than 1 if the user would like blank space in the background.

`coord_geo_polar` manually generates the `r` axis, meaning it does not support changing the guide features of ggplot v. 2.5.0 or later. However, the `deeptime.axis.line.r`, `deeptime.axis.text.r`, `deeptime.axis.ticks.r`, and `deeptime.axis.ticks.length.r` ggplot2 theme elements can be modified just like their x and y counterparts to change the appearance of the radius axis. The default settings work well for a horizontal axis pointing towards the right, but these theme settings will need to be modified for other orientations. The default value for `deeptime.axis.line.r` is `element_line()`. The default value for `deeptime.axis.text.r` is `element_text(size = 3.5, vjust = -2, hjust = -0.5)`. The default value for `deeptime.axis.ticks.r` is `element_line()`. The default value for `deeptime.axis.ticks.length.r` is `unit(1.5, "points")`. However, note that the units for this element are meaningless and only the numeric value will be used (but a `unit` must still be used).

Care must be taken when adding labels to plots, as they are very likely to overlap with the plot under the default settings. The `textpath_args` argument can be used to adjust the settings for the plotting of the labels. See `geomtextpath::geom_textpath()` for details about the available arguments. Also note that the curvature of the labels may vary based on the distance from the origin. This is why `abbrv` is set to `TRUE` by default.

Life cycle

This function is soft-deprecated in favor of `coord_geo_radial()` as of **deeptime** version 1.1.0. There is currently no plan to remove this function, but users are strongly encouraged to migrate to the new function for enhanced polar functionality.

Examples

```
library(ggplot2)

library(ggtree)
set.seed(1)
tree <- rtree(100)
# single scale
revts(ggtree(tree)) +
  coord_geo_polar(dat = "stages")

# multiple scales
revts(ggtree(tree)) +
  coord_geo_polar(
    dat = list("stages", "periods"), alpha = .5,
    prop = list(0.75, .25), start = pi / 4, lty = "dashed"
  ) +
  scale_y_continuous(expand = expansion(mult = c(0.02, 0.02))) +
  theme(deeptime.axis.text.r = element_text(size = 3.5, hjust = .75,
                                            vjust = .75))


library(ggplot2)
library(paleotree)
data(RaiaCopesRule)
ggtree(ceratopsianTreeRaia,
       position = position_nudge(x = -ceratopsianTreeRaia$root.time)) +
  coord_geo_polar(dat = "stages")
```

`coord_geo_radial` *Enhanced polar coordinate system with geological timescale*

Description

`coord_geo_radial` behaves similarly to `ggplot2::coord_radial()` in that it occurs after statistical transformation and will affect the visual appearance of geoms. The main difference is that it also adds a geological timescale to the background of the plot. `coord_geo_radial` is similar to `coord_geo_polar()` but has more options related to the polar coordinate plotting that are inherited from `ggplot2::coord_radial()` (e.g., `end`, `r_axis_inside`, `inner.radius`). Furthermore, unlike `coord_geo_polar`, `coord_geo_radial` uses the ggplot2 internals to draw the `r` and `theta` axes, gridlines, etc. This means that users can tweak the guide and theme settings for these features (see examples).

Usage

```
coord_geo_radial(
  dat = "periods",
  theta = "y",
  start = -0.5 * pi,
  end = 1.25 * pi,
  expand = TRUE,
  direction = 1,
  reverse = "none",
  r_axis_inside = NULL,
  inner.radius = 0.05,
  fill = NULL,
  alpha = 1,
  lwd = 0.25,
  color = "grey80",
  lty = "solid",
  lab = FALSE,
  abbrv = TRUE,
  skip = c("Quaternary", "Holocene", "Late Pleistocene"),
  neg = TRUE,
  prop = 1,
  textpath_args = list(),
  clip = "off",
  rotate_angle = FALSE
)
```

Arguments

`dat`	Either A) a string indicating a built-in dataframe with interval data from the ICS ("periods", "epochs", "stages", "eons", or "eras"), B) a string indicating a timescale from macrostrat (see list here: `https://macrostrat.org/api/`

	`defs/timescales?all`), or C) a custom data.frame of time interval boundaries (see Details).
`theta`	variable to map angle to (`x` or `y`)
`start`	Offset of starting point from 12 o'clock in radians. Offset is applied clockwise or anticlockwise depending on value of `direction`.
`end`	Position from 12 o'clock in radians where plot ends, to allow for partial polar coordinates. The default, `NULL`, is set to `start + 2 * pi`.
`expand`	If `TRUE`, the default, adds a small expansion factor to the limits to prevent overlap between data and axes. If `FALSE`, limits are taken directly from the scale.
`direction`	1, clockwise; -1, anticlockwise
`reverse`	A string giving which directions to reverse. `"none"` (default) keep directions as is. `"theta"` reverses the angle and `"r"` reverses the radius. `"thetar"` reverses both the angle and the radius.
`r_axis_inside`, `rotate_angle`	**[Deprecated]**
`inner.radius`	A `numeric` between 0 and 1 setting the size of a inner radius hole.
`fill`	The fill color of the background. The default is to use the `color` column included in `dat`. If a custom dataset is provided with `dat` without a `color` column and without fill, a greyscale will be used. Custom fill colors can be provided with this option (overriding the `color` column) and will be recycled if/as necessary.
`alpha`	The transparency of the fill colors.
`lwd`	Line width for lines between intervals. Set to `NULL` to remove lines.
`color`	The color of the lines between intervals.
`lty`	Line type for lines between intervals.
`lab`	Whether to include labels. Requires the `geomtextpath` package.
`abbrv`	If including labels, whether to use abbreviations instead of full interval names.
`skip`	A vector of interval names indicating which intervals should not be labeled. If `abbrv` is `TRUE`, this can also include interval abbreviations.
`neg`	Set this to true if your theta-axis is using negative values. This is usually true if you are using `ggtree`.
`prop`	This is the rotational proportion of the background that the scale takes up.
`textpath_args`	A list of named arguments to provide to `geomtextpath::geom_textpath()`. Only used if `lab` is set to `TRUE`. Useful arguments include `color` (font color), `family` (font family), `fontface`, `hjust` (radial adjustment), and `size` (font size).
`clip`	Should drawing be clipped to the extent of the plot panel? A setting of `"on"` (the default) means yes, and a setting of `"off"` means no. For details, please see `coord_cartesian()`.

Details

If a custom data.frame is provided (with `dat`), it should consist of at least 2 columns of data. See `data(periods)` for an example.

- The `max_age` column lists the oldest boundary of each time interval.
- The `min_age` column lists the youngest boundary of each time interval.
- The `abbr` column is optional and lists abbreviations that may be used as labels.
- The `color` column is optional and lists a color for the background for each time interval.

`dat` may also be a list of values and/or dataframes if multiple time scales should be added to the background. Scales will be added sequentially starting at `start` and going in the specified `direction`. By default the scales will all be equal in circular/rotational proportion, but this can be overridden with `prop`. If `dat` is a list, `fill`, `alpha`, `lwd`, `color`, `lty`, `lab`, `abbrv`, `skip`, `neg`, `prop`, and `textpath_args` can also be lists (N.B. `textpath_args` would be a list of lists). If these lists are not as long as `dat`, the elements will be recycled. If individual values (or vectors) are used for these parameters, they will be applied to all time scales (and recycled as necessary).

If the sum of the `prop` values is greater than 1, the proportions will be scaled such that they sum to 1. However, the `prop` values may sum to less than 1 if the user would like blank space in the background.

Care must be taken when adding labels to plots, as they are very likely to overlap with the plot under the default settings. The `textpath_args` argument can be used to adjust the settings for the plotting of the labels. See `geomtextpath::geom_textpath()` for details about the available arguments. Also note that the curvature of the labels may vary based on the distance from the origin. This is why `abbrv` is set to `TRUE` by default.

Examples

```
library(ggplot2)

library(ggtree)
set.seed(1)
tree <- rtree(100)
# single scale
revts(ggtree(tree)) +
  coord_geo_radial(dat = "stages") +
  scale_y_continuous(guide = "none", breaks = NULL) +
  theme_gray()

# multiple scales
revts(ggtree(tree)) +
  coord_geo_radial(
    dat = list("stages", "periods"), alpha = .5,
    prop = list(0.75, .25), start = pi / 4, end = 2 * pi, lty = "dashed"
  ) +
  scale_y_continuous(expand = expansion(mult = c(0.02, 0.02)),
                     guide = "none", breaks = NULL) +
  theme_gray()
```

```
library(ggplot2)
library(paleotree)
data(RaiaCopesRule)
ggtree(ceratopsianTreeRaia,
       position = position_nudge(x = -ceratopsianTreeRaia$root.time)) +
  coord_geo_radial(dat = "stages") +
  scale_y_continuous(guide = "none", breaks = NULL) +
  theme_classic()
```

`coord_trans_flip` *Transformed and flipped Cartesian coordinate system*

Description

`coord_trans_flip` behaves similarly to `ggplot2::coord_trans()` in that it occurs after statistical transformation and will affect the visual appearance of geoms. The main difference is that it also flips the x and y coordinates like `ggplot2::coord_flip()`.

Usage

```
coord_trans_flip(
  x = "identity",
  y = "identity",
  xlim = NULL,
  ylim = NULL,
  clip = "on",
  expand = TRUE
)
```

Arguments

`x`, `y`	Transformers for x and y axes or their names.
`xlim`, `ylim`	Limits for the x and y axes.
`clip`	Should drawing be clipped to the extent of the plot panel? A setting of `"on"` (the default) means yes, and a setting of `"off"` means no. In most cases, the default of `"on"` should not be changed, as setting `clip = "off"` can cause unexpected results. It allows drawing of data points anywhere on the plot, including in the plot margins. If limits are set via `xlim` and `ylim` and some data points fall outside those limits, then those data points may show up in places such as the axes, the legend, the plot title, or the plot margins.
`expand`	If `TRUE`, the default, adds a small expansion factor to the limits to ensure that data and axes don't overlap. If `FALSE`, limits are taken exactly from the data or `xlim`/`ylim`. Giving a logical vector will separately control the expansion for the four directions (top, left, bottom and right). The `expand` argument will be recycled to length 4 if necessary. Alternatively, can be a named logical vector to control a single direction, e.g. `expand = c(bottom = FALSE)`.

Examples

```
library(ggplot2)
ggplot(mtcars, aes(disp, wt)) +
  geom_point() +
  coord_trans_flip(x = "log10", y = "log10")
```

`coord_trans_xy` *Transformed XY Cartesian coordinate system*

Description

`coord_trans_xy` behaves similarly to `ggplot2::coord_trans()` in that it occurs after statistical transformation and will affect the visual appearance of geoms. The main difference is that it takes a single transformer that is applied to the x and y axes simultaneously. Any transformers produced by `ggforce::linear_trans()` that have x and y arguments should work, but any other transformers produced using `scales::trans_new()` that take x and y arguments should also work. Axis limits will be adjusted to account for transformation unless limits are specified with `xlim` or `ylim`.

Usage

```
coord_trans_xy(
  trans = NULL,
  xlim = NULL,
  ylim = NULL,
  expand = FALSE,
  default = FALSE,
  clip = "on"
)
```

Arguments

`trans`	Transformer for x and y axes.
`xlim`, `ylim`	Limits for the x and y axes.
`expand`	If `TRUE`, the default, adds a small expansion factor to the limits to ensure that data and axes don't overlap. If `FALSE`, limits are taken exactly from the data or `xlim`/`ylim`. Giving a logical vector will separately control the expansion for the four directions (top, left, bottom and right). The `expand` argument will be recycled to length 4 if necessary. Alternatively, can be a named logical vector to control a single direction, e.g. `expand = c(bottom = FALSE)`.
`default`	Is this the default coordinate system? If `FALSE` (the default), then replacing this coordinate system with another one creates a message alerting the user that the coordinate system is being replaced. If `TRUE`, that warning is suppressed.
`clip`	Should drawing be clipped to the extent of the plot panel? A setting of `"on"` (the default) means yes, and a setting of `"off"` means no. In most cases, the default of `"on"` should not be changed, as setting `clip = "off"` can cause unexpected results. It allows drawing of data points anywhere on the plot, including in

the plot margins. If limits are set via `xlim` and `ylim` and some data points fall outside those limits, then those data points may show up in places such as the axes, the legend, the plot title, or the plot margins.

Details

This coordinate system only works with geoms where all points are defined with x and y coordinates (e.g., `ggplot2::geom_point()`, `ggplot2::geom_polygon()`). This does not currently work with geoms where point coordinates are extrapolated (e.g., `ggplot2::geom_rect()`). Furthermore, when used with ggplot2 3.5.0 and later, some transformation edge cases may cause problems with rendering axis lines. This includes not currently support "capping" axes. I hope to support all of these geoms, edge cases, and features in the future.

Examples

```
# make transformer
library(ggforce)
trans <- linear_trans(shear(2, 0), rotate(-pi / 3))

# set up data to be plotted
square <- data.frame(x = c(0, 0, 4, 4), y = c(0, 1, 1, 0))
points <- data.frame(x = runif(100, 0, 4), y = runif(100, 0, 1))

# plot data normally
library(ggplot2)
ggplot(data = points, aes(x = x, y = y)) +
  geom_polygon(data = square, fill = NA, color = "black") +
  geom_point(color = "black") +
  coord_cartesian(expand = FALSE) +
  theme_classic()

# plot data with transformation
ggplot(data = points, aes(x = x, y = y)) +
  geom_polygon(data = square, fill = NA, color = "black") +
  geom_point(color = "black") +
  coord_trans_xy(trans = trans, expand = FALSE) +
  theme_classic()
```

`disparity_through_time`

Disparity through time plot using lattice

Description

Plots points on 2-D surfaces within a a 3-D framework. See `lattice::wireframe()` and `lattice::panel.cloud()` for customization options.

Usage

```
disparity_through_time(
  x,
  data,
  groups,
  pch = 16,
  col.point = c("blue"),
  scales = list(arrows = FALSE, distance = 1, col = "black", z = list(rot = 90)),
  colorkey = FALSE,
  screen = list(z = 90, x = 70, y = 180),
  aspect = c(1.5, 4),
  drape = TRUE,
  col.regions = c("white"),
  alpha.regions = c(1),
  perspective = FALSE,
  R.mat = matrix(c(1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1), 4, 4),
  par.settings = list(axis.line = list(col = "transparent"), layout.heights =
   list(top.padding = 0, main.key.padding = 0, key.axis.padding = 0, axis.xlab.padding =
   0, xlab.key.padding = 0, key.sub.padding = 0, bottom.padding = 0), layout.widths =
   list(left.padding = 0, key.ylab.padding = 0, ylab.axis.padding = 0, axis.key.padding
     = 0, right.padding = 0)),
  lattice.options = list(axis.padding = list(factor = 0)),
  ...
)
```

Arguments

`x`	a formula (most likely of the form `z ~ x * y`)
`data`	a data frame in which variables in the formula are to be evaluated
`groups`	a variable in `data` to be used as a grouping variable (this is probably the z variable)
`pch`	the point type
`col.point`	color(s) for points on surfaces
`scales`	a list specifying how the axes are drawn (see `lattice::xyplot()` for details)
`colorkey`	logical, should a legend be drawn (or a list describing the legend; see `lattice::levelplot()` for details)
`screen`	a list of the rotations that should be applied to each axis
`aspect`	a numeric vector of length 2, giving the relative aspects of the y-size/x-size and z-size/x-size of the enclosing cube
`drape`	logical, whether the surfaces should be colored based on `col.regions` and `alpha.regions`
`col.regions`	color(s) for surfaces
`alpha.regions`	alpha value(s) for surfaces
`perspective`	logical, whether to plot a perspective view

`R.mat`	a transformational matrix that is applied to the orientation of the axes
`par.settings`	plotting settings (see `lattice::trellis.par.set()`)
`lattice.options`	lattice settings (see `lattice::lattice.options()`)
`...`	Other arguments passed to `lattice::wireframe()`

Value

An object of class `"trellis"`, as output by `lattice::wireframe()`.

Examples

```
g <- data.frame(
  x = runif(100, 0, 60), y = runif(100, 0, 10),
  z = factor(rep(periods$name[1:5], each = 20),
    levels = periods$name[1:5]
  )
)
disparity_through_time(z ~ x * y,
  data = g, groups = z, aspect = c(1.5, 2),
  xlim = c(0, 60), ylim = c(0, 10), col.regions = "lightgreen",
  col.point = c("red", "blue")
)
```

`eons` *Eon data from the International Commission on Stratigraphy (v2024/12)*

Description

A dataset containing the boundary ages, abbreviations, and colors for the eons of the Geologic Time Scale. Based on The ICS International Chronostratigraphic Chart (v2024/12), by Cohen, Finney, Gibbard, and Fan.

Usage

```
eons
```

Format

A data frame with 3 rows and 5 variables:

name eon name

max_age maximum age, in millions of years

min_age minimum age, in millions of years

abbr eon name abbreviations

color the colors for each eon, according to the Commission for the Geological Map of the World

lab_color the label colors for each eon, either white or black, whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union

Source

`https://stratigraphy.org` via `https://macrostrat.org/api/v2/defs/intervals?timescale=international%20eons`

See Also

Other built-in timescales: `epochs`, `eras`, `periods`, `stages`

`epochs` *Epoch data from the International Commission on Stratigraphy (v2024/12)*

Description

A dataset containing the boundary ages, abbreviations, and colors for the epochs of the Geologic Time Scale. Based on The ICS International Chronostratigraphic Chart (v2024/12), by Cohen, Finney, Gibbard, and Fan.

Usage

```
epochs
```

Format

A data frame with 34 rows and 5 variables:

name epoch name

max_age maximum age, in millions of years

min_age minimum age, in millions of years

abbr epoch name abbreviations

color the colors for each epoch, according to the Commission for the Geological Map of the World

lab_color the label colors for each epoch, either white or black, whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union

Source

`https://stratigraphy.org` via `https://macrostrat.org/api/v2/defs/intervals?timescale=international%20epochs`

See Also

Other built-in timescales: `eons`, `eras`, `periods`, `stages`

`eras` *Era data from the International Commission on Stratigraphy (v2024/12)*

Description

A dataset containing the boundary ages, abbreviations, and colors for the eras of the Geologic Time Scale. Based on The ICS International Chronostratigraphic Chart (v2024/12), by Cohen, Finney, Gibbard, and Fan.

Usage

```
eras
```

Format

A data frame with 10 rows and 5 variables:

name era name

max_age maximum age, in millions of years

min_age minimum age, in millions of years

abbr era name abbreviations

color the colors for each era, according to the Commission for the Geological Map of the World

lab_color the label colors for each era, either white or black, whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union

Source

`https://stratigraphy.org` via `https://macrostrat.org/api/v2/defs/intervals?timescale=international%20eras`

See Also

Other built-in timescales: `eons`, `epochs`, `periods`, `stages`

`facet_grid_color` *Lay out panels in a grid with colored strips*

Description

`facet_grid_color` behaves similarly to `ggplot2::facet_grid()` in that it forms a matrix of panels defined by row and column faceting variables. The main difference is that it also allows the user to specify the background and label colors of the individual facet strips using the `colors` and `lab_colors` arguments. If you have only one variable with many levels, try `facet_wrap_color()`.

Usage

```
facet_grid_color(
  colors,
  rows = NULL,
  cols = NULL,
  scales = "fixed",
  space = "fixed",
  shrink = TRUE,
  labeller = "label_value",
  lab_colors = "auto",
  as.table = TRUE,
  switch = NULL,
  drop = TRUE,
  margins = FALSE,
  axes = "margins",
  axis.labels = "all"
)

facet_grid_geo(
  colors = stages,
  rows = NULL,
  cols = NULL,
  scales = "fixed",
  space = "fixed",
  shrink = TRUE,
  labeller = "label_value",
  lab_colors = "auto",
  as.table = TRUE,
  switch = NULL,
  drop = TRUE,
  margins = FALSE,
  axes = "margins",
  axis.labels = "all"
)
```

Arguments

`colors`	Specifies which colors to use to replace the strip backgrounds. Either A) a function that returns a color for a given strip label, B) the character name of a function that does the same, C) a named character vector with names matching strip labels and values indicating the desired colors, or D) a data.frame representing a lookup table with columns named "name" (matching strip labels) and "color" (indicating desired colors). If the function returns `NA`, the default background color will be used.
`rows, cols`	A set of variables or expressions quoted by `vars()` and defining faceting groups on the rows or columns dimension. The variables can be named (the names are passed to `labeller`). For compatibility with the classic interface, `rows` can also be a formula with the rows (of the tabular display) on the LHS and the columns (of the tabular display) on the RHS; the dot in the formula is used to indicate there should be no faceting on this dimension (either row or column).
`scales`	Are scales shared across all facets (the default, `"fixed"`), or do they vary across rows (`"free_x"`), columns (`"free_y"`), or both rows and columns (`"free"`)?
`space`	If `"fixed"`, the default, all panels have the same size. If `"free_y"` their height will be proportional to the length of the y scale; if `"free_x"` their width will be proportional to the length of the x scale; or if `"free"` both height and width will vary. This setting has no effect unless the appropriate scales also vary.
`shrink`	If `TRUE`, will shrink scales to fit output of statistics, not raw data. If `FALSE`, will be range of raw data before statistical summary.
`labeller`	A function that takes one data frame of labels and returns a list or data frame of character vectors. Each input column corresponds to one factor. Thus there will be more than one with `vars(cyl, am)`. Each output column gets displayed as one separate line in the strip label. This function should inherit from the "labeller" S3 class for compatibility with `labeller()`. You can use different labeling functions for different kind of labels, for example use `label_parsed()` for formatting facet labels. `label_value()` is used by default, check it for more details and pointers to other options.
`lab_colors`	Specifies which colors to use for the strip labels. Either A) a function that returns a color for a given strip label, B) the character name of a function that does the same, C) a named character vector with names matching strip labels and values indicating the desired colors, D) a data.frame representing a lookup table with columns named "name" (matching strip labels) and "lab_color" (indicating desired colors), or E) "auto" (the default), which set the labels to black or white, whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union. If the function returns `NA`, the default label color will be used.
`as.table`	If `TRUE`, the default, the facets are laid out like a table with highest values at the bottom-right. If `FALSE`, the facets are laid out like a plot with the highest value at the top-right.
`switch`	By default, the labels are displayed on the top and right of the plot. If `"x"`, the top labels will be displayed to the bottom. If `"y"`, the right-hand side labels will be displayed to the left. Can also be set to `"both"`.

`drop`	If `TRUE`, the default, all factor levels not used in the data will automatically be dropped. If `FALSE`, all factor levels will be shown, regardless of whether or not they appear in the data.
`margins`	Either a logical value or a character vector. Margins are additional facets which contain all the data for each of the possible values of the faceting variables. If `FALSE`, no additional facets are included (the default). If `TRUE`, margins are included for all faceting variables. If specified as a character vector, it is the names of variables for which margins are to be created.
`axes`	Determines which axes will be drawn. When `"margins"` (default), axes will be drawn at the exterior margins. `"all_x"` and `"all_y"` will draw the respective axes at the interior panels too, whereas `"all"` will draw all axes at all panels.
`axis.labels`	Determines whether to draw labels for interior axes when the `axes` argument is not `"margins"`. When `"all"` (default), all interior axes get labels. When `"margins"`, only the exterior axes get labels and the interior axes get none. When `"all_x"` or `"all_y"`, only draws the labels at the interior axes in the x- or y-direction respectively.

Details

`facet_grid_geo(...)` is an alias of `facet_grid_color()` with the default of `colors` set to `stages`.

See Also

Other faceting functions: `facet_nested_color()`, `facet_nested_wrap_color()`, `facet_wrap_color()`

Examples

```
library(ggplot2)
df <- data.frame(x = 1:10, y = 1:10, period = c("Permian", "Triassic"))
ggplot(df) +
  geom_point(aes(x, y)) +
  facet_grid_color(cols = vars(period), colors = periods)
```

`facet_nested_color` *Layout panels in a grid with nested colored strips*

Description

`facet_nested_color` behaves similarly to `ggh4x::facet_nested()` in that it forms a matrix of panels defined by row and column faceting variables and nests grouped facets. The main difference is that it also allows the user to specify the background and label colors of the individual facet strips using the `colors` and `lab_colors` arguments.

Usage

```
facet_nested_color(
  colors,
  rows = NULL,
  cols = NULL,
  scales = "fixed",
  space = "fixed",
  axes = "margins",
  remove_labels = "none",
  independent = "none",
  shrink = TRUE,
  labeller = "label_value",
  lab_colors = "auto",
  as.table = TRUE,
  switch = NULL,
  drop = TRUE,
  margins = FALSE,
  nest_line = element_line(inherit.blank = TRUE),
  solo_line = FALSE,
  resect = unit(0, "mm"),
  render_empty = TRUE,
  strip = strip_nested(),
  bleed = NULL
)

facet_nested_geo(
  colors = rbind(periods, stages),
  rows = NULL,
  cols = NULL,
  scales = "fixed",
  space = "fixed",
  axes = "margins",
  remove_labels = "none",
  independent = "none",
  shrink = TRUE,
  labeller = "label_value",
  lab_colors = "auto",
  as.table = TRUE,
  switch = NULL,
  drop = TRUE,
  margins = FALSE,
  nest_line = element_line(inherit.blank = TRUE),
  solo_line = FALSE,
  resect = unit(0, "mm"),
  render_empty = TRUE,
  strip = strip_nested(),
  bleed = NULL
)
```

Arguments

`colors`	Specifies which colors to use to replace the strip backgrounds. Either A) a function that returns a color for a given strip label, B) the character name of a function that does the same, C) a named character vector with names matching strip labels and values indicating the desired colors, or D) a data.frame representing a lookup table with columns named "name" (matching strip labels) and "color" (indicating desired colors). If the function returns `NA`, the default background color will be used.
`rows, cols`	A set of variables or expressions quoted by `vars()` and defining faceting groups on the rows or columns dimension. The variables can be named (the names are passed to `labeller`). For compatibility with the classic interface, `rows` can also be a formula with the rows (of the tabular display) on the LHS and the columns (of the tabular display) on the RHS; the dot in the formula is used to indicate there should be no faceting on this dimension (either row or column).
`scales`	A `character(1)` or `logical(1)` whether scales are shared across facets or allowed to vary. Interacts with the `independent` argument. One of the following: `"fixed"` **or** `FALSE` Scales are shared across all facets (default). `"free_x"` x-scales are allowed to vary across rows. `"free_y"` y-scales are allowed to vary across columns. `"free"` **or** `TRUE` Scales can vary across rows and columns.
`space`	A `character(1)` or `logical(1)` determining whether the size of panels are proportional to the length of the scales. When the `independent` argument allows for free scales in a dimension, the panel sizes cannot be proportional. Note that the `scales` argument must be free in the same dimension as the `space` argument to have an effect.One of the following: `"fixed"` **or** `FALSE` All panels have the same size (default). `"free_x"` Panel widths are proportional to the x-scales. `"free_y"` Panel heights are proportional to the y-scales. `"free"` **or** `TRUE` Both the widths and heights vary according to scales.
`axes`	A `character(1)` or `logical(1)` where axes should be drawn. One of the following: `"margins"` **or** `FALSE` Only draw axes at the outer margins (default). `"x"` Draw axes at the outer margins and all inner x-axes too. `"y"` Draw axes at the outer margins and all inner y-axes too. `"all"` **or** `TRUE` Draw the axes for every panel.
`remove_labels`	A `character(1)` or `logical(1)` determining whether axis text is displayed at inner panels. One of the following: `"none"` **or** `FALSE` Display axis text at all axes (default). `"x"` Display axis text at outer margins and all inner y-axes. `"y"` Display axis text at outer margins and all inner x-axes. `"all"` **or** `TRUE` Only display axis text at the outer margins.

`independent`	A `character(1)` or `logical(1)` determining whether scales can vary within a row or column of panels, like they can be in ggplot2::facet_wrap. The `scales` argument must be free for the same dimension before they can be set to independent. One of the following: `"none"` **or** `FALSE` All y-scales should be fixed in a row and all x-scales are fixed in a column (default). `"x"` x-scales are allowed to vary within a column. `"y"` y-scales are allowed to vary within a row. `"all"` **or** `TRUE` Both x- and y-scales are allowed to vary within a column or row respectively.
`shrink`	If `TRUE`, will shrink scales to fit output of statistics, not raw data. If `FALSE`, will be range of raw data before statistical summary.
`labeller`	A function that takes one data frame of labels and returns a list or data frame of character vectors. Each input column corresponds to one factor. Thus there will be more than one with `vars(cyl, am)`. Each output column gets displayed as one separate line in the strip label. This function should inherit from the "labeller" S3 class for compatibility with `labeller()`. You can use different labeling functions for different kind of labels, for example use `label_parsed()` for formatting facet labels. `label_value()` is used by default, check it for more details and pointers to other options.
`lab_colors`	Specifies which colors to use for the strip labels. Either A) a function that returns a color for a given strip label, B) the character name of a function that does the same, C) a named character vector with names matching strip labels and values indicating the desired colors, D) a data.frame representing a lookup table with columns named "name" (matching strip labels) and "lab_color" (indicating desired colors), or E) "auto" (the default), which set the labels to black or white, whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union. If the function returns `NA`, the default label color will be used.
`as.table`	If `TRUE`, the default, the facets are laid out like a table with highest values at the bottom-right. If `FALSE`, the facets are laid out like a plot with the highest value at the top-right.
`switch`	By default, the labels are displayed on the top and right of the plot. If `"x"`, the top labels will be displayed to the bottom. If `"y"`, the right-hand side labels will be displayed to the left. Can also be set to `"both"`.
`drop`	If `TRUE`, the default, all factor levels not used in the data will automatically be dropped. If `FALSE`, all factor levels will be shown, regardless of whether or not they appear in the data.
`margins`	Either a logical value or a character vector. Margins are additional facets which contain all the data for each of the possible values of the faceting variables. If `FALSE`, no additional facets are included (the default). If `TRUE`, margins are included for all faceting variables. If specified as a character vector, it is the names of variables for which margins are to be created.
`nest_line`	a theme element, either `element_blank()` or inheriting from `ggplot2::element_line()`. Lines are drawn between layers of strips indicating hierarchy. The element inherits from the `ggh4x.facet.nestline` element in the theme.

`solo_line`	A `logical(1)` indicating whether parent strips with a single child should be drawn with a `nest_line` (`TRUE`) or the line only applies to parents with multiple children (`FALSE`, default). Only relevant when `nest_line` is drawn.
`resect`	a `unit` vector of length 1, indicating how much the nesting line should be shortened.
`render_empty`	A `logical(1)`: whether to draw panels without any data (`TRUE`, default) or display these as blanks (`FALSE`).
`strip`	An object created by a call to a strip function, such as `strip_nested()`.
`bleed`	**[Deprecated]** the `bleed` argument has moved to the `strip_nested()` function.

Details

`facet_nested_geo(...)` is an alias of `facet_nested_color()` with the default of `colors` set to `rbind(periods, stages)`.

See Also

Other faceting functions: `facet_grid_color()`, `facet_nested_wrap_color()`, `facet_wrap_color()`

Examples

```
library(ggplot2)
df <- data.frame(x = 1:10, y = 1:10,
                 period = factor(c("Permian", "Triassic", "Jurassic",
                                   "Cretaceous", "Paleogene"),
                                 levels = c("Permian", "Triassic",
                                            "Jurassic", "Cretaceous",
                                            "Paleogene")),
                 era = factor(c("Paleozoic", "Mesozoic", "Mesozoic",
                                "Mesozoic", "Cenozoic"),
                              levels = c("Paleozoic", "Mesozoic",
                                         "Cenozoic")))
ggplot(df, aes(x, y)) +
  geom_point() +
  facet_nested_color(~ era + period, colors = rbind(periods, eras))
```

`facet_nested_wrap_color`

Ribbon of panels with nested colored strips

Description

`facet_nested_wrap_color` behaves similarly to `ggh4x::facet_nested_wrap()` in that it wraps a sequence of panels onto a two-dimensional layout, and nests grouped facets where possible.. The main difference is that it also allows the user to specify the background and label colors of the individual facet strips using the `colors` and `lab_colors` arguments.

Usage

```
facet_nested_wrap_color(
  facets,
  colors,
  nrow = NULL,
  ncol = NULL,
  scales = "fixed",
  axes = "margins",
  remove_labels = "none",
  shrink = TRUE,
  labeller = "label_value",
  lab_colors = "auto",
  as.table = TRUE,
  drop = TRUE,
  dir = "h",
  strip.position = "top",
  nest_line = element_line(inherit.blank = TRUE),
  solo_line = FALSE,
  resect = unit(0, "mm"),
  trim_blank = TRUE,
  strip = strip_nested(),
  bleed = NULL
)

facet_nested_wrap_geo(
  facets,
  colors = rbind(periods, stages),
  nrow = NULL,
  ncol = NULL,
  scales = "fixed",
  axes = "margins",
  remove_labels = "none",
  shrink = TRUE,
  labeller = "label_value",
  lab_colors = "auto",
  as.table = TRUE,
  drop = TRUE,
  dir = "h",
  strip.position = "top",
  nest_line = element_line(inherit.blank = TRUE),
  solo_line = FALSE,
  resect = unit(0, "mm"),
  trim_blank = TRUE,
  strip = strip_nested(),
  bleed = NULL
)
```

Arguments

`facets`	A set of variables or expressions quoted by `vars()` and defining faceting groups on the rows or columns dimension. The variables can be named (the names are passed to `labeller`). For compatibility with the classic interface, can also be a formula or character vector. Use either a one sided formula, `~a + b`, or a character vector, `c("a", "b")`.
`colors`	Specifies which colors to use to replace the strip backgrounds. Either A) a function that returns a color for a given strip label, B) the character name of a function that does the same, C) a named character vector with names matching strip labels and values indicating the desired colors, or D) a data.frame representing a lookup table with columns named "name" (matching strip labels) and "color" (indicating desired colors). If the function returns `NA`, the default background color will be used.
`nrow, ncol`	Number of rows and columns.
`scales`	A `character(1)` or `logical(1)` whether scales are shared across facets or allowed to vary. One of the following: `"fixed"` **or** `FALSE` Scales are shared across all facets (default). `"free_x"` x-scales are allowed to vary. `"free_y"` y-scales are allowed to vary. `"free"` **or** `TRUE` Both scales can vary
`axes`	A `character(1)` or `logical(1)` where axes should be drawn. One of the following: `"margins"` **or** `FALSE` Only draw axes at the outer margins (default). `"x"` Draw axes at the outer margins and all inner x-axes too. `"y"` Draw axes at the outer margins and all inner y-axes too. `"all"` **or** `TRUE` Draw the axes for every panel.
`remove_labels`	A `character(1)` or `logical(1)` determining whether axis text is displayed at inner panels. One of the following: `"none"` **or** `FALSE` Display axis text at all axes (default). `"x"` Display axis text at outer margins and all inner y-axes. `"y"` Display axis text at outer margins and all inner x-axes. `"all"` **or** `TRUE` Only display axis text at the outer margins.
`shrink`	If `TRUE`, will shrink scales to fit output of statistics, not raw data. If `FALSE`, will be range of raw data before statistical summary.
`labeller`	A function that takes one data frame of labels and returns a list or data frame of character vectors. Each input column corresponds to one factor. Thus there will be more than one with `vars(cyl, am)`. Each output column gets displayed as one separate line in the strip label. This function should inherit from the "labeller" S3 class for compatibility with `labeller()`. You can use different labeling functions for different kind of labels, for example use `label_parsed()` for formatting facet labels. `label_value()` is used by default, check it for more details and pointers to other options.

`lab_colors`	Specifies which colors to use for the strip labels. Either A) a function that returns a color for a given strip label, B) the character name of a function that does the same, C) a named character vector with names matching strip labels and values indicating the desired colors, D) a data.frame representing a lookup table with columns named "name" (matching strip labels) and "lab_color" (indicating desired colors), or E) "auto" (the default), which set the labels to black or white, whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union. If the function returns `NA`, the default label color will be used.
`as.table`	If `TRUE`, the default, the facets are laid out like a table with highest values at the bottom-right. If `FALSE`, the facets are laid out like a plot with the highest value at the top-right.
`drop`	If `TRUE`, the default, all factor levels not used in the data will automatically be dropped. If `FALSE`, all factor levels will be shown, regardless of whether or not they appear in the data.
`dir`	Direction: either `"h"` for horizontal, the default, or `"v"`, for vertical.
`strip.position`	By default, the labels are displayed on the top of the plot. Using `strip.position` it is possible to place the labels on either of the four sides by setting `strip.position = c("top", "bottom", "left", "right")`
`nest_line`	a theme element, either `element_blank()` or inheriting from `ggplot2::element_line()`. Lines are drawn between layers of strips indicating hierarchy. The element inherits from the `ggh4x.facet.nestline` element in the theme.
`solo_line`	A `logical(1)` indicating whether parent strips with a single child should be drawn with a `nest_line` (`TRUE`) or the line only applies to parents with multiple children (`FALSE`, default). Only relevant when `nest_line` is drawn.
`resect`	a `unit` vector of length 1, indicating how much the nesting line should be shortened.
`trim_blank`	A `logical(1)`. When `TRUE` (default), does not draw rows and columns containing no panels. When `FALSE`, the `nrow` and `ncol` arguments are taken literally, even when there are more than needed to fit all panels.
`strip`	An object created by a call to a strip function, such as `strip_nested()`.
`bleed`	**[Deprecated]** the `bleed` argument has moved to the `strip_nested()` function.

Details

`facet_nested_wrap_geo(...)` is an alias of `facet_nested_wrap_color()` with the default of `colors` set to `rbind(periods, stages)`.

See Also

Other faceting functions: `facet_grid_color()`, `facet_nested_color()`, `facet_wrap_color()`

Examples

```
library(ggplot2)
df <- data.frame(x = 1:10, y = 1:10,
```

```
                 period = factor(c("Permian", "Triassic", "Jurassic",
                                   "Cretaceous", "Paleogene"),
                                 levels = c("Permian", "Triassic",
                                            "Jurassic", "Cretaceous",
                                            "Paleogene")),
                 era = factor(c("Paleozoic", "Mesozoic", "Mesozoic",
                                "Mesozoic", "Cenozoic"),
                              levels = c("Paleozoic", "Mesozoic",
                                         "Cenozoic")))
ggplot(df, aes(x, y)) +
  geom_point() +
  facet_nested_wrap_color(~ era + period, colors = rbind(periods, eras))
```

`facet_wrap_color` *Wrap a 1d ribbon of panels into 2d with colored strips*

Description

`facet_wrap_color` behaves similarly to `ggplot2::facet_wrap()` in that it wraps a 1d sequence of panels into 2d. The main difference is that it also allows the user to specify the background and label colors of the individual facet strips using the `colors` and `lab_colors` arguments. This is generally a better use of screen space than `facet_grid_color()` because most displays are roughly rectangular.

Usage

```
facet_wrap_color(
  facets,
  colors,
  nrow = NULL,
  ncol = NULL,
  scales = "fixed",
  shrink = TRUE,
  labeller = "label_value",
  lab_colors = "auto",
  as.table = TRUE,
  drop = TRUE,
  dir = "h",
  strip.position = "top",
  axes = "margins",
  axis.labels = "all"
)

facet_wrap_geo(
  facets,
  colors = stages,
  nrow = NULL,
  ncol = NULL,
```

```
  scales = "fixed",
  shrink = TRUE,
  labeller = "label_value",
  lab_colors = "auto",
  as.table = TRUE,
  drop = TRUE,
  dir = "h",
  strip.position = "top",
  axes = "margins",
  axis.labels = "all"
)
```

Arguments

`facets`	A set of variables or expressions quoted by `vars()` and defining faceting groups on the rows or columns dimension. The variables can be named (the names are passed to `labeller`). For compatibility with the classic interface, can also be a formula or character vector. Use either a one sided formula, `~a + b`, or a character vector, `c("a", "b")`.
`colors`	Specifies which colors to use to replace the strip backgrounds. Either A) a function that returns a color for a given strip label, B) the character name of a function that does the same, C) a named character vector with names matching strip labels and values indicating the desired colors, or D) a data.frame representing a lookup table with columns named "name" (matching strip labels) and "color" (indicating desired colors). If the function returns `NA`, the default background color will be used.
`nrow, ncol`	Number of rows and columns.
`scales`	Should scales be fixed (`"fixed"`, the default), free (`"free"`), or free in one dimension (`"free_x"`, `"free_y"`)?
`shrink`	If `TRUE`, will shrink scales to fit output of statistics, not raw data. If `FALSE`, will be range of raw data before statistical summary.
`labeller`	A function that takes one data frame of labels and returns a list or data frame of character vectors. Each input column corresponds to one factor. Thus there will be more than one with `vars(cyl, am)`. Each output column gets displayed as one separate line in the strip label. This function should inherit from the "labeller" S3 class for compatibility with `labeller()`. You can use different labeling functions for different kind of labels, for example use `label_parsed()` for formatting facet labels. `label_value()` is used by default, check it for more details and pointers to other options.
`lab_colors`	Specifies which colors to use for the strip labels. Either A) a function that returns a color for a given strip label, B) the character name of a function that does the same, C) a named character vector with names matching strip labels and values indicating the desired colors, D) a data.frame representing a lookup table with columns named "name" (matching strip labels) and "lab_color" (indicating desired colors), or E) "auto" (the default), which set the labels to black or white,

	whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union. If the function returns `NA`, the default label color will be used.
`as.table`	**[Superseded]** The `as.table` argument is now absorbed into the `dir` argument via the two letter options. If `TRUE`, the facets are laid out like a table with highest values at the bottom-right. If `FALSE`, the facets are laid out like a plot with the highest value at the top-right.
`drop`	If `TRUE`, the default, all factor levels not used in the data will automatically be dropped. If `FALSE`, all factor levels will be shown, regardless of whether or not they appear in the data.
`dir`	Direction: either `"h"` for horizontal, the default, or `"v"`, for vertical. When `"h"` or `"v"` will be combined with `as.table` to set final layout. Alternatively, a combination of `"t"` (top) or `"b"` (bottom) with `"l"` (left) or `"r"` (right) to set a layout directly. These two letters give the starting position and the first letter gives the growing direction. For example `"rt"` will place the first panel in the top-right and starts filling in panels right-to-left.
`strip.position`	By default, the labels are displayed on the top of the plot. Using `strip.position` it is possible to place the labels on either of the four sides by setting `strip.position = c("top", "bottom", "left", "right")`
`axes`	Determines which axes will be drawn in case of fixed scales. When `"margins"` (default), axes will be drawn at the exterior margins. `"all_x"` and `"all_y"` will draw the respective axes at the interior panels too, whereas `"all"` will draw all axes at all panels.
`axis.labels`	Determines whether to draw labels for interior axes when the scale is fixed and the `axis` argument is not `"margins"`. When `"all"` (default), all interior axes get labels. When `"margins"`, only the exterior axes get labels, and the interior axes get none. When `"all_x"` or `"all_y"`, only draws the labels at the interior axes in the x- or y-direction respectively.

Details

`facet_wrap_geo(...)` is an alias of `facet_wrap_color()` with the default of `colors` set to `stages`.

See Also

Other faceting functions: `facet_grid_color()`, `facet_nested_color()`, `facet_nested_wrap_color()`

Examples

```
library(ggplot2)
df <- data.frame(x = 1:10, y = 1:10, period = c("Permian", "Triassic"))
ggplot(df) +
  geom_point(aes(x, y)) +
  facet_wrap_color(vars(period), colors = periods)
```

`geom_phylomorpho` *Plot a 2-D phylomorphospace in ggplot2*

Description

This behaves similar to `phytools::phylomorphospace()`, but is for plotting a 2-D phylomorphospace with `ggplot2::ggplot()`. This function works like any other `ggplot2` geom; it can be combined with other geoms (see the example below), and the output can be modified using scales, themes, etc.

Usage

```
geom_phylomorpho(
  tree,
  mapping = NULL,
  data = NULL,
  position = "identity",
  ...,
  seg_args = list(),
  point_args = list(),
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
  linejoin = "round",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

`tree`	An object of class "phylo".
`mapping`	Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
`data`	The data to be displayed in this layer. There are three options: If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`. A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created. A `function` will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A `function` can be created from a `formula` (e.g. `~ head(.x, 10)`).

`position`	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The `position` argument accepts the following: • The result of calling a position function, such as `position_jitter()`. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the `position_` prefix. For example, to use `position_jitter()`, give the position as `"jitter"`.
`...`	Other arguments passed on to both `ggplot2::geom_segment()` and `ggplot2::geom_point()`.
`seg_args`	A list of arguments passed only to `ggplot2::geom_segment()`.
`point_args`	A list of arguments passed only to `ggplot2::geom_point()`.
`arrow`	specification for arrow heads, as created by `grid::arrow()`.
`arrow.fill`	fill colour to use for the arrow head (if closed). `NULL` means use `colour` aesthetic.
`lineend`	Line end style (round, butt, square).
`linejoin`	Line join style (round, mitre, bevel).
`na.rm`	If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.
`show.legend`	logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use `TRUE`. If `NA`, all levels are shown in legend, but unobserved levels are omitted.
`inherit.aes`	If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. `borders()`.

Details

The ancestral states are estimated using `phytools::fastAnc()`. Note that `phytools` is not necessarily installed with `deeptime`, but it is required to use this function. Following the estimation of the ancestral states, the nodes are connected using `ggplot2::geom_segment()`, while the tips are indicated using `ggplot2::geom_point()`.

The default expectation is that the order of the data is the same order as the tip labels of the tree (`tree$tip.label`). However, if this is not the case, you can map the optional `label` aesthetic to a column in the data that contains the tip names (see example below).

Examples

```
library(ggplot2)

library(ape)
tr <- rtree(10)
dat <- data.frame(
  x = runif(10), y = runif(10), label = tr$tip.label,
  row.names = tr$tip.label
```

```
)
ggplot(dat, aes(x = x, y = y, label = label)) +
  geom_phylomorpho(tr) +
  geom_label(size = 5)
```

`geom_points_range` *Display points and their range*

Description

This geom is like `ggplot2::geom_pointrange()` in that it draws points and lines. However, unlike `ggplot2::geom_pointrange()`, this geom takes in sets of x-y points and calculates the ranges/intervals based on those. It then plots both the original points and the ranges using `ggplot2::geom_linerange()`. In cases where not all points are connected (because of grouping due to aesthetics), the `background_line` argument can be used to add lines that span the entire point range for each `x` or `y` category.

Usage

```
geom_points_range(
  mapping = NULL,
  data = NULL,
  stat = "points_range",
  position = "identity",
  ...,
  na.rm = FALSE,
  orientation = NA,
  background_line = NULL,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_points_range(
  mapping = NULL,
  data = NULL,
  geom = "points_range",
  position = "identity",
  ...,
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

`mapping`	Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

`data`	The data to be displayed in this layer. There are three options: If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`. A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created. A `function` will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A `function` can be created from a `formula` (e.g. `~ head(.x, 10)`).
`stat`	The statistical transformation to use on the data for this layer. When using a `geom_*()` function to construct a layer, the `stat` argument can be used the override the default coupling between geoms and stats. The `stat` argument accepts the following: • A `Stat` ggproto subclass, for example `StatCount`. • A string naming the stat. To give the stat as a string, strip the function name of the `stat_` prefix. For example, to use `stat_count()`, give the stat as `"count"`.
`position`	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The `position` argument accepts the following: • The result of calling a position function, such as `position_jitter()`. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the `position_` prefix. For example, to use `position_jitter()`, give the position as `"jitter"`.
`...`	Arguments passed on to both `ggplot2::geom_linerange()` and `ggplot2::geom_point()`.
`na.rm`	If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.
`orientation`	The orientation of the layer. The default (`NA`) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting `orientation` to either `"x"` or `"y"`. See the *Orientation* section for more detail.
`background_line`	A named list of aesthetic values to use for plotted line segments that span the entire `y` or `x` range for each `x` or `y` category. The default aesthetics will be used for any aesthetics that are not specified in the list. This can be useful if the plotted groups of points don't overlap but you want a continuous line connecting all points for a given `x` or `y` category. If NULL (the default), no line segments will be plotted.
`show.legend`	logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use `TRUE`. If `NA`, all levels are shown in legend, but unobserved levels are omitted.

`inherit.aes`	If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. `borders()`.
`geom`	The geometric object to use to display the data for this layer. When using a `stat_*()` function to construct a layer, the `geom` argument can be used to override the default coupling between stats and geoms. The `geom` argument accepts the following: • A `Geom` ggproto subclass, for example `GeomPoint`. • A string naming the geom. To give the geom as a string, strip the function name of the `geom_` prefix. For example, to use `geom_point()`, give the geom as `"point"`.

Aesthetics

`geom_points_range()` understands the following aesthetics (required aesthetics are in bold):

- **x**
- **y**
- size
- color/colour
- fill
- shape
- alpha
- group
- linetype
- linewidth

Computed variables

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation. `stat_points_range()` provides the following variables, some of which depend on the orientation:

- `after_stat(ymin)` *or* `after_stat(xmin)`
  the minimum extent of the point range
- `after_stat(ymax)` *or* `after_stat(xmax)`
  the maximum extent of the point range

Orientation

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the `orientation` parameter, which can be either `"x"` or `"y"`. The value gives the axis that the geom should run along, `"x"` being the default orientation you would expect for the geom.

Examples

```
library(ggplot2)

library(palaeoverse)
data(tetrapods)
tetrapod_names <- tetrapods$accepted_name[1:50]
beds_sampled <- sample.int(n = 10, size = 50, replace = TRUE)
occdf <- data.frame(taxon = tetrapod_names, bed = beds_sampled)
ggplot(occdf, aes(y = reorder(taxon, bed, min), x = bed)) +
  geom_points_range()
```

`geom_text_phylo` *Label nodes on a phylogenetic tree plotted with ggtree*

Description

This geom adds labels to all or a subset of the nodes of a phylogenetic tree that has been plotted using `ggtree::ggtree()`. It is therefore very similar to `ggtree::geom_tiplab()`, `ggtree::geom_tiplab2()`, `ggtree::geom_nodelab()`, and `ggtree::geom_nodelab2()`. However, unlike those geoms, this geom is intended to work with all coordinate systems, including `coord_geo()` and `coord_geo_radial()`.

Usage

```
geom_text_phylo(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  parse = FALSE,
  nudge_x = 0,
  nudge_y = 0,
  node_type = "tip",
  auto_adjust = TRUE,
  check_overlap = FALSE,
  size.unit = "mm",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

`mapping`	Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

`data`	The data to be displayed in this layer. There are three options: If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`. A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created. A `function` will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A `function` can be created from a `formula` (e.g. `~ head(.x, 10)`).
`stat`	The statistical transformation to use on the data for this layer. When using a `geom_*()` function to construct a layer, the `stat` argument can be used the override the default coupling between geoms and stats. The `stat` argument accepts the following: • A `Stat` ggproto subclass, for example `StatCount`. • A string naming the stat. To give the stat as a string, strip the function name of the `stat_` prefix. For example, to use `stat_count()`, give the stat as `"count"`.
`position`	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The `position` argument accepts the following: • The result of calling a position function, such as `position_jitter()`. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the `position_` prefix. For example, to use `position_jitter()`, give the position as `"jitter"`.
`...`	Other arguments passed on to `layer()`'s `params` argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the `position` argument, or aesthetics that are required can *not* be passed through `...`. Unknown arguments that are not part of the 4 categories below are ignored. • Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, `colour = "red"` or `linewidth = 3`. The geom's documentation has an **Aesthetics** section that lists the available options. The 'required' aesthetics cannot be passed on to the `params`. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data. • When constructing a layer using a `stat_*()` function, the `...` argument can be used to pass on parameters to the `geom` part of the layer. An example of this is `stat_density(geom = "area", outline.type = "both")`. The geom's documentation lists which parameters it can accept. • Inversely, when constructing a layer using a `geom_*()` function, the `...` argument can be used to pass on parameters to the `stat` part of the layer. An example of this is `geom_area(stat = "density", adjust = 0.5)`. The stat's documentation lists which parameters it can accept. • The `key_glyph` argument of `layer()` may also be passed on through `...`. This can be one of the functions described as key glyphs, to change the display of the layer in the legend.

`parse`	If `TRUE`, the labels will be parsed into expressions and displayed as described in `?plotmath`.
`nudge_x`, `nudge_y`	Horizontal and vertical adjustment to nudge labels by. Useful for offsetting text from points, particularly on discrete scales. Cannot be jointly specified with `position`.
`node_type`	Determines the subset of nodes to label. Valid options are "tip" for tip nodes, "internal" for non-tip nodes, and "all" for all nodes.
`auto_adjust`	Should upside-down text labels automatically be rotated 180° to improve readability?
`check_overlap`	If `TRUE`, text that overlaps previous text in the same layer will not be plotted. `check_overlap` happens at draw time and in the order of the data. Therefore data should be arranged by the label column before calling `geom_text()`. Note that this argument is not supported by `geom_label()`.
`size.unit`	How the `size` aesthetic is interpreted: as millimetres (`"mm"`, default), points (`"pt"`), centimetres (`"cm"`), inches (`"in"`), or picas (`"pc"`).
`na.rm`	If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.
`show.legend`	logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use `TRUE`. If `NA`, all levels are shown in legend, but unobserved levels are omitted.
`inherit.aes`	If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. `borders()`.

Details

Each label will be plotted with the same angle as the branch/edge leading to its node by default. The `angle`, `hjust`, and `vjust` aesthetics can be used to adjust this. If custom `angle` values are specified, these will be **added** to the default angle as calculated as described above.

As with `ggplot2::geom_text()`, the limits of axes will not be expanded to accommodate the new labels, so you may need to extend them manually using the `limits` or `expand` arguments within `scale_` or `coord_` functions. Note that `coord_geo()` by default sets `expand = FALSE`.

Aesthetics

`geom_text_phylo()` understands the following aesthetics (required aesthetics are in bold):

- **x** (pulled from the phylogeny by default)
- **y** (pulled from the phylogeny by default)
- **label** (pulled from the phylogeny by default)
- alpha
- angle

- color/colour
- family
- fontface
- group
- hjust
- lineheight
- size
- vjust

Alignment

You can modify text alignment with the `vjust` and `hjust` aesthetics. These can either be a number between 0 (left/bottom) and 1 (right/top) or a character (`"left"`, `"middle"`, `"right"`, `"bottom"`, `"center"`, `"top"`). There are two special alignments: `"inward"` and `"outward"`. Inward always aligns text towards the center, and outward aligns it away from the center.

Examples

```
library(ggplot2)

library(ape)
library(ggtree)
tr <- rtree(10)
revts(ggtree(tr)) +
  geom_text_phylo() +
  coord_geo_radial("epochs")
```

`geo_pattern` *Get a FGDC geologic plotting pattern*

Description

Retrieve a single geologic pattern as defined in the FGDC Digital Cartographic Standard for Geologic Map Symbolization by the U.S. Geological Survey and the Geologic Data Subcommittee (GDS) of the Federal Geographic Data Committee (FGDC).

Usage

```
geo_pattern(
  code,
  scale = 2,
  col = NULL,
  fill = NULL,
  alpha = NULL,
  bg = "white"
```

```
)

geo_grob(code, col = NULL, fill = NULL, alpha = NULL, bg = "white")
```

Arguments

`code`	The number corresponding to the pattern to return. Strings and numbers are permitted.
`scale`	The visual scale of the pattern (higher values mean the pattern is more zoomed in).
`col`	The color to use for the lines of the pattern.
`fill`	The color used to fill various closed shapes (e.g., circles) in the pattern.
`alpha`	The transparency to use for the fill of the pattern.
`bg`	The background color to use for the pattern.

Details

For specific codes, see the "pattern numbers" in the full pattern chart for valid code values. Daven Quinn has also assembled more accessible documentation of the map patterns/codes and lithology patterns/codes. `rmacrostrat::def_lithologies()` can also be used to look up pattern codes for various lithologies (see the "fill" column). Note that codes associated with color variants (e.g., "101-M") are supported but will result in the default color variant instead (usually black and white, e.g., "101-K").

These patterns were originally processed and optimized by Daven Quinn and are hosted on GitHub.

Value

`geo_grob()` returns a grob object with a single instance of the desired pattern. `geo_pattern()` returns a GridPattern object with a repeated instance of the desired pattern.

See Also

FGDC patterns: `grid.pattern_geo()`, `scale_fill_geopattern()`

Examples

```
library(grid)
# Get a generic igneous pattern
pattern1 <- geo_pattern(code = "313-K")
# Get the pattern for a sandstone
pattern2 <- geo_pattern(code = "607")

# plot the two patterns
grid.newpage()
grid.draw(rectGrob(gp = gpar(fill = pattern1)))
grid.newpage()
grid.draw(rectGrob(gp = gpar(fill = pattern2)))
```

`get_scale_data` *Get geological timescale data*

Description

This function takes a name of a geological timescale and returns data for the timescale. Valid names include those of built-in `data.frames` (`periods()`, `epochs()`, `stages()`, `eons()`, or `eras()`), partial matches of those names (e.g., "per" or "age"), and partial or exact matches to those hosted by Macrostrat (see Details below). Note that the colors in the built-in `data.frames` are according to the Commission for the Geological Map of the World. If you would like to obtain custom Macrostrat colors that are better for mapping, you should specify the full name of a timescale (e.g., "international periods") and set `true_colors` to `FALSE`. Note that these colors only vary for the Precambrian.

Usage

```
get_scale_data(name, true_colors = TRUE)
```

Arguments

`name`	The name of the desired timescale.
`true_colors`	Return original international time scale colors? (as opposed to custom Macrostrat plotting colors)

Details

The following timescales are available from the Macrostrat API as of 2025-06-18:

- international ages
- international epochs
- international periods
- calcareous nannoplankton zones
- New Zealand ages
- custom COSUNA
- North American land mammal ages
- international intervals
- COSUNA
- international eras
- international eons
- Trilobite Zonation - Laurentia
- Conodont Zonation
- North American Regional
- Ammonite Zonation - Boreal

- Ammonite Zonation - Western Interior
- international intervals covering all time
- Scotese Reconstruction
- Geomagnetic Polarity Chron
- Geomagnetic Polarity Subchron
- Planktic foraminiferal Primary Biozones
- Planktic foraminiferal Secondary Biozones
- Planktic foraminiferal datums
- Martian Periods
- Martian Epochs
- Cretaceous Planktic foraminifer zonations
- Low latitude radiolarian zonation
- Neogene North Pacific Diatom Biochronology
- Neogene North Pacific Diatom Biochronology Subzones
- Siberian Regional
- Australian Regional
- Western Europe Regional
- Russian Platform Regional Stages
- Russian Precambrian Eras
- Russian Precambrian Eons
- Russian Epochs
- Russian Stages

The most up-to-date list can be found via the Macrostrat API here.

Value

A `data.frame` with the following columns:

`name`	the names of the time intervals
`max_age`	the oldest boundaries of the time intervals, in millions of years
`min_age`	the youngest boundaries of the time intervals, in millions of years
`abbr`	either traditional abbreviations of the names of the time intervals (if they exist) or custom abbreviations created with R
`color`	hex color codes associated with the time intervals (if applicable)
`lab_color`	default label colors for the time interals, either white or black, whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union

---

`ggarrange2` *Combine and arrange multiple ggplot-like objects*

Description

Arrange multiple ggplot, grobified ggplot, or geo_scale objects on a page, aligning the plot panels, axes, and axis titles.

Usage

```
ggarrange2(
  ...,
  plots = list(...),
  layout = NULL,
  nrow = NULL,
  ncol = NULL,
  widths = NULL,
  heights = NULL,
  byrow = TRUE,
  top = NULL,
  bottom = NULL,
  left = NULL,
  right = NULL,
  padding = unit(0.5, "line"),
  margin = unit(0.5, "line"),
  clip = "on",
  draw = TRUE,
  newpage = TRUE,
  debug = FALSE,
  labels = NULL,
  label.args = list(gp = gpar(font = 4, cex = 1.2))
)
```

Arguments

`...`	ggplot, grobified ggplot (gtable), or geo_scale objects
`plots`	list of ggplot, gtable, or geo_scale objects
`layout`	a matrix of integers specifying where each plot should go, like `mat` in `graphics::layout()`; `NA` or a value less than 0 or greater than the number of plots indicates a blank plot; overrides nrow/ncol/byrow
`nrow`	number of rows
`ncol`	number of columns
`widths`	list of requested widths
`heights`	list of requested heights
`byrow`	logical, fill by rows

`top`	optional string, or grob
`bottom`	optional string, or grob
`left`	optional string, or grob
`right`	optional string, or grob
`padding`	unit of length one, margin around annotations
`margin`	vector of units of length 4: top, right, bottom, left (as in `gtable::gtable_add_padding()`)
`clip`	argument of gtable
`draw`	logical: draw or return a grob
`newpage`	logical: draw on a new page
`debug`	logical, show layout with thin lines
`labels`	character labels used for annotation of subfigures (should be in the same order as `plots`)
`label.args`	label list of parameters for the formatting of labels

Value

gtable of aligned plots

Examples

```
library(ggplot2)
p1 <- ggplot(mtcars, aes(mpg, wt, colour = factor(cyl))) +
  geom_point()
p2 <- ggplot(mtcars, aes(mpg, wt, colour = factor(cyl))) +
  geom_point() +
  facet_wrap(~cyl, ncol = 2, scales = "free") +
  guides(colour = "none") +
  theme()
ggarrange2(p1, p2, widths = c(2, 1), labels = c("a", "b"))

p3 <- ggplot() +
  geom_point(aes(y = runif(1000, 0, 8), x = runif(1000, 0, 1000))) +
  scale_x_reverse() +
  coord_geo(xlim = c(1000, 0), ylim = c(0, 8)) +
  theme_classic()
ggarrange2(ggarrange2(p1, p2, widths = c(2, 1), draw = FALSE), p3, nrow = 2)
```

`grid.pattern_geo` *Plot an individual FGDC pattern using grid*

Description

This function can be used to plot a single geologic pattern as defined in the FGDC Digital Cartographic Standard for Geologic Map Symbolization by the U.S. Geological Survey and the Geologic Data Subcommittee (GDS) of the Federal Geographic Data Committee (FGDC). The pattern is plotted on the existing canvas (i.e., use `grid::grid.newpage()` to make a new canvas).

Usage

```
grid.pattern_geo(params, boundary_df, aspect_ratio, legend = FALSE)
```

Arguments

`params`	A list of pattern parameters to customize the plotted pattern (see "Details").
`boundary_df`	A `data.frame` consisting of three columns: "x" (x-coordinates), "y" (y-coordinates), and "id" (polygon group ID). This `data.frame` defines the boundary (as a closed polygon) of the plotted pattern.
`aspect_ratio`	Unused.
`legend`	Unused.

Details

The following `params` are accepted:

`pattern_alpha` Alpha transparency for pattern. default: 1

`pattern_colour` Color used for strokes and points in the pattern. default: 'black'

`pattern_fill` Color used to fill various closed shapes (e.g., circles) in the pattern. default: `NA`

`pattern_scale` Scale. default: 2

`pattern_type` Code for the FGDC pattern to use. See `geo_pattern()` for more details. default: "101"

`fill` Color used for the background. default: "white"

Warning

Pattern fills are not supported on all graphics devices. Not all devices are under active development, and such devices are unlikely to add support for new features (such as pattern fills). The new features have only been implemented on a subset of graphics devices so far: `cairo_pdf()`, `cairo_ps()`, `x11(type="cairo")`, `png(type="cairo")`, `jpeg(type="cairo")`, `tiff(type="cairo")`, `svg()`, and `pdf()`. Although there is no support yet for `quartz()` or `windows()`, almost all of the graphics devices above will work on all major platforms. Further, the ragg and svglite packages contain graphics devices that support patterns. When using a graphics device where patterns are not supported, closed shapes will be rendered with a transparent fill. Note that, at least on Windows machines, the default device in RStudio and in the knitr package is `png()`, which does not support patterns. In RStudio, you can go to 'Tools > Global Options > General > Graphics' and choose the 'Cairo PNG' device from the dropdown menu to display patterns. Similar issues may arise when using RStudio on other operating systems.

See Also

FGDC patterns: `geo_pattern()`, `scale_fill_geopattern()`

Examples

```
# use the function directly to make a hexagon with the pattern
library(grid)
x <- 0.5 + 0.5 * cos(seq(2 * pi / 4, by = 2 * pi / 6, length.out = 6))
y <- 0.5 + 0.5 * sin(seq(2 * pi / 4, by = 2 * pi / 6, length.out = 6))
grid.newpage()
grid.pattern_geo(params = list(pattern_type = "633", pattern_scale = 4),
                 boundary_df = data.frame(x, y, id = 1))

# use the function via ggpattern by specifying `pattern = 'geo'`
library(ggplot2)
library(ggpattern)
df <- data.frame(trt = c("a", "b", "c"), outcome = c(2.3, 1.9, 3.2))
ggplot(df, aes(trt, outcome)) +
  geom_col_pattern(aes(color = trt, pattern_type = trt), pattern = 'geo',
  pattern_color = "black", fill = "white", pattern_fill = "white") +
  scale_pattern_type_manual(values = c("101", "313", "634")) +
  scale_color_viridis_d() +
  theme(legend.key.size = unit(1.5, 'cm'))
```

`gtable_frame2` *Decompose a ggplot gtable*

Description

Reformat the gtable associated with a ggplot object into a 7x7 gtable where the central cell corresponds to the plot panel(s), the rectangle of cells around that corresponds to the axes, and the rectangle of cells around that corresponds to the axis titles.

Usage

```
gtable_frame2(
  g,
  width = unit(1, "null"),
  height = unit(1, "null"),
  debug = FALSE
)
```

Arguments

`g`	gtable
`width`	requested width
`height`	requested height
`debug`	logical draw gtable cells

Value

7x7 gtable wrapping the plot

Examples

```
library(grid)
library(gridExtra)
library(ggplot2)
p1 <- ggplot(mtcars, aes(mpg, wt, colour = factor(cyl))) +
  geom_point()

p2 <- ggplot(mtcars, aes(mpg, wt, colour = factor(cyl))) +
  geom_point() +
  facet_wrap(~cyl, ncol = 2, scales = "free") +
  guides(colour = "none") +
  theme()

p3 <- ggplot(mtcars, aes(mpg, wt, colour = factor(cyl))) +
  geom_point() +
  facet_grid(. ~ cyl, scales = "free")

g1 <- ggplotGrob(p1)
g2 <- ggplotGrob(p2)
g3 <- ggplotGrob(p3)
fg1 <- gtable_frame2(g1)
fg2 <- gtable_frame2(g2)
fg12 <- gtable_frame2(gtable_rbind(fg1, fg2), width = unit(2, "null"),
                      height = unit(1, "null"))
fg3 <- gtable_frame2(g3, width = unit(1, "null"), height = unit(1, "null"))
grid.newpage()
combined <- gtable_cbind(fg12, fg3)
grid.draw(combined)
```

`guide_geo` *Geological timescale axis guide*

Description

`guide_geo` behaves similarly to `ggplot2::guide_axis()` in that it modifies the visual appearance of the axis. The main difference is that it adds a geological timescale instead of an axis.

Usage

```
guide_geo(
  dat = "periods",
  fill = NULL,
  alpha = 1,
  height = unit(2, "line"),
  bord = c("left", "right", "top", "bottom"),
```

```
  lwd = 0.25,
  color = "black",
  lab = TRUE,
  lab_color = NULL,
  rot = 0,
  family = "sans",
  fontface = "plain",
  size = 5,
  skip = c("Quaternary", "Holocene", "Late Pleistocene"),
  abbrv = TRUE,
  neg = FALSE,
  end_labels = "center",
  dat_is_discrete = FALSE,
  fittext_args = list(),
  theme = NULL,
  title = waiver(),
  order = 0,
  position = waiver()
)
```

Arguments

`dat`	Either A) a string indicating a built-in dataframe with interval data from the ICS ("periods", "epochs", "stages", "eons", or "eras"), B) a string indicating a timescale from macrostrat (see list here: `https://macrostrat.org/api/defs/timescales?all`), or C) a custom data.frame of time interval boundaries (see Details).
`fill`	The fill color of the boxes. The default is to use the `color` column included in `dat`. If a custom dataset is provided with `dat` without a `color` column and without fill, a greyscale will be used. Custom fill colors can be provided with this option (overriding the `color` column) and will be recycled if/as necessary.
`alpha`	The transparency of the fill colors.
`height`	The height (or width if `pos` is `left` or `right`) of the scale.
`bord`	A vector specifying on which sides of the scale to add borders (same options as `pos`).
`lwd`	Line width.
`color`	The outline color of the interval boxes.
`lab`	Whether to include labels.
`lab_color`	The color of the labels. The default is to use the `lab_color` column included in `dat`. If a custom dataset is provided with `dat` without a `lab_color` column and without fill, all labels will be black. Custom label colors can be provided with this option (overriding the `lab_color` column) and will be recycled if/as necessary.
`rot`	The amount of counter-clockwise rotation to add to the labels (in degrees).
`family`	The font family to use for the labels. There are only three fonts that are guaranteed to work everywhere: “sans” (the default), “serif”, or “mono”.

`fontface`	The font face to use for the labels. The standard options are "plain" (default), "bold", "italic", and "bold.italic".
`size`	Label size. Either a number as you would specify in `ggplot2::geom_text()` or `"auto"` to use `ggfittext::geom_fit_text()`.
`skip`	A vector of interval names indicating which intervals should not be labeled. If `abbrv` is `TRUE`, this can also include interval abbreviations.
`abbrv`	If including labels, should the labels be abbreviated? If `TRUE`, the `abbr` column will be used for the labels. If `FALSE`, the `name` column will be used for the labels. If `"auto"`, the `abbreviate()` function will be used to abbreviate the values in the `name` column. Note that the built-in data and data retrieved via `get_scale_data()` already have built-in abbreviations. However, using the `"auto"` option here will create new unique abbreviations based on only the intervals that are being plotted. In many cases, this may result in abbreviations that are shorter in length because there are fewer similar interval names to abbreviate.
`neg`	Set this to `TRUE` if your x-axis is using negative values.
`end_labels`	How should labels for intervals at the ends of the guide be treated? "center", the default, centers the labels within the visible part of the label. "clip" removes the labels if their midpoint is beyond the axis limits. "keep" plots the labels in the midpoint of the full interval.
`dat_is_discrete`	Are the ages in `dat` already converted for a discrete scale?
`fittext_args`	A list of named arguments to provide to `ggfittext::geom_fit_text()`. Only used if `size` is set to `"auto"`.
`theme`	A `theme` object to style the guide individually or differently from the plot's theme settings. The `theme` argument in the guide partially overrides, and is combined with, the plot's theme.
`title`	A character string or expression indicating a title of guide. If `NULL`, the title is not shown. By default (`waiver()`), the name of the scale object or the name specified in `labs()` is used for the title.
`order`	A positive `integer` of length 1 that specifies the order of this guide among multiple guides. This controls in which order guides are merged if there are multiple guides for the same position. If 0 (default), the order is determined by a secret algorithm.
`position`	Where this guide should be drawn: one of top, bottom, left, or right.

Details

If a custom data.frame is provided (with `dat`), it should consist of at least 3 columns of data. See `data(periods)` for an example.

- The `name` column lists the names of each time interval. These will be used as labels if no abbreviations are provided.
- The `max_age` column lists the oldest boundary of each time interval.
- The `min_age` column lists the youngest boundary of each time interval.

- The `abbr` column is optional and lists abbreviations that may be used as labels.
- The `color` column is also optional and lists a color for the background for each time interval.
- The `lab_color` column is also optional and lists a color for the label for each time interval.

If the axis of the time scale is discrete, `max_age` and `min_age` will automatically be converted to the discrete scale. In this case, the categories of the discrete axis should match the values in the `name` column. If the ages within `dat` are already discretized, you can set `dat_is_discrete` to `TRUE` to prevent this automatic conversion. This can be useful for adding a time scale where categories and time intervals are not 1:1.

Since this guide only plots the timescale and not ticks or an axis line, a call to this function should almost always be combined with a call to `ggplot2::guide_axis()` within a call to `ggplot2::guide_axis_stack()` (see Examples). Note that in most cases this has the same end result as a single call to `coord_geo()`; however, there are some use cases in which this may be more useful or allow for more customization. For example, users may wish to combine this guide in unique ways with other guides. Further, since `coord_geo()` doesn't work with radial/fan phylogenies (and `coord_geo_radial()` is quite different visually), this guide can be used to achieve the look of `coord_geo()` on a radial/fan phylogeny.

Examples

```
library(ggplot2)
# reproduce the coord_geo() appearance
ggplot() +
  geom_point(aes(y = runif(1000, 0, 8), x = runif(1000, 0, 1000))) +
  scale_x_reverse(guide = guide_axis_stack(guide_geo(), "axis",
                  spacing = unit(0, "npc"))) +
  coord_cartesian(xlim = c(1000, 0), ylim = c(0, 8)) +
  theme_classic()

# the coord_geo() look on a radial phylogeny
library(ggtree)
library(paleotree)
data(RaiaCopesRule)
ggtree(ceratopsianTreeRaia,
       position = position_nudge(x = -ceratopsianTreeRaia$root.time)) +
  coord_geo_radial(dat = "stages", fill = c("grey80", "grey95"),
                   end = 1.25 * pi) +
  guides(
    r = guide_axis_stack(guide_geo(rot = -90, neg = TRUE,
                                   height = unit(0.5, "line")),
                        "axis", spacing = unit(0, "npc"))
  ) +
  scale_y_continuous(guide = "none", breaks = NULL) +
  theme_classic()
```

`panel.disparity` *Combined wireframe and cloud panel*

Description

Plots the provided data on 2-D surfaces within a 3-D framework. See `disparity_through_time()`.

Usage

```
panel.disparity(x, y, z, groups, subscripts, ...)
```

Arguments

`x, y, z, groups, subscripts, ...`	Same as for `lattice::panel.cloud()`

Value

No return value, plots the results of both `lattice::panel.cloud()` and `lattice::panel.wireframe()`.

`periods` *Period data from the International Commission on Stratigraphy (v2024/12)*

Description

A dataset containing the boundary ages, abbreviations, and colors for the periods of the Geologic Time Scale. Based on The ICS International Chronostratigraphic Chart (v2024/12), by Cohen, Finney, Gibbard, and Fan.

Usage

```
periods
```

Format

A data frame with 22 rows and 5 variables:

name period name

max_age maximum age, in millions of years

min_age minimum age, in millions of years

abbr period name abbreviations

color the colors for each period, according to the Commission for the Geological Map of the World

lab_color the label colors for each period, either white or black, whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union

Source

https://stratigraphy.org via https://macrostrat.org/api/v2/defs/intervals?timescale=international%20periods

See Also

Other built-in timescales: `eons`, `epochs`, `eras`, `stages`

`scale_color_geo` *Geological Time Scale color scales*

Description

Color scales using the colors in the Geological Time Scale graphics.

Usage

```
scale_color_geo(dat, ...)

scale_fill_geo(dat, ...)

scale_discrete_geo(dat, aesthetics, ...)
```

Arguments

`dat`	Either A) a string indicating a built-in dataframe with interval data from the ICS ("periods", "epochs", "stages", "eons", or "eras"), B) a string indicating a timescale from macrostrat (see list here: https://macrostrat.org/api/defs/timescales?all), or C) a custom data.frame of time interval boundaries (see `coord_geo()`).
`...`	Arguments passed on to `ggplot2::discrete_scale` `scale_name` **[Deprecated]** The name of the scale that should be used for error messages associated with this scale. `name` The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted. `minor_breaks` One of: • `NULL` for no minor breaks • `waiver()` for the default breaks (none for discrete, one minor break between each major break for continuous) • A numeric vector of positions • A function that given the limits returns a vector of minor breaks. Also accepts rlang lambda function notation. When the function has two arguments, it will be given the limits and major break positions.

`labels` One of the options below. Please note that when `labels` is a vector, it is highly recommended to also set the `breaks` argument as a vector to protect against unintended mismatches.

- `NULL` for no labels
- `waiver()` for the default labels computed by the transformation object
- A character vector giving labels (must be same length as `breaks`)
- An expression vector (must be the same length as breaks). See ?plotmath for details.
- A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

`limits` One of:

- `NULL` to use the default scale values
- A character vector that defines possible values of the scale and their order
- A function that accepts the existing (automatic) values and returns new ones. Also accepts rlang lambda function notation.

`na.translate` Unlike continuous scales, discrete scales can easily show missing values, and do so by default. If you want to remove missing values from a discrete scale, specify `na.translate = FALSE`.

`na.value` If `na.translate = TRUE`, what aesthetic value should the missing values be displayed as? Does not apply to position scales where `NA` is always placed at the far right.

`drop` Should unused factor levels be omitted from the scale? The default, `TRUE`, uses the levels that appear in the data; `FALSE` includes the levels in the factor. Please note that to display every level in a legend, the layer should use `show.legend = TRUE`.

`guide` A function used to create a guide or its name. See `guides()` for more information.

`call` The `call` used to construct the scale for reporting messages.

`super` The super class to use for the constructed scale

`aesthetics`	Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the `colour` and `fill` aesthetics at the same time, via `aesthetics = c("colour", "fill")`.

Examples

```
library(ggplot2)
df <- data.frame(
  x = runif(1000, 0, 10), y = runif(1000, 0, 10),
  color = sample(periods$name, 1000, TRUE), shape = 21
)
ggplot(df) +
  geom_point(aes(x = x, y = y, fill = color), shape = 21) +
  scale_fill_geo("periods", name = "Period") +
  theme_classic()
```

```
# cut continuous variable into discrete
df <- data.frame(x = runif(1000, 0, 1000), y = runif(1000, 0, 8))
df$color <- cut(df$x, c(periods$min_age, periods$max_age[22]), periods$name)
ggplot(df) +
  geom_point(aes(x = x, y = y, color = color)) +
  scale_x_reverse() +
  scale_color_geo("periods", name = "Period") +
  coord_geo(xlim = c(1000, 0), ylim = c(0, 8)) +
  theme_classic()
```

`scale_fill_geopattern` *Geologic pattern fill scale*

Description

Fill scale using the FGDC Digital Cartographic Standard for Geologic Map Symbolization. Fill values should correspond to specific pattern codes (see "Details").

Usage

```
scale_fill_geopattern(na.value = "grey50", ...)
```

Arguments

`na.value`	The aesthetic value to use for missing (NA) values. May be either a color or a GridPattern object (such as that returned by `geo_pattern()`).
`...`	Arguments passed on to `ggplot2::discrete_scale`

`scale_name` **[Deprecated]** The name of the scale that should be used for error messages associated with this scale.

`name` The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted.

`breaks` One of:

- `NULL` for no breaks
- `waiver()` for the default breaks (the scale limits)
- A character vector of breaks
- A function that takes the limits as input and returns breaks as output. Also accepts rlang lambda function notation.

`minor_breaks` One of:

- `NULL` for no minor breaks
- `waiver()` for the default breaks (none for discrete, one minor break between each major break for continuous)
- A numeric vector of positions
- A function that given the limits returns a vector of minor breaks. Also accepts rlang lambda function notation. When the function has two arguments, it will be given the limits and major break positions.

`labels` One of the options below. Please note that when `labels` is a vector, it is highly recommended to also set the `breaks` argument as a vector to protect against unintended mismatches.

- `NULL` for no labels
- `waiver()` for the default labels computed by the transformation object
- A character vector giving labels (must be same length as `breaks`)
- An expression vector (must be the same length as breaks). See ?plotmath for details.
- A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

`limits` One of:

- `NULL` to use the default scale values
- A character vector that defines possible values of the scale and their order
- A function that accepts the existing (automatic) values and returns new ones. Also accepts rlang lambda function notation.

`na.translate` Unlike continuous scales, discrete scales can easily show missing values, and do so by default. If you want to remove missing values from a discrete scale, specify `na.translate = FALSE`.

`drop` Should unused factor levels be omitted from the scale? The default, `TRUE`, uses the levels that appear in the data; `FALSE` includes the levels in the factor. Please note that to display every level in a legend, the layer should use `show.legend = TRUE`.

`guide` A function used to create a guide or its name. See `guides()` for more information.

`call` The `call` used to construct the scale for reporting messages.

Details

For specific codes, see the "pattern numbers" in the full pattern chart for valid `code` values. Daven Quinn has also assembled more accessible documentation of the map patterns/codes and lithology patterns/codes. `rmacrostrat::def_lithologies()` can also be used to look up pattern codes for various lithologies (see the "fill" column). Note that codes associated with color variants (e.g., "101-M") are supported but will result in the default color variant instead (usually black and white, e.g., "101-K").

These patterns were originally processed and optimized by Daven Quinn and are hosted on GitHub.

Warning

Pattern fills are not supported on all graphics devices. Not all devices are under active development, and such devices are unlikely to add support for new features (such as pattern fills). The new features have only been implemented on a subset of graphics devices so far: `cairo_pdf()`, `cairo_ps()`, `x11(type="cairo")`, `png(type="cairo")`, `jpeg(type="cairo")`, `tiff(type="cairo")`, `svg()`, and `pdf()`. Although there is no support yet for `quartz()` or `windows()`, almost all of the graphics devices above will work on all major platforms. Further, the ragg and svglite packages contain graphics devices that support patterns. When using a graphics device where patterns are not supported, closed shapes will be rendered with a transparent fill. Note that, at least on Windows machines, the default device in RStudio and in the knitr package is `png()`, which does not support patterns. In RStudio, you can go to 'Tools > Global Options > General > Graphics' and choose the 'Cairo PNG' device from the dropdown menu to display patterns. Similar issues may arise when using RStudio on other operating systems.

See Also

FGDC patterns: `geo_pattern()`, `grid.pattern_geo()`

Examples

```
library(ggplot2)
vals <- c("101", "313", "603", "733")
ggplot(mpg, aes(factor(cyl), fill = vals[factor(cyl)])) +
  geom_bar() +
  scale_fill_geopattern(name = NULL)
```

`stages` *Stage data from the International Commission on Stratigraphy (v2024/12)*

Description

A dataset containing the boundary ages, abbreviations, and colors for the stages of the Geologic Time Scale. Based on The ICS International Chronostratigraphic Chart (v2024/12), by Cohen, Finney, Gibbard, and Fan.

Usage

```
stages
```

Format

A data frame with 102 rows and 5 variables:

name stage name

max_age maximum age, in millions of years

min_age minimum age, in millions of years

abbr stage name abbreviations

color the colors for each stage, according to the Commission for the Geological Map of the World

lab_color the label colors for each stage, either white or black, whichever has better contrast with the background color, based on recommendations by the International Telecommunication Union

Source

`https://stratigraphy.org` via `https://macrostrat.org/api/v2/defs/intervals?timescale=international%20ages`

See Also

Other built-in timescales: `eons`, `epochs`, `eras`, `periods`

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