Package: ordr (via r-universe)

October 25, 2026

Title A 'Tidyverse' Extension for Ordinations and Biplots

Version 0.2.0.0002

Description Ordination comprises several multivariate exploratory and explanatory techniques with theoretical foundations in geometric data analysis; see Podani (2000, ISBN:90-5782-067-6) for techniques and applications and Le Roux & Rouanet (2005) <doi:10.1007/1-4020-2236-0> for foundations. Greenacre (2010, ISBN:978-84-923846) shows how the most established of these, including principal components analysis, correspondence analysis, multidimensional scaling, factor analysis, and discriminant analysis, rely on eigen-decompositions or singular value decompositions of pre-processed numeric matrix data. These decompositions give rise to a set of shared coordinates along which the row and column elements can be measured. The overlay of their scatterplots on these axes, introduced by Gabriel (1971) <doi:10.1093/biomet/58.3.453>, is called a biplot. 'ordr' provides inspection, extraction, manipulation, and visualization tools for several popular ordination classes supported by a set of recovery methods. It is inspired by and designed to integrate into 'Tidyverse' workflows provided by Wickham et al (2019) <doi:10.21105/joss.01686>.

Depends R (>= 3.3.0), ggplot2

Imports rlang, cli, crayon, pillar, MASS, stringr, tidyselect, scales, generics, magrittr, tibble, tidyr, dplyr, purrr, labeling, ggrepel, gggda (>= 0.2.0-1)

Suggests testthat, sessioninfo, gridExtra, mlpack, ddalpha, knitr, rmarkdown

License GPL-3

Encoding UTF-8

LazyData true

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BugReports https://github.com/corybrunson/ordr/issues

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`annotation` *Annotate factors of 'tbl_ord' objects*

Description

These functions annotate the matrix factors of tbl_ords with additional variables, and retrieve these annotations.

The unexported `annotation_*()` and `set_annotation_*()` functions assign and retrieve values of the `"*_annotation"` attributes of `x`, which must have the same number of rows as `get_*(x)`.

Arguments

`annot`	A data.frame having the same number of rows as `get_*(x)`.

See Also

augmentation methods that must interface with annotation.

`augmentation` *Augment factors and coordinates of 'tbl_ord' objects*

Description

These functions return data associated with the cases, variables, and coordinates of an ordination object, and attach it to the object.

Usage

```
recover_aug_rows(x)

recover_aug_cols(x)

recover_aug_coord(x)

augment_ord(x, .matrix = "dims")
```

Arguments

`x`	An object of class 'tbl_ord'.
`.matrix`	A character string partially matched (lowercase) to several indicators for one or both matrices in a matrix decomposition used for ordination. The standard values are `"rows"`, `"cols"`, and `"dims"` (for both).

Details

The `recover_aug_*()` S3 methods produce tibbles of values associated with the rows, columns, and artificial coordinates of an object of class 'tbl_ord'. The first field of each tibble is `name`, which contains the row, column, or coordinate names. Additional fields contain information about the rows, columns, or coordinates extracted from the ordination object.

The function `augment_ord()` returns the ordination with either or both matrix factors annotated with the result of `recover_aug_*()`. In this way `augment_ord()` works like `generics::augment()`, as popularized by the **broom** package, by extracting information about the rows and columns, but it differs in returning an annotated 'tbl_ord' rather than a 'tbl_df' object. The advantage of implementing separate methods for the rows, columns, and artificial coordinates is that more information contained in the original object becomes accessible to the user.

Value

The `recover_aug_*()` functions return tibbles having the same numbers of rows as `recover_*()`. `augment_ord()` returns an augmented tbl_ord with the wrapped model unchanged.

See Also

tidiers and annotation methods that interface with augmentation.

Other generic recoverers: conference, recoverers, supplementation

---

biplot-geoms *Convenience geoms for row and column matrix factors*

Description

These geometric element layers (geoms) pair conventional **ggplot2** geoms with stat_rows() or stat_cols() in order to render elements for one or the other matrix factor of a tbl_ord. They understand the same aesthetics as their corresponding conventional geoms.

Usage

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

geom_cols_point(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_path(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
```

```
  linejoin = "round",
  linemitre = 10,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_path(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_polygon(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  rule = "evenodd",
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_polygon(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  rule = "evenodd",
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
```

```
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_contour(
  mapping = NULL,
  data = NULL,
  stat = "contour",
  position = "identity",
  ...,
  bins = NULL,
  binwidth = NULL,
  breaks = NULL,
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_contour(
  mapping = NULL,
  data = NULL,
  stat = "contour",
  position = "identity",
  ...,
  bins = NULL,
  binwidth = NULL,
  breaks = NULL,
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_density_2d(
  mapping = NULL,
  data = NULL,
  stat = "density_2d",
  position = "identity",
```

```
  ...,
  contour_var = "density",
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_density_2d(
  mapping = NULL,
  data = NULL,
  stat = "density_2d",
  position = "identity",
  ...,
  contour_var = "density",
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_density_2d_filled(
  mapping = NULL,
  data = NULL,
  stat = "density_2d_filled",
  position = "identity",
  ...,
  contour_var = "density",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_density_2d_filled(
  mapping = NULL,
  data = NULL,
  stat = "density_2d_filled",
  position = "identity",
  ...,
  contour_var = "density",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```
geom_rows_text(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "nudge",
  ...,
  parse = FALSE,
  check_overlap = FALSE,
  size.unit = "mm",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_text(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "nudge",
  ...,
  parse = FALSE,
  check_overlap = FALSE,
  size.unit = "mm",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_label(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "nudge",
  ...,
  parse = FALSE,
  label.padding = unit(0.25, "lines"),
  label.r = unit(0.15, "lines"),
  label.size = deprecated(),
  border.colour = NULL,
  border.color = NULL,
  text.colour = NULL,
  text.color = NULL,
  size.unit = "mm",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```
geom_cols_label(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "nudge",
  ...,
  parse = FALSE,
  label.padding = unit(0.25, "lines"),
  label.r = unit(0.15, "lines"),
  label.size = deprecated(),
  border.colour = NULL,
  border.color = NULL,
  text.colour = NULL,
  text.color = NULL,
  size.unit = "mm",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_text_repel(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  parse = FALSE,
  ...,
  box.padding = 0.25,
  point.padding = 1e-06,
  min.segment.length = 0.5,
  arrow = NULL,
  force = 1,
  force_pull = 1,
  max.time = 0.5,
  max.iter = 10000,
  max.overlaps = getOption("ggrepel.max.overlaps", default = 10),
  nudge_x = 0,
  nudge_y = 0,
  xlim = c(NA, NA),
  ylim = c(NA, NA),
  na.rm = FALSE,
  show.legend = NA,
  direction = c("both", "y", "x"),
  seed = NA,
  verbose = getOption("verbose", default = FALSE),
  inherit.aes = TRUE
)
```

```
geom_cols_text_repel(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  parse = FALSE,
  ...,
  box.padding = 0.25,
  point.padding = 1e-06,
  min.segment.length = 0.5,
  arrow = NULL,
  force = 1,
  force_pull = 1,
  max.time = 0.5,
  max.iter = 10000,
  max.overlaps = getOption("ggrepel.max.overlaps", default = 10),
  nudge_x = 0,
  nudge_y = 0,
  xlim = c(NA, NA),
  ylim = c(NA, NA),
  na.rm = FALSE,
  show.legend = NA,
  direction = c("both", "y", "x"),
  seed = NA,
  verbose = getOption("verbose", default = FALSE),
  inherit.aes = TRUE
)

geom_rows_label_repel(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  parse = FALSE,
  ...,
  box.padding = 0.25,
  label.padding = 0.25,
  point.padding = 1e-06,
  label.r = 0.15,
  label.size = 0.25,
  min.segment.length = 0.5,
  arrow = NULL,
  force = 1,
  force_pull = 1,
  max.time = 0.5,
  max.iter = 10000,
  max.overlaps = getOption("ggrepel.max.overlaps", default = 10),
```

```
  nudge_x = 0,
  nudge_y = 0,
  xlim = c(NA, NA),
  ylim = c(NA, NA),
  na.rm = FALSE,
  show.legend = NA,
  direction = c("both", "y", "x"),
  seed = NA,
  verbose = getOption("verbose", default = FALSE),
  inherit.aes = TRUE
)

geom_cols_label_repel(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  parse = FALSE,
  ...,
  box.padding = 0.25,
  label.padding = 0.25,
  point.padding = 1e-06,
  label.r = 0.15,
  label.size = 0.25,
  min.segment.length = 0.5,
  arrow = NULL,
  force = 1,
  force_pull = 1,
  max.time = 0.5,
  max.iter = 10000,
  max.overlaps = getOption("ggrepel.max.overlaps", default = 10),
  nudge_x = 0,
  nudge_y = 0,
  xlim = c(NA, NA),
  ylim = c(NA, NA),
  na.rm = FALSE,
  show.legend = NA,
  direction = c("both", "y", "x"),
  seed = NA,
  verbose = getOption("verbose", default = FALSE),
  inherit.aes = TRUE
)

geom_rows_axis(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
```

```
  axis_labels = TRUE,
  axis_ticks = TRUE,
  axis_text = TRUE,
  by = NULL,
  num = NULL,
  axis.type = c("interpolative", "predictive"),
  tick_length = 0.025,
  text_dodge = 0.03,
  label_dodge = 0.03,
  label_placement = c("positive", "negative", "peripheral"),
  ...,
  axis.linewidth = sync(),
  axis.linetype = sync(),
  axis.colour = sync(),
  axis.color = NULL,
  axis.alpha = sync(),
  label.size = sync(),
  label.angle = 0,
  label.hjust = sync(),
  label.vjust = sync(),
  label.family = sync(),
  label.fontface = sync(),
  label.colour = sync(),
  label.color = NULL,
  label.alpha = sync(),
  tick.linewidth = 0.25,
  tick.linetype = "solid",
  tick.colour = sync(),
  tick.color = NULL,
  tick.alpha = sync(),
  text.size = 2.6,
  text.angle = 0,
  text.hjust = sync(),
  text.vjust = sync(),
  text.family = sync(),
  text.fontface = sync(),
  text.colour = sync(),
  text.color = NULL,
  text.alpha = sync(),
  parse = FALSE,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_axis(
  mapping = NULL,
```

```
  data = NULL,
  stat = "identity",
  position = "identity",
  axis_labels = TRUE,
  axis_ticks = TRUE,
  axis_text = TRUE,
  by = NULL,
  num = NULL,
  axis.type = c("interpolative", "predictive"),
  tick_length = 0.025,
  text_dodge = 0.03,
  label_dodge = 0.03,
  label_placement = c("positive", "negative", "peripheral"),
  ...,
  axis.linewidth = sync(),
  axis.linetype = sync(),
  axis.colour = sync(),
  axis.color = NULL,
  axis.alpha = sync(),
  label.size = sync(),
  label.angle = 0,
  label.hjust = sync(),
  label.vjust = sync(),
  label.family = sync(),
  label.fontface = sync(),
  label.colour = sync(),
  label.color = NULL,
  label.alpha = sync(),
  tick.linewidth = 0.25,
  tick.linetype = "solid",
  tick.colour = sync(),
  tick.color = NULL,
  tick.alpha = sync(),
  text.size = 2.6,
  text.angle = 0,
  text.hjust = sync(),
  text.vjust = sync(),
  text.family = sync(),
  text.fontface = sync(),
  text.colour = sync(),
  text.color = NULL,
  text.alpha = sync(),
  parse = FALSE,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```
geom_rows_pointranges(
  mapping = NULL,
  data = NULL,
  stat = "center",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_pointranges(
  mapping = NULL,
  data = NULL,
  stat = "center",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_lineranges(
  mapping = NULL,
  data = NULL,
  stat = "center",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_lineranges(
  mapping = NULL,
  data = NULL,
  stat = "center",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_isoline(
  mapping = NULL,
  data = NULL,
```

```
  stat = "identity",
  position = "identity",
  isoline_text = TRUE,
  by = NULL,
  num = NULL,
  text_dodge = 0.06,
  ...,
  text.size = 3.18,
  text.angle = 0,
  text.hjust = sync(),
  text.vjust = sync(),
  text.family = sync(),
  text.fontface = sync(),
  text.colour = sync(),
  text.color = NULL,
  text.alpha = sync(),
  parse = FALSE,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_isoline(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  isoline_text = TRUE,
  by = NULL,
  num = NULL,
  text_dodge = 0.06,
  ...,
  text.size = 3.18,
  text.angle = 0,
  text.hjust = sync(),
  text.vjust = sync(),
  text.family = sync(),
  text.fontface = sync(),
  text.colour = sync(),
  text.color = NULL,
  text.alpha = sync(),
  parse = FALSE,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```
geom_rows_text_radiate(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  parse = FALSE,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_text_radiate(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  parse = FALSE,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_vector(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  arrow = default_arrow,
  lineend = "round",
  linejoin = "mitre",
  vector_labels = TRUE,
  ...,
  label.colour = NULL,
  label.color = NULL,
  label.alpha = NULL,
  parse = FALSE,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_vector(
```

```
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  arrow = default_arrow,
  lineend = "round",
  linejoin = "mitre",
  vector_labels = TRUE,
  ...,
  label.colour = NULL,
  label.color = NULL,
  label.alpha = NULL,
  parse = FALSE,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_bagplot(
  mapping = NULL,
  data = NULL,
  stat = "bagplot",
  position = "identity",
  outlier_points = !outlier_labels,
  outlier_labels = FALSE,
  ...,
  bag.linewidth = sync(),
  bag.linetype = sync(),
  bag.colour = "black",
  bag.color = NULL,
  bag.fill = sync(),
  bag.alpha = NA,
  median.shape = 21L,
  median.stroke = sync(),
  median.size = 5,
  median.colour = sync(),
  median.color = NULL,
  median.fill = "white",
  median.alpha = NA,
  fence.linewidth = 0.25,
  fence.linetype = 0L,
  fence.colour = sync(),
  fence.color = NULL,
  fence.fill = sync(),
  fence.alpha = 0.25,
  outlier.shape = sync(),
  outlier.stroke = sync(),
```

```
  outlier.size = sync(),
  outlier.colour = sync(),
  outlier.color = NULL,
  outlier.fill = NA,
  outlier.alpha = NA,
  text.size = 3.88,
  text.colour = sync(),
  text.color = sync(),
  text.alpha = sync(),
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_bagplot(
  mapping = NULL,
  data = NULL,
  stat = "bagplot",
  position = "identity",
  outlier_points = !outlier_labels,
  outlier_labels = FALSE,
  ...,
  bag.linewidth = sync(),
  bag.linetype = sync(),
  bag.colour = "black",
  bag.color = NULL,
  bag.fill = sync(),
  bag.alpha = NA,
  median.shape = 21L,
  median.stroke = sync(),
  median.size = 5,
  median.colour = sync(),
  median.color = NULL,
  median.fill = "white",
  median.alpha = NA,
  fence.linewidth = 0.25,
  fence.linetype = 0L,
  fence.colour = sync(),
  fence.color = NULL,
  fence.fill = sync(),
  fence.alpha = 0.25,
  outlier.shape = sync(),
  outlier.stroke = sync(),
  outlier.size = sync(),
  outlier.colour = sync(),
  outlier.color = NULL,
  outlier.fill = NA,
  outlier.alpha = NA,
```

```
  text.size = 3.88,
  text.colour = sync(),
  text.color = sync(),
  text.alpha = sync(),
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_rule(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  axis_labels = TRUE,
  axis_ticks = TRUE,
  axis_text = TRUE,
  by = NULL,
  num = NULL,
  axis.type = c("interpolative", "predictive"),
  snap_rule = TRUE,
  tick_length = 0.025,
  text_dodge = 0.03,
  label_dodge = 0.03,
  ...,
  axis.linewidth = sync(),
  axis.linetype = sync(),
  axis.colour = sync(),
  axis.color = NULL,
  axis.alpha = sync(),
  label.size = sync(),
  label.angle = 0,
  label.hjust = sync(),
  label.vjust = sync(),
  label.family = sync(),
  label.fontface = sync(),
  label.colour = sync(),
  label.color = NULL,
  label.alpha = sync(),
  tick.linewidth = 0.25,
  tick.linetype = "solid",
  tick.colour = sync(),
  tick.color = NULL,
  tick.alpha = sync(),
  text.size = 2.6,
  text.angle = 0,
  text.hjust = sync(),
  text.vjust = sync(),
```

```
    text.family = sync(),
    text.fontface = sync(),
    text.colour = sync(),
    text.color = NULL,
    text.alpha = sync(),
    parse = FALSE,
    check_overlap = FALSE,
    na.rm = FALSE,
    show.legend = NA,
    inherit.aes = TRUE
  )

  geom_cols_rule(
    mapping = NULL,
    data = NULL,
    stat = "identity",
    position = "identity",
    axis_labels = TRUE,
    axis_ticks = TRUE,
    axis_text = TRUE,
    by = NULL,
    num = NULL,
    axis.type = c("interpolative", "predictive"),
    snap_rule = TRUE,
    tick_length = 0.025,
    text_dodge = 0.03,
    label_dodge = 0.03,
    ...,
    axis.linewidth = sync(),
    axis.linetype = sync(),
    axis.colour = sync(),
    axis.color = NULL,
    axis.alpha = sync(),
    label.size = sync(),
    label.angle = 0,
    label.hjust = sync(),
    label.vjust = sync(),
    label.family = sync(),
    label.fontface = sync(),
    label.colour = sync(),
    label.color = NULL,
    label.alpha = sync(),
    tick.linewidth = 0.25,
    tick.linetype = "solid",
    tick.colour = sync(),
    tick.color = NULL,
    tick.alpha = sync(),
    text.size = 2.6,
```

```
  text.angle = 0,
  text.hjust = sync(),
  text.vjust = sync(),
  text.family = sync(),
  text.fontface = sync(),
  text.colour = sync(),
  text.color = NULL,
  text.alpha = sync(),
  parse = FALSE,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_rows_interpolation(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  new_data = NULL,
  type = c("centroid", "sequence"),
  arrow = default_arrow,
  ...,
  point.fill = NA,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_cols_interpolation(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  new_data = NULL,
  type = c("centroid", "sequence"),
  arrow = default_arrow,
  ...,
  point.fill = NA,
  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 to 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"`.
- For more information and other ways to specify the stat, see the layer stat documentation.

`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"`.
- For more information and other ways to specify the position, see the layer position documentation.

`...` Additional arguments passed to `ggplot2::layer()`.

`na.rm` Passed to `ggplot2::layer()`.

`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. `annotation_borders()`.

`arrow` Arrow specification, 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).

`linemitre` Line mitre limit (number greater than 1).

`rule` Either `"evenodd"` or `"winding"`. If polygons with holes are being drawn (using the `subgroup` aesthetic) this argument defines how the hole coordinates are interpreted. See the examples in `grid::pathGrob()` for an explanation.

`bins` Number of contour bins. Overridden by `breaks`.

`binwidth` The width of the contour bins. Overridden by `bins`.

`breaks` One of:

- Numeric vector to set the contour breaks
- A function that takes the range of the data and binwidth as input and returns breaks as output. A function can be created from a formula (e.g. ~ fullseq(.x, .y)).

Overrides `binwidth` and `bins`. By default, this is a vector of length ten with `pretty()` breaks.

`contour_var` Character string identifying the variable to contour by. Can be one of `"density"`, `"ndensity"`, or `"count"`. See the section on computed variables for details.

`parse` If `TRUE`, the labels will be parsed into expressions and displayed as described in `?plotmath`.

`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"`).

`label.padding` Amount of padding around label. Defaults to 0.25 lines.

`label.r` Radius of rounded corners. Defaults to 0.15 lines.

`label.size` **[Deprecated]** Replaced by the `linewidth` aesthetic. Size of label border, in mm.

`border.colour`, `border.color`
Colour of label border. When `NULL` (default), the `colour` aesthetic determines the colour of the label border. `border.color` is an alias for `border.colour`.

`text.colour`, `text.color`
Colour of the text. When `NULL` (default), the `colour` aesthetic determines the colour of the text. `text.color` is an alias for `text.colour`.

`box.padding` Amount of padding around bounding box, as unit or number. Defaults to 0.25. (Default unit is lines, but other units can be specified by passing `unit(x, "units")`).

`point.padding` Amount of padding around labeled point, as unit or number. Defaults to 0. (Default unit is lines, but other units can be specified by passing `unit(x, "units")`).

`min.segment.length`
Skip drawing segments shorter than this, as unit or number. Defaults to 0.5. (Default unit is lines, but other units can be specified by passing `unit(x, "units")`).

`force` Force of repulsion between overlapping text labels. Defaults to 1.

force_pull Force of attraction between a text label and its corresponding data point. Defaults to 1.

max.time Maximum number of seconds to try to resolve overlaps. Defaults to 0.5.

max.iter Maximum number of iterations to try to resolve overlaps. Defaults to 10000.

max.overlaps Exclude text labels when they overlap too many other things. For each text label, we count how many other text labels or other data points it overlaps, and exclude the text label if it has too many overlaps. Defaults to 10.

nudge_x, nudge_y
Horizontal and vertical adjustments to nudge the starting position of each text label. The units for nudge_x and nudge_y are the same as for the data units on the x-axis and y-axis.

xlim, ylim Limits for the x and y axes. Text labels will be constrained to these limits. By default, text labels are constrained to the entire plot area.

direction direction of stairs: 'vh' for vertical then horizontal, 'hv' for horizontal then vertical, or 'mid' for step half-way between adjacent x-values.

seed Random seed passed to set.seed. Defaults to NA, which means that set.seed will not be called.

verbose If TRUE, some diagnostics of the repel algorithm are printed

axis_labels, axis_ticks, axis_text
Logical; whether to include labels, tick marks, and text value marks along the axes.

by, num Intervals between elements or number of elements; specify only one.

tick_length Numeric; the length of the tick marks, as a proportion of the minimum of the plot width and height.

text_dodge Numeric; the orthogonal distance of tick mark text from the axis, as a proportion of the minimum of the plot width and height.

label_dodge Numeric; the orthogonal distance of the axis label from the axis, as a proportion of the minimum of the plot width and height.

label_placement
Character; how to place the labels along the axes. Matched to "positive" (the default; at the increasing end of the axis), "negative" (at the decreasing end), "peripheral" (at the end farther from the origin).

axis.linewidth, axis.linetype, axis.colour, axis.color, axis.alpha
Default aesthetics for axes. Set to NULL to inherit from the data's aesthetics.

label.colour, label.color, label.alpha
Default aesthetics for labels. Set to NULL to inherit from the data's aesthetics.

tick.linewidth, tick.linetype, tick.colour, tick.color, tick.alpha
Default aesthetics for tick marks. Set to NULL to inherit from the data's aesthetics.

isoline_text Logical; whether to include text value marks along the isolines.

vector_labels Logical; whether to include labels radiating outward from the vectors.

outlier_points Logical; whether to plot outlier markers. Defaults to ! outlier_labels.

outlier_labels Logical; whether to plot outlier labels. Defaults to FALSE.

`bag.linetype`, `bag.linewidth`, `bag.colour`, `bag.color`, `bag.fill`, `bag.alpha`
: Default aesthetics for bags. Set to `sync()` to inherit from the data's aesthetics or to `NULL` to use the data's aesthetics.

`median.shape`, `median.stroke`, `median.size`, `median.colour`, `median.color`, `median.fill`, `median.alpha`
: Default aesthetics for medians. Set to `sync()` to inherit from the data's aesthetics or to `NULL` to use the data's aesthetics.

`fence.linetype`, `fence.linewidth`, `fence.colour`, `fence.color`, `fence.fill`, `fence.alpha`
: Default aesthetics for fences. Set to `sync()` to inherit from the data's aesthetics or to `NULL` to use the data's aesthetics.

`outlier.shape`, `outlier.stroke`, `outlier.size`, `outlier.colour`, `outlier.color`, `outlier.fill`, `outlier.alpha`
: Default aesthetics for outliers. Set to `sync()` to inherit from the data's aesthetics or to `NULL` to use the data's aesthetics.

`snap_rule`
: Logical; whether to snap rule segments to grid values.

`new_data`
: A list (best structured as a data.frame) of row (`geom_cols_interpolation()`) or column (`geom_rows_interpolation()`) values to interpolate.

`type`
: Character value matched to `"centroid"` or `"sequence"`; the type of operations used to visualize interpolation.

`point.fill`
: Default aesthetics for markers. Set to NULL to inherit from the data's aesthetics.

Value

A ggproto layer.

See Also

Other biplot layers: `biplot-stats`, `stat_rows()`

Examples

```
# compute log-ratio analysis of Freestone primary class composition measurements
glass %>%
  ordinate(cols = c(SiO2, Al2O3, CaO, FeO, MgO),
           model = lra, compositional = TRUE) %>%
  confer_inertia("rows") %>%
  print() -> glass_lra
# row-principal biplot with ordinate-wise standard deviations
glass_lra %>%
  ggbiplot(aes(color = Site), sec.axes = "cols") +
  theme_biplot() +
  scale_color_brewer(type = "qual", palette = 6) +
  geom_cols_text(stat = "chull", aes(label = name), color = "#444444") +
  geom_rows_lineranges(fun.data = mean_sdl, linewidth = .75) +
  geom_rows_point(alpha = .5) +
  ggtitle(
    "Row-principal LRA biplot of Freestone glass measurements",
    "Ranges 2 sample standard deviations from centroids"
  )
```

```
# principal components analysis of glass composition measurements
glass[, c(5L, 7L, 8L, 10L, 11L)] %>%
  princomp(cor = TRUE) %>%
  as_tbl_ord() %>%
  cbind_rows(site = glass$Site, form = glass$Form) %>%
  augment_ord() %>%
  print() -> glass_pca
# note that column standard coordinates are unit vectors
rowSums(get_cols(glass_pca) ^ 2)
# plot column standard coordinates with a unit circle underlaid
glass_pca %>%
  ggbiplot(aes(label = name), sec.axes = "cols") +
  theme_biplot() +
  geom_rows_point(aes(color = site, shape = form), elements = "score") +
  geom_unit_circle(alpha = .5, scale.factor = 3) +
  geom_cols_vector()
```

`biplot-stats` *Convenience stats for row and column matrix factors*

Description

These statistical transformations (stats) adapt conventional **ggplot2** stats to one or the other matrix factor of a tbl_ord, in lieu of `stat_rows()` or `stat_cols()`. They accept the same parameters as their corresponding conventional stats.

Usage

```
stat_rows_density_2d(
  mapping = NULL,
  data = NULL,
  geom = "density_2d",
  position = "identity",
  ...,
  contour = TRUE,
  contour_var = "density",
  h = NULL,
  adjust = c(1, 1),
  n = 100,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_cols_density_2d(
  mapping = NULL,
  data = NULL,
```

```
  geom = "density_2d",
  position = "identity",
  ...,
  contour = TRUE,
  contour_var = "density",
  h = NULL,
  adjust = c(1, 1),
  n = 100,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_rows_density_2d_filled(
  mapping = NULL,
  data = NULL,
  geom = "density_2d_filled",
  position = "identity",
  ...,
  contour = TRUE,
  contour_var = "density",
  h = NULL,
  adjust = c(1, 1),
  n = 100,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_cols_density_2d_filled(
  mapping = NULL,
  data = NULL,
  geom = "density_2d_filled",
  position = "identity",
  ...,
  contour = TRUE,
  contour_var = "density",
  h = NULL,
  adjust = c(1, 1),
  n = 100,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_rows_ellipse(
  mapping = NULL,
  data = NULL,
```

```
  geom = "path",
  position = "identity",
  ...,
  type = "t",
  level = 0.95,
  segments = 51,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_cols_ellipse(
  mapping = NULL,
  data = NULL,
  geom = "path",
  position = "identity",
  ...,
  type = "t",
  level = 0.95,
  segments = 51,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_rows_center(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  ...,
  fun.data = NULL,
  fun = NULL,
  fun.center = NULL,
  fun.min = NULL,
  fun.max = NULL,
  fun.ord = NULL,
  fun.args = list()
)

stat_cols_center(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  show.legend = NA,
```

```
  inherit.aes = TRUE,
  ...,
  fun.data = NULL,
  fun = NULL,
  fun.center = NULL,
  fun.min = NULL,
  fun.max = NULL,
  fun.ord = NULL,
  fun.args = list()
)

stat_rows_star(
  mapping = NULL,
  data = NULL,
  geom = "segment",
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  ...,
  fun.data = NULL,
  fun = NULL,
  fun.center = NULL,
  fun.ord = NULL,
  fun.args = list()
)

stat_cols_star(
  mapping = NULL,
  data = NULL,
  geom = "segment",
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  ...,
  fun.data = NULL,
  fun = NULL,
  fun.center = NULL,
  fun.ord = NULL,
  fun.args = list()
)

stat_rows_chull(
  mapping = NULL,
  data = NULL,
  geom = "polygon",
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
```

```
  ...
)

stat_cols_chull(
  mapping = NULL,
  data = NULL,
  geom = "polygon",
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_rows_peel(
  mapping = NULL,
  data = NULL,
  geom = "polygon",
  position = "identity",
  num = NULL,
  by = 1L,
  breaks = c(0.5),
  cut = c("above", "below"),
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_cols_peel(
  mapping = NULL,
  data = NULL,
  geom = "polygon",
  position = "identity",
  num = NULL,
  by = 1L,
  breaks = c(0.5),
  cut = c("above", "below"),
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_rows_cone(
  mapping = NULL,
  data = NULL,
  geom = "path",
  position = "identity",
  origin = FALSE,
  show.legend = NA,
```

```
  inherit.aes = TRUE,
  ...
)

stat_cols_cone(
  mapping = NULL,
  data = NULL,
  geom = "path",
  position = "identity",
  origin = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_rows_depth(
  mapping = NULL,
  data = NULL,
  geom = "contour",
  position = "identity",
  contour = TRUE,
  contour_var = "depth",
  notion = "zonoid",
  notion_params = list(),
  n = 100L,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_cols_depth(
  mapping = NULL,
  data = NULL,
  geom = "contour",
  position = "identity",
  contour = TRUE,
  contour_var = "depth",
  notion = "zonoid",
  notion_params = list(),
  n = 100L,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_rows_depth_filled(
  mapping = NULL,
  data = NULL,
```

```
  geom = "contour_filled",
  position = "identity",
  contour = TRUE,
  contour_var = "depth",
  notion = "zonoid",
  notion_params = list(),
  n = 100L,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_cols_depth_filled(
  mapping = NULL,
  data = NULL,
  geom = "contour_filled",
  position = "identity",
  contour = TRUE,
  contour_var = "depth",
  notion = "zonoid",
  notion_params = list(),
  n = 100L,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_rows_scale(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  ...,
  mult = 1
)

stat_cols_scale(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  ...,
  mult = 1
)
```

```
stat_rows_spantree(
  mapping = NULL,
  data = NULL,
  geom = "segment",
  position = "identity",
  engine = "mlpack",
  method = "euclidean",
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_cols_spantree(
  mapping = NULL,
  data = NULL,
  geom = "segment",
  position = "identity",
  engine = "mlpack",
  method = "euclidean",
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_rows_bagplot(
  mapping = NULL,
  data = NULL,
  geom = "bagplot",
  position = "identity",
  fraction = 0.5,
  coef = 3,
  median = TRUE,
  fence = TRUE,
  outliers = TRUE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_cols_bagplot(
  mapping = NULL,
  data = NULL,
  geom = "bagplot",
  position = "identity",
  fraction = 0.5,
  coef = 3,
  median = TRUE,
```

```
  fence = TRUE,
  outliers = TRUE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

stat_rows_rule(
  mapping = NULL,
  data = NULL,
  geom = "rule",
  position = "identity",
  fun.lower = "minpp",
  fun.upper = "maxpp",
  fun.offset = "minabspp",
  fun.args = list(),
  axis.type = c("interpolative", "predictive"),
  referent = NULL,
  show.legend = NA,
  inherit.aes = TRUE,
  ref_subset = NULL,
  ref_elements = "active",
  ...
)

stat_cols_rule(
  mapping = NULL,
  data = NULL,
  geom = "rule",
  position = "identity",
  fun.lower = "minpp",
  fun.upper = "maxpp",
  fun.offset = "minabspp",
  fun.args = list(),
  axis.type = c("interpolative", "predictive"),
  referent = NULL,
  show.legend = NA,
  inherit.aes = TRUE,
  ref_subset = NULL,
  ref_elements = "active",
  ...
)

stat_rows_projection(
  mapping = NULL,
  data = NULL,
  geom = "segment",
  position = "identity",
```

```
  referent = NULL,
  ref_subset = NULL,
  ref_elements = "active",
  ...,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_cols_projection(
  mapping = NULL,
  data = NULL,
  geom = "segment",
  position = "identity",
  referent = NULL,
  ref_subset = NULL,
  ref_elements = "active",
  ...,
  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)).
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". • For more information and other ways to specify the geom, see the layer geom documentation.
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"`.
- For more information and other ways to specify the position, see the layer position documentation.

`...` Additional arguments passed to `ggplot2::layer()`.

`contour` If `TRUE`, contour the results of the 2d density estimation.

`contour_var` Character string identifying the variable to contour by. Can be one of `"density"`, `"ndensity"`, or `"count"`. See the section on computed variables for details.

`h` Bandwidth (vector of length two). If `NULL`, estimated using `MASS::bandwidth.nrd()`.

`adjust` A multiplicative bandwidth adjustment to be used if 'h' is 'NULL'. This makes it possible to adjust the bandwidth while still using the a bandwidth estimator. For example, `adjust = 1/2` means use half of the default bandwidth.

`n` Number of grid points in each direction.

`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. `annotation_borders()`.

`type` The type of ellipse. The default `"t"` assumes a multivariate t-distribution, and `"norm"` assumes a multivariate normal distribution. `"euclid"` draws a circle with the radius equal to `level`, representing the euclidean distance from the center. This ellipse probably won't appear circular unless `coord_fixed()` is applied.

`level` The level at which to draw an ellipse, or, if `type="euclid"`, the radius of the circle to be drawn.

`segments` The number of segments to be used in drawing the ellipse.

`fun.data` A function that is given the complete data and should return a data frame with variables `ymin`, `y`, and `ymax`.

`fun.center` Deprecated alias to `fun`.

`fun.min`, `fun`, `fun.max`
Alternatively, supply three individual functions that are each passed a vector of values and should return a single number.

`fun.ord` Alternatively to the `ggplot2::stat_summary_bin()` parameters, supply a summary function that takes a matrix as input and returns a named column summary vector. Overridden by `fun.data` and `fun`, cannot be used together with `fun.min` and `fun.max`.

fun.args	Optional additional arguments passed on to the functions.
num	A positive integer; the number of hulls to peel. Pass Inf for all hulls.
by	A positive integer; with what frequency to include consecutive hulls, pairs with num.
breaks	A numeric vector of fractions (between 0 and 1) of the data to contain in each hull; overridden by num.
cut	Character; one of "above" and "below", indicating whether each hull should contain at least or at most breaks of the data, respectively.
origin	Logical; whether to include the origin with the transformed data. Defaults to FALSE.
notion	Character; the name of the depth function (passed to ddalpha::depth.()).
notion_params	List of additional parameters passed via ... to ddalpha::depth.().
mult	Numeric value used to scale the coordinates.
engine	A single character string specifying the package implementation to use; "mlpack", "vegan", or "ade4".
method	Passed to stats::dist() if engine is "vegan" or "ade4", ignored if "mlpack".
fraction	Fraction of the data to include in the bag.
coef	Scale factor of the fence relative to the bag.
median, fence, outliers	Logical indicators whether to include median, fence, and outliers in the composite output.
fun.lower, fun.upper, fun.offset	Functions used to determine the limits of the rules and the translations of the axes from the projections of referent onto the axes and onto their normal vectors.
referent	The reference data set, admitting the same 3 options as data; see Details.
ref_elements, ref_subset	Analogues of elements and subset applied to referent.

Value

A ggproto layer.

Ordination aesthetics

This statistical transformation is compatible with the convenience function ord_aes().

Some transformations (e.g. stat_center()) commute with projection to the lower (1 or 2)-dimensional biplot space. If they detect aesthetics of the form ..coord[0-9]+, then ..coord1 and ..coord2 are converted to x and y while any remaining are ignored.

Other transformations (e.g. stat_spantree()) yield different results in a lower-dimensional biplot when they are computed before versus after projection. If the stat layer detects these aesthetics, then the transformation is performed before projection, and the results in the first two dimensions are returned as x and y.

A small number of transformations (stat_rule()) are incompatible with ordination aesthetics but will accept ord_aes() without warning.

See Also

Other biplot layers: biplot-geoms, stat_rows()

Examples

```
iris_pca <- ordinate(iris, prcomp, cols = seq(4), scale. = TRUE)
# NB: Non-standard aesthetics are handled as in version > 3.5.1; see:
# https://github.com/tidyverse/ggplot2/issues/6191
# This prevents `scale_color_discrete(aesthetics = ...)` from synching them.
ggbiplot(iris_pca) +
  stat_rows_bagplot(
    aes(fill = Species),
    median_gp = list(color = sync()),
    fence_gp = list(linewidth = 0.25),
    outlier_gp = list(shape = "asterisk")
  ) +
  scale_color_discrete(name = "Species", aesthetics = c("color", "fill")) +
  geom_cols_vector(aes(label = name))
ggbiplot(iris_pca) +
  stat_rows_bagplot(
    aes(fill = Species, color = Species),
    median_gp = list(color = sync()),
    fence_gp = list(linewidth = 0.25),
    outlier_gp = list(shape = "asterisk")
  ) +
  geom_cols_vector(aes(label = name))

# scaled PCA of Anderson iris measurements
iris[, -5] %>%
  princomp(cor = TRUE) %>%
  as_tbl_ord() %>%
  mutate_rows(species = iris$Species) %>%
  print() -> iris_pca
# row-principal biplot with depth median-based stars
iris_pca %>%
  ggbiplot(aes(color = species)) +
  theme_bw() +
  scale_color_brewer(type = "qual", palette = 2) +
  stat_rows_star(alpha = .5, fun.ord = "depth_median") +
  geom_rows_point(alpha = .5) +
  stat_rows_center(fun.ord = "depth_median", size = 4, shape = 1L) +
  ggtitle(
    "Row-principal PCA biplot of Anderson iris measurements",
    "Segments connect each observation to its within-species depth median"
  )

# correspondence analysis of combined female and male hair and eye color data
HairEyeColor %>%
  rowSums(dims = 2L) %>%
  MASS::corresp(nf = 2L) %>%
  as_tbl_ord() %>%
  augment_ord() %>%
```

```
  print() -> hec_ca
# inertia across artificial coordinates (all singular values < 1)
get_inertia(hec_ca)
# in row-principal biplot, row coordinates are weighted averages of columns
# (and vice-versa)
hec_ca %>%
  confer_inertia("rows") %>%
  ggbiplot(aes(color = .matrix, fill = .matrix, shape = .matrix)) +
  theme_bw() +
  stat_cols_chull(alpha = .1) +
  geom_cols_point() +
  geom_rows_point() +
  ggtitle("Row-principal CA of hair & eye color")

# centered principal components analysis of U.S. personal expenditure data
USPersonalExpenditure %>%
  prcomp() %>%
  as_tbl_ord() %>%
  augment_ord() %>%
  # allow radiating text to exceed plotting window
  ggbiplot(aes(label = name), clip = "off",
           sec.axes = "cols", scale.factor = 50) +
  geom_rows_label(size = 3) +
  # omit labels in the conical hull without the origin
  geom_cols_vector(vector_labels = FALSE) +
  stat_cols_cone(linetype = "dotted") +
  geom_cols_vector(stat = "cone", vector_labels = TRUE, color = "transparent") +
  ggtitle(
    "U.S. Personal Expenditure data, 1940-1960",
    "Row-principal biplot of centered PCA"
  )
# compute row-principal components of scaled iris measurements
iris[, -5] %>%
  prcomp(scale = TRUE) %>%
  as_tbl_ord() %>%
  mutate_rows(species = iris$Species) %>%
  print() -> iris_pca
# row-principal biplot with centroids and confidence elliptical disks
iris_pca %>%
  ggbiplot(aes(color = species)) +
  theme_bw() +
  geom_rows_point() +
  geom_polygon(
    aes(fill = species),
    color = NA, alpha = .25, stat = "rows_ellipse"
  ) +
  geom_cols_vector(color = "#444444") +
  scale_color_brewer(
    type = "qual", palette = 2,
    aesthetics = c("color", "fill")
  ) +
  ggtitle(
    "Row-principal PCA biplot of Anderson iris measurements",
```

```
    "Overlaid with 95% confidence disks"
  )

# hull peeling with breaks below
judge_pca <- ordinate(USJudgeRatings, princomp, cols = -c(1, 12))
ggbiplot(judge_pca) +
  geom_cols_axis(axis.type = "predictive") +
  geom_rows_point(elements = "score") +
  stat_rows_peel(
    aes(alpha = after_stat(hull)), color = "black", elements = "score",
    breaks = c(.9, .5, .1), cut = "below"
  )

# hull peeling by groups
iris_pca <- ordinate(iris, cols = 1:4, model = prcomp)
ggbiplot(iris_pca) +
  geom_rows_point(aes(color = Species), shape = "circle open") +
  stat_rows_peel(
    aes(fill = Species, alpha = after_stat(hull)),
    num = 3
  )

# unscaled PCA
iris_pca <- ordinate(iris, cols = 1:4, model = prcomp)
# biplot canvas
iris_biplot <-
  iris_pca %>%
  ggbiplot(aes(color = Species, label = name)) +
  geom_rows_point() +
  geom_cols_axis(aes(center = center), axis.type = "predictive")
# print select cases
top_cases <- c(1, 51, 101)
iris[top_cases, ]
# subset variables
length_vars <- c(1, 3)
iris[, length_vars] %>%
  aggregate(by = iris[, "Species", drop = FALSE], FUN = mean)

# project all cases onto all axes
iris_biplot + stat_rows_projection()
# project all cases onto select axes
iris_biplot + stat_rows_projection(ref_subset = length_vars)

# project select cases onto all axes
iris_biplot + stat_rows_projection(subset = top_cases)
# project select cases onto select axes
iris_biplot + stat_rows_projection(subset = top_cases, ref_subset = length_vars)

# project select cases onto manually provided axes
iris_cols <- as.data.frame(get_cols(iris_pca))[c(1, 2), ]
iris_biplot + stat_rows_projection(subset = top_cases, referent = iris_cols)

# project selected cases onto selected axes in full-dimensional space
```

```
iris_pca %>%
  ggbiplot(ord_aes(iris_pca, color = Species, label = name)) +
  geom_rows_point() +
  geom_cols_axis(aes(center = center), axis.type = "predictive") +
  stat_rows_projection(subset = top_cases, ref_subset = length_vars)

# default (standardized) linear discriminant analysis
glass_lda <- MASS::lda(Site ~ SiO2 + Al2O3 + FeO + MgO + CaO, glass)
# bestow 'tbl_ord' class & augment observation, centroid, and variable fields
as_tbl_ord(glass_lda) %>%
  augment_ord() %>%
  print() -> glass_lda
# row-standard biplot
glass_lda %>%
  confer_inertia(1) %>%
  ggbiplot(aes(shape = grouping)) +
  theme_bw() + theme_biplot() +
  geom_rows_point(size = 4) +
  geom_rows_point(elements = "score") +
  stat_cols_rule(
    aes(label = name), color = "#888888", num = 8L,
    ref_elements = "score", fun.offset = function(x) minabspp(x, p = .1),
    text.size = 2.5, label_dodge = .04
  ) +
  scale_shape_manual(values = c(2L, 3L, 0L, 5L)) +
  ggtitle(
    "LDA of Freestone glass measurements",
    "Row-standard biplot of standardized LDA"
  )
# contribution LDA of sites on measurements
glass_lda <-
  lda_ord(Site ~ SiO2 + Al2O3 + FeO + MgO + CaO, glass,
          axes.scale = "contribution")
# bestow 'tbl_ord' class & augment observation, centroid, and variable fields
as_tbl_ord(glass_lda) %>%
  augment_ord() %>%
  print() -> glass_lda
# symmetric biplot
glass_lda %>%
  confer_inertia(.5) %>%
  ggbiplot(aes(shape = grouping)) +
  theme_bw() + theme_biplot() +
  geom_rows_point() +
  stat_rows_density_2d(elements = "score", alpha = .5, color = "#444444") +
  stat_cols_rule(
    aes(label = name), geom = "axis", color = "#888888", num = 8L,
    ref_elements = "active", fun.offset = function(x) minabspp(x, p = .1),
    label_dodge = 0.04, text.size = 2.5, text_dodge = .025
  ) +
  scale_shape_manual(values = c(16L, 17L, 15L, 18L)) +
  ggtitle(
    "LDA of Freestone glass measurements",
    "Symmetric biplot of contribution LDA"
```

```
  )

## Not run:
# classical multidimensional scaling of road distances between European cities
euro_mds <- ordinate(eurodist, cmdscale_ord, k = 11)
# monoplot of city locations
euro_plot <- euro_mds %>%
  negate_ord("PCo2") %>%
  ggbiplot() +
  geom_cols_text(aes(label = name), size = 3)
print(euro_plot)
# biplot with minimal spanning tree based on plotting window distances
euro_plot +
  stat_cols_spantree(
    engine = "mlpack",
    alpha = .5, linetype = "dotted"
  )
# biplot with minimal spanning tree based on full-dimensional distances
euro_plot +
  stat_cols_spantree(
    ord_aes(euro_mds), engine = "mlpack",
    alpha = .5, linetype = "dotted"
  )

## End(Not run)
```

`conference` *Confer inertia to factors of a 'tbl_ord' object*

Description

Re-distribute inertia between rows and columns in an ordination.

Usage

```
recover_conference(x)

## Default S3 method:
recover_conference(x)

get_conference(x)

revert_conference(x)

confer_inertia(x, p)
```

Arguments

`x`	A tbl_ord.

p — Numeric vector of length 1 or 2. If length 1, the proportion of the inertia assigned to the cases, with the remainder 1 - p assigned to the variables. If length 2, the proportions of the inertia assigned to the cases and to the variables, respectively.

Details

The *inertia* of a singular value decomposition $X = UDV'$ consists in the squares of the singular values (the diagonal elements of D), and represents the variance, likened to the physical inertia, in the directions of the orthogonal singular vectors (the columns of U or of V). Biplots superimpose the projections of the rows and the columns of X onto these coordinate vectors, scaled by some proportion of the total inertia: UD^p and VD^q. A biplot is *balanced* if $p + q = 1$. Read Orlov (2013) for more on conferring inertia in PCA.

`recover_conference()`, like the other recoverers, is an S3 method that is exported for convenience but not intended to be used directly.

Note: In case the `"inertia"` *attribute is a rectangular matrix, one may only be able to confer it entirely to the cases (*`p = 1`*) or entirely to the variables (*`p = 0`*).*

Value

`recover_conference()` returns the (statically implemented) distribution of inertia between the rows and the columns as stored in the model. `confer_inertia()` returns a tbl_ord with a specified distribution of inertia but the wrapped model unchanged. `get_conference()` returns the distribution currently conferred.

References

Orlov K (2013) *Answer to* "Algebra of LDA. Fisher discrimination power of a variable and Linear Discriminant Analysis". CrossValidated, accessed 2019-07-26. https://stats.stackexchange.com/a/83114/68743

See Also

Other generic recoverers: `augmentation`, `recoverers`, `supplementation`

Examples

```
# illustrative ordination: correspondence analysis of hair & eye data
haireye_ca <- ordinate(
  as.data.frame(rowSums(HairEyeColor, dims = 2L)),
  cols = everything(), model = MASS::corresp
)
print(haireye_ca)

# check distribution of inertia
get_conference(haireye_ca)
# confer inertia to rows, then to columns
confer_inertia(haireye_ca, "rows")
confer_inertia(haireye_ca, "columns")
# confer inertia symmetrically
(haireye_ca <- confer_inertia(haireye_ca, "symmetric"))
```

```
# check redistributed inertia
get_conference(haireye_ca)
# restore default distribution of inertia
revert_conference(haireye_ca)
```

---

coord_scaffold *Convenience coordinate system for scaffolding axes*

Description

2- (and 3-) dimensional biplots require that coordinates lie on the same scale but may additionally benefit from a square plotting window. While `CoordRect` provides control of coordinate and window aspect ratios, the convenience `CoordScaffold` system also fixes the coordinate aspect ratio at 1 and gives the user control only of the plotting window.

Usage

```
coord_scaffold(
  window_ratio = 1,
  xlim = NULL,
  ylim = NULL,
  expand = TRUE,
  clip = "on"
)
```

Arguments

`window_ratio`	aspect ratio of plotting window

Examples

```
# resize the plot to see that the specified aspect ratio is maintained
p <- ggplot(mtcars, aes(mpg, hp/10)) + geom_point()
p + coord_scaffold()
p + coord_scaffold(window_ratio = 2)

# prevent rescaling in response to `theme()` aspect ratio
p <- ggplot(mtcars, aes(mpg, hp/5)) + geom_point()
p + coord_equal() + theme(aspect.ratio = 1)
p + coord_scaffold() + theme(aspect.ratio = 1)

# NB: `theme(aspect.ratio = )` overrides `Coord*$aspect`:
p + coord_fixed(ratio = 1) + theme(aspect.ratio = 1)
p + coord_scaffold(window_ratio = 2) + theme(aspect.ratio = 1)
```

dplyr-verbs **dplyr** *verbs for tbl_ord factors*

Description

These functions adapt dplyr verbs to the factors of a tbl_ord.

The raw verbs are not defined for tbl_ords; instead, each verb has two analogues, corresponding to the two matrix factors. They each rely on a common workhorse function, which takes the composition of the **dplyr** verb with `annotation_*`, applied to the factor, removes any variables corresponding to coordinates or already annotated, and only then assigns it as the new `"*_annotation"` attribute of `.data` (see annotation). Note that these functions are not generics and so cannot be extended to other classes.

Usage

```
pull_factor(.data, var = -1, .matrix)

pull_rows(.data, var = -1)

pull_cols(.data, var = -1)

rename_rows(.data, ...)

rename_cols(.data, ...)

select_rows(.data, ...)

select_cols(.data, ...)

mutate_rows(.data, ...)

mutate_cols(.data, ...)

transmute_rows(.data, ...)

transmute_cols(.data, ...)

cbind_rows(.data, ..., elements = "all")

cbind_cols(.data, ..., elements = "all")

left_join_rows(.data, ...)

left_join_cols(.data, ...)
```

Arguments

.data	An object of class 'tbl_ord'.
var	A variable specified as in dplyr::pull().
.matrix	A character string partially matched (lowercase) to several indicators for one or both matrices in a matrix decomposition used for ordination. The standard values are "rows", "cols", and "dims" (for both).
...	Comma-separated unquoted expressions as in, e.g., dplyr::select().
elements	Character vector; which elements of each factor for which to render graphical elements. One of "active" (the default) or any supplementary element type defined by the specific class methods (e.g. "score" for 'factanal', 'lda_ord', and 'cancord_ord' and "intraset" and "interset" for 'cancor_ord'), via partial matching.

Value

A tbl_ord; the wrapped model is unchanged.

Examples

```
# illustrative ordination: LDA of iris data
(iris_lda <- ordinate(iris, cols = 1:4, lda_ord, grouping = iris$Species))

# extract a coordinate or annotation
head(pull_rows(iris_lda, Species))
pull_cols(iris_lda, LD2)

# rename an annotation
rename_cols(iris_lda, species = name)

# select annotations
select_rows(iris_lda, species = name, .element)

# create, modify, and delete annotations
mutate_cols(iris_lda, vec.length = sqrt(LD1^2 + LD2^2))
transmute_cols(iris_lda, vec.length = sqrt(LD1^2 + LD2^2))

# bind data frames of annotations
iris_medians <-
  stats::aggregate(iris[, 1:4], median, by = iris[, 5, drop = FALSE])
# TODO: Requirement of `.elements` for matching is fragile.
iris_lda %>%
  # retain '.element' in order to match by `elements`
  select_rows(.element) %>%
  cbind_rows(iris_medians, elements = "active")
iris_lda %>%
  select_rows(name, Species) %>%
  left_join_rows(iris_medians, by = c("name" = "Species"))
```

draw-key *Biplot key drawing functions*

Description

These key drawing functions supplement those built into **ggplot2** for producing legends suitable to biplots.

Usage

```
draw_key_line(data, params, size)

draw_key_crosslines(data, params, size)

draw_key_crosspoint(data, params, size)
```

Arguments

data	A single row data frame containing the scaled aesthetics to display in this key
params	A list of additional parameters supplied to the geom.
size	Width and height of key in mm.

Details

`draw_key_line()` is a horizontal counterpart to `ggplot2::draw_key_vline()`. `draw_key_crosslines()` superimposes these two keys, and `draw_key_crosspoint()` additionally superimposes an oversized `ggplot2::draw_key_point()`.

Value

A grid grob.

See Also

ggplot2::draw_key for key glyphs installed with **ggplot2**.

Examples

```
# scaled PCA of Anderson iris data with ranges and confidence intervals
iris[, -5] %>%
  prcomp(scale = TRUE) %>%
  as_tbl_ord() %>%
  confer_inertia(1) %>%
  augment_ord() %>%
  mutate_rows(species = iris$Species) %>%
  ggbiplot(aes(color = species)) +
  theme_bw() +
  scale_color_brewer(type = "qual", palette = 2) +
```

```
geom_rows_lineranges(fun.data = mean_sdl, linewidth = .75) +
geom_rows_density_2d(contour = TRUE, alpha = .5) +
geom_cols_vector(aes(label = name), color = "#444444", size = 3) +
ggtitle(
  "Row-principal PCA biplot of Anderson iris data",
  "Ranges 2 sample standard deviations from centroids"
)
```

`facet_ord` *Arrange biplots of all pairs of ordination coordinates*

Description

Facet biplots using all ordered pairs of scaffolding coordinates in an ordination object.

Usage

```
facet_ord(coords = NULL, scales = NULL, space = NULL)
```

Arguments

`coords`	Coordinates to include, in one of several formats: • `NULL` (default): all coordinates • Integer scalar: number of first coordinates • Integer vector: subset of coordinates • Character scalar: single coordinate name • Character vector: subset of coordinate names
`scales`	A character scalar indicating whether all panels share the same x and y coordinate scales (`"fixed"`) or whether the x and y scales are free to differ between panels (`"free"`). By default, `NULL`. Unlike `ggplot2::facet_grid()`, no x- or y-specific values are available.
`space`	A character scalar indicating whether all panels are the same size (`"fixed"`) or whether each panel is sized proportionally to the ranges of its coordinate scales (`"free"`). By default, `NULL`. Unlike `facet_grid()`, no x- or y-specific values are available.

Details

`facet_ord()` is intended to be added to a plot produced by `ggbiplot()`, which stores the recovered ordination coordinates in the fortified data of each layer. Adding `facet_ord()` replaces the x and y mappings with internal panel-specific columns, so that the coordinates mapped in the original call are used only to set the coordinate system.

As in `ggplot2::facet_grid()`, the `scales` and `space` parameters control the scales and sizes of the panels. Setting either parameter to a value also sets the other to the same value, unless both are set; if neither is set, both default to `"fixed"`. Setting `scales = "fixed"` obtains the same plot regardless of `space`. Pairing `scales = "free"` with `space = "fixed"` warps aspect ratios away from 1 and is discouraged though not warned against.

Value

A FacetOrd ggproto object to be added to a ggbiplot().

See Also

ggbiplot(), ggplot2::facet_grid()

Examples

```
# scaled PCA of Anderson iris measurements
iris[, -5] %>%
  prcomp(scale = TRUE) %>%
  as_tbl_ord() %>%
  confer_inertia(1) %>%
  augment_ord() %>%
  mutate_rows(species = iris$Species) %>%
  print() -> iris_pca

# facet the first three principal components (by default fixed space and scales)
iris_pca %>%
  ggbiplot() +
  facet_ord(coords = 3) +
  geom_rows_point(aes(color = species)) +
  geom_cols_vector(aes(label = name), color = "#444444") +
  ggtitle(
    "PCA biplot of Anderson iris measurements",
    "Faceted pairs with fixed scales and space"
  )

# free space (by default frees the scales)
iris_pca %>%
  ggbiplot() +
  facet_ord(coords = 3, space = "free") +
  geom_rows_point(aes(color = species)) +
  geom_cols_vector(aes(label = name), color = "#444444") +
  ggtitle(
    "PCA biplot of Anderson iris measurements",
    "Faceted pairs with free scales and space"
  )

# free scales, fixed space: panel scales determined by coordinates (discouraged)
iris_pca %>%
  ggbiplot() +
  facet_ord(coords = 3, scales = "free", space = "fixed") +
  geom_rows_point(aes(color = species)) +
  geom_cols_vector(aes(label = name), color = "#444444") +
  ggtitle(
    "PCA biplot of Anderson iris measurements",
    "Faceted pairs with free scales and fixed space"
  )
# correspondence analysis of combined hair and eye color data
haireye <- as.data.frame(rowSums(HairEyeColor, dims = 2L))
```

```
haireye %>%
  ordinate(MASS::corresp, cols = everything(), nf = 3L) %>%
  confer_inertia("symmetric") %>%
  print() -> hec_ca

# facet the first three correspondence coordinates
hec_ca %>%
  ggbiplot() +
  facet_ord(coords = 3) +
  geom_rows_text(aes(label = name), color = "#D55E00", size = 3) +
  geom_cols_text(aes(label = name), color = "#0072B2", size = 3) +
  ggtitle(
    "CA biplot of Snee hair & eye colors",
    "Faceted pairs with fixed scales and space"
  )

# facet specific correspondence coordinates by index
hec_ca %>%
  ggbiplot() +
  facet_ord(coords = c(1, 3)) +
  geom_rows_text(aes(label = name), color = "#D55E00", size = 3) +
  geom_cols_text(aes(label = name), color = "#0072B2", size = 3) +
  ggtitle(
    "CA biplot of Snee hair & eye colors",
    "Faceted pairs with specific coordinates by index"
  )

# facet specific correspondence coordinates by name
hec_ca %>%
  ggbiplot() +
  facet_ord(coords = c("Can1", "Can3")) +
  geom_rows_text(aes(label = name), color = "#D55E00", size = 3) +
  geom_cols_text(aes(label = name), color = "#0072B2", size = 3) +
  ggtitle(
    "CA biplot of Snee hair & eye colors",
    "Faceted pairs with specific coordinates by name"
  )
```

`format` *Format a tbl_ord for printing*

Description

These methods of `base::format()` and `base::print()` render a (usually more) tidy readout of a tbl_ord that is consistent across all original ordination classes.

Usage

```
.by
```

```
## S3 method for class 'tbl_ord'
format(
  x,
  width = NULL,
  ...,
  n = NULL,
  max_extra_cols = NULL,
  max_footer_lines = NULL
)

## S3 method for class 'tbl_ord'
print(
  x,
  width = NULL,
  ...,
  n = NULL,
  max_extra_cols = NULL,
  max_footer_lines = NULL
)
```

Arguments

x	A tbl_ord.
width	Width of text output to generate. This defaults to NULL, which means use the width option.
...	Additional arguments.
n	Number(s) of rows to show from each matrix factor, handled as by tibble::format.tbl(). If length 1, will apply to both matrix factors. To pass NULL to only one factor, be sure to pass as a list, e.g. n = list(6, NULL).
max_extra_cols, max_footer_lines	As in tibble::format.tbl, applied to each matrix factor separately.

Details

The base::format() and base::print() methods for class 'tbl_ord' are adapted from those for class 'tbl_df' and for class 'tbl_graph' from the **tidygraph** package.

NB: The format.tbl_ord() method is tedious but cannot be easily modularized without invoking recoverers, annotation, and augmentation multiple times, thereby significantly reducing performance. It calls upon **pillar** for tbl_df formatting then revises the results per tbl_ord.

Value

The format() method returns a vector of strings that are more elegantly printed by the print() method, which itself returns the tbl_ord invisibly.

Examples

```
iris_pca <- ordinate(iris[1:4], prcomp)
```

```
# single value applies to both factors
print(iris_pca, n = 2)
print(iris_pca, n = 10)

# double values apply to factors in order
print(iris_pca, n = c(6, 2))

# use `list()` to pass `NULL` (for default) to only one factor
print(iris_pca, n = list(2, NULL))
print(iris_pca, n = list(NULL, 2))

# too narrow width for all coordinates
print(iris_pca, width = 22)

iris_lda <- ordinate(iris[1:4], lda_ord, grouping = iris$Species)

# supplementary elements appear below active elements
print(iris_lda)

# too many annotations to print within console width
print(iris_lda, width = 40)

# annotations too wide to print are summarized in footers
print(iris_pca, width = 30)

# cap the number of lines of each factor's footer note
print(iris_pca, width = 30, max_footer_lines = 2)

haireye_ca <- ordinate(
  as.data.frame(rowSums(HairEyeColor, dims = 2L)),
  cols = everything(), model = MASS::corresp, nf = 3
)

# default conference: standard coordinates for both factors
print(haireye_ca)

# column-principal coordinates, very narrow width
print(confer_inertia(haireye_ca, "cols"), width = 18)

# symmetric coordinates
print(confer_inertia(haireye_ca, "symmetric"), max_extra_cols = 1)
```

`geom_interpolation` *Render interpolation of new rows from columns (or vice-versa)*

Description

`geom_interpolation()` renders a geometric construction that interpolates a new data matrix (row or column) element from its entries to its artificial coordinates.

Usage

```
geom_interpolation(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  new_data = NULL,
  type = c("centroid", "sequence"),
  arrow = default_arrow,
  ...,
  point.fill = NA,
  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 to 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". • For more information and other ways to specify the stat, see the layer stat documentation.
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"`.
- For more information and other ways to specify the position, see the layer position documentation.

`new_data`	A list (best structured as a data.frame) of row (`geom_cols_interpolation()`) or column (`geom_rows_interpolation()`) values to interpolate.
`type`	Character value matched to `"centroid"` or `"sequence"`; the type of operations used to visualize interpolation.
`arrow`	Specification for arrows, as created by `grid::arrow()`, or else `NULL` for no arrows.
`...`	Additional arguments passed to `ggplot2::layer()`.
`point.fill`	Default aesthetics for markers. Set to NULL to inherit from the data's aesthetics.
`na.rm`	Passed to `ggplot2::layer()`.
`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. `annotation_borders()`.

Details

Interpolation answers the following question: Given a new data element that might have appeared as a row (respectively, column) in the singular-value-decomposed data matrix, where should we expect the marker for this element to appear in the biplot? The solution is the vector sum of the column (row) units weighted by their values in the new row (column). Gower, Gardner–Lubbe, & le Roux (2011) provide two visualizations of this calculation: a tail-to-head sequence of weighted units (`type = "sequence"`), and a centroid of the weighted units scaled by the number of units (`type = "centroid"`).

WARNING: This layer is appropriate only with axes in standard coordinates (usually `confer_inertia(p = "rows")`) and interpolative calibration, the default `axis.type` of `geom_axis()`.

Biplot layers

`ggbiplot()` uses `ggplot2::fortify()` internally to produce a single data frame with a `.matrix` column distinguishing the subjects (`"rows"`) and variables (`"cols"`). The stat layers `stat_rows()` and `stat_cols()` simply filter the data frame to one of these two.

The geom layers `geom_rows_*()` and `geom_cols_*()` call the corresponding stat in order to render plot elements for the corresponding factor matrix. `geom_dims_*()` selects a default matrix based on common practice, e.g. points for rows and arrows for columns.

Aesthetics

geom_interpolation() requires the custom interpolate aesthetic, which tells the internals which columns of the new_data parameter contain the variables to be used for interpolation. Except in rare cases, new_data should contain the same rows or columns as the ordinated data and interpolate should be set to name (procured by augment_ord()). geom_interpolation() additionally understands the following aesthetics (required aesthetics are in bold):

- alpha
- colour
- linetype
- size
- fill
- shape
- stroke
- center, scale
- group

References

Gower JC, Gardner–Lubbe S, & le Roux NJ (2011) *Understanding Biplots*. Wiley, ISBN: 978-0-470-01255-0. https://www.wiley.com/go/biplots

See Also

Other geom layers: geom_origin()

Examples

```
iris[, -5] %>%
  prcomp(scale = TRUE) %>%
  as_tbl_ord() %>%
  print() -> iris_pca
iris_pca <- mutate_rows(iris_pca, species = iris$Species)
iris_pca <- augment_ord(iris_pca)

# sample of one of each species, with some missing measurements
new_data <- iris[c(42, 61, 110), seq(5, 1), drop = FALSE]
new_data[3L, "Sepal.Width"] <- NA
new_data[1L, "Petal.Length"] <- NA
print(new_data)

# centroid interpolation method
iris_pca %>%
  augment_ord() %>%
  mutate_rows(obs = dplyr::row_number()) %>%
  mutate_cols(measure = name) %>%
  ggbiplot() +
  theme_bw() +
```

```
  scale_color_brewer(type = "qual", palette = 2) +
  geom_origin(marker = "cross", alpha = .5) +
  geom_cols_interpolation(
    aes(center = center, scale = scale, interpolate = name), size = 3,
    new_data = new_data, type = "centroid", alpha = .5
  ) +
  geom_rows_text(aes(label = obs, color = species), alpha = .5, size = 3)

# missing an entire variable
new_data$Petal.Length <- NULL

# sequence interpolation method
iris_pca %>%
  augment_ord() %>%
  mutate_rows(obs = dplyr::row_number()) %>%
  mutate_cols(measure = name) %>%
  ggbiplot() +
  theme_bw() +
  scale_color_brewer(type = "qual", palette = 2) +
  geom_origin(marker = "circle", alpha = .5) +
  geom_cols_interpolation(
    aes(center = center, scale = scale, interpolate = name,
        linetype = measure),
    new_data = new_data, type = "sequence", alpha = .5
  ) +
  geom_rows_text(aes(label = obs, color = species), alpha = .5, size = 3)
```

`geom_origin` *Marker or unit circle at the origin*

Description

`geom_origin()` renders a symbol, either a set of crosshairs or a circle, at the origin. `geom_unit_circle()` renders the unit circle, centered at the origin with radius 1.

Usage

```
geom_origin(
  mapping = NULL,
  data = NULL,
  marker = "crosshairs",
  radius = unit(0.04, "snpc"),
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = FALSE
)

geom_unit_circle(
```

```
  mapping = NULL,
  data = NULL,
  segments = 60,
  scale.factor = 1,
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = FALSE
)
```

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)).
marker	The symbol to be drawn at the origin; matched to "crosshairs" or "circle".
radius	A grid::unit() object that sets the radius of the crosshairs or of the circle.
...	Additional arguments passed to ggplot2::layer().
na.rm	Passed to ggplot2::layer().
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. annotation_borders().
segments	The number of segments to be used in drawing the circle.
scale.factor	The circle radius; should remain at its default value 1 or passed the same value as ggbiplot(). (This is an imperfect fix that may be changed in a future version.)

Value

A ggproto layer.

Biplot layers

ggbiplot() uses ggplot2::fortify() internally to produce a single data frame with a .matrix column distinguishing the subjects ("rows") and variables ("cols"). The stat layers stat_rows() and stat_cols() simply filter the data frame to one of these two.

The geom layers geom_rows_*() and geom_cols_*() call the corresponding stat in order to render plot elements for the corresponding factor matrix. geom_dims_*() selects a default matrix based on common practice, e.g. points for rows and arrows for columns.

Aesthetics

geom_origin() accepts no aesthetics. geom_unit_circle() understands the following aesthetics (none required):

- linetype
- linewidth
- colour
- alpha

See Also

Other geom layers: geom_interpolation()

Examples

```
ggplot() +
  theme_void() +
  geom_origin() +
  geom_point(data = seals, aes(delta_long, delta_lat), alpha = .25)
# center each group separately
iris %>%
  split(~ Species) %>%
  lapply(subset, select = -c(Species)) %>%
  lapply(scale, center = TRUE, scale = FALSE) %>%
  lapply(as.data.frame) %>%
  unsplit(iris$Species) %>%
  transform(Species = iris$Species) ->
  iris_ctr
ggplot(iris_ctr, aes(Petal.Width, Petal.Length)) +
  coord_equal() +
  facet_wrap(vars(Species)) +
  geom_unit_circle() +
  geom_point()
# scale group mean differences uniformly
iris_ctr %>%
  subset(select = -c(Species)) %>%
  scale(center = FALSE, scale = TRUE) %>%
  transform(Species = iris$Species) %>%
  ggplot(aes(Petal.Width, Petal.Length)) +
  coord_equal() +
  facet_wrap(vars(Species)) +
```

```
  geom_unit_circle() +
  geom_point()
```

---

ggbiplot *Biplots following the grammar of graphics*

Description

Build a biplot visualization from ordination data wrapped as a tbl_ord object.

Usage

```
ggbiplot(
  ordination = NULL,
  mapping = aes(x = 1, y = 2),
  xlim = NULL,
  ylim = NULL,
  expand = TRUE,
  clip = "on",
  axis.percents = TRUE,
  sec.axes = NULL,
  scale.factor = "inertia",
  scale_rows = NULL,
  scale_cols = NULL,
  ...
)

ord_aes(ordination, ...)
```

Arguments

ordination	A tbl_ord.
mapping	List of default aesthetic mappings to use for the biplot. The default assigns the first two coordinates to the aesthetics x and y. Other assignments must be supplied in each layer added to the plot.
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).
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.

`axis.percents` Whether to concatenate default axis labels with inertia percentages.

`sec.axes` Matrix factor character to specify a secondary set of axes.

`scale.factor` Either a numeric value, used to scale the secondary axes against the primary axes, or the name of a harmonizing function (currently `"range"` or `"inertia"`); ignored if `sec.axes` is not specified.

`scale_rows, scale_cols`
Either the character name of a numeric variable in `get_*(ordination)` or a numeric vector of length `nrow(get_*(ordination))`, used to scale the coordinates of the matrix factors.

`...` Additional arguments passed to `ggplot2::fortify()`; see `fortify.tbl_ord()`.

Details

`ggbiplot()` produces a ggplot object from a tbl_ord object `ordination`. The baseline object is the default unadorned `"ggplot"`-class object p with the following differences from what `ggplot2::ggplot()` returns:

- `p$mapping` is augmented with `.matrix = .matrix`, which expects either `.matrix = "rows"` or `.matrix = "cols"` from the biplot.
- `p$coordinates` is defaulted to `ggplot2::coord_equal()` in order to faithfully render the geometry of an ordination. The optional parameters `xlim`, `ylim`, `expand`, and `clip` are passed to `coord_equal()` and default to its **ggplot2** defaults.
- When `x` or `y` are mapped to coordinates of `ordination`, and if `axis.percents` is `TRUE`, `p$labels$x` or `p$labels$y` are defaulted to the coordinate names concatenated with the percentages of inertia captured by the coordinates.
- p is assigned the class `"ggbiplot"` in addition to `"ggplot"`. This serves no functional purpose currently.

Furthermore, the user may feed single integer values to the `x` and `y` aesthetics, which will be interpreted as the corresponding coordinates in the ordination. Currently only 2-dimensional biplots are supported, so both `x` and `y` must take coordinate values.

`ord_aes()` is a convenience function that generates a full-rank set of coordinate aesthetics `..coord1`, `..coord2`, etc. mapped to the shared coordinates of the ordination object, along with any additional aesthetics that are processed internally by `ggplot2::aes()`.

Predictive axes are scaled inversely by the squared norm. By default, this is computed from `x` and `y` (or from the full model space if obtained by `ord_aes()`). If the data contain an `axis.ss` column, it is used instead. Gower & Hand (1996) and Gower, Gardner–Lubbe, & le Roux (2011) thoroughly explain the construction and interpretation of predictive biplots. (Predictive calibration was previously handled by `ggbiplot(axis.type)` but has been transferred to `gggda::geom_axis(axis.type)`.)

Value

A ggplot object.

Biplot layers

`ggbiplot()` uses `ggplot2::fortify()` internally to produce a single data frame with a `.matrix` column distinguishing the subjects (`"rows"`) and variables (`"cols"`). The stat layers `stat_rows()` and `stat_cols()` simply filter the data frame to one of these two.

The geom layers `geom_rows_*()` and `geom_cols_*()` call the corresponding stat in order to render plot elements for the corresponding factor matrix. `geom_dims_*()` selects a default matrix based on common practice, e.g. points for rows and arrows for columns.

References

Gower JC & Hand DJ (1996) *Biplots*. Chapman & Hall, ISBN: 0-412-71630-5.

Gower JC, Gardner–Lubbe S, & le Roux NJ (2011) *Understanding Biplots*. Wiley, ISBN: 978-0-470-01255-0. https://www.wiley.com/go/biplots

See Also

`ggplot2::ggplot2()`, on which `ggbiplot()` is built

Examples

```
# compute PCA of Anderson iris measurements
iris[, -5] %>%
  princomp(cor = TRUE) %>%
  as_tbl_ord() %>%
  confer_inertia(1) %>%
  mutate_rows(species = iris$Species) %>%
  mutate_cols(measure = gsub("\\.", " ", tolower(names(iris)[-5]))) %>%
  print() -> iris_pca

# row-principal biplot with range-harmonized secondary axis
iris_pca %>%
  ggbiplot(aes(color = species), sec.axes = "cols", scale.factor = "range") +
  theme_bw() +
  scale_color_brewer(type = "qual", palette = 2) +
  geom_rows_point() +
  geom_cols_vector(aes(label = measure), color = "#444444") +
  ggtitle(
    "Row-principal PCA biplot of Anderson iris measurements",
    "Variable loadings scaled to secondary axes"
  ) +
  expand_limits(y = c(-1, 3.5))

# row-principal biplot with manually rescaled secondary axis
iris_pca %>%
  ggbiplot(aes(color = species), sec.axes = "cols", scale.factor = 2) +
  theme_bw() +
  scale_color_brewer(type = "qual", palette = 2) +
  geom_rows_point() +
  geom_cols_vector(aes(label = measure), color = "#444444") +
  ggtitle(
```

```
    "Row-principal PCA biplot of Anderson iris measurements",
    "Variable loadings scaled to secondary axes"
  ) +
  expand_limits(y = c(-1, 3.5))
# Performance measures can be regressed on the artificial coordinates of
# ordinated vehicle specs. Because the ordination of specs ignores performance,
# these coordinates will probably not be highly predictive. The gradient of each
# performance measure along the artificial axes is visualized by projecting the
# regression coefficients onto the ordination biplot.

# scaled principal components analysis of vehicle specs
mtcars_specs_pca <- ordinate(
  mtcars, cols = c(cyl, disp, hp, drat, wt, vs, carb),
  model = ~ princomp(., cor = TRUE)
)
# data frame of vehicle performance measures
mtcars %>%
  subset(select = c(mpg, qsec)) %>%
  as.matrix() %>%
  print() -> mtcars_perf
# regress performance measures on principal components
lm(mtcars_perf ~ get_rows(mtcars_specs_pca)) %>%
  as_tbl_ord() %>%
  augment_ord() %>%
  print() -> mtcars_pca_lm
# regression biplot
ggbiplot(mtcars_specs_pca, aes(label = name),
         sec.axes = "rows", scale.factor = .5) +
  theme_minimal() +
  geom_rows_text(size = 3) +
  geom_cols_vector(data = mtcars_pca_lm) +
  expand_limits(x = c(-2.5, 2))

# multidimensional scaling based on a scaled cosine distance of vehicle specs
cosine_dist <- function(x) {
  x <- as.matrix(x)
  num <- x %*% t(x)
  denom_rt <- as.matrix(rowSums(x^2))
  denom <- sqrt(denom_rt %*% t(denom_rt))
  as.dist(1 - num / denom)
}
mtcars %>%
  subset(select = c(cyl, disp, hp, drat, wt, vs, carb)) %>%
  scale() %>%
  cosine_dist() %>%
  cmdscale() %>%
  as.data.frame() ->
  mtcars_specs_cmds
# names must be consistent with `cmdscale_ord()` below
names(mtcars_specs_cmds) <- c("PCo1", "PCo2")
# regress performance measures on principal coordinates
lm(mtcars_perf ~ as.matrix(mtcars_specs_cmds)) %>%
  as_tbl_ord() %>%
```

```
  augment_ord() %>%
  print() -> mtcars_cmds_lm
# multidimensional scaling using `cmdscale_ord()`
mtcars %>%
  subset(select = c(cyl, disp, hp, drat, wt, vs, carb)) %>%
  scale() %>%
  cosine_dist() %>%
  cmdscale_ord() %>%
  as_tbl_ord() %>%
  augment_ord() %>%
  print() -> mtcars_specs_cmds_ord
# regression biplot
ggbiplot(mtcars_specs_cmds_ord, aes(label = name),
         sec.axes = "rows", scale.factor = 3) +
  theme_minimal() +
  geom_rows_text(size = 3) +
  geom_cols_vector(data = mtcars_cmds_lm) +
  expand_limits(x = c(-2.25, 1.25), y = c(-2, 1.5))
# PCA of iris data
iris_pca <- ordinate(iris, cols = 1:4, prcomp, scale = TRUE)

# row-principal predictive biplot
iris_pca %>%
  ggbiplot() +
  theme_bw() +
  scale_color_brewer(type = "qual", palette = 2) +
  geom_cols_axis(
    aes(label = name, center = center, scale = scale),
    axis.type = "predictive"
  ) +
  geom_rows_point(aes(color = Species), alpha = .5) +
  ggtitle("Predictive biplot of Anderson iris measurements")

# with two calibrated axes
iris_pca %>%
  ggbiplot() +
  theme_bw() +
  scale_color_brewer(type = "qual", palette = 2) +
  geom_origin() +
  stat_cols_rule(
    subset = c(2, 4), axis.type = "predictive",
    fontface = "bold", text.fontface = "plain",
    aes(label = name, center = center, scale = scale)
  ) +
  geom_rows_point(aes(color = Species), alpha = .5) +
  expand_limits(x = c(-5, 5), y = c(-5, 5)) +
  ggtitle("Predictive biplot of Anderson iris measurements")
```

`glass` *Glass composition data*

Description

Sites, types, and compositions of glass samples from archaeological sites in Israel.

Usage

```
data(glass)
```

Format

A tibble with 68 cases and 16 variables:

`Site` site at which sample was found

`Anal` analysis identifier

`Context` furnace identifier

`Form` type of sample

`SiO2, TiO2, Al2O3, FeO, MnO, MgO, CaO, Na2O, K2O, P2O5, Cl, SO3` normalized weight percent oxide of each component

Details

Chunks of unformed glass from several furnaces found at the primary Byzantine-era site of Bet Eli'ezer, along with samples from other sites with weaker evidence of glass-making (Apollonia and Dor) and and from an Islamic-era site (Banias), were analyzed using X-ray spectrometry to determine their major components.

Baxter & Freestone (2006) used these data to illustrate log-ratio analysis.

Source

Freestone &al (2000), Table 2.

References

Freestone IC, Gorin-Rosen Y, & Hughes MJ (2000) "Primary glass from Israel and the production of glass in Late Antiquity and the early Islamic period". *La route du verre: Ateliers primaires et secondaires du second millénaire av. J.-C. au Moyen Âge*: 65–83. https://pascal-francis.inist.fr/vibad/index.php?action=getRecordDetail&idt=1158762

Baxter MJ & Freestone IC (2006) "Log-Ratio Compositional Data Analysis in Archaeometry". *Archaeometry*, **48**(3): 511–531. doi:10.1111/j.14754754.2006.00270.x

Examples

```
# subset glass data to one site and major components
head(glass)
glass_main <- subset(
  glass,
  Site == "Bet Eli'ezer",
  select = c("SiO2", "Na2O", "CaO", "Al2O3", "MgO", "K2O")
)
```

```
# format as a data frame with row names
glass_main <- as.data.frame(glass_main)
rownames(glass_main) <- subset(glass, Site == "Bet Eli'ezer")$Anal

# perform log-ratio analysis
glass_lra <- lra(glass_main, compositional = TRUE, weighted = FALSE)
# inspect LRA row and column coordinates
head(glass_lra$row.coords)
glass_lra$column.coords
# inspect singular values of LRA
glass_lra$sv

# plot samples and measurements in a biplot
biplot(
  x = glass_lra$row.coords %*% diag(glass_lra$sv),
  y = glass_lra$column.coords,
  xlab = "Sample (principal coord.)", ylab = ""
)
mtext("Component (standard coord.)", side = 4L, line = 3L)
```

---

goodness-of-fit *Measures of goodness of fit of ordination models*

Description

Compute the quality, adequacy, and predictivity of a 'tbl_ord' object from the retrieved matrix factors.

Usage

```
ord_quality(x, rank = NULL)

ord_adequacy(x, .matrix, rank = NULL)

ord_predictivity(x, .matrix, rank = NULL)
```

Arguments

x	A 'tbl_ord' object.
rank	The maximum rank for which to compute statistics; the default, NULL computes statistics up to the rank of the model.
.matrix	A character string partially matched (lowercase) to several indicators for one or both matrices in a matrix decomposition used for ordination. The standard values are "rows", "cols", and "dims" (for both).

Details

Gower, Gardner–Lubbe, & le Roux (2011) detail several measures of fit for biplots, most prominently

- the *quality* of the r-dimensional biplot, measured as the proportion of variance in the plot, calculated as the quotient of the traces of $\Lambda_r = {D_r}^2$ and of $\Lambda = D^2$.
- the *adequacy* of the representation of the j-th row (respectively, column) in the r-dimensional biplot, calculated as the j-th diagonal element of $U_r \ {U_r}^\top$ (respectively, $V_r \ {V_r}^\top$), understood as the fidelity of the projections of the standard coordinates.
- the *predictivity* of the j-th row (respectively, column) in the r-dimensional biplot, measured as the quotient of the j-th diagonal elements of $U_r \ \Lambda_r \ {U_r}^\top$ and of $U \ \Lambda \ U^\top$ (respectively, of $V_r \ \Lambda_r \ {V_r}^\top$ and of $V \ \Lambda \ V^\top$), understood as the fidelity of the projections of the principal coordinates.

These can be calculated directly from any SVD or EVD and interpreted for any technique based on them. In some cases they may also be calculated for supplementary elements.

Value

A vector, matrix, or list of matrices of numeric goodness-of-fit statistics. If no items are found, a matrix will have zero rows.

References

Gower JC, Gardner–Lubbe S, & le Roux NJ (2011) *Understanding Biplots*. Wiley, ISBN: 978-0-470-01255-0. https://www.wiley.com/go/biplots

Examples

```
# log-ratio analysis of Apollonia glass composition data
glass_apollonia <- subset(
  glass,
  Site == "Apollonia",
  select = c("SiO2", "Na2O", "CaO", "Al2O3", "MgO", "K2O")
)
glass_lra <- lra(glass_apollonia, weighted = FALSE)

# quality (cumulative proportion of inertia included)
ord_quality(glass_lra)
# adequacy (fidelity of projections to standard coordinates)
ord_adequacy(glass_lra, "rows", rank = 3)
ord_adequacy(glass_lra, "cols", rank = 3)
# predictivity (fidelity of projections to principal coordinates)
ord_predictivity(glass_lra, "dims", rank = 2)

# principal components analysis of setosa iris data
iris_pca <- princomp(iris3[, , "Setosa"])

# quality (cumulative proportion of inertia included)
ord_quality(iris_pca)
```

```
# adequacy (fidelity of projections to standard coordinates)
ord_adequacy(iris_pca, "both")
# predictivity (fidelity of projections to principal coordinates)
ord_predictivity(iris_pca, "f")
ord_predictivity(iris_pca, "g")
```

---

lda-ord *Augmented implementation of linear discriminant analysis*

Description

This function replicates MASS::lda() with options and defaults to retain elements useful to the tbl_ord class and biplot calculations.

Usage

```
lda_ord(x, ...)

## S3 method for class 'formula'
lda_ord(formula, data, ..., subset, na.action)

## S3 method for class 'data.frame'
lda_ord(x, ...)

## S3 method for class 'matrix'
lda_ord(x, grouping, ..., subset, na.action)

## Default S3 method:
lda_ord(
  x,
  grouping,
  prior = proportions,
  tol = 1e-04,
  method = c("moment", "mle", "mve", "t"),
  CV = FALSE,
  nu = 5,
  ...,
  ret.x = TRUE,
  ret.grouping = TRUE,
  axes.scale = "unstandardized"
)

## S3 method for class 'lda_ord'
predict(
  object,
  newdata,
  prior = object$prior,
```

```
  dimen,
  method = c("plug-in", "predictive", "debiased"),
  ...
)

## S3 method for class 'lda_ord'
model.frame(formula, ...)
```

Arguments

x	(required if no formula is given as the principal argument.) a matrix or data frame or Matrix containing the explanatory variables.
...	arguments passed to or from other methods.
formula	A formula of the form groups ~ x1 + x2 + ... That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	An optional data frame, list or environment from which variables specified in formula are preferentially to be taken.
subset	An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
na.action	A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is na.omit, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)
grouping	(required if no formula principal argument is given.) a factor specifying the class for each observation.
prior	the prior probabilities of class membership. If unspecified, the class proportions for the training set are used. If present, the probabilities should be specified in the order of the factor levels.
tol	A tolerance to decide if a matrix is singular; it will reject variables and linear combinations of unit-variance variables whose variance is less than tol^2.
method	"moment" for standard estimators of the mean and variance, "mle" for MLEs, "mve" to use cov.mve, or "t" for robust estimates based on a t distribution.
CV	If true, returns results (classes and posterior probabilities) for leave-one-out cross-validation. Note that if the prior is estimated, the proportions in the whole dataset are used.
nu	degrees of freedom for method = "t".
ret.x, ret.grouping	Logical; whether to retain as attributes the data matrix (x) and the class assignments (grouping) on which LDA is performed. Methods like predict() access these objects by name in the parent environment, and retaining them as attributes prevents errors that arise if these objects are reassigned.
axes.scale	Character string indicating how to left-transform the scaling value when rendering biplots using ggbiplot(). Options include "unstandardized", "standardized", and "contribution".
object	object of class "lda"

newdata	data frame of cases to be classified or, if object has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If newdata is missing, an attempt will be made to retrieve the data used to fit the lda object.
dimen	the dimension of the space to be used. If this is less than min(p, ng-1), only the first dimen discriminant components are used (except for method="predictive"), and only those dimensions are returned in x.

Details

Linear discriminant analysis relies on an eigendecomposition of the product $W^{-1}B$ of the inverse of the within-class covariance matrix W by the between-class covariance matrix B. This eigendecomposition can be motivated as the right (V) half of the singular value decomposition of the matrix of *Mahalanobis distances* between the cases after "sphering" (linearly transforming them so that the within-class covariance is the identity matrix). LDA are not traditionally represented as biplots, with some exceptions (Gardner & le Roux, 2005; Greenacre, 2010, p. 109–117).

LDA is implemented as MASS::lda() in the **MASS** package, in which the variables are transformed by a sphering matrix S (Venables & Ripley, 2003, p. 331–333). The returned element scaling contains the unstandardized *discriminant coefficients*, which define the discriminant scores of the cases and their centroids as linear combinations of the original variables.

The discriminant coefficients constitute one of several possible choices of axes for a biplot representation of the LDA. The slightly modified function lda_ord() provides additional options:

- The *standardized discriminant coefficients* are obtained by (re)scaling the coefficients by the variable standard deviations. These coefficients indicate the contributions of the variables to the discriminant scores after controlling for their variances (Orlov, 2013).
- The variables' *contributions* to the Mahalanobis variance along each discriminant axis are obtained by transforming the coefficients by the inverse of the sphering matrix S. Because the contribution biplot derives from the eigendecomposition of the Mahalanobis distance matrix, the projections of the centroids and cases onto the variable axes approximate their variable values after centering and sphering (Greenacre, 2013).

Finally, in contrast to MASS::lda(), lda_ord() defaults both ret.x and ret.grouping to TRUE, so that these elements can be used to compute and annotate case scores as supplementary elements.

Value

Output from MASS::lda() with an additional preceding class 'lda_ord' and up to three attributes:

- the input data x, if ret.x = TRUE
- the class assignments grouping, if ret.grouping = TRUE
- if the parameter axes.scale is not 'unstandardized', a matrix axes.scale that encodes the transformation of the row space

References

Gardner S & le Roux NJ (2005) "Extensions of Biplot Methodology to Discriminant Analysis". *Journal of Classification* **22**(1): 59–86. doi:10.1007/s0035700500067 https://link.springer.com/article/10.1007/s00357-005-0006-7

Greenacre MJ (2010) *Biplots in Practice*. Fundacion BBVA, ISBN: 978-84-923846. https://www.fbbva.es/microsite/multivariate-statistics/biplots.html

Venables WN & Ripley BD (2003) *Modern Applied Statistics with S*, Fourth Edition. Springer Science & Business Media, ISBN: 0387954570, 9780387954578. https://www.mimuw.edu.pl/~pokar/StatystykaMgr/Books/VenablesRipley_ModernAppliedStatisticsS02.pdf

Orlov K (2013) *Answer to* "Algebra of LDA. Fisher discrimination power of a variable and Linear Discriminant Analysis". CrossValidated, accessed 2019-07-26. https://stats.stackexchange.com/a/83114/68743

Greenacre M (2013) "Contribution Biplots". *Journal of Computational and Graphical Statistics*, **22**(1): 107–122. https://www.tandfonline.com/doi/abs/10.1080/10618600.2012.702494

See Also

`MASS::lda()`, from which `lda_ord()` is adapted

Examples

```
# Anderson iris species data centroid
iris_centroid <- t(apply(iris[, 1:4], 2, mean))
# unstandardized discriminant coefficients: the discriminant axes are linear
# combinations of the centered variables
iris_lda <- lda_ord(iris[, 1:4], iris[, 5], axes.scale = "unstandardized")
# linear combinations of centered variables
print(sweep(iris_lda$means, 2, iris_centroid, "-") %*% get_cols(iris_lda))
# discriminant centroids
print(get_rows(iris_lda, elements = "active"))

# unstandardized coefficient LDA biplot
iris_lda %>%
  as_tbl_ord() %>%
  augment_ord() %>%
  ggbiplot() +
  theme_bw() +
  coord_scaffold() +
  geom_rows_point(aes(color = grouping), elements = "score", alpha = 1/3) +
  geom_rows_point(aes(color = grouping), size = 3) +
  geom_cols_vector(aes(label = name), color = "#888888", size = 3) +
  scale_color_brewer(type = "qual", palette = 2) +
  ggtitle("Unstandardized coefficient biplot of iris LDA")

# standardized discriminant coefficients: permit comparisons across the
# variables
iris_lda <- lda_ord(iris[, 1:4], iris[, 5], axes.scale = "standardized")
# standardized variable contributions to discriminant axes
iris_lda %>%
  as_tbl_ord() %>%
  augment_ord() %>%
  fortify(.matrix = "cols") %>%
  dplyr::mutate(variable = name) %>%
  tidyr::gather(discriminant, coefficient, LD1, LD2) %>%
  ggplot(aes(x = discriminant, y = coefficient, fill = variable)) +
```

```
  geom_bar(position = "dodge", stat = "identity") +
  labs(y = "Standardized coefficient", x = "Linear discriminant") +
  theme_bw() +
  coord_flip()
# standardized coefficient LDA biplot
iris_lda %>%
  as_tbl_ord() %>%
  augment_ord() %>%
  ggbiplot() +
  theme_bw() +
  coord_scaffold() +
  geom_rows_point(aes(color = grouping), elements = "score", alpha = 1/3) +
  geom_rows_point(aes(color = grouping), size = 3) +
  geom_cols_vector(aes(label = name), color = "#888888", size = 3) +
  scale_color_brewer(type = "qual", palette = 2) +
  ggtitle("Standardized coefficient biplot of iris LDA")

# variable contributions (de-sphered discriminant coefficients): recover the
# inner product relationship with the centered class centroids
iris_lda <- lda_ord(iris[, 1:4], iris[, 5], axes.scale = "contribution")
# symmetric square root of within-class covariance
C_W_eig <- eigen(cov(iris[, 1:4] - iris_lda$means[iris[, 5], ]))
C_W_sqrtinv <-
  C_W_eig$vectors %*% diag(1/sqrt(C_W_eig$values)) %*% t(C_W_eig$vectors)
# product of matrix factors (scores and loadings)
print(get_rows(iris_lda, elements = "active") %*% t(get_cols(iris_lda)))
# "asymmetric" square roots of Mahalanobis distances between variables
print(sweep(iris_lda$means, 2, iris_centroid, "-") %*% C_W_sqrtinv)
# contribution LDA biplot
iris_lda %>%
  as_tbl_ord() %>%
  augment_ord() %>%
  ggbiplot() +
  theme_bw() +
  coord_scaffold() +
  geom_rows_point(aes(color = grouping), elements = "score", alpha = 1/3) +
  geom_rows_point(aes(color = grouping), size = 3) +
  geom_cols_vector(aes(label = name), color = "#888888", size = 3) +
  scale_color_brewer(type = "qual", palette = 2) +
  ggtitle("Contribution biplot of iris LDA")
```

`lra-ord` *Log-ratio analysis*

Description

Represent log-ratios between variables based on their values on a population of cases.

Usage

```
lra(x, compositional = FALSE, weighted = TRUE)

## S3 method for class 'lra'
print(x, nd = length(x$sv), n = 6L, ...)

## S3 method for class 'lra'
screeplot(x, main = deparse1(substitute(x)), ...)

## S3 method for class 'lra'
biplot(
  x,
  choices = c(1L, 2L),
  scale = c(0, 0),
  main = deparse1(substitute(x)),
  var.axes = FALSE,
  ...
)

## S3 method for class 'lra'
plot(x, main = deparse1(substitute(x)), ...)
```

Arguments

x	A numeric matrix or rectangular data set.
compositional	Logical; whether to normalize rows of x to sum to 1.
weighted	Logical; whether to weight rows and columns by their sums.
nd	Integer; number of shared dimensions to include in print.
n	Integer; number of rows of each factor to print.
main, var.axes, ...	Parameters passed to other plotting methods (in the case of main, after being force()d.
choices	Integer; length-2 vector specifying the components to plot.
scale	Numeric; values between 0 and 1 that control how inertia is conferred unto the points: Row (i = 1L) and column (i = 2L) coordinates are scaled by sv ^ scale[[i]]. If a single value scale is passed, it is assigned to the rows while 1 - scale is assigned to the columns.

Details

Log-ratio analysis (LRA) is based on a double-centering of log-transformed data, usually weighted by row and column totals. The technique is suitable for positive-valued variables on a common scale (e.g. percentages). The distances between variables' coordinates (in the full-dimensional space) are their pairwise log-ratios. The distances between cases' coordinates are called their *log-ratio distances*, and the total variance is the weighted sum of their squares.

LRA is not implemented in standard R distributions but is a useful member of the ordination toolkit. This is a minimal implementation following Greenacre's (2010) exposition in Chapter 7.

Value

Given an $n * p$ data matrix and setting $r = min(n, p)$, `lra()` returns a list of class `"lra"` containing three elements:

`sv` The $r - 1$ singular values

`row.coords` The $n * (r - 1)$ matrix of row standard coordinates.

`column.coords` The $p * (r - 1)$ matrix of column standard coordinates.

`row.weights` The weights used to scale the row coordinates.

`column.weights` The weights used to scale the column coordinates.

References

Greenacre MJ (2010) *Biplots in Practice*. Fundacion BBVA, ISBN: 978-84-923846. https://www.fbbva.es/microsite/multivariate-statistics/biplots.html

Examples

```
# U.S. 1973 violent crime arrests
head(USArrests)
# row and column subsets
state_examples <- c("Hawaii", "Mississippi", "North Dakota")
arrests <- c(1L, 2L, 4L)

# pairwise log-ratios of violent crime arrests for two states
arrest_pairs <- combn(arrests, 2L)
arrest_ratios <-
  USArrests[, arrest_pairs[1L, ]] / USArrests[, arrest_pairs[2L, ]]
colnames(arrest_ratios) <- paste(
  colnames(USArrests)[arrest_pairs[1L, ]], "/",
  colnames(USArrests)[arrest_pairs[2L, ]], sep = ""
)
arrest_logratios <- log(arrest_ratios)
arrest_logratios[state_examples, ]

# non-compositional log-ratio analysis
(arrests_lra <- lra(USArrests[, arrests]))
screeplot(arrests_lra)
biplot(arrests_lra, scale = c(1, 0), cex = c(2/3, 1))

# compositional log-ratio analysis
(arrests_lra <- lra(USArrests[, arrests], compositional = TRUE))
biplot(arrests_lra, scale = c(1, 0), cex = c(2/3, 1))
```

`methods-cancor` *Functionality for canonical correlations*

Description

These methods extract data from, and attribute new data to, objects of class `"cancor_ord"`. This is a class introduced in this package to identify objects returned by `cancor_ord()`, which wraps `stats::cancor()`.

Usage

```
## S3 method for class 'cancor_ord'
as_tbl_ord(x)

## S3 method for class 'cancor_ord'
recover_rows(x)

## S3 method for class 'cancor_ord'
recover_cols(x)

## S3 method for class 'cancor_ord'
recover_inertia(x)

## S3 method for class 'cancor_ord'
recover_coord(x)

## S3 method for class 'cancor_ord'
recover_conference(x)

## S3 method for class 'cancor_ord'
recover_supp_rows(x)

## S3 method for class 'cancor_ord'
recover_supp_cols(x)

## S3 method for class 'cancor_ord'
recover_aug_rows(x)

## S3 method for class 'cancor_ord'
recover_aug_cols(x)

## S3 method for class 'cancor_ord'
recover_aug_coord(x)
```

Arguments

`x`	An ordination object.

Details

The canonical coefficients (loadings) are obtained directly from the underlying singular value decomposition and constitute the active elements. If canonical scores are returned, then they and the structure correlations are made available as supplementary elements. **ordr** takes rows and columns from the intraset correlations `$xstructure` and `$ystructure`, on which no intertia is conferred; the interset correlations can be obtained by conferring inertia onto these.

A biplot of the canonical coefficients can be interpreted as approximating the X-Y inner product matrix, inversely weighted by the X and Y variances. The canonical scores and structure coefficients are available as supplementary points if returned by `cancor_ord()`. These can be used to create biplots of the case scores as linear combinations of loadings (the coefficients, in standard coordinates, overlaid with the scores) or of intraset and interset correlations with respect to either data set (the correlations with inertia conferred entirely onto rows or onto columns). Greenacre (1984) and ter Braak (1990) describe these families, though ter Braak recommends against the first.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

References

Greenacre MJ (1984) *Theory and applications of correspondence analysis*. London: Academic Press, ISBN 0-12-299050-1. http://www.carme-n.org/?sec=books5

ter Braak CJF (1990) "Interpreting canonical correlation analysis through biplots of structure correlations and weights". *Psychometrika* 55(3), 519–531. doi:10.1007/BF02294765

See Also

Other methods for singular value decomposition-based techniques: `methods-correspondence`, `methods-lda`, `methods-lra`, `methods-mca`, `methods-prcomp`, `methods-svd`

Other models from the stats package: `methods-cmds`, `methods-factanal`, `methods-kmeans`, `methods-lm`, `methods-prcomp`, `methods-princomp`

Examples

```
# data frame of life-cycle savings across countries
class(LifeCycleSavings)
head(LifeCycleSavings)
savings_pop <- LifeCycleSavings[, c("pop15", "pop75")]
savings_oec <- LifeCycleSavings[, c("sr", "dpi", "ddpi")]

# canonical correlation analysis with scores and correlations included
savings_cca <- cancor_ord(savings_pop, savings_oec, scores = TRUE)
savings_cca <- augment_ord(as_tbl_ord(savings_cca))
```

```
head(get_cols(savings_cca))
head(get_cols(savings_cca, elements = "score"))
get_rows(savings_cca, elements = "structure")
get_cols(savings_cca, elements = "structure")

# biplot of interset and intraset correlations with the population data
# NB: `contour = TRUE` is not automatically set as in `geom_density_2d()`
savings_cca %>%
  confer_inertia("cols") %>%
  ggbiplot(aes(label = name, color = .matrix)) +
  theme_bw() + theme_scaffold() +
  geom_unit_circle() +
  geom_rows_density_2d(elements = "score", color = "grey", contour = TRUE) +
  geom_rows_vector(arrow = NULL, elements = "structure") +
  geom_cols_vector(arrow = NULL, elements = "structure", linetype = "dashed") +
  geom_rows_text(elements = "structure", hjust = "outward") +
  geom_cols_text(elements = "structure", hjust = "outward") +
  scale_color_brewer(limits = c("rows", "cols"), type = "qual") +
  expand_limits(x = c(-1, 1), y = c(-1, 1))

# situate country scores along financial variables
# (inner product interpretation requires that scores be in population units)
savings_cca %>%
  confer_inertia("cols") %>%
  ggbiplot(aes(label = name, center = center)) +
  theme_scaffold() +
  geom_cols_axis(elements = "active") +
  geom_rows_text(elements = "score") +
  stat_rows_projection(elements = "score", subset = 49)
# the model predicts much higher disposable income in Libya than was measured
```

`methods-cmds` *Functionality for classical multidimensional scaling objects*

Description

These methods extract data from, and attribute new data to, objects of class `"cmds_ord"`. This is a class introduced in this package to identify objects returned by `cmdscale_ord()`, which wraps `stats::cmdscale()`.

Usage

```
## S3 method for class 'cmds_ord'
as_tbl_ord(x)

## S3 method for class 'cmds_ord'
recover_rows(x)

## S3 method for class 'cmds_ord'
```

```
recover_cols(x)

## S3 method for class 'cmds_ord'
recover_inertia(x)

## S3 method for class 'cmds_ord'
recover_coord(x)

## S3 method for class 'cmds_ord'
recover_conference(x)

## S3 method for class 'cmds_ord'
recover_aug_rows(x)

## S3 method for class 'cmds_ord'
recover_aug_cols(x)

## S3 method for class 'cmds_ord'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

See Also

Other methods for eigen-decomposition-based techniques: `methods-eigen`, `methods-factanal`, `methods-princomp`

Other models from the stats package: `methods-cancor`, `methods-factanal`, `methods-kmeans`, `methods-lm`, `methods-prcomp`, `methods-princomp`

Examples

```
# 'dist' object (matrix of road distances) of large American cities
class(UScitiesD)
print(UScitiesD)

# use multidimensional scaling to infer artificial planar coordinates
UScitiesD %>%
  cmdscale_ord(k = 2) %>%
```

```
  as_tbl_ord() %>%
  print() -> usa_mds

# recover (equivalent) matrices of row and column artificial coordinates
get_rows(usa_mds)
get_cols(usa_mds)

# augment ordination with point names
(usa_mds <- augment_ord(usa_mds))

# reorient biplot to conventional compass
usa_mds %>%
  negate_ord(c(1, 2)) %>%
  ggbiplot() +
  geom_cols_text(aes(label = name), size = 3) +
  ggtitle("MDS biplot of distances between U.S. cities")
```

`methods-correspondence` *Functionality for correspondence analysis ('correspondence') objects*

Description

These methods extract data from, and attribute new data to, objects of class `"correspondence"` from the **MASS** package.

Usage

```
## S3 method for class 'correspondence'
as_tbl_ord(x)

## S3 method for class 'correspondence'
recover_rows(x)

## S3 method for class 'correspondence'
recover_cols(x)

## S3 method for class 'correspondence'
recover_inertia(x)

## S3 method for class 'correspondence'
recover_conference(x)

## S3 method for class 'correspondence'
recover_coord(x)

## S3 method for class 'correspondence'
recover_aug_rows(x)
```

```
## S3 method for class 'correspondence'
recover_aug_cols(x)

## S3 method for class 'correspondence'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

See Also

Other methods for singular value decomposition-based techniques: `methods-cancor`, `methods-lda`, `methods-lra`, `methods-mca`, `methods-prcomp`, `methods-svd`

Other models from the MASS package: `methods-lda`, `methods-mca`

Examples

```
# table of hair and eye color data collapsed by sex
data(quine, package = "MASS")
class(quine)
head(quine)

# use correspondence analysis to construct row and column profiles
(quine_ca <- MASS::corresp(~ Age + Eth, data = quine))
(quine_ca <- as_tbl_ord(quine_ca))

# recover row and column profiles
get_rows(quine_ca)
get_cols(quine_ca)

# augment profiles with names, masses, distances, and inertias
(quine_ca <- augment_ord(quine_ca))
```

methods-eigen *Functionality for eigen-decompositions*

Description

These methods extract data from, and attribute new data to, objects of class "eigen" returned by base::eigen() when the parameter only.values is set to FALSE or of class "eigen_ord" returned by eigen_ord().

Usage

```
## S3 method for class 'eigen'
as_tbl_ord(x)

## S3 method for class 'eigen'
recover_rows(x)

## S3 method for class 'eigen'
recover_cols(x)

## S3 method for class 'eigen'
recover_inertia(x)

## S3 method for class 'eigen'
recover_coord(x)

## S3 method for class 'eigen'
recover_conference(x)

## S3 method for class 'eigen'
recover_aug_rows(x)

## S3 method for class 'eigen'
recover_aug_cols(x)

## S3 method for class 'eigen'
recover_aug_coord(x)

## S3 method for class 'eigen_ord'
as_tbl_ord(x)

## S3 method for class 'eigen_ord'
recover_rows(x)

## S3 method for class 'eigen_ord'
recover_cols(x)
```

```
## S3 method for class 'eigen_ord'
recover_inertia(x)

## S3 method for class 'eigen_ord'
recover_coord(x)

## S3 method for class 'eigen_ord'
recover_conference(x)

## S3 method for class 'eigen_ord'
recover_aug_rows(x)

## S3 method for class 'eigen_ord'
recover_aug_cols(x)

## S3 method for class 'eigen_ord'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Details

`base::eigen()` usually returns an object of class `"eigen"`, which contains the numerical eigendecomposition without annotations such as row and column names. To facilitate downstream analysis, `eigen_ord()` returns a modified 'eigen' object with row names taken (if available) from the original data and column names indicating the integer index of each eigenvector.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

See Also

Other methods for eigen-decomposition-based techniques: `methods-cmds`, `methods-factanal`, `methods-princomp`

Other models from the base package: `methods-svd`

Examples

```
# eigendecompose covariance matrix of ability tests
gi_eigen <- eigen(ability.cov$cov)
```

```
# recover eigenvectors
get_rows(gi_eigen)
identical(get_cols(gi_eigen), get_rows(gi_eigen))

# wrap as a 'tbl_ord'
as_tbl_ord(gi_eigen)

# same eigendecomposition, preserving names
gi_eigen <- eigen_ord(ability.cov$cov)

# wrap as a 'tbl_ord' and augment with dimension names
augment_ord(as_tbl_ord(gi_eigen))

# decomposition returns pure eigenvectors
get_conference(gi_eigen)
```

`methods-factanal` *Functionality for factor analysis ('factanal') objects*

Description

These methods extract data from, and attribute new data to, objects of class `"factanal"` as returned by `stats::factanal()`.

Usage

```
## S3 method for class 'factanal'
as_tbl_ord(x)

## S3 method for class 'factanal'
recover_rows(x)

## S3 method for class 'factanal'
recover_cols(x)

## S3 method for class 'factanal'
recover_inertia(x)

## S3 method for class 'factanal'
recover_coord(x)

## S3 method for class 'factanal'
recover_conference(x)

## S3 method for class 'factanal'
recover_supp_rows(x)

## S3 method for class 'factanal'
```

```
recover_aug_rows(x)

## S3 method for class 'factanal'
recover_aug_cols(x)

## S3 method for class 'factanal'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Details

Factor analysis of a data matrix relies on an an eigendecomposition of its correlation matrix, whose eigenvectors (up to weighting) comprise the variable loadings. For this reason, both row and column recoverers retrieve the loadings and inertia is evenly distributed between them. When computed and returned by `stats::factanal()`, the case scores are accessible as supplementary elements. Redistribution of inertia commutes through both score calculations.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

See Also

Other methods for eigen-decomposition-based techniques: `methods-cmds`, `methods-eigen`, `methods-princomp`

Other models from the stats package: `methods-cancor`, `methods-cmds`, `methods-kmeans`, `methods-lm`, `methods-prcomp`, `methods-princomp`

Examples

```
# data frame of Swiss fertility and socioeconomic indicators
class(swiss)
head(swiss)
# perform factor analysis
swiss_fa <- factanal(~ ., factors = 2L, data = swiss, scores = "regression")

# wrap as a 'tbl_ord' object
(swiss_fa <- as_tbl_ord(swiss_fa))

# recover loadings
get_rows(swiss_fa, elements = "active")
get_cols(swiss_fa)
# recover scores
```

```
head(get_rows(swiss_fa, elements = "score"))

# augment column loadings with uniquenesses
(swiss_fa <- augment_ord(swiss_fa))

# symmetric biplot
swiss_fa %>%
  ggbiplot() +
  theme_bw() +
  geom_cols_vector(aes(color = uniqueness, label = name)) +
  expand_limits(x = c(-2, 2.5), y = c(-1.5, 2))
```

`methods-kmeans` *Functionality for k-means clustering ('kmeans') objects*

Description

These methods extract data from, and attribute new data to, objects of class `"kmeans"` as returned by `stats::kmeans()`.

Usage

```
## S3 method for class 'kmeans'
as_tbl_ord(x)

## S3 method for class 'kmeans'
recover_rows(x)

## S3 method for class 'kmeans'
recover_cols(x)

## S3 method for class 'kmeans'
recover_coord(x)

## S3 method for class 'kmeans'
recover_aug_rows(x)

## S3 method for class 'kmeans'
recover_aug_cols(x)

## S3 method for class 'kmeans'
recover_aug_coord(x)
```

Arguments

`x`	An ordination object.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

See Also

Other methods for idiosyncratic techniques: `methods-lm`

Other models from the stats package: `methods-cancor`, `methods-cmds`, `methods-factanal`, `methods-lm`, `methods-prcomp`, `methods-princomp`

Examples

```
# data frame of Anderson iris species measurements
class(iris)
head(iris)
# compute 3-means clustering on scaled iris measurements
set.seed(5601L)
iris %>%
  subset(select = -Species) %>%
  scale() %>%
  kmeans(centers = 3) %>%
  print() -> iris_km

# visualize clusters using PCA
iris %>%
  subset(select = -Species) %>%
  prcomp() %>%
  as_tbl_ord() %>%
  mutate_rows(cluster = iris_km$cluster) %>%
  ggbiplot() +
  geom_rows_point(aes(color = factor(as.character(as.integer(cluster)),
                                     levels = as.character(seq(3L))))) +
  scale_color_brewer(type = "qual", name = "cluster")

# wrap as a 'tbl_ord' object
(iris_km_ord <- as_tbl_ord(iris_km))

# augment everything with names, observations with cluster assignment
(iris_km_ord <- augment_ord(iris_km_ord))

# summarize clusters with standard deviation
iris_km_ord %>%
  tidy() %>%
  transform(sdev = sqrt(withinss / size))

# discriminate between clusters 2 and 3
iris_km_ord %>%
```

```
ggbiplot(aes(x = `2`, y = `3`), color = factor(.cluster)) +
geom_jitter(stat = "rows", aes(shape = cluster), width = .2, height = .2) +
geom_cols_axis(aes(color = `1`, label = name),
               text.size = 2, text_dodge = .1,
               size = 3, label.alpha = .5) +
scale_x_continuous(expand = expansion(mult = .8)) +
scale_y_continuous(expand = expansion(mult = .5)) +
ggtitle(
  "Measurement loadings onto clusters 2 and 3",
  "Color indicates loadings onto cluster 1"
)
```

`methods-lda` *Functionality for linear discriminant analysis ('lda') objects*

Description

These methods extract data from, and attribute new data to, objects of class `"lda"` and `"lda_ord"` as returned by `MASS::lda()` and `lda_ord()`.

Usage

```
## S3 method for class 'lda'
as_tbl_ord(x)

## S3 method for class 'lda_ord'
as_tbl_ord(x)

## S3 method for class 'lda'
recover_rows(x)

## S3 method for class 'lda_ord'
recover_rows(x)

## S3 method for class 'lda'
recover_cols(x)

## S3 method for class 'lda_ord'
recover_cols(x)

## S3 method for class 'lda'
recover_inertia(x)

## S3 method for class 'lda_ord'
recover_inertia(x)

## S3 method for class 'lda'
recover_coord(x)
```

```
## S3 method for class 'lda_ord'
recover_coord(x)

## S3 method for class 'lda'
recover_conference(x)

## S3 method for class 'lda_ord'
recover_conference(x)

## S3 method for class 'lda'
recover_aug_rows(x)

## S3 method for class 'lda_ord'
recover_aug_rows(x)

## S3 method for class 'lda'
recover_aug_cols(x)

## S3 method for class 'lda_ord'
recover_aug_cols(x)

## S3 method for class 'lda'
recover_aug_coord(x)

## S3 method for class 'lda_ord'
recover_aug_coord(x)

## S3 method for class 'lda'
recover_supp_rows(x)

## S3 method for class 'lda_ord'
recover_supp_rows(x)
```

Arguments

x	An ordination object.

Details

See lda-ord for details.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the

recoverers and hence to the model components.

See Also

Other methods for singular value decomposition-based techniques: methods-cancor, methods-correspondence, methods-lra, methods-mca, methods-prcomp, methods-svd

Other models from the MASS package: methods-correspondence, methods-mca

Examples

```
# data frame of Anderson iris species measurements
class(iris)
head(iris)

# default (unstandardized discriminant) coefficients
lda_ord(iris[, 1:4], iris[, 5]) %>%
  as_tbl_ord() %>%
  print() -> iris_lda

# recover centroid coordinates and measurement discriminant coefficients
get_rows(iris_lda, elements = "active")
head(get_rows(iris_lda, elements = "score"))
get_cols(iris_lda)

# augment ordination with centroid and measurement names
augment_ord(iris_lda)
```

---

methods-lm *Functionality for linear model objects*

Description

These methods extract data from, and attribute new data to, objects of class "lm", "glm", and "mlm" as returned by stats::lm() and stats::glm().

Usage

```
## S3 method for class 'lm'
as_tbl_ord(x)

## S3 method for class 'lm'
recover_rows(x)

## S3 method for class 'lm'
recover_cols(x)

## S3 method for class 'lm'
recover_coord(x)
```

```
## S3 method for class 'lm'
recover_aug_rows(x)

## S3 method for class 'lm'
recover_aug_cols(x)

## S3 method for class 'lm'
recover_aug_coord(x)

## S3 method for class 'glm'
recover_aug_rows(x)

## S3 method for class 'mlm'
recover_rows(x)

## S3 method for class 'mlm'
recover_cols(x)

## S3 method for class 'mlm'
recover_coord(x)

## S3 method for class 'mlm'
recover_aug_rows(x)

## S3 method for class 'mlm'
recover_aug_cols(x)

## S3 method for class 'mlm'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

See Also

Other methods for idiosyncratic techniques: `methods-kmeans`

Other models from the stats package: `methods-cancor`, `methods-cmds`, `methods-factanal`, `methods-kmeans`, `methods-prcomp`, `methods-princomp`

Examples

```
# Motor Trend design and performance data
head(mtcars)
# regression analysis of performance measures on design specifications
mtcars_centered <- scale(mtcars, scale = FALSE)
mtcars_centered %>%
  as.data.frame() %>%
  lm(formula = mpg ~ wt + cyl) %>%
  print() -> mtcars_lm

# wrap as a 'tbl_ord' object
(mtcars_lm_ord <- as_tbl_ord(mtcars_lm))
# augment everything with names, predictors with observation stats
augment_ord(mtcars_lm_ord)
# calculate influences as the squares of weighted residuals
mutate_rows(augment_ord(mtcars_lm_ord), influence = wt.res^2)

# regression biplot with performance isolines
mtcars_lm_ord %>%
  augment_ord() %>%
  mutate_cols(center = attr(mtcars_centered, "scaled:center")[name]) %>%
  mutate_rows(influence = wt.res^2) %T>% print() %>%
  ggbiplot(aes(x = wt, y = cyl, intercept = `(Intercept)`)) +
  #theme_biplot() +
  geom_origin(marker = "circle", radius = unit(0.02, "snpc")) +
  geom_rows_point(aes(color = influence)) +
  geom_cols_vector() +
  geom_cols_isoline(aes(center = center), by = .5, hjust = -.1) +
  ggtitle(
    "Weight isolines with data colored by importance",
    "Regressing gas mileage onto weight and number of cylinders"
  )
```

`methods-lra` *Functionality for log-ratio analysis ('lra') objects*

Description

These methods extract data from, and attribute new data to, objects of class `"lra"`, a class introduced in this package to organize the singular value decomposition of a double-centered log-transformed data matrix output by `lra()`.

Usage

```
## S3 method for class 'lra'
as_tbl_ord(x)

## S3 method for class 'lra'
recover_rows(x)
```

```
## S3 method for class 'lra'
recover_cols(x)

## S3 method for class 'lra'
recover_inertia(x)

## S3 method for class 'lra'
recover_coord(x)

## S3 method for class 'lra'
recover_conference(x)

## S3 method for class 'lra'
recover_aug_rows(x)

## S3 method for class 'lra'
recover_aug_cols(x)

## S3 method for class 'lra'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

See Also

Other methods for singular value decomposition-based techniques: `methods-cancor`, `methods-correspondence`, `methods-lda`, `methods-mca`, `methods-prcomp`, `methods-svd`

Examples

```
# data frame of violent crime arrests in the United States
class(USArrests)
head(USArrests)
# get state abbreviation data
state <- data.frame(
  name = state.name,
  abb = state.abb
)
```

```
# compute (non-compositional, unweighted) log-ratio analysis
USArrests %>%
  subset(select = -UrbanPop) %>%
  lra() %>%
  as_tbl_ord() %>%
  print() -> arrests_lra

# augment log-ratio profiles with names and join state abbreviations
arrests_lra %>%
  augment_ord() %>%
  left_join_rows(state, by = "name") %>%
  print() -> arrests_lra

# recover state and arrest profiles
head(get_rows(arrests_lra))
get_cols(arrests_lra)
# initially, inertia is conferred on neither factor
get_conference(arrests_lra)

# row-principal biplot
arrests_lra %>%
  confer_inertia("rows") %>%
  ggbiplot(aes(color = .matrix), sec.axes = "cols", scale.factor = 1/20) +
  scale_color_manual(values = c("tomato4", "turquoise4")) +
  theme_bw() + theme_biplot() +
  geom_rows_text(aes(label = abb), size = 3, alpha = .75) +
  geom_cols_polygon(fill = NA, linetype = "dashed") +
  geom_cols_text(aes(label = name, size = weight), fontface = "bold") +
  scale_size_area(guide = "none") +
  ggtitle(
    "Violent crime arrest rates",
    "Non-compositional LRA"
  ) +
  coord_scaffold() +
  guides(color = "none")
```

`methods-mca` *Functionality for multiple correspondence analysis ('mca') objects*

Description

These methods extract data from, and attribute new data to, objects of class `"mca"` from the **MASS** package.

Usage

```
## S3 method for class 'mca'
as_tbl_ord(x)
```

```
## S3 method for class 'mca'
recover_rows(x)

## S3 method for class 'mca'
recover_cols(x)

## S3 method for class 'mca'
recover_inertia(x)

## S3 method for class 'mca'
recover_conference(x)

## S3 method for class 'mca'
recover_coord(x)

## S3 method for class 'mca'
recover_supp_rows(x)

## S3 method for class 'mca'
recover_aug_rows(x)

## S3 method for class 'mca'
recover_aug_cols(x)

## S3 method for class 'mca'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Details

Multiple correspondence analysis (MCA) relies on a singular value decomposition of the indicator matrix X of a table of several categorical variables, scaled by its column totals. `MASS::mca()` returns the SVD factors UD and V as the row weights `$fs`, on which the inertia is conferred, and the column coordinates `$cs`. The row coordinates `$rs` are obtained as XV and accessible as supplementary elements.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

See Also

Other methods for singular value decomposition-based techniques: methods-cancor, methods-correspondence, methods-lda, methods-lra, methods-prcomp, methods-svd

Other models from the MASS package: methods-correspondence, methods-lda

Examples

```
# table of admissions and rejections from UC Berkeley
class(UCBAdmissions)
ucb_admissions <- as.data.frame(UCBAdmissions)
ucb_admissions <-
  ucb_admissions[rep(seq(nrow(ucb_admissions)), ucb_admissions$Freq), -4L]
head(ucb_admissions)
# perform multiple correspondence analysis
ucb_admissions %>%
  MASS::mca() %>%
  as_tbl_ord() %>%
  # augment profiles with names, masses, distances, and inertias
  augment_ord() %>%
  print() -> admissions_mca

# recover row and column coordinates and row weights
head(get_rows(admissions_mca, elements = "score"))
get_cols(admissions_mca)
head(get_rows(admissions_mca))

# column-standard biplot of factor levels
admissions_mca %>%
  ggbiplot() +
  theme_bw() + theme_biplot() +
  geom_origin() +
  #geom_rows_point(stat = "unique") +
  geom_cols_point(aes(color = factor, shape = factor)) +
  geom_cols_text_repel(aes(label = level, color = factor),
                       show.legend = FALSE) +
  scale_color_brewer(palette = "Dark2") +
  scale_size_area(guide = "none") +
  labs(color = "Factor level", shape = "Factor level")
```

---

methods-prcomp *Functionality for principal components analysis ('prcomp') objects*

Description

These methods extract data from, and attribute new data to, objects of class "prcomp" as returned by stats::prcomp().

Usage

```
## S3 method for class 'prcomp'
as_tbl_ord(x)

## S3 method for class 'prcomp'
recover_rows(x)

## S3 method for class 'prcomp'
recover_cols(x)

## S3 method for class 'prcomp'
recover_inertia(x)

## S3 method for class 'prcomp'
recover_coord(x)

## S3 method for class 'prcomp'
recover_conference(x)

## S3 method for class 'prcomp'
recover_aug_rows(x)

## S3 method for class 'prcomp'
recover_aug_cols(x)

## S3 method for class 'prcomp'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

Author(s)

Emily Paul

See Also

Other methods for singular value decomposition-based techniques: `methods-cancor`, `methods-correspondence`, `methods-lda`, `methods-lra`, `methods-mca`, `methods-svd`

Other models from the stats package: methods-cancor, methods-cmds, methods-factanal, methods-kmeans, methods-lm, methods-princomp

Examples

```
# data frame of Anderson iris species measurements
class(iris)
head(iris)

# compute scaled row-principal components of scaled measurements
iris[, -5] %>%
  prcomp(scale = TRUE) %>%
  as_tbl_ord() %>%
  print() -> iris_pca

# recover observation principal coordinates and measurement standard coordinates
head(get_rows(iris_pca))
get_cols(iris_pca)

# augment measurements with names and scaling parameters
(iris_pca <- augment_ord(iris_pca))
```

---

methods-princomp *Functionality for principal components analysis ('princomp') objects*

Description

These methods extract data from, and attribute new data to, objects of class "princomp" as returned by stats::princomp().

Usage

```
## S3 method for class 'princomp'
as_tbl_ord(x)

## S3 method for class 'princomp'
recover_rows(x)

## S3 method for class 'princomp'
recover_cols(x)

## S3 method for class 'princomp'
recover_inertia(x)

## S3 method for class 'princomp'
recover_coord(x)

## S3 method for class 'princomp'
recover_conference(x)
```

```
## S3 method for class 'princomp'
recover_supp_rows(x)

## S3 method for class 'princomp'
recover_aug_rows(x)

## S3 method for class 'princomp'
recover_aug_cols(x)

## S3 method for class 'princomp'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Details

Principal components analysis (PCA), as performed by `stats::princomp()`, relies on an eigenvalue decomposition (EVD) of the covariance matrix $X^T X$ of a data set X. `stats::princomp()` returns the EVD factor V as the loadings `$loadings`. The scores `$scores` are obtained as XV and are accessible as supplementary elements.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

Author(s)

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See Also

Other methods for eigen-decomposition-based techniques: `methods-cmds`, `methods-eigen`, `methods-factanal`

Other models from the stats package: `methods-cancor`, `methods-cmds`, `methods-factanal`, `methods-kmeans`, `methods-lm`, `methods-prcomp`

Examples

```
# data frame of Anderson iris species measurements
class(iris)
head(iris)

# compute unscaled row-principal components of scaled measurements
```

```
iris[, -5] %>%
  princomp() %>%
  as_tbl_ord() %>%
  print() -> iris_pca

# recover observation principal coordinates and measurement standard coordinates
head(get_rows(iris_pca))
get_cols(iris_pca)

# augment measurement coordinates with names and scaling parameters
(iris_pca <- augment_ord(iris_pca))
```

`methods-svd` *Functionality for singular value decompositions*

Description

These methods extract data from, and attribute new data to, objects of class `"svd_ord"` returned by `svd_ord()`.

Usage

```
## S3 method for class 'svd_ord'
as_tbl_ord(x)

## S3 method for class 'svd_ord'
recover_rows(x)

## S3 method for class 'svd_ord'
recover_cols(x)

## S3 method for class 'svd_ord'
recover_inertia(x)

## S3 method for class 'svd_ord'
recover_coord(x)

## S3 method for class 'svd_ord'
recover_conference(x)

## S3 method for class 'svd_ord'
recover_aug_rows(x)

## S3 method for class 'svd_ord'
recover_aug_cols(x)

## S3 method for class 'svd_ord'
recover_aug_coord(x)
```

Arguments

x	An ordination object.

Value

The recovery generics `recover_*()` return core model components, distribution of inertia, supplementary elements, and intrinsic metadata; but they require methods for each model class to tell them what these components are.

The generic `as_tbl_ord()` returns its input wrapped in the 'tbl_ord' class. Its methods determine what model classes it is allowed to wrap. It then provides 'tbl_ord' methods with access to the recoverers and hence to the model components.

See Also

Other methods for singular value decomposition-based techniques: `methods-cancor`, `methods-correspondence`, `methods-lda`, `methods-lra`, `methods-mca`, `methods-prcomp`

Other models from the base package: `methods-eigen`

Examples

```
# matrix of U.S. personal expenditure data
class(USPersonalExpenditure)
print(USPersonalExpenditure)
# singular value decomposition into row and column coordinates
USPersonalExpenditure %>%
  svd_ord() %>%
  as_tbl_ord() %>%
  print() -> spend_svd

# recover matrices of row and column coordinates
get_rows(spend_svd)
get_cols(spend_svd)

# augment with row and column names
augment_ord(spend_svd)
# initial matrix decomposition confers no inertia to coordinates
get_conference(spend_svd)
```

`negation` *Negation of ordination axes*

Description

Negate the coordinates of a subset of ordination axes in both row and column singular vectors.

Usage

```
get_negation(x)

revert_negation(x)

negate_ord(x, negation = NULL)

negate_to_first_orthant(x, .matrix)
```

Arguments

x	A tbl_ord.
negation	Integer vector of coordinates to negate.
.matrix	A character string partially matched (lowercase) to several indicators for one or both matrices in a matrix decomposition used for ordination. The standard values are "rows", "cols", and "dims" (for both).

Details

For purposes of comparison and visualization, it can be useful to negate the (already artificial) coordinates of an ordination, either by fixed criteria or to better align with another basis (matrix) of coordinates. negate_ord() allows the user to negate specified coordinates of an ordination.

get_negation() accesses the negations of an ordination, an integer vector of 1s and -1s stored as a "negate" attribute.

Value

negate_ord() and negate_to_first_orthant() return a tbl_ord with certain axes negated but the wrapped model unchanged. get_negation() returns the current negations. revert_negation() returns the tbl_ord without any manual negations.

A tbl_ord; the wrapped model is unchanged.

Examples

```
(pca <- ordinate(iris, cols = 1:4, prcomp))
ggbiplot(pca) + geom_rows_point() + geom_cols_vector()

# manually negate second coordinate
(pca_neg <- negate_ord(pca, 2))
ggbiplot(pca_neg) + geom_rows_point() + geom_cols_vector()

# NB: 'prcomp' method takes precedence; negations are part of the wrapper
biplot(pca)
biplot(pca_neg)

# negate to the first orthant
(pca_orth <- negate_to_first_orthant(pca, "v"))
get_negation(pca_orth)
```

`ordinate` *Fit an ordination model to a data object*

Description

This is a convenience function to fit an ordination model to a data object, wrap the result as a tbl_ord, and annotate this output with metadata from the model and possibly from the data.

Usage

```
ordinate(x, model, ...)

## Default S3 method:
ordinate(x, model, ...)

## S3 method for class 'array'
ordinate(x, model, ...)

## S3 method for class 'table'
ordinate(x, model, ...)

## S3 method for class 'data.frame'
ordinate(x, model, cols, augment, ...)

## S3 method for class 'dist'
ordinate(x, model, ...)
```

Arguments

`x`	A data object to be passed to the `model`, such as an array, table, data.frame, or stats::dist.
`model`	An ordination function whose output is coercible to class 'tbl_ord', or a symbol or character string (handled by `match.fun()`). Alternatively, a formula ~ `fun(., ...)` where `fun` is such a function and other arguments are explicit, which will be evaluated with `x` in place of `.`.
`...`	Additional arguments passed to `model`.
`cols`	<`tidy-select`> If `x` is a data frame, columns to pass to `model`. If missing, all columns are used.
`augment`	<`tidy-select`> If `x` is a data frame, columns to augment to the row data of the ordination. If missing, all columns not included in `cols` will be augmented.

Details

The default method fits the specified model to the provided data object, wraps the result as a tbl_ord, and augments this output with any intrinsic metadata from the model via `augment_ord()`.

The default method is used for most classes, though this may change in future. The data.frame method allows the user to specify what columns to include in the model and what columns with which to annotate the output.

Value

An augmented tbl_ord.

Examples

```
# LRA of arrest data
ordinate(USArrests, cols = c(Murder, Rape, Assault), lra)

# CMDS of inter-city distance data
ordinate(UScitiesD, cmdscale_ord, k = 3L)

# PCA of iris data
ordinate(iris, princomp, cols = -Species, augment = c(Sepal.Width, Species))
ordinate(iris, cols = 1:4, ~ prcomp(., center = TRUE, scale. = TRUE))

# CA of hair & eye color data
haireye <- as.data.frame(rowSums(HairEyeColor, dims = 2L))
ordinate(haireye, MASS::corresp, cols = everything())

# FA of Swiss social data
ordinate(swiss, model = factanal, factors = 2L, scores = "Bartlett")

# LDA of iris data
ordinate(iris, ~ lda_ord(.[, 1:4], .[, 5]))

# CCA of savings data
ordinate(
  LifeCycleSavings[, c("pop15", "pop75")],
  # second data set must be handled as an additional parameter to `model`
  y = LifeCycleSavings[, c("sr", "dpi", "ddpi")],
  model = cancor_ord, scores = TRUE
)
```

---

ordr-ggproto *ggproto classes created and adapted for ordr*

Description

In addition to geometric element layers (geoms) based on base-**ggplot2** layers like `geom_point()` but specified to matrix factors as `geom_row_point()`, **ordr** introduces ggproto classes for some additional geometric elements commonly used in biplots. The factor-specific geoms invoke the statistical transformation layers (stats) `stat_rows()` and `stat_cols()`, which specify the matrix factor. Because each ggplot layer consists of only one stat and one geom, this necessitates that ggproto classes for new stats must also come in `*Rows` and `*Cols` flavors.

See Also

ggplot2::ggplot2-ggproto and ggplot2::ggproto for explanations of base ggproto classes in **ggplot2** and how to create new ones.

`plot.tbl_ord` *Plot and biplot methods for 'tbl_ord' objects*

Description

Adapt **stats** 'prcomp' and 'princomp' methods for `plot()`, `screeplot()`, and `biplot()` generics to 'tbl_ord' objects.

Usage

```
## S3 method for class 'tbl_ord'
plot(x, main = deparse(substitute(x)), ...)

## S3 method for class 'tbl_ord'
screeplot(x, main = deparse(substitute(x)), ...)

## S3 method for class 'tbl_ord'
biplot(x, main = deparse(substitute(x)), ...)
```

Arguments

`x`	A 'tbl_ord' object.
`main`	A main title for the plot, passed to other methods (included to enable parsing of object name).
`...`	Additional arguments passed to other methods.

Details

These methods defer to any `plot()` and `biplot()` methods for the original, underlying model classes of 'tbl_ord' objects. If none are found: Following the examples of `stats::plot.prcomp()` and `stats::plot.princomp()`, `plot.tbl_ord()` calls on `stats::screeplot()` to produce a scree plot of the decomposition of variance in the singular value decomposition. Similarly following `stats::biplot.prcomp()` and `stats::biplot.princomp()`, `biplot.tbl_ord()` produces a biplot of both rows and columns, using text labels when available and markers otherwise, with rows and columns distinguished by color and no additional annotation (e.g. vectors). The biplot confers inertia according to `get_conference()` unless the proportions do not sum to 1, in which case it produces a symmetric biplot (inertia conferred equally to rows and columns).

Value

Nothing, but a plot is produced on the current graphics device.

Examples

```
# note: behavior depends on installed packages with class-specific methods

# class 'prcomp'
iris_pca <- prcomp(iris[, -5L], scale = TRUE)
iris_pca_ord <- as_tbl_ord(iris_pca)
plot(iris_pca)
plot(iris_pca_ord)
screeplot(iris_pca)
screeplot(iris_pca_ord)
biplot(iris_pca)
biplot(iris_pca_ord)

# class 'correspondence'
haireye_ca <- MASS::corresp(rowSums(HairEyeColor, dims = 2L), nf = 2L)
haireye_ca_ord <- as_tbl_ord(haireye_ca)
plot(haireye_ca)
plot(haireye_ca_ord)
# no `screeplot()` method for class 'correspondence'
screeplot(haireye_ca_ord)
biplot(haireye_ca)
biplot(haireye_ca_ord)
```

---

qswur_usa *U.S. university rankings*

Description

Classifications and rankings of U.S. universities for the years 2017–2020.

Usage

```
data(qswur_usa)
```

Format

A tibble of 13 variables on 612 cases:

`year` year of rankings

`institution` institution of higher learning

`size` size category of institution

`focus` subject range of institution

`res` research intensity of institution

`age` age classification of institution

`status` status of institution

`rk_academic` rank by academic reputation

`rk_employer` rank by employer reputation

`rk_ratio` rank by faculty–student ratio

`rk_citations` rank by citations per faculty

`rk_intl_faculty` rank by international faculty ratio

`rk_intl_students` rank by international student ratio

Details

Ranking data were obtained from the public QS website.

Source

Quacquarelli Symonds (2021).

References

Quacquarelli Symonds (2021) "University Rankings". TopUniversities.com https://www.topuniversities.com/university-rankings.

Examples

```
# subset QS data to rank variables
head(qswur_usa)
qs_ranks <- subset(
  qswur_usa,
  complete.cases(qswur_usa),
  select = 8:13
)
# calculate Kendall correlation matrix
qs_cor <- cor(qs_ranks, method = "kendall")

# calculate eigendecomposition
qs_eigen <- eigen_ord(qs_cor)
# view correlations as cosines of biplot vectors
biplot(x = qs_eigen$vectors, y = qs_eigen$vectors, col = c(NA, "black"))
```

---

recoverers *Access factors, coordinates, and metadata from ordination objects*

Description

These functions return information about the matrix factorization underlying an ordination.

Usage

```
recover_rows(x)

recover_cols(x)

## Default S3 method:
recover_rows(x)

## Default S3 method:
recover_cols(x)

## S3 method for class 'data.frame'
recover_rows(x)

## S3 method for class 'data.frame'
recover_cols(x)

get_rows(x, elements = "all")

get_cols(x, elements = "all")

## S3 method for class 'tbl_ord'
as.matrix(x, ..., .matrix, elements = "all")

recover_inertia(x)

## Default S3 method:
recover_inertia(x)

recover_coord(x)

## Default S3 method:
recover_coord(x)

## S3 method for class 'data.frame'
recover_coord(x)

get_coord(x)

get_inertia(x)

## S3 method for class 'tbl_ord'
dim(x)
```

Arguments

x	An object of class 'tbl_ord'.
elements	Character vector; which elements of each factor for which to render graphical

elements. One of "active" (the default) or any supplementary element type defined by the specific class methods (e.g. "score" for 'factanal', 'lda_ord', and 'cancord_ord' and "intraset" and "interset" for 'cancor_ord'), via partial matching.

... Additional arguments from base::as.matrix(); ignored.

.matrix A character string partially matched (lowercase) to several indicators for one or both matrices in a matrix decomposition used for ordination. The standard values are "rows", "cols", and "dims" (for both).

Details

The recover_*() S3 methods extract one or both of the row and column matrix factors that constitute the original ordination. These are interpreted as the case scores (rows) and the variable loadings (columns). The get_*() functions optionally (and by default) include any supplemental observations (see supplementation).

The recover_*() functions are generics that require methods for each ordination class. They are not intended to be called directly but are exported so that users can query methods("recover_*").

get_coord() retrieves the names of the coordinates shared by the matrix factors on which the original data were ordinated, and get_inertia() retrieves a vector of the inertia with these names. dim() retrieves the dimensions of the row and column factors, which reflect the dimensions of the matrix they reconstruct—**not** the original data matrix. (This matters for techniques that rely on eigendecomposition, for which the decomposed matrix is square.)

Value

The recover_*() functions are generics whose methods return base R objects retrieved from the model wrapped in the 'tbl_ord' class:

- rows: the row matrix as stored in the model
- cols: the column matrix as stored in the model
- inertia: the vector of eigen-values or squared singular values, often known by other names depending on the model
- coord: names for the artificial axes, from the model if available The get_*() functions (which are not generics) return modifications of these objects:
- rows: the recovered rows, adjusted according to any negation of axes or conference of inertia
- cols: the recovered columns, adjusted according to any negation of axes or conference of inertia
- inertia: the recovered inertia, named by the recovered coordinates
- coord: the recovered coordinates (unmodified) dim() returns the dimensions of the decomposed matrix, i.e. the numbers of rows of recover_rows() and of recover_cols().

See Also

Other generic recoverers: augmentation, conference, supplementation

Examples

```
# example ordination: LRA of U.S. arrests data
arrests_lra <- ordinate(USArrests, cols = c(Murder, Rape, Assault), lra)

# extract matrix factors
as.matrix(arrests_lra, .matrix = "rows")
as.matrix(arrests_lra, .matrix = "cols")
# special named functions
get_rows(arrests_lra)
get_cols(arrests_lra)
# get dimensions of underlying matrix factorization (not of original data)
dim(arrests_lra)

# get names of artificial / latent coordinates
get_coord(arrests_lra)
# get distribution of inertia
get_inertia(arrests_lra)
```

`stat_projection` *Project rows onto columns or vice-versa*

Description

Compute projections of vectors from one matrix factor onto those of the other.

Usage

```
stat_projection(
  mapping = NULL,
  data = NULL,
  geom = "segment",
  position = "identity",
  referent = NULL,
  ...,
  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)).

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".
- For more information and other ways to specify the geom, see the layer geom documentation.

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".
- For more information and other ways to specify the position, see the layer position documentation.

referent — The reference data set, admitting the same 3 options as data; see Details.

... — Additional arguments passed to ggplot2::layer().

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. annotation_borders().

Details

An ordination model of continuous data can be used to predict values along one dimension from those along the other, using the artificial axes as intermediaries. The predictions correspond geometrically to projections of elements of one matrix factor in principal coordinates onto those of the other factor in standard coordinates. In the most familiar setting of PCA biplots, variable (column) values are predicted from case (row) locations along PC1 and PC2. This transformation obtains the axis projections as xend,yend and pairs them with original points x,y to demarcate segments visualizing the projections.

WARNING: This layer is appropriate only with axes in standard coordinates (usually `confer_inertia(p = "rows")`) and predictive calibration, e.g. `geom_cols_axis(axis.type = "predictive")`.

Use the same mapped coordinates for the projection layer and the axes. When `ord_aes()` maps more than two coordinates, projections and axes are computed from all mapped model coordinates; when only `x` and `y` are mapped, both use the plot-plane coordinates.

Value

A ggproto layer.

Referential stats

This statistical transformation is done with respect to reference data passed to `referent` (ignored if `NULL`, the default, possibly resulting in empty output). See `gggda::stat_referent()` for more details. This relies on a sleight of hand through a new undocumented `LayerRef` class and associated `ggplot2::ggplot_add()` method. As a result, only layers constructed using this `stat_*()` shortcut will pass the necessary positional aesthetics to the `$setup_params()` step, making them available to pre-process `referent` data.

The biplot shortcuts automatically substitute the complementary matrix factor for `referent = NULL` and will use an integer vector to select a subset from this factor. These uses do not require the mapping passage.

Biplot layers

`ggbiplot()` uses `ggplot2::fortify()` internally to produce a single data frame with a `.matrix` column distinguishing the subjects (`"rows"`) and variables (`"cols"`). The stat layers `stat_rows()` and `stat_cols()` simply filter the data frame to one of these two.

The geom layers `geom_rows_*()` and `geom_cols_*()` call the corresponding stat in order to render plot elements for the corresponding factor matrix. `geom_dims_*()` selects a default matrix based on common practice, e.g. points for rows and arrows for columns.

Ordination aesthetics

This statistical transformation is compatible with the convenience function `ord_aes()`.

Some transformations (e.g. `stat_center()`) commute with projection to the lower (1 or 2)-dimensional biplot space. If they detect aesthetics of the form `..coord[0-9]+`, then `..coord1` and `..coord2` are converted to `x` and `y` while any remaining are ignored.

Other transformations (e.g. `stat_spantree()`) yield different results in a lower-dimensional biplot when they are computed before versus after projection. If the stat layer detects these aesthetics, then the transformation is performed before projection, and the results in the first two dimensions are returned as `x` and `y`.

A small number of transformations (`stat_rule()`) are incompatible with ordination aesthetics but will accept `ord_aes()` without warning.

Computed variables

These are calculated during the statistical transformation and can be accessed with delayed evaluation.

`xend,yend` projections onto (specified) vectors

Examples

```
# simplify the Motor Trends data to two predictors legible at aspect ratio 1
mtcars %>%
  transform(hp00 = hp/100) %>%
  subset(select = c(mpg, hp00, wt)) ->
  subcars
# compute the gradient of `mpg` against these two predictors
lm(mpg ~ hp00 + wt, subcars) %>%
  coefficients() %>%
  as.list() %>% as.data.frame() ->
  grad
# project the data onto the gradient axis (with a reversed gradient vector)
ggplot(subcars, aes(x = hp00, y = wt)) +
  coord_equal() +
  geom_point(shape = "circle open") +
  geom_vector(data = -grad) +
  stat_projection(referent = grad)
```

`stat_rows` *Render plot elements for one matrix of an ordination*

Description

These stats merely tell `ggplot2::ggplot()` which factor of an ordination to pull data from for a plot layer. They are invoked internally by the various `geom_*_*()` layers.

Usage

```
stat_rows(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  subset = NULL,
  elements = "active",
  ...,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_cols(
  mapping = NULL,
  data = NULL,
  geom = "axis",
  position = "identity",
  subset = NULL,
```

```
  elements = "active",
  ...,
  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)).
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". • For more information and other ways to specify the geom, see the layer geom documentation.
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". • For more information and other ways to specify the position, see the layer position documentation.
subset	An integer, logical, or character vector indicating a subset of rows or columns for which to render graphical elements. NB: Internally, the subset will be taken from the rows of the fortified 'tbl_ord' comprising rows from only one of the matrix factors. It is still possible to pass a formula to the data parameter, but it will act on the fortified data *before* it has been restricted to one matrix factor.

elements	Character vector; which elements of each factor for which to render graphical elements. One of "active" (the default) or any supplementary element type defined by the specific class methods (e.g. "score" for 'factanal', 'lda_ord', and 'cancord_ord' and "intraset" and "interset" for 'cancor_ord'), via partial matching.
...	Additional arguments passed to ggplot2::layer().
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. annotation_borders().

Value

A ggproto layer.

Biplot layers

ggbiplot() uses ggplot2::fortify() internally to produce a single data frame with a .matrix column distinguishing the subjects ("rows") and variables ("cols"). The stat layers stat_rows() and stat_cols() simply filter the data frame to one of these two.

The geom layers geom_rows_*() and geom_cols_*() call the corresponding stat in order to render plot elements for the corresponding factor matrix. geom_dims_*() selects a default matrix based on common practice, e.g. points for rows and arrows for columns.

See Also

Other biplot layers: biplot-geoms, biplot-stats

Examples

```
# FA of Swiss social data
swiss_fa <-
  ordinate(swiss, model = factanal, factors = 2L, scores = "regression")
# active and supplementary elements
get_rows(swiss_fa, elements = "active")
head(get_rows(swiss_fa, elements = "score"))

# biplot using matrix stats and element filter
ggbiplot(swiss_fa) +
  stat_rows(elements = "score") +
  stat_cols(geom = "vector", aes(label = name))

# biplot using element filter and item selection
# (note that filter precedes selection)
ggbiplot(swiss_fa) +
```

```
  geom_rows_point(elements = "score") +
  geom_rows_label(aes(label = name), elements = "score", subset = c(1, 4, 18)) +
  scale_alpha_manual(values = c(0, 1), guide = "none") +
  geom_cols_vector(aes(label = name))
```

`supplementation` *Supplement 'tbl_ord' objects with new data*

Description

These functions attach supplementary rows or columns to an ordination object.

Usage

```
recover_supp_rows(x)

## Default S3 method:
recover_supp_rows(x)

recover_supp_cols(x)

## Default S3 method:
recover_supp_cols(x)
```

Arguments

`x`	An object of class 'tbl_ord'.

Details

The `recover_supp_*()` S3 methods produce matrices of supplemental rows or columns of a tbl_ord object from the object itself. The motivating example is linear discriminant analysis, which produces a natural biplot of class discriminant centroids and variable axes but is usually supplemented with case discriminant scores. The supplementary values are augmented with an `.element` column whose value indicates their source and can be incorporated into a tidied form. If no supplementary rows of a factor are produced, the functions return `NULL`.

Value

Matrices having the same numbers of columns as returned by `recover_rows()` and `recover_cols()`.

See Also

Other generic recoverers: `augmentation`, `conference`, `recoverers`

tbl_ord *A unified ordination object class*

Description

These functions wrap ordination objects in the class tbl_ord, create tbl_ords directly from matrices, and test for the class and basic structure.

Usage

```
as_tbl_ord(x)

## S3 method for class 'tbl_ord'
as_tbl_ord(x)

make_tbl_ord(rows = NULL, cols = NULL, ...)

is_tbl_ord(x)

is.tbl_ord(x)

valid_tbl_ord(x)

un_tbl_ord(x)
```

Arguments

x	An ordination object.
rows, cols	Matrices to be used as factors of a tbl_ord.
...	Additional elements of a custom tbl_ord.

Details

The tbl_ord class wraps around a range of ordination classes, making available a suite of ordination tools that specialize to each original object class. These tools include `format()` and `ggplot2::fortify()` methods, which facilitate the `print()` method and the `ggbiplot()` function.

No default method is provided for `as_tbl_ord()`, despite most defined methods being equivalent (simply appending 'tbl_ord' to the vector of object classes). This prevents objects for which other methods are not defined from being re-classed as tbl_ords.

The function `make_tbl_ord()` creates a tbl_ord structured as a list of two matrices, `u` and `v`, which must have the same number of columns and the same column names.

`is_tbl_ord()` checks an object `x` for the tbl_ord class; `valid_tbl_ord()` additionally checks for consistency between `recover_coord(x)` and the columns of `recover_rows(x)` and `recover_cols(x)`, using the recoverers. `un_tbl_ord()` removes attributes associated with the tbl_ord class in order to restore an object that was originally passed to `as_tbl_ord`.

Value

A tbl_ord (`as*()`, `make*()`), an S3-class model object that can be wrapped as one (`un*()`), or a logical value (`is*()`, `value*()`).

Examples

```
# illustrative ordination: FA of Swiss social data
swiss_fa <- factanal(swiss, factors = 3L, scores = "regression")
print(swiss_fa)

# add the 'tbl_ord' wrapper
swiss_fa_ord <- as_tbl_ord(swiss_fa)
# inspect wrapped model
is_tbl_ord(swiss_fa_ord)
print(swiss_fa_ord)
valid_tbl_ord(swiss_fa_ord)
# unwrap the model
un_tbl_ord(swiss_fa_ord)

# create a 'tbl_ord' directly from row and column factors
# (missing inertia & other attributes)
swiss_fa_ord2 <- make_tbl_ord(rows = swiss_fa$scores, cols = swiss_fa$loadings)
# inspect wrapped factors
is_tbl_ord(swiss_fa_ord2)
print(swiss_fa_ord2)
valid_tbl_ord(swiss_fa_ord2)
# unwrap factors
un_tbl_ord(swiss_fa_ord2)
```

---

theme_scaffold *Scaffolding theme*

Description

Omit cartesian coordinate visual aids.

Usage

```
theme_scaffold()

theme_biplot()
```

Details

Geometric data analysis concerns the intrinsic geometry of data. Analyses often use artificial or arbitrary coordinate systems that carry no useful interpretation but instead serve as scaffolding, especially for graphical elements like axes that represent other variables (Gardner, 2001). In such cases, the visual aids (tick marks and labels, grid lines) used to recover the coordinates of the row and column markers would add unnecessary clutter and should be omitted. This partial theme

updates the current theme by removing these elements. The biplot theme is an alias included for convenience and backward compatibility.

Value

A ggplot theme.

References

Gardner S (2001) *Extensions of biplot methodology to discriminant analysis with applications of non-parametric principal components*. PhD thesis, Stellenbosch University. https://scholar.sun.ac.za/items/279f7958-0b54-43f1-8c75-da652f65db3f

---

`tidiers` *Tidiers for 'tbl_ord' objects*

Description

These functions return tibbles that summarize an object of class 'tbl_ord'. `tidy()` output contains one row per artificial coordinate and `glance()` output contains one row for the whole ordination.

Usage

```
## S3 method for class 'tbl_ord'
tidy(x, ...)

## S3 method for class 'tbl_ord'
glance(x, ...)

## S3 method for class 'tbl_ord'
fortify(model, data, ..., .matrix = "dims", elements = "all")
```

Arguments

`x`, `model`	An object of class 'tbl_ord'.
`...`	Additional arguments allowed by generics; currently ignored.
`data`	Passed to generic methods; currently ignored.
`.matrix`	A character string partially matched (lowercase) to several indicators for one or both matrices in a matrix decomposition used for ordination. The standard values are `"rows"`, `"cols"`, and `"dims"` (for both).
`elements`	Character vector; which elements of each factor for which to render graphical elements. One of `"active"` (the default) or any supplementary element type defined by the specific class methods (e.g. `"score"` for 'factanal', 'lda_ord', and 'cancord_ord' and `"intraset"` and `"interset"` for 'cancor_ord'), via partial matching.

Details

Three generics popularized by the **ggplot2** and **broom** packages make use of the augmentation methods:

- The `generics::tidy()` method summarizes information about model components, which here are the artificial coordinates created by ordinations. The output can be passed to `ggplot2::ggplot()` to generate scree plots. The returned columns are
  - `name`: (the name of) the coordinate
  - other columns extracted from the model, usually a single additional column of the singular or eigen values
  - `inertia`: the multidimensional variance
  - `prop_var`: the proportion of inertia
  - `quality`: the cumulative proportion of variance
- The `generics::glance()` method reports information about the entire model, here always treated as one of a broader class of ordination models. The returned columns are
  - `rank`: the rank of the ordination model, i.e. the number of ordinates
  - `n.row`,`n.col`: the dimensions of the decomposed matrix
  - `inertia`: the total inertia in the ordination
  - `prop.var.*`: the proportion of variance in the first 2 ordinates
  - `class`: the class of the wrapped model object
- The `ggplot2::fortify()` method augments and collapses row and/or column data, depending on `.matrix` and `.element`, into a single tibble, in preparation for `ggplot2::ggplot()`. Its output resembles that of `generics::augment()`, though rows in the output may correspond to rows, columns, or both of the original data. If `.matrix` is passed `"rows"`, `"cols"`, or `"dims"` (for both), then `fortify()` returns a tibble whose fields are obtained, in order, via `get_*()`, `recover_aug_*()`, and `annotation_*()`.

The tibble is assigned a `"coordinates"` attribute whose value is obtained via `get_coord()`. This facilitates some downstream functionality that relies on more than those coordinates used as position aesthetics in a biplot, in particular `stat_spantree()`.

Value

A tibble.

See Also

augmentation methods that must interface with tidiers.

Examples

```
# illustrative ordination: PCA of iris data
iris_pca <- ordinate(iris, ~ prcomp(., center = TRUE, scale. = TRUE), seq(4L))

# use `tidy()` to summarize distribution of inertia
tidy(iris_pca)
# this facilitates scree plots
```

```
tidy(iris_pca) %>%
  ggplot(aes(x = name, y = prop_var)) +
  geom_col() +
  scale_y_continuous(labels = scales::percent) +
  labs(x = NULL, y = "Proportion of variance")

# use `fortify()` to prepare either matrix factor for `ggplot()`
fortify(iris_pca, .matrix = "V") %>%
  ggplot(aes(x = name, y = PC1)) +
  geom_col() +
  coord_flip() +
  labs(x = "Measurement")
iris_pca %>%
  fortify(.matrix = "U") %>%
  ggplot(aes(x = PC1, fill = Species)) +
  geom_histogram() +
  labs(y = NULL)
# ... or to prepare both for `ggbiplot()`
fortify(iris_pca)

# use `glance()` to summarize the model as an ordination
glance(iris_pca)
# this enables comparisons to other models
rbind(
  glance(ordinate(subset(iris, Species == "setosa"), prcomp, seq(4L))),
  glance(ordinate(subset(iris, Species == "versicolor"), prcomp, seq(4L))),
  glance(ordinate(subset(iris, Species == "virginica"), prcomp, seq(4L)))
)
```

---

wrap-ord *Wrappers for lossy ordination methods*

Description

These *_ord functions wrap core R functions with modifications for use with 'tbl_ord' methods. Some parameters are hidden from the user and set to settings required for these methods, some matrix outputs are given row or column names to be used by them, and new '*_ord' S3 class attributes are added to enable them.

Usage

```
eigen_ord(x, symmetric = isSymmetric.matrix(x))

svd_ord(x, nu = min(dim(x)), nv = min(dim(x)))

cmdscale_ord(d, k = 2, add = FALSE)

cancor_ord(x, y, xcenter = TRUE, ycenter = TRUE, scores = FALSE)
```

Arguments

x	a numeric or complex matrix whose spectral decomposition is to be computed. Logical matrices are coerced to numeric.
symmetric	if TRUE, the matrix is assumed to be symmetric (or Hermitian if complex) and only its lower triangle (diagonal included) is used. If symmetric is not specified, isSymmetric(x) is used.
nu	the number of left singular vectors to be computed. This must between 0 and n = nrow(x).
nv	the number of right singular vectors to be computed. This must be between 0 and p = ncol(x).
d	a distance structure such as that returned by dist or a full symmetric matrix containing the dissimilarities.
k	the maximum dimension of the space which the data are to be represented in; must be in $\{1, 2, \ldots, n-1\}$.
add	logical indicating if an additive constant $c*$ should be computed, and added to the non-diagonal dissimilarities such that the modified dissimilarities are Euclidean.
y	numeric matrix ($n \times p_2$), containing the y coordinates.
xcenter	logical or numeric vector of length p_1, describing any centering to be done on the x values before the analysis. If TRUE (default), subtract the column means. If FALSE, do not adjust the columns. Otherwise, a vector of values to be subtracted from the columns.
ycenter	analogous to xcenter, but for the y values.
scores	Logical; whether to return canonical scores and structure correlations.

Details

The following table summarizes the wrapped functions:

Original function	Hide params	New params	Add names	New class
base::eigen()	Yes	No	Yes	Yes
base::svd()	Yes	No	Yes	Yes
stats::cmdscale()	Yes	No	No	Yes
stats::cancor()	No	Yes	No	Yes

NB: eigen_ord() is deprecated in favor of eigen(), which for some time has returned an S3 class (with recovery methods in **ordr**).

By default, cancor_ord() returns the same data as stats::cancor(): the canonical correlations (cor), the canonical coefficients ($xcoef and $ycoef), and the variable means ($xcenter, $ycenter). If scores = TRUE, then cancor_ord() also returns the scores $xscores and $yscores calculated from the (appropriately centered) data and the coefficients and the intraset structure correlations $xstructure and $ystructure between these and the data. These modifications are inspired by the cancor() function in **candisc**, though two caveats should be noted: First, the canonical coefficients (hence the canonical scores) are scaled by $n - 1$ compared to these, though the intraset structure correlations are the same. Second, the *interset* structure correlations are not returned, as these may be obtained by conferring inertia unto the intraset ones.

Value

Objects slightly modified from the outputs of the original functions, with new '*-ord' classes.

Examples

```
# glass composition data from one furnace
glass_banias <- subset(
  glass,
  Context == "L.15;B.166",
  select = c("SiO2", "Na2O", "CaO", "Al2O3", "MgO", "K2O")
)
# eigendecomposition of a covariance matrix
(glass_cov <- cov(glass_banias))
eigen_ord(glass_cov)
# singular value decomposition of a data matrix
svd_ord(glass_banias)
# classical multidimensional scaling of a distance matrix
cmdscale_ord(dist(glass_banias))

# canonical correlation analysis with trace components
glass_banias_minor <- subset(
  glass,
  Context == "L.15;B.166",
  select = c("TiO2", "FeO", "MnO", "P2O5", "Cl", "SO3")
)
# impute value just below smallest recorded value
glass_banias_minor$TiO2[[1L]] <- 0.5
cancor_ord(glass_banias, glass_banias_minor)

# calculate canonical scores and structure correlations
glass_cca <-
  cancor_ord(glass_banias[, 1:3], glass_banias_minor[, 1:3], scores = TRUE)
# scores
glass_cca$xscores
# intraset correlations
glass_cca$xstructure
# interset correlations
glass_cca$xstructure %*% diag(glass_cca$cor)
```

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