

Package: tidypaleo (via r-universe)

September 7, 2024

Title Tidy Tools for Paleoenvironmental Archives

Version 0.1.3.9000

Description Provides a set of functions with a common framework for age-depth model management, stratigraphic visualization, and common statistical transformations. The focus of the package is stratigraphic visualization, for which 'ggplot2' components are provided to reproduce the scales, geometries, facets, and theme elements commonly used in publication-quality stratigraphic diagrams. Helpers are also provided to reproduce the exploratory statistical summaries that are frequently included on stratigraphic diagrams. See Dunnington et al. (2021) <doi:10.18637/jss.v101.i07>.

Depends R (>= 3.4.0)

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Suggests testthat, knitr, rmarkdown, vegan, patchwork, forcats, vdiff

URL <https://paleolimbot.github.io/tidypaleo/>,
<https://github.com/paleolimbot/tidypaleo>

BugReports <https://github.com/paleolimbot/tidypaleo/issues>

Imports rlang, tidyselect, dplyr, vctrs, tibble, scales, ggplot2 (>= 3.0.0), styler, purrr, ggstance, stringr, withr, tidyr (>= 1.0.2), digest, rioja

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

Repository <https://paleolimbot.r-universe.dev>

RemoteUrl <https://github.com/paleolimbot/tidypaleo>

RemoteRef HEAD

RemoteSha 4c5114026119fc7fd40ae5b017456f950fd578db

Contents

age_depth_as_sec_axis	2
age_depth_interpolate	3
age_depth_model	4
alta_lake_210Pb_ages	5
as_trans_factory	6
facet_abundanceh	7
geom_col_segsh	10
geom_lineh	11
geom_point_exaggerate	12
geom_ribbonh	14
halifax_lakes_plottable	15
keji_lakes_plottable	16
kellys_lake_cladocera	17
label_geochem	17
label_species	18
layer_dendrogram	19
layer_scores	21
long_lake_14C_ages	22
nested_analysis	23
nested_data	24
nested_hclust	25
nested_pcomp	27
plot.age_depth_model	28
plot.nested_analysis	29
predict.age_depth_model	30
rotated_facet_labels	31
scale_x_abundance	32
scale_y_depth_age	33
sequential_layer_facets	35
stat_nested_hclust	35
theme_paleo	37
Index	38

age_depth_as_sec_axis *Use an age depth model as a second ggplot axis*

Description

Use an age depth model as a second ggplot axis

Usage

```
age_depth_as_sec_axis(x, primary = c("depth", "age"), ...)
```

Arguments

x	An age_depth_model
primary	Specify the primary axis as 'age' or 'depth'
...	Passed to sec_axis

Value

A ggplot2 [sec_axis](#) for use in [scale_x_continuous](#), [scale_y_continuous](#), or their reverse variants.

Examples

```
library(ggplot2)
alta_lake_adm <- age_depth_model(
  alta_lake_210Pb_ages,
  depth = depth_cm,
  age = age_year_ad
)

ggplot(alta_lake_210Pb_ages, aes(y = depth_cm, x = age_year_ad)) +
  geom_path() +
  geom_point() +
  scale_y_reverse(sec.axis = age_depth_as_sec_axis(alta_lake_adm))
```

age_depth_interpolate *Age-depth model interpolators/extrapolators*

Description

Age-depth model interpolators/extrapolators

Usage

```
age_depth_interpolate(x, y)

age_depth_extrapolate(x, y, x0 = last, y0 = last, slope = NULL)

age_depth_exact(x, y)

age_depth_na(x, y)
```

Arguments

x	A paired vector of x values
y	A paired vector of y values
x0	The x value to anchor the transform
y0	The y value to anchor the transform
slope	The slope (in units of y/x) to use for the transform

Value

A list with component functions `trans` and `inverse`

Examples

```
age_depth_model(
  alta_lake_210Pb_ages,
  depth = depth_cm, age = age_year_ad,
  age_max = age_year_ad + age_error_yr,
  age_min = age_year_ad - age_error_yr,
  extrapolate_age_below = ~age_depth_extrapolate(
    tail(.x, 3), tail(.y, 3), x0 = dplyr::last, y0 = dplyr::last
  ),
  extrapolate_age_above = ~age_depth_extrapolate(
    head(.x, 3), head(.y, 3), x0 = dplyr::first, y0 = dplyr::first
  )
)
```

age_depth_model	<i>Create age depth models</i>
-----------------	--------------------------------

Description

Create age depth models

Usage

```
age_depth_model(
  .data = NULL,
  depth,
  age,
  age_min = NA_real_,
  age_max = NA_real_,
  interpolate_age = age_depth_interpolate,
  extrapolate_age_below = ~age_depth_extrapolate(.x, .y, x0 = last, y0 = last),
  extrapolate_age_above = ~age_depth_extrapolate(.x, .y, x0 = first, y0 = first),
  interpolate_age_limits = age_depth_exact,
  extrapolate_age_limits_below = age_depth_na,
  extrapolate_age_limits_above = age_depth_na
)
```

Arguments

<code>.data</code>	A data frame
<code>depth, age, age_min, age_max</code>	Expressions evaluated in <code>.data</code> that provide the known depths, known ages, and error information if available. These expressions are evaluated like they are within <code>mutate</code> if <code>.data</code> is present.

interpolate_age, extrapolate_age_below, extrapolate_age_above

These arguments provide the rules for interpolating and extrapolating ages based on depths.

interpolate_age_limits, extrapolate_age_limits_below,
extrapolate_age_limits_above

These arguments provide the rules for interpolating and extrapolating age min and max values based on depths.

Value

An age depth model object.

Examples

```
age_depth_model(
  alta_lake_210Pb_ages,
  depth = depth_cm, age = age_year_ad,
  age_max = age_year_ad + age_error_yr,
  age_min = age_year_ad - age_error_yr
)
```

alta_lake_210Pb_ages *Alta Lake Lead-210 and Carbon-14 Ages*

Description

The `alta_lake_210Pb_ages` object contains raw depths and ages for Alta Lake (Whistler, British Columbia, Canada) core AL-GC2 (Dunnington et al. 2016; Dunnington 2015). For these values, ages were calculated from Lead-210 activities using the constant rate of supply (CRS) model (Appleby and Oldfield 1983). The `alta_lake_14C_ages` object contains one uncalibrated Carbon-14 measurement from the same core. The `alta_lake_bacon_ages` object contains the combined result of the Lead-210 and the Carbon-14 ages as modelled by the `rbacon` package (Blaauw and Christen 2011).

Usage

`alta_lake_210Pb_ages`

`alta_lake_14C_ages`

`alta_lake_bacon_ages`

`alta_lake_geochem`

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 9 rows and 5 columns.

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 1 rows and 5 columns.

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 58 rows and 5 columns.

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 192 rows and 9 columns.

References

Appleby, P. G., and F. Oldfield. "The Assessment of 210Pb Data from Sites with Varying Sediment Accumulation Rates." *Hydrobiologia* 103, no. 1 (July 1, 1983): 29–35. doi:10.1007/BF00028424.

Blaauw, Maarten, and J. Andrés Christen. "Flexible Paleoclimate Age-Depth Models Using an Autoregressive Gamma Process." *Bayesian Analysis* 6, no. 3 (September 2011): 457–74. doi:10.1214/ba/1339616472.

Dunnington, Dewey W., Ian S. Spooner, Chris E. White, R. Jack Cornett, Dave Williamson, and Mike Nelson. "A Geochemical Perspective on the Impact of Development at Alta Lake, British Columbia, Canada." *Journal of Paleolimnology* 56, no. 4 (November 2016): 315–330. doi:10.1007/s109330169919x.

Dunnington, Dewey W. "A 500-Year Applied Paleolimnological Assessment of Environmental Change at Alta Lake, Whistler, British Columbia, Canada." M.Sc. Thesis, Acadia University, 2015. <https://scholar.acadiau.ca/islandora/object/theses:411>.

Examples

```
alta_lake_210Pb_ages
alta_lake_14C_ages
alta_lake_bacon_ages
```

as_trans_factory

Coerce and validate transforms and functions that produce them

Description

Coerce and validate transforms and functions that produce them

Usage

```
as_trans_factory(factory, env = parent.frame())
```

```
validate_trans_factory(factory, x = 1:3, y = 1:3)
```

```
validate_trans(trans, x = 1:3, y = 1:3)
```

Arguments

factory	A function that produces a transform object
env	The calling environment, for transform factories that are calls or rlang lambda-style functions.
x	The test x data
y	The test y data
trans	A transform object

Value

The input, invisibly.

Examples

```
as_trans_factory(age_depth_interpolate)
```

facet_abundanceh	<i>Facet for relative abundance data</i>
------------------	--

Description

Provides a number of modifications to the plot that are necessary for relative abundance plots of a number of species. See [scale_x_abundance](#), [facet_grid](#), [facet_grid](#), [label_species](#), [label_geochem](#), and [rotated_facet_labels](#) [rotated_axis_labels](#) for examples of how to customize the default behaviour.

Usage

```
facet_abundanceh(
  taxon,
  grouping = NULL,
  rotate_facet_labels = 45,
  labeller = label_species,
  scales = "free_x",
  space = "free_x",
  dont_italicize = c("\\(.*?\\)", "spp?\\.\"", "-complex", "[Oo]ther"),
  ...
)
```

```
facet_abundance(
  taxon,
  grouping = NULL,
  rotate_facet_labels = 0,
  labeller = label_species,
  scales = "free_y",
```

```

space = "free_y",
dont_italicize = c("\\(. *?\\)", "spp?\\.", "-complex", "[Oo]ther"),
...
)

facet_geochem_wrap(
  param,
  grouping = NULL,
  rotate_axis_labels = 90,
  scales = "free_x",
  labeller = label_geochem,
  renamers = c(`^d([0-9]+)([HCNOS])$` = "paste(delta ^ \\1, \\2)", `^210Pb$` =
    "paste({}^210, Pb)", `^Pb210$` = "paste({}^210, Pb)"),
  units = character(0),
  default_units = NA_character_,
  ...
)

facet_geochem_wrap(
  param,
  grouping = NULL,
  scales = "free_y",
  labeller = label_geochem,
  renamers = c(`^d([0-9]+)([HCNOS])$` = "paste(delta ^ \\1, \\2)", `^210Pb$` =
    "paste({}^210, Pb)", `^Pb210$` = "paste({}^210, Pb)"),
  units = character(0),
  default_units = NA_character_,
  ...
)

facet_geochem_grid(
  param,
  grouping = NULL,
  rotate_axis_labels = 0,
  scales = "free_y",
  space = "fixed",
  labeller = label_geochem,
  renamers = c(`^d([0-9]+)([HCNOS])$` = "paste(delta ^ \\1, \\2)", `^210Pb$` =
    "paste({}^210, Pb)", `^Pb210$` = "paste({}^210, Pb)"),
  units = character(0),
  default_units = NA_character_,
  ...
)

facet_geochem_gridh(
  param,
  grouping = NULL,
  rotate_axis_labels = 90,

```



```

scales = "free_x",
space = "fixed",
labeller = label_geochem,
renamers = c(`^d([0-9]+)([HCNOS])$` = "paste(delta ^ \\1, \\2)", `^210Pb$` =
  "paste({}^210, Pb)", `^Pb210$` = "paste({}^210, Pb)"),
units = character(0),
default_units = NA_character_,
...
)

```

Arguments

taxon, param A call to [vars](#), defining the column that identifies the taxon (parameter).
grouping A call to [vars](#), identifying additional grouping columns
rotate_facet_labels, rotate_axis_labels Facet (axis) label rotation (degrees)
labeller Labeller to process facet names. Use [label_species](#) to italicize species names, [label_geochem](#) to perform common formatting and units, or [label_value](#) to suppress.
space, scales Modify default scale freedom behaviour
dont_italicize Regular expressions that should not be italicized
... Passed to [facet_grid](#) (abundance) or [facet_wrap](#) (geochem).
renamers Search and replace operations to perform in the form search = replace. Replace text can (should) contain backreferences, and will be parsed as an expression (see [plotmath](#)). Use NULL to suppress renaming.
units A named list of values = unit
default_units The default units to apply

Value

A subclass of [ggplot2::facet_grid\(\)](#) or [ggplot2::facet_wrap\(\)](#).

Examples

```

library(ggplot2)

ggplot(keji_lakes_plottable, aes(x = rel_abund, y = depth)) +
  geom_col_segsh() +
  scale_y_reverse() +
  facet_abundanceh(vars(taxon), grouping = vars(location)) +
  labs(y = "Depth (cm)")

ggplot(keji_lakes_plottable, aes(y = rel_abund, x = depth)) +
  geom_col_segs() +
  scale_x_reverse() +
  facet_abundance(vars(taxon), grouping = vars(location)) +
  labs(x = "Depth (cm)")

```

```
ggplot(alta_lake_geochem, aes(x = value, y = depth)) +
  geom_lineh() +
  geom_point() +
  scale_y_reverse() +
  facet_geochem_wrap(vars(param), units = c(C = "%", Cu = "ppm", Ti = "ppm"), nrow = 1) +
  labs(x = NULL, y = "Depth (cm)")
```

```
ggplot(alta_lake_geochem, aes(x = value, y = depth)) +
  geom_lineh() +
  geom_point() +
  scale_y_reverse() +
  facet_geochem_gridh(vars(param), units = c(C = "%", Cu = "ppm", Ti = "ppm")) +
  labs(x = NULL, y = "Depth (cm)")
```

```
ggplot(alta_lake_geochem, aes(y = value, x = depth)) +
  geom_line() +
  geom_point() +
  scale_x_reverse() +
  facet_geochem_grid(vars(param), units = c(C = "%", Cu = "ppm", Ti = "ppm")) +
  labs(y = NULL, x = "Depth (cm)")
```

 geom_col_segsh

Useful geometries for strat diagrams

Description

Useful geometries for strat diagrams

Usage

```
geom_col_segsh(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  xend = 0,
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
  linejoin = "round",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```
geom_col_segsh(
  mapping = NULL,
```

```

data = NULL,
stat = "identity",
position = "identity",
...,
yend = 0,
arrow = NULL,
arrow.fill = NULL,
lineend = "butt",
linejoin = "round",
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE
)

```

GeomColSegsh

GeomColSegs

GeomLineh

Arguments

mapping, data, stat, position, arrow, arrow.fill, lineend, linejoin, na.rm, show.legend, inherit.aes, ...

See [geom_segment](#).

xend, yend The end of the horizontal or vertical segment bars, respectively.

Format

An object of class GeomColSegsh (inherits from GeomSegment, Geom, ggproto, gg) of length 4.

An object of class GeomColSegs (inherits from GeomSegment, Geom, ggproto, gg) of length 4.

An object of class GeomLineh (inherits from GeomPath, Geom, ggproto, gg) of length 2.

Value

A ggplot2 layer

geom_lineh

Connect observations in the vertical direction

Description

Connect observations in the vertical direction

Usage

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

Arguments

mapping, data, stat, position, na.rm, show.legend, inherit.aes, ...
See [geom_line](#).

Value

A ggplot2 layer.

geom_point_exaggerate *Exaggerated geometries that do not train scales*

Description

Exaggerated geometries that do not train scales

Usage

```
geom_point_exaggerate(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",  
  position = "identity",  
  ...,  
  exaggerate_x = 1,  
  exaggerate_y = 1,  
  na.rm = FALSE,  
  show.legend = NA,  
  inherit.aes = TRUE  
)
```

```
geom_line_exaggerate(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",
```

```
    position = "identity",  
    ...,  
    exaggerate_x = 1,  
    exaggerate_y = 1,  
    na.rm = FALSE,  
    show.legend = NA,  
    inherit.aes = TRUE  
  )
```

```
geom_lineh_exaggerate(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",  
  position = "identity",  
  ...,  
  exaggerate_x = 1,  
  exaggerate_y = 1,  
  na.rm = FALSE,  
  show.legend = NA,  
  inherit.aes = TRUE  
)
```

```
geom_area_exaggerate(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",  
  position = "identity",  
  ...,  
  exaggerate_x = 1,  
  exaggerate_y = 1,  
  na.rm = FALSE,  
  show.legend = NA,  
  inherit.aes = TRUE  
)
```

```
geom_areah_exaggerate(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",  
  position = "identity",  
  ...,  
  exaggerate_x = 1,  
  exaggerate_y = 1,  
  na.rm = FALSE,  
  show.legend = NA,  
  inherit.aes = TRUE  
)
```

Arguments

mapping, data, stat, position, na.rm, show.legend, inherit.aes, ...
 See parent geometries
 exaggerate_x, exaggerate_y
 The factor by which to exaggerate x or y values

Value

A subclass of `ggplot2::Geom`.

Examples

```
library(ggplot2)

ggplot(keji_lakes_plottable, aes(x = rel_abund, y = depth)) +
  geom_lineh_exaggerate(exaggerate_x = 2, lty = 2) +
  geom_col_segsh() +
  scale_y_reverse() +
  facet_abundanceh(vars(taxon), grouping = vars(location)) +
  labs(y = "Depth (cm)")
```

 geom_ribbonh

Vertical ribbons and area plots

Description

Vertical ribbons and area plots

Usage

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

GeomRibbonh

```
geom_areah(
  mapping = NULL,
  data = NULL,
```

```

    stat = "identity",
    position = "stackv",
    na.rm = FALSE,
    show.legend = NA,
    inherit.aes = TRUE,
    ...
  )

  GeomAreah

```

Arguments

mapping, data, stat, position, na.rm, show.legend, inherit.aes, ...
 See [geom_ribbon](#).

Format

An object of class `GeomRibbonh` (inherits from `Geom`, `ggproto`, `gg`) of length 6.
 An object of class `GeomAreah` (inherits from `GeomRibbonh`, `Geom`, `ggproto`, `gg`) of length 4.

Examples

```

library(ggplot2)

# Generate data
huron <- data.frame(year = 1875:1972, level = as.vector(LakeHuron))
h <- ggplot(huron, aes(y = year))

h + geom_ribbonh(aes(xmin=0, xmax=level))
h + geom_areah(aes(x = level))

# Add aesthetic mappings
h +
  geom_ribbonh(aes(xmin = level - 1, xmax = level + 1), fill = "grey70") +
  geom_lineh(aes(x = level))

```

halifax_lakes_plottable

Halifax lakes water chemistry and top/bottom diatom counts

Description

A subset of well-labeled, clean diatom count data for 44 Halifax-area (Nova Scotia) lakes, an analysis of which has been published by Ginn et al. (2015).

Usage

```
halifax_lakes_plottable
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 114 rows and 5 columns.

Source

Neotoma paleoecology database (<https://www.neotomadb.org>)

References

Ginn, Brian K., Thiyake Rajaratnam, Brian F. Cumming, and John P. Smol. "Establishing Realistic Management Objectives for Urban Lakes Using Paleolimnological Techniques: An Example from Halifax Region (Nova Scotia, Canada)." *Lake and Reservoir Management* 31, no. 2 (April 3, 2015): 92-108. doi:10.1080/10402381.2015.1013648.

Examples

```
halifax_lakes_plottable
```

```
keji_lakes_plottable  Keji lakes core diatom counts
```

Description

A subset of well-labeled, clean diatom count data for 3 Keji-area (Nova Scotia) lakes, which form part of the analysis in Ginn et al. (2007).

Usage

```
keji_lakes_plottable
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 202 rows and 5 columns.

Source

Neotoma paleoecology database (<https://www.neotomadb.org>)

References

Ginn, Brian K., Brian F. Cumming, and John P. Smol. "Long-Term Lake Acidification Trends in High- and Low-Sulphate Deposition Regions from Nova Scotia, Canada." *Hydrobiologia* 586, no. 1 (July 1, 2007): 261-75. doi:10.1007/s1075000706443.

Examples

```
keji_lakes_plottable
```

kellys_lake_cladocera *Kellys Lake Data*

Description

Geochemistry measurements and Cladocera counts from Kellys Lake, Cape Breton Island, Nova Scotia, Canada.

Usage

kellys_lake_cladocera

kellys_lake_geochem

kellys_lake_ages

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 300 rows and 5 columns.

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 305 rows and 9 columns.

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 14 rows and 5 columns.

References

Joshua Kurek, Ian Spooner, and Dewey Dunnington (unpublished data).

label_geochem *Geochem facet labelers*

Description

Geochem facet labelers

Usage

```
label_geochem(
  labels,
  units = character(),
  default_units = NA_character_,
  geochem_facet = 1,
  renamers = c(`^[0-9]+([HCNOS])$` = "paste(delta ^ \\1, \\2)", `^210Pb$` =
    "paste({}^210, Pb)", `^Pb210$` = "paste({}^210, Pb)"),
  multi_line = TRUE
)
```

Arguments

labels	A data.frame of facet label values
units	A named list of values = unit
default_units	The default units to apply
geochem_facet	Which facet to apply formatting
renamers	Search and replace operations to perform in the form search = replace. Replace text can (should) contain backreferences, and will be parsed as an expression (see plotmath). Use NULL to suppress renaming.
multi_line	See label_parsed

Value

A `ggplot2::labeller()`

Examples

```
library(ggplot2)

ggplot(alta_lake_geochem, aes(x = value, y = depth)) +
  geom_lineh() +
  geom_point() +
  scale_y_reverse() +
  facet_wrap(
    vars(param),
    labeller = purrr::partial(label_geochem, geochem_facet = "param"),
    nrow = 1,
    scales = "free_x"
  ) +
  labs(x = NULL, y = "Depth (cm)")
```

label_species	<i>Species facet labellers</i>
---------------	--------------------------------

Description

Use these to label species with partial italic formatting. See [label_parsed](#).

Usage

```
label_species(
  labels,
  dont_italicize = c("\\(..*?\\)", "spp?\\.\\.", "-complex", "[Oo]ther"),
  species_facet = 1,
  multi_line = TRUE
)
```

Arguments

labels A data.frame of facet label values
dont_italicize Regular expressions that should not be italicized
species_facet Which facet(s) contain species values
multi_line See [label_parsed](#)

Value

A `ggplot2::labeller()`

Examples

```
library(ggplot2)

ggplot(keji_lakes_plottable, aes(x = rel_abund, y = depth)) +
  geom_col_segsh() +
  scale_y_reverse() +
  facet_grid(
    cols = vars(taxon),
    rows = vars(location),
    scales = "free_x",
    space = "free_x",
    labeller = purrr::partial(label_species, species_facet = "taxon")
  ) +
  labs(y = "Depth (cm)")
```

layer_dendrogram	<i>Add a dendrogram as a layer or facet</i>
------------------	---

Description

Add a dendrogram as a layer or facet

Usage

```
layer_dendrogram(
  object,
  mapping,
  ...,
  colour = "black",
  size = 0.5,
  linetype = 1,
  alpha = NA,
  sequential_facets = TRUE
)
```

```

plot_layer_dendrogram(object, mapping, ..., panel_label = "CONISS")

layer_zone_boundaries(
  object,
  mapping,
  ...,
  linetype = 2,
  alpha = 0.7,
  colour = "black",
  size = 0.5
)

```

Arguments

object	A nested_hclust object.
mapping	Map at least one axis (x or y) to a qualifier, like <code>aes(x = depth)</code> or similar.
...	Use <code>facet_var = "CONISS"</code> or similar to name the panel
linetype, alpha, colour, size	Customize the appearance of boundary/dendrogram segment lines
sequential_facets	TRUE will result in the panel containing the dendrogram added to the right of the plot.
panel_label	Use to label a pane on a standalone dendrogram plot

Value

A `ggplot2::layer()`

Examples

```

library(ggplot2)
library(dplyr, warn.conflicts = FALSE)

alta_coniss <- nested_data(
  alta_lake_geochem,
  qualifiers = c(age, depth, zone),
  key = param,
  value = value,
  trans = scale
) %>%
  nested_chclust_coniss()

ggplot() +
  layer_dendrogram(alta_coniss, aes(y = depth)) +
  scale_y_reverse()

```

layer_scores	<i>Add scores to a plot</i>
--------------	-----------------------------

Description

Add scores to a plot

Usage

```
layer_scores(
  object,
  mapping = NULL,
  which = "PC1",
  key = "param",
  value = "value",
  scores_geom = list(ggplot2::geom_path(), ggplot2::geom_point()),
  sequential_facets = TRUE
)
```

```
plot_layer_scores(
  object,
  mapping,
  which = "PC1",
  key = "param",
  value = "value",
  ...
)
```

Arguments

object	A nested_prcomp or similar object
mapping	A mapping created with aes
which	Which principal components to plot
key	The column name to use for the principal component names
value	The column name to use for the principal component score values
scores_geom	One or more geometries to which scores should be applied.
sequential_facets	TRUE will result in the panel containing the dendrogram added to the right of the plot.
...	Passed to <code>layer_scores()</code>

Value

A `list()` that can be added to a `ggplot2::ggplot()`

Examples

```
library(ggplot2)
library(dplyr, warn.conflicts = FALSE)

alta_pca <- nested_data(
  alta_lake_geochem,
  qualifiers = c(age, depth, zone),
  key = param,
  value = value,
  trans = scale
) %>%
  nested_prcomp()

ggplot() +
  layer_scores(alta_pca, aes(value, depth), which = "PC1") +
  scale_y_reverse()

plot_layer_scores(alta_pca, aes(y = depth), which = c("PC1", "PC2")) +
  scale_y_reverse()
```

long_lake_14C_ages *Long Lake Carbon-14 Ages*

Description

This object contains several uncalibrated Carbon-14 measurements from Long Lake (Nova Scotia-New Brunswick Border Region, Canada) core LL-PC2 (Dunnington et al. 2017; White 2012). The `long_lake_bacon_ages` object contains the result of the Carbon-14 ages as modelled by the `rbacon` package (Blaauw and Christen 2011).

Usage

```
long_lake_14C_ages

long_lake_bacon_ages

long_lake_plottable
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 5 rows and 5 columns.
An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 86 rows and 5 columns.
An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 51 rows and 10 columns.

References

Blaauw, Maarten, and J. Andrés Christen. "Flexible Paleoclimate Age-Depth Models Using an Autoregressive Gamma Process." *Bayesian Analysis* 6, no. 3 (September 2011): 457–74. doi:10.1214/ba/1339616472.

Dunnington, Dewey W., Hilary White, Ian S. Spooner, Mark L. Mallory, Chris White, Nelson J. O’Driscoll, and Nic R. McLellan. "A Paleolimnological Archive of Metal Sequestration and Release in the Cumberland Basin Marshes, Atlantic Canada." *FACETS* 2, no. 1 (May 23, 2017): 440–60. doi:10.1139/facets20170004.

White, Hilary E. "Paleolimnological Records of Post-Glacial Lake and Wetland Evolution from the Isthmus of Chignecto Region, Eastern Canada." M.Sc. Thesis, Acadia University, 2012. <https://scholar.acadiau.ca/islandora/object/theses:247>.

Examples

```
long_lake_14C_ages
long_lake_bacon_ages
long_lake_plottable
```

nested_analysis	<i>Perform an analysis on a nested data matrix</i>
-----------------	--

Description

Perform an analysis on a nested data matrix

Usage

```
nested_analysis(
  .data,
  .fun,
  ...,
  .output_column = "model",
  .reserved_names = NULL,
  .env = parent.frame()
)
```

Arguments

.data	A data frame with a list column of data frames, possibly created using nested_data .
.fun	A model function
...	Passed to fun
.output_column	A column name in which the output of .fun should be stored.
.reserved_names	Names that should not be allowed as columns in any data frame within this object
.env	Passed to as_function

Value

.data with an additional list column of fun output

Examples

```
nd <- nested_data(
  alta_lake_geochem,
  qualifiers = c(age, depth, zone),
  key = param,
  value = value,
  trans = scale
)

na <- nested_analysis(nd, vegan::rda, X = data)
plot(na)
```

 nested_data

Prepare a parameter-long data frame for statistical analysis

Description

Prepare a parameter-long data frame for statistical analysis

Usage

```
nested_data(
  .data,
  qualifiers = NULL,
  key = NULL,
  value,
  fill = NA,
  select_if = ~TRUE,
  filter_all = any_vars(TRUE),
  trans = identity,
  groups = NULL
)

unnested_data(.data, ...)
```

Arguments

.data	Data in parameter-long form
qualifiers	Columns that add context to observations (e.g., depth, zone, core)
key	The column name that contains the column names of the data matrix
value	The column name that contains the values

fill	If a key/value combination doesn't exist in the input, this value will be assigned in the data matrix. Generally, using NA for geochemical data and 0 for relative abundance data is advised.
select_if	Use <code>~TRUE</code> to keep all columns; use <code>~all(is.finite(.))</code> to keep columns with all finite values. See select_if .
filter_all	Use <code>any_vars(TRUE)</code> to keep all observations; use <code>all_vars(is.finite(.))</code> to keep only observations with finite (non-missing) values. See filter_all .
trans	A function that will be applied to all columns, column-wise. Use identity to perform no transformation, use scale to scale each column to a mean of zero and variance of 1. See mutate_all .
groups	Use group_by or this argument to group by one or more columns (e.g., core or lake)
...	One or more columns to unnest.

Value

A nested data matrix, which is composed of a `tibble::tibble()` with tibble list-columns data, `discarded_rows`, `discarded_columns`, and `qualifiers`.

Examples

```
nested_data(
  alta_lake_geochem,
  qualifiers = c(age, depth, zone),
  key = param,
  value = value,
  trans = scale
)
```

nested_hclust	<i>Nested (Constrained) hierarchical clustering</i>
---------------	---

Description

Powered by [chclust](#) and [hclust](#); broken stick using [bstick](#).

Usage

```
nested_hclust(
  .data,
  data_column = "data",
  qualifiers_column = "qualifiers",
  distance_fun = stats::dist,
  n_groups = NULL,
  ...,

```

```

    .fun = stats::hclust,
    .reserved_names = character(0)
  )

  nested_chclust_conslink(
    .data,
    data_column = "data",
    qualifiers_column = "qualifiers",
    distance_fun = stats::dist,
    n_groups = NULL,
    ...
  )

  nested_chclust_coniss(
    .data,
    data_column = "data",
    qualifiers_column = "qualifiers",
    distance_fun = stats::dist,
    n_groups = NULL,
    ...
  )

```

Arguments

<code>.data</code>	A data frame with a list column of data frames, possibly created using nested_data .
<code>data_column</code>	An expression that evaluates to the data object within each row of <code>.data</code>
<code>qualifiers_column</code>	The column that contains the qualifiers
<code>distance_fun</code>	A distance function like dist or vegdist .
<code>n_groups</code>	The number of groups to use (can be a vector or expression using vars in <code>.data</code>)
<code>...</code>	Passed to chclust or hclust .
<code>.fun</code>	Function powering the clustering. Must return an <code>hclust</code> object of some kind.
<code>.reserved_names</code>	Names that should not be allowed as columns in any data frame within this object

Value

`.data` with additional columns

References

Bennett, K. (1996) Determination of the number of zones in a biostratigraphic sequence. *New Phytologist*, 132, 155-170. doi:[10.1111/j.14698137.1996.tb04521.x](https://doi.org/10.1111/j.14698137.1996.tb04521.x) (Broken stick)

Grimm, E.C. (1987) CONISS: A FORTRAN 77 program for stratigraphically constrained cluster analysis by the method of incremental sum of squares. *Computers & Geosciences*, 13, 13-35. doi:[10.1016/00983004\(87\)900227](https://doi.org/10.1016/00983004(87)900227)

Juggins, S. (2017) rioja: Analysis of Quaternary Science Data, R package version (0.9-15.1). (<https://cran.r-project.org/package=rioja>).

See [hclust](#) for hierarchical clustering references

Examples

```
library(tidyr)
library(dplyr, warn.conflicts = FALSE)

nested_coniss <- keji_lakes_plottable %>%
  group_by(location) %>%
  nested_data(depth, taxon, rel_abund, fill = 0) %>%
  nested_chclust_coniss()

# plot the dendrograms using base graphics
plot(nested_coniss, main = location, ncol = 1)

# plot broken stick dispersion to verify number of plausible groups
library(ggplot2)

nested_coniss %>%
  select(location, broken_stick) %>%
  unnest(broken_stick) %>%
  tidyr::gather(type, value, broken_stick_dispersion, dispersion) %>%
  ggplot(aes(x = n_groups, y = value, col = type)) +
  geom_line() +
  geom_point() +
  facet_wrap(vars(location))
```

nested_prcomp

Nested Principal Components Analysis (PCA)

Description

Powered by [prcomp](#). When creating the [nested_data](#), the data should be scaled (i.e, trans = scale) if all variables are not in the same unit.

Usage

```
nested_prcomp(.data, data_column = .data$data, ...)
```

Arguments

<code>.data</code>	A data frame with a list column of data frames, possibly created using nested_data .
<code>data_column</code>	An expression that evaluates to the data object within each row of <code>.data</code>
<code>...</code>	Passed to prcomp .

Value

.data with additional columns 'model', 'loadings', 'variance' and 'scores'

Examples

```
library(dplyr, warn.conflicts = FALSE)

nested_pca <- alta_lake_geochem %>%
  nested_data(
    qualifiers = c(depth, zone),
    key = param,
    value = value,
    trans = scale
  ) %>%
  nested_prcomp()

# get variance info
nested_pca %>% unnested_data(variance)

# get loadings info
nested_pca %>% unnested_data(loadings)

# scores, requalified
nested_pca %>% unnested_data(c(qualifiers, scores))
```

plot.age_depth_model *Plot an age depth model using base graphics*

Description

Plot an age depth model using base graphics

Usage

```
## S3 method for class 'age_depth_model'
plot(
  x,
  xlab = "depth",
  ylab = "age",
  xlim = NULL,
  ylim = NULL,
  add = FALSE,
  ...
)
```

Arguments

x	An age_depth_model
xlab, ylab	Axis labels
xlim, ylim	Axis limits
add	Pass TRUE to skip creating a new plot
...	Passed to points to customize points display

Value

The input, invisibly

Examples

```
adm <- age_depth_model(
  alta_lake_210Pb_ages,
  depth = depth_cm, age = age_year_ad,
  age_max = age_year_ad + age_error_yr,
  age_min = age_year_ad - age_error_yr
)

plot(adm)
```

plot.nested_analysis *Plot a nested analysis*

Description

Calls [plot](#) or another (base) plotting function on all models, arranging the output in subplots.

Usage

```
## S3 method for class 'nested_analysis'
plot(x, ..., main = "", nrow = NULL, ncol = NULL)

plot_nested_analysis(
  .x,
  .fun,
  ...,
  nrow = NULL,
  ncol = NULL,
  .model_column = .data$model,
  .output_column = NULL
)

## S3 method for class 'nested_prcomp'
biplot(x, ..., nrow = NULL, ncol = NULL)
```

Arguments

x, .x	A nested_analysis object (or subclass)
...	Passed to the plot function. Tidy evaluation is supported, and arguments are evaluated within a transposed version of x for each row.
main	The plot title
nrow, ncol	Force a number of rows or columns in the output
.fun	A function that produces graphical output
.model_column	The column containing the model
.output_column	The column in which the output of the plot function should be placed

Value

the input, invisibly

Examples

```
nd <- nested_data(  
  alta_lake_geochem,  
  qualifiers = c(age, depth, zone),  
  key = param,  
  value = value,  
  trans = scale  
)  
  
na <- nested_analysis(nd, vegan::rda, X = data)  
plot(na)
```

predict.age_depth_model

Predict age and depth values

Description

Predict age and depth values

Usage

```
## S3 method for class 'age_depth_model'  
predict(object, .data = NULL, depth = NULL, age = NULL, ...)  
  
predict_depth(object, age)  
  
predict_age(object, depth)
```

Arguments

object	An <code>age_depth_model</code> object
.data	Optional input data frame
depth, age	Specify exactly one of these to predict the other.
...	Unused

Value

A data frame with the same number of observations as the input age or depth vector.

Examples

```
adm <- age_depth_model(
  alta_lake_210Pb_ages,
  depth = depth_cm, age = age_year_ad,
  age_max = age_year_ad + age_error_yr,
  age_min = age_year_ad - age_error_yr
)

predict(adm, depth = 1:5)
```

rotated_facet_labels *Common plot modifications for stratigraphic plots*

Description

Common plot modifications for stratigraphic plots

Usage

```
rotated_facet_labels(
  angle = 45,
  direction = "x",
  remove_label_background = TRUE
)

rotated_axis_labels(angle = 90, direction = "x")
```

Arguments

angle	The angle at which labels should be rotated
direction	The axes along which the operations should be performed
remove_label_background	Whether or not label backgrounds should be removed along rotated label axes

Value

An object or list of objects that can be added to a [ggplot](#)

Examples

```
library(ggplot2)

ggplot(mpg, aes(cty, hwy)) +
  geom_point() +
  facet_wrap(vars(class)) +
  rotated_facet_labels(45, "x")
```

scale_x_abundance *Scales for relative abundance values*

Description

Continuous scales that (1) always start at 0, (2) always have the same breaks, and (3) expand using a constant rather than a percentage. These scales assume that data are in percentages (i.e., range 0 to 100 rather than 0 to 1).

Usage

```
scale_x_abundance(
  ...,
  limits = c(0, NA),
  breaks = seq(10, 90, 30),
  minor_breaks = seq(0, 100, 10),
  expand = c(0, 1)
)

scale_y_abundance(
  ...,
  limits = c(0, NA),
  breaks = seq(10, 90, 30),
  minor_breaks = seq(0, 100, 10),
  expand = c(0, 1)
)
```

Arguments

...	Passed to scale_y_continuous or scale_x_continuous
limits	Limits for the scale
breaks	Where to place labels on the scale
minor_breaks	Where to place minor breaks
expand	A vector of expansion constants

Value

A [scale_y_continuous](#) or [scale_x_continuous](#)

Examples

```
library(dplyr, warn.conflicts = FALSE)
library(ggplot2)

keji_lakes_plottable %>%
  filter(taxon == "Other", location == "Beaverskin Lake") %>%
  ggplot(aes(rel_abund, depth)) +
  geom_col_segsh() +
  scale_x_abundance() +
  scale_y_reverse()
```

scale_y_depth_age	<i>Age-depth scales</i>
-------------------	-------------------------

Description

Age-depth scales

Usage

```
scale_y_depth_age(
  model = NULL,
  age_name = "age",
  age_breaks = waiver(),
  age_labels = waiver(),
  ...
)

scale_y_age_depth(
  model = NULL,
  reversed = FALSE,
  depth_name = "depth",
  depth_breaks = waiver(),
  depth_labels = waiver(),
  ...
)

scale_x_depth_age(
  model = NULL,
  age_name = "age",
  age_breaks = waiver(),
  age_labels = waiver(),
```

```

    ...
  )

scale_x_age_depth(
  model = NULL,
  reversed = FALSE,
  depth_name = "depth",
  depth_breaks = waiver(),
  depth_labels = waiver(),
  ...
)

```

Arguments

model	An age-depth model, or NULL to suppress the second axis
age_name, depth_name	Label for the second axis
age_breaks, depth_breaks	Breaks for the second axis
age_labels, depth_labels	Labels for each break on the second axis
...	Passed to scale_y_continuous or scale_x_continuous
reversed	Reverse the primary age axis (for years BP or similar)

Value

A [scale_y_continuous](#) or [scale_x_continuous](#)

Examples

```

library(ggplot2)
library(dplyr, warn.conflicts = FALSE)

adm <- age_depth_model(
  alta_lake_210Pb_ages,
  depth = depth_cm, age = age_year_ad
)

alta_lake_geochem %>%
  filter(param == "Cu") %>%
  ggplot(aes(value, depth)) +
  geom_point() +
  scale_y_depth_age(adm)

```

`sequential_layer_facets`*Change facet ordering behaviour*

Description

Normally, facets are ordered using `as.factor` on all values that occur within layer data, which means that when adding additional layers, any ordering is not preserved unless the factor levels are identical on all factors. This function changes this behaviour such that facet levels are combined in layer order. This is useful when adding standalone layers to a plot without disturbing the existing order.

Usage

```
sequential_layer_facets(reverse = FALSE)
```

Arguments

`reverse` Use TRUE to process layers in reverse order

Value

An object that can be added to a `ggplot2::ggplot()`

Examples

```
library(ggplot2)

p <- ggplot(mapping = aes(x, y)) +
  geom_point(data = data.frame(x = 1:5, y = 1:5, facet = "b")) +
  geom_point(data = data.frame(x = 1:5, y = 1:5, facet = "a")) +
  facet_wrap(vars(facet))

p
p + sequential_layer_facets()
```

`stat_nested_hclust`*Display a dendrogram as a ggplot2 layer*

Description

Display a dendrogram as a ggplot2 layer

Usage

```
stat_nested_hclust(
  mapping = NULL,
  data = NULL,
  geom = "segment",
  position = "identity",
  ...,
  inherit.aes = TRUE,
  show.legend = NA
)
```

StatNestedHclust

Arguments

mapping	A mapping created using aes . Must map x OR y to a qualifier.
data	A nested_hclust object
geom	Any geom that takes x, xend, y, and yend. Probably geom_segment is the only one that makes sense.
position	Position adjustment
...	Passed to the the stat/geom (see geom_segment)
inherit.aes	Inherit aesthetics from ggplot()?
show.legend	Show mapped aesthetics in the legend?

Format

An object of class StatNestedHclust (inherits from Stat, ggproto, gg) of length 4.

Value

A [ggplot2::Stat](#)

Examples

```
library(ggplot2)
library(dplyr, warn.conflicts = FALSE)

alta_coniss <- nested_data(
  alta_lake_geochem,
  qualifiers = c(age, depth, zone),
  key = param,
  value = value,
  trans = scale
) %>%
  nested_chclust_coniss()

ggplot(alta_coniss) +
  stat_nested_hclust(aes(model = model, y = depth)) +
```

```
scale_y_reverse()
```

theme_paleo	<i>A Paleo-friendly ggplot2 theme</i>
-------------	---------------------------------------

Description

Essentially, this is `ggplot2::theme_bw()` with a few modifications

Usage

```
theme_paleo(...)
```

Arguments

... Passed to `ggplot2::theme_bw()`

Value

A complete `ggplot2::theme()`

Examples

```
library(ggplot2)

ggplot(mpg, aes(cty, hwy)) +
  geom_point() +
  theme_paleo()
```

Index

- * **datasets**
 - alta_lake_210Pb_ages, 5
 - geom_col_segsh, 10
 - geom_ribbonh, 14
 - halifax_lakes_plottable, 15
 - keji_lakes_plottable, 16
 - kellys_lake_cladocera, 17
 - long_lake_14C_ages, 22
 - stat_nested_hclust, 35
- aes, 21, 36
- age_depth_as_sec_axis, 2
- age_depth_exact
 - (age_depth_interpolate), 3
- age_depth_extrapolate
 - (age_depth_interpolate), 3
- age_depth_interpolate, 3
- age_depth_model, 3, 4, 29, 31
- age_depth_na (age_depth_interpolate), 3
- alta_lake_14C_ages
 - (alta_lake_210Pb_ages), 5
- alta_lake_210Pb_ages, 5
- alta_lake_bacon_ages
 - (alta_lake_210Pb_ages), 5
- alta_lake_geochem
 - (alta_lake_210Pb_ages), 5
- as.factor, 35
- as_function, 23
- as_trans_factory, 6
- biplot.nested_prcomp
 - (plot.nested_analysis), 29
- bstick, 25
- chclust, 25, 26
- dist, 26
- facet_abundance (facet_abundanceh), 7
- facet_abundanceh, 7
- facet_geochem_grid (facet_abundanceh), 7
- facet_geochem_gridh (facet_abundanceh), 7
- facet_geochem_wrap (facet_abundanceh), 7
- facet_geochem_wrapp (facet_abundanceh), 7
- facet_grid, 7, 9
- facet_wrap, 9
- filter_all, 25
- geom_area_exaggerate
 - (geom_point_exaggerate), 12
- geom_areah (geom_ribbonh), 14
- geom_areah_exaggerate
 - (geom_point_exaggerate), 12
- geom_col_segs (geom_col_segsh), 10
- geom_col_segsh, 10
- geom_line, 12
- geom_line_exaggerate
 - (geom_point_exaggerate), 12
- geom_lineh, 11
- geom_lineh_exaggerate
 - (geom_point_exaggerate), 12
- geom_point_exaggerate, 12
- geom_ribbon, 15
- geom_ribbonh, 14
- geom_segment, 11, 36
- GeomAreah (geom_ribbonh), 14
- GeomColSegs (geom_col_segsh), 10
- GeomColSegsh (geom_col_segsh), 10
- GeomLineh (geom_col_segsh), 10
- GeomRibbonh (geom_ribbonh), 14
- ggplot, 32
- ggplot2::facet_grid(), 9
- ggplot2::facet_wrap(), 9
- ggplot2::Geom, 14
- ggplot2::ggplot(), 21, 35
- ggplot2::labeller(), 18, 19
- ggplot2::layer(), 20
- ggplot2::Stat, 36
- ggplot2::theme(), 37

- ggplot2::theme_bw(), 37
- group_by, 25
- halifax_lakes_plottable, 15
- hclust, 25–27
- identity, 25
- keji_lakes_plottable, 16
- kellys_lake_ages
 - (kellys_lake_cladocera), 17
- kellys_lake_cladocera, 17
- kellys_lake_geochem
 - (kellys_lake_cladocera), 17
- label_geochem, 7, 9, 17
- label_parsed, 18, 19
- label_species, 7, 9, 18
- label_value, 9
- layer_dendrogram, 19
- layer_scores, 21
- layer_zone_boundaries
 - (layer_dendrogram), 19
- long_lake_14C_ages, 22
- long_lake_bacon_ages
 - (long_lake_14C_ages), 22
- long_lake_plottable
 - (long_lake_14C_ages), 22
- mutate, 4
- mutate_all, 25
- nested_analysis, 23, 30
- nested_chclust_coniss (nested_hclust), 25
- nested_chclust_conslink
 - (nested_hclust), 25
- nested_data, 23, 24, 26, 27
- nested_hclust, 20, 25, 36
- nested_prcomp, 21, 27
- plot, 29
- plot.age_depth_model, 28
- plot.nested_analysis, 29
- plot_layer_dendrogram
 - (layer_dendrogram), 19
- plot_layer_scores (layer_scores), 21
- plot_nested_analysis
 - (plot.nested_analysis), 29
- plotmath, 9, 18
- points, 29
- prcomp, 27
- predict.age_depth_model, 30
- predict_age (predict.age_depth_model), 30
- predict_depth
 - (predict.age_depth_model), 30
- rotated_axis_labels, 7
- rotated_axis_labels
 - (rotated_facet_labels), 31
- rotated_facet_labels, 7, 31
- scale, 25
- scale_x_abundance, 7, 32
- scale_x_age_depth (scale_y_depth_age), 33
- scale_x_continuous, 3, 32–34
- scale_x_depth_age (scale_y_depth_age), 33
- scale_y_abundance (scale_x_abundance), 32
- scale_y_age_depth (scale_y_depth_age), 33
- scale_y_continuous, 3, 32–34
- scale_y_depth_age, 33
- sec_axis, 3
- select_if, 25
- sequential_layer_facets, 35
- stat_nested_hclust, 35
- StatNestedHclust (stat_nested_hclust), 35
- theme_paleo, 37
- tibble::tibble(), 25
- unnested_data (nested_data), 24
- validate_trans (as_trans_factory), 6
- validate_trans_factory
 - (as_trans_factory), 6
- vars, 9
- vegdist, 26