Package 'ssdtools'

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Title Species Sensitivity Distributions

Version 2.6.0

Description Species sensitivity distributions are cumulative probability distributions which are fitted to toxicity concentrations for different species as described by Posthuma et al.(2001) <isbn:9781566705783>. The ssdtools package uses Maximum Likelihood to fit distributions such as the gamma, log-logistic, log-normal and log-normal log-normal mixture. Multiple distributions can be averaged using Akaike Information Criteria. Confidence intervals on hazard concentrations and proportions are produced by bootstrapping.

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URL https://github.com/bcgov/ssdtools, https://bcgov.github.io/ssdtools/

BugReports https://github.com/bcgov/ssdtools/issues

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Contents

augment.fitdists *Augmented Data from fitdists Object*

Description

Get a tibble of the original data with augmentation.

Usage

```
## S3 method for class 'fitdists'
augment(x, ...)
```

Arguments

x	The object.
...	Unused.

Value

A tibble of the agumented data.

See Also

ssd_data()

Other generics: glance.fitdists(), tidy.fitdists()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
augment(fits)
```

autoplot.fitdists *Plot a fitdists Object*

Description

A wrapper on ssd_plot_cdf().

Usage

```
## S3 method for class 'fitdists'
autoplot(object, ...)
```

Arguments

object	The object.
...	Unused.

Value

A ggplot object.

See Also

ssd_plot_cdf()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
autoplot(fits)
```

---

coef.fitdists *Turn a fitdists Object into a Tidy Tibble*

Description

A wrapper on tidy.fitdists().

Usage

```
## S3 method for class 'fitdists'
coef(object, ...)
```

Arguments

object	The object.
...	Unused.

See Also

tidy.fitdists()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
coef(fits)
```

estimates.fitdists *Estimates for fitdists Object*

Description

Gets a named list of the estimated weights and parameters.

Usage

```
## S3 method for class 'fitdists'
estimates(x, all_estimates = FALSE, ...)
```

Arguments

x	The object.
all_estimates	A flag specifying whether to calculate estimates for all implemented distributions.
...	Unused.

Value

A named list of the estimates.

See Also

tidy.fitdists(), ssd_match_moments(), ssd_hc() and ssd_plot_cdf()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
estimates(fits)
```

geom_hcintersect *Species Sensitivity Hazard Concentration Intersection*

Description

Plots the intersection between each xintercept and yintercept value.

Usage

```
geom_hcintersect(
  mapping = NULL,
  data = NULL,
  ...,
  xintercept,
  yintercept,
  na.rm = FALSE,
  show.legend = NA
)
```

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)).
...	Other arguments passed on to layer()'s params argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the position argument, or aesthetics that are required can *not* be passed through .... Unknown arguments that are not part of the 4 categories below are ignored. • Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, colour = "red" or linewidth = 3. The geom's documentation has an **Aesthetics** section that lists the available options. The 'required' aesthetics cannot be passed on to the params. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data. • When constructing a layer using a stat_*() function, the ... argument can be used to pass on parameters to the geom part of the layer. An example of this is stat_density(geom = "area", outline.type = "both"). The geom's documentation lists which parameters it can accept. • Inversely, when constructing a layer using a geom_*() function, the ... argument can be used to pass on parameters to the stat part of the layer. An example of this is geom_area(stat = "density", adjust = 0.5). The stat's documentation lists which parameters it can accept. • The key_glyph argument of layer() may also be passed on through .... This can be one of the functions described as key glyphs, to change the display of the layer in the legend.

xintercept	The x-value for the intersect.
yintercept	The y-value for the intersect.
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.

See Also

ssd_plot_cdf()

Other ggplot: geom_ssdpoint(), geom_ssdsegment(), geom_xribbon(), scale_colour_ssd(), ssd_pal()

Examples

```
ggplot2::ggplot(ssddata::ccme_boron, ggplot2::aes(x = Conc)) +
  geom_ssdpoint() +
  geom_hcintersect(xintercept = 1.5, yintercept = 0.05)
```

---

geom_ssdpoint *Species Sensitivity Data Points*

Description

Uses the empirical cumulative distribution to create scatterplot of points x.

Usage

```
geom_ssdpoint(
  mapping = NULL,
  data = NULL,
  stat = "ssdpoint",
  position = "identity",
  ...,
  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.
...	Other arguments passed on to layer()'s params argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the position argument, or aesthetics that are required can *not* be passed through .... Unknown arguments that are not part of the 4 categories below are ignored. • Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, colour = "red" or linewidth = 3. The geom's documentation has an **Aesthetics** section that lists the available options. The 'required' aesthetics cannot be passed on to the params. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data.

- When constructing a layer using a `stat_*()` function, the `...` argument can be used to pass on parameters to the geom part of the layer. An example of this is `stat_density(geom = "area", outline.type = "both")`. The geom's documentation lists which parameters it can accept.
- Inversely, when constructing a layer using a `geom_*()` function, the `...` argument can be used to pass on parameters to the `stat` part of the layer. An example of this is `geom_area(stat = "density", adjust = 0.5)`. The stat's documentation lists which parameters it can accept.
- The `key_glyph` argument of `layer()` may also be passed on through `....` This can be one of the functions described as key glyphs, to change the display of the layer in the legend.

`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.

See Also

`ssd_plot_cdf()`

Other ggplot: `geom_hcintersect()`, `geom_ssdsegment()`, `geom_xribbon()`, `scale_colour_ssd()`, `ssd_pal()`

Examples

```
ggplot2::ggplot(ssddata::ccme_boron, ggplot2::aes(x = Conc)) +
  geom_ssdpoint()
```

---

geom_ssdsegment *Species Sensitivity Censored Segments*

Description

Uses the empirical cumulative distribution to draw lines between points `x` and `xend`.

Usage

```
geom_ssdsegment(
  mapping = NULL,
  data = NULL,
  stat = "ssdsegment",
  position = "identity",
  ...,
```

```
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
  linejoin = "round",
  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.
...	Other arguments passed on to layer()'s params argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the position argument, or aesthetics that are required can *not* be passed through .... Unknown arguments that are not part of the 4 categories below are ignored.

- Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, `colour = "red"` or `linewidth = 3`. The geom's documentation has an **Aesthetics** section that lists the available options. The 'required' aesthetics cannot be passed on to the `params`. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data.
- When constructing a layer using a `stat_*()` function, the `...` argument can be used to pass on parameters to the `geom` part of the layer. An example of this is `stat_density(geom = "area", outline.type = "both")`. The geom's documentation lists which parameters it can accept.
- Inversely, when constructing a layer using a `geom_*()` function, the `...` argument can be used to pass on parameters to the `stat` part of the layer. An example of this is `geom_area(stat = "density", adjust = 0.5)`. The stat's documentation lists which parameters it can accept.
- The `key_glyph` argument of `layer()` may also be passed on through `...`. This can be one of the functions described as key glyphs, to change the display of the layer in the legend.

`arrow` specification for arrow heads, as created by `grid::arrow()`.

`arrow.fill` fill colour to use for the arrow head (if closed). `NULL` means use `colour` aesthetic.

`lineend` Line end style (round, butt, square).

`linejoin` Line join style (round, mitre, bevel).

`na.rm` If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.

`show.legend` logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use `TRUE`. If `NA`, all levels are shown in legend, but unobserved levels are omitted.

`inherit.aes` If `FALSE`, overrides the default aesthetics, rather than combining with them.

See Also

`ssd_plot_cdf()`

Other ggplot: `geom_hcintersect()`, `geom_ssdpoint()`, `geom_xribbon()`, `scale_colour_ssd()`, `ssd_pal()`

Examples

```
ggplot2::ggplot(ssddata::ccme_boron, ggplot2::aes(x = Conc, xend = Conc * 2)) +
  geom_ssdsegment()
```

geom_xribbon *Ribbon on X-Axis*

Description

Plots the x interval defined by xmin and xmax.

Usage

```
geom_xribbon(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  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.

... — Other arguments passed on to layer()'s params argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the position argument, or aesthetics that are required can *not* be passed through .... Unknown arguments that are not part of the 4 categories below are ignored.

- Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, colour = "red" or linewidth = 3. The geom's documentation has an **Aesthetics** section that lists the available options. The 'required' aesthetics cannot be passed on to the params. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data.
- When constructing a layer using a stat_*() function, the ... argument can be used to pass on parameters to the geom part of the layer. An example of this is stat_density(geom = "area", outline.type = "both"). The geom's documentation lists which parameters it can accept.
- Inversely, when constructing a layer using a geom_*() function, the ... argument can be used to pass on parameters to the stat part of the layer. An example of this is geom_area(stat = "density", adjust = 0.5). The stat's documentation lists which parameters it can accept.
- The key_glyph argument of layer() may also be passed on through .... This can be one of the functions described as key glyphs, to change the display of the layer in the legend.

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.

See Also

ssd_plot_cdf()

Other ggplot: geom_hcintersect(), geom_ssdpoint(), geom_ssdsegment(), scale_colour_ssd(), ssd_pal()

Examples

```
gp <- ggplot2::ggplot(boron_pred) +
  geom_xribbon(ggplot2::aes(xmin = lcl, xmax = ucl, y = proportion))
```

`glance.fitdists` *Get a tibble summarizing each distribution*

Description

Gets a tibble with a single row for each distribution.

Usage

```
## S3 method for class 'fitdists'
glance(x, ..., wt = FALSE)
```

Arguments

`x`	The object.
`...`	Unused.
`wt`	A flag specifying whether to return the Akaike weight as "wt" instead of "weight".

Value

A tidy tibble of the distributions.

See Also

`ssd_gof()`

Other generics: `augment.fitdists()`, `tidy.fitdists()`

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
glance(fits, wt = TRUE)
```

is.fitdists *Is fitdists Object*

Description

Tests whether x is a fitdists Object.

Usage

```
is.fitdists(x)
```

Arguments

x	The object.

Value

A flag specifying whether x is a fitdists Object.

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
is.fitdists(fits)
```

predict.fitburrlioz *Predict Hazard Concentrations of fitburrlioz Object*

Description

A wrapper on `ssd_hc()` that by default calculates all hazard concentrations from 1 to 99%.

Usage

```
## S3 method for class 'fitburrlioz'
predict(
  object,
  percent,
  proportion = 1:99/100,
  ...,
  ci = FALSE,
  level = 0.95,
  nboot = 1000,
  min_pboot = 0.8,
  parametric = TRUE
)
```

Arguments

object	The object.
percent	A numeric vector of percent values to estimate hazard concentrations for. Deprecated for proportion = 0.05. **[Deprecated]**
proportion	A numeric vector of proportion values to estimate hazard concentrations for.
...	Unused.
ci	A flag specifying whether to estimate confidence intervals (by bootstrapping).
level	A number between 0 and 1 of the confidence level of the interval.
nboot	A count of the number of bootstrap samples to use to estimate the confidence limits. A value of 10,000 is recommended for official guidelines.
min_pboot	A number between 0 and 1 of the minimum proportion of bootstrap samples that must successfully fit (return a likelihood) to report the confidence intervals.
parametric	A flag specifying whether to perform parametric bootstrapping as opposed to non-parametrically resampling the original data with replacement.

Details

It is useful for plotting purposes.

See Also

ssd_hc() and ssd_plot()

Examples

```
fits <- ssd_fit_burrlioz(ssddata::ccme_boron)
predict(fits)
```

---

predict.fitdists *Predict Hazard Concentrations of fitdists Object*

Description

A wrapper on ssd_hc() that by default calculates all hazard concentrations from 1 to 99%.

Usage

```
## S3 method for class 'fitdists'
predict(
  object,
  percent,
  proportion = 1:99/100,
  ...,
  average = TRUE,
  ci = FALSE,
```

```
  level = 0.95,
  nboot = 1000,
  min_pboot = 0.8,
  est_method = "multi",
  ci_method = "weighted_samples",
  parametric = TRUE,
  delta = 9.21,
  control = NULL
)
```

Arguments

object	The object.
percent	A numeric vector of percent values to estimate hazard concentrations for. Deprecated for proportion = 0.05. **[Deprecated]**
proportion	A numeric vector of proportion values to estimate hazard concentrations for.
...	Unused.
average	A flag specifying whether to provide model averaged values as opposed to a value for each distribution.
ci	A flag specifying whether to estimate confidence intervals (by bootstrapping).
level	A number between 0 and 1 of the confidence level of the interval.
nboot	A count of the number of bootstrap samples to use to estimate the confidence limits. A value of 10,000 is recommended for official guidelines.
min_pboot	A number between 0 and 1 of the minimum proportion of bootstrap samples that must successfully fit (return a likelihood) to report the confidence intervals.
est_method	A string specifying whether to estimate directly from the model-averaged cumulative distribution function (est_method = 'multi') or to take the arithmetic mean of the estimates from the individual cumulative distribution functions weighted by the AICc derived weights (est_method = 'arithmetic') or or to use the geometric mean instead (est_method = 'geometric').
ci_method	A string specifying which method to use for estimating the standard error and confidence limits from the bootstrap samples. The default and recommended value is still ci_method = "weighted_samples" which takes bootstrap samples from each distribution proportional to its AICc based weights and calculates the confidence limits (and SE) from this single set. ci_method = "multi_fixed" and ci_method = "multi_free" generate the bootstrap samples using the model-averaged cumulative distribution function but differ in whether the model weights are fixed at the values for the original dataset or re-estimated for each bootstrap sample dataset. The value ci_method = "MACL" (was ci_method = "weighted_arithmetic"), which is only included for historical reasons, takes the weighted arithmetic mean of the confidence limits while ci_method = GMACL which takes the weighted geometric mean of the confidence limits was added for completeness but is also not recommended. Finally ci_method = "arithmetic_samples" and ci_method = "geometric_samples" take the weighted arithmetic or geometric mean of the values for each bootstrap iteration across all the distributions and then calculate the confidence limits (and SE) from the single set of samples.

parametric	A flag specifying whether to perform parametric bootstrapping as opposed to non-parametrically resampling the original data with replacement.
delta	A non-negative number specifying the maximum absolute AIC difference cutoff. Distributions with an absolute AIC difference greater than delta are excluded from the calculations.
control	A list of control parameters passed to stats::optim().

Details

It is useful for plotting purposes.

See Also

ssd_hc() and ssd_plot()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
predict(fits)
```

---

scale_colour_ssd *Discrete color-blind scale for SSD Plots*

Description

The functions were designed for coloring different groups in a plot of SSD data.

Usage

```
scale_colour_ssd(...)

scale_color_ssd(...)

scale_fill_ssd(...)
```

Arguments

...	Arguments passed to ggplot2::discrete_scale().

Functions

- scale_color_ssd(): Discrete color-blind scale for SSD Plots
- scale_fill_ssd(): Discrete color-blind scale for SSD Plots

See Also

Other ggplot: geom_hcintersect(), geom_ssdpoint(), geom_ssdsegment(), geom_xribbon(), ssd_pal()

Examples

```
# Use the color-blind palette for a SSD plot
ssd_plot(ssddata::ccme_boron, boron_pred, shape = "Group", color = "Group") +
  scale_colour_ssd()
# Use the color-blind palette for a histogram of concentrations
ggplot2::ggplot(ssddata::ccme_boron, ggplot2::aes(x = Species, y = Conc, fill = Group)) +
  ggplot2::geom_col() +
  scale_fill_ssd() +
  ggplot2::theme(axis.text.x = ggplot2::element_text(angle = 90, vjust = 0.5, hjust = 1))
```

---

ssdtools-ggproto *ggproto Classes for Plotting Species Sensitivity Data and Distributions*

Description

ggproto Classes for Plotting Species Sensitivity Data and Distributions

Usage

```
StatSsdpoint

StatSsdsegment

GeomSsdpoint

GeomSsdsegment

GeomHcintersect

GeomXribbon
```

Format

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

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

An object of class `GeomSsdpoint` (inherits from `GeomPoint`, `Geom`, `ggproto`, gg) of length 1.

An object of class `GeomSsdsegment` (inherits from `GeomSegment`, `Geom`, `ggproto`, gg) of length 1.

An object of class `GeomHcintersect` (inherits from `Geom`, `ggproto`, gg) of length 5.

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

See Also

`ggplot2::ggproto()` and `ssd_plot_cdf()`

ssd_at_boundary *Is At Boundary*

Description

Generic function to test if one or more parameters is at boundary.

Usage

```
ssd_at_boundary(x, ...)

## S3 method for class 'tmbfit'
ssd_at_boundary(x, ...)

## S3 method for class 'fitdists'
ssd_at_boundary(x, ...)
```

Arguments

x	The object.
...	Unused.

Value

A flag for each distribution indicating if one or more parameters at boundary.

A flag indicating if one or more parameters at boundary.

A logical vector for each distribution indicating if one or more parameters at boundary.

Methods (by class)

- ssd_at_boundary(tmbfit): Is At Boundary for tmbfit Object
- ssd_at_boundary(fitdists): Is At Boundary for fitdists Object

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron,
  dists = c("lnorm", "lnorm_lnorm", "burrIII3")
)
ssd_at_boundary(fits$lnorm)
ssd_at_boundary(fits$lnorm_lnorm)
ssd_at_boundary(fits$burrIII3)

fits <- ssd_fit_dists(ssddata::ccme_boron,
  dists = c("lnorm", "lnorm_lnorm", "burrIII3")
)
ssd_at_boundary(fits)
```

ssd_censor_data *Censor Data*

Description

Censors data to a specified range based on the `censoring` argument. The function is useful for creating test data sets.

Usage

```
ssd_censor_data(data, left = "Conc", ..., right = left, censoring = c(0, Inf))
```

Arguments

`data`	A data frame.
`left`	A string of the column in data with the concentrations.
`...`	Unused.
`right`	A string of the column in data with the right concentration values.
`censoring`	A numeric vector of the left and right censoring values.

Value

A tibble of the censored data.

Examples

```
ssd_censor_data(ssddata::ccme_boron, censoring = c(2.5, Inf))
```

ssd_computable *Is Computable Standard Errors*

Description

Generic function to test if all parameters have numerically computable standard errors.

Usage

```
ssd_computable(x, ...)

## S3 method for class 'tmbfit'
ssd_computable(x, ...)

## S3 method for class 'fitdists'
ssd_computable(x, ...)
```

Arguments

x	The object.
...	Unused.

Value

A flag for each distribution indicating if all parameters have numerically computable standard errors.

A flag indicating if all parameters have numerically computable standard errors.

A logical vector for each distribution indicating if all parameters have numerically computable standard errors.

Methods (by class)

- `ssd_computable(tmbfit)`: Is Computable Standard for tmbfit Object
- `ssd_computable(fitdists)`: Is At Boundary for fitdists Object

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron,
  dists = c("lnorm", "lnorm_lnorm", "burrIII3")
)
ssd_computable(fits$lnorm)
ssd_computable(fits$lnorm_lnorm)
ssd_computable(fits$burrIII3)

fits <- ssd_fit_dists(ssddata::ccme_boron,
  dists = c("lnorm", "lnorm_lnorm", "burrIII3")
)
ssd_computable(fits)
```

`ssd_data` *Data from fitdists Object*

Description

Get a tibble of the original data.

Usage

```
ssd_data(x)
```

Arguments

x	The object.

Value

A tibble of the original data.

See Also

augment.fitdists(), ssd_ecd_data() and ssd_sort_data()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
ssd_data(fits)
```

---

ssd_dists *Species Sensitivity Distributions*

Description

Gets a character vector of the names of the available distributions.

Usage

```
ssd_dists(bcanz = NULL, ..., tails = NULL, npars = 2:5, valid = TRUE)
```

Arguments

bcanz	A flag or NULL specifying whether to only include distributions in the set that is approved by BC, Canada, Australia and New Zealand for official guidelines.
...	Unused.
tails	A flag or NULL specifying whether to only include distributions with both tails.
npars	A whole numeric vector specifying which distributions to include based on the number of parameters.
valid	A flag or NULL specifying whether to include distributions with valid likelihoods that allows them to be fit with other distributions for modeling averaging.

Value

A unique, sorted character vector of the distributions.

See Also

Other dists: dist_data, ssd_dists_all(), ssd_dists_shiny()

Examples

```
ssd_dists()
ssd_dists(bcanz = TRUE)
ssd_dists(tails = FALSE)
ssd_dists(npars = 5)
```

ssd_dists_all *All Species Sensitivity Distributions*

Description

Gets a character vector of the names of all the available distributions.

Usage

```
ssd_dists_all(valid = TRUE)
```

Arguments

valid	A flag or NULL specifying whether to include distributions with valid likelihoods that allows them to be fit with other distributions for modeling averaging.

Value

A unique, sorted character vector of the distributions.

See Also

Other dists: dist_data, ssd_dists(), ssd_dists_shiny()

Examples

```
ssd_dists_all()
```

ssd_dists_bcanz *BCANZ Distributions*

Description

Gets a character vector of the names of the distributions adopted by BC, Canada, Australia and New Zealand for official guidelines.

Usage

```
ssd_dists_bcanz(npars = c(2L, 5L))
```

Arguments

npars	A whole numeric vector specifying which distributions to include based on the number of parameters.

Value

A unique, sorted character vector of the distributions.

See Also

`ssd_dists()`

Examples

```
ssd_dists_bcanz()
ssd_dists_bcanz(npars = 2)
```

`ssd_dists_shiny` *All Shiny Species Sensitivity Distributions*

Description

Gets a character vector of the names of all the available distributions in the shinyssdtools.

Usage

```
ssd_dists_shiny()
```

Value

A unique, sorted character vector of the distributions.

See Also

Other dists: `dist_data`, `ssd_dists()`, `ssd_dists_all()`

Examples

```
ssd_dists_shiny()
```

ssd_eburrIII3 *Default Parameter Estimates*

Description

Default Parameter Estimates

Usage

```
ssd_eburrIII3()

ssd_egamma()

ssd_egompertz()

ssd_einvpareto()

ssd_elgumbel()

ssd_elgumbel()

ssd_ellogis_llogis()

ssd_ellogis()

ssd_elnorm_lnorm()

ssd_elnorm()

ssd_emulti()

ssd_eweibull()
```

Functions

- `ssd_eburrIII3()`: Default Parameter Values for BurrIII Distribution
- `ssd_egamma()`: Default Parameter Values for Gamma Distribution
- `ssd_egompertz()`: Default Parameter Values for Gompertz Distribution
- `ssd_einvpareto()`: Default Parameter Values for Inverse Pareto Distribution
- `ssd_elgumbel()`: Default Parameter Values for Log-Gumbel Distribution
- `ssd_elgumbel()`: Default Parameter Values for log-Gumbel Distribution
- `ssd_ellogis_llogis()`: Default Parameter Values for Log-Logistic/Log-Logistic Mixture Distribution
- `ssd_ellogis()`: Default Parameter Values for Log-Logistic Distribution

- ssd_elnorm_lnorm(): Default Parameter Values for Log-Normal/Log-Normal Mixture Distribution
- ssd_elnorm(): Default Parameter Values for Log-Normal Distribution
- ssd_emulti(): Default Parameter Values for Multiple Distributions
- ssd_eweibull(): Default Parameter Values for Log-Normal Distribution

See Also

ssd_p and ssd_q

Examples

```
ssd_eburrIII3()

ssd_egamma()

ssd_egompertz()

ssd_einvpareto()

ssd_einvpareto()

ssd_elgumbel()

ssd_ellogis_llogis()

ssd_ellogis()

ssd_elnorm_lnorm()

ssd_elnorm()

ssd_emulti()

ssd_eweibull()
```

---

ssd_ecd *Empirical Cumulative Density*

Description

Empirical Cumulative Density

Usage

```
ssd_ecd(x, ties.method = "first")
```

Arguments

x	a numeric, complex, character or logical vector.
ties.method	a character string specifying how ties are treated, see 'Details'; can be abbreviated.

Value

A numeric vector of the empirical cumulative density.

Examples

```
ssd_ecd(1:10)
```

---

ssd_ecd_data *Empirical Cumulative Density for Species Sensitivity Data*

Description

Empirical Cumulative Density for Species Sensitivity Data

Usage

```
ssd_ecd_data(
  data,
  left = "Conc",
  right = left,
  ...,
  bounds = c(left = 1, right = 1)
)
```

Arguments

data	A data frame.
left	A string of the column in data with the concentrations.
right	A string of the column in data with the right concentration values.
...	Unused.
bounds	A named non-negative numeric vector of the left and right bounds for uncensored missing (0 and Inf) data in terms of the orders of magnitude relative to the extremes for non-missing values.

Value

A numeric vector of the empirical cumulative density for the rows in data.

See Also

ssd_ecd() and ssd_data()

Examples

```
ssd_ecd_data(ssddata::ccme_boron)
```

`ssd_exposure` *Proportion Exposure*

Description

Calculates average proportion exposed based on log-normal distribution of concentrations.

Usage

```
ssd_exposure(x, meanlog = 0, sdlog = 1, ..., nboot = 1000)
```

Arguments

`x`	The object.
`meanlog`	The mean of the exposure concentrations on the log scale.
`sdlog`	The standard deviation of the exposure concentrations on the log scale.
`...`	Unused.
`nboot`	The number of samples to use to calculate the exposure.

Value

The proportion exposed.

Examples

```
## Not run:
fits <- ssd_fit_dists(ssddata::ccme_boron, dists = "lnorm")
withr::with_seed(50, {
  ssd_exposure(fits)
  ssd_exposure(fits, meanlog = 1)
  ssd_exposure(fits, meanlog = 1, sdlog = 1)
})

## End(Not run)
```

`ssd_fit_bcanz` *Fit BCANZ Distributions*

Description

Fits distributions using settings adopted by BC, Canada, Australia and New Zealand for official guidelines.

Usage

```
ssd_fit_bcanz(
  data,
  left = "Conc",
  ...,
  dists = ssd_dists_bcanz(),
  rescale = FALSE,
  silent = FALSE
)
```

Arguments

`data`	A data frame.
`left`	A string of the column in data with the concentrations.
`...`	Unused.
`dists`	A character vector of the distribution names.
`rescale`	A flag specifying whether to leave the values unchanged (FALSE) or to rescale concentration values by dividing by the geometric mean of the minimum and maximum positive finite values (TRUE).
`silent`	A flag indicating whether fits should fail silently.

Value

An object of class fitdists.

See Also

`ssd_fit_dists()`

Other BCANZ: `ssd_hc_bcanz()`, `ssd_hp_bcanz()`

Examples

```
ssd_fit_bcanz(ssddata::ccme_boron)
```

`ssd_fit_burrlioz` *Fit Burrlioz Distributions*

Description

Fits 'burrIII3' distribution. If shape1 parameter is at boundary returns 'lgumbel' (which is equivalent to inverse Weibull). Else if shape2 parameter is at a boundary returns 'invpareto'. Otherwise returns 'burrIII3'

Usage

```
ssd_fit_burrlioz(
  data,
  left = "Conc",
  ...,
  rescale = FALSE,
  control = list(),
  silent = FALSE
)
```

Arguments

`data`	A data frame.
`left`	A string of the column in data with the concentrations.
`...`	Unused.
`rescale`	A flag specifying whether to leave the values unchanged (FALSE) or to rescale concentration values by dividing by the geometric mean of the minimum and maximum positive finite values (TRUE) or a string specifying whether to leave the values unchanged ("no") or to rescale concentration values by dividing by the geometric mean of the minimum and maximum positive finite values ("geomean") or to logistically transform ("odds").
`control`	A list of control parameters passed to `stats::optim()`.
`silent`	A flag indicating whether fits should fail silently.

Value

An object of class fitdists.

See Also

`ssd_fit_dists()`

Examples

```
ssd_fit_burrlioz(ssddata::ccme_boron)
```

`ssd_fit_dists` *Fit Distributions*

Description

Fits one or more distributions to species sensitivity data.

Usage

```
ssd_fit_dists(
  data,
  left = "Conc",
  ...,
  right = left,
  weight = NULL,
  dists = ssd_dists_bcanz(),
  nrow = 6L,
  rescale = FALSE,
  odds_max = 0.999,
  reweight = FALSE,
  computable = FALSE,
  at_boundary_ok = TRUE,
  all_dists = FALSE,
  min_pmix = ssd_min_pmix(nrow(data)),
  range_shape1 = c(0.05, 20),
  range_shape2 = range_shape1,
  control = list(),
  silent = FALSE
)
```

Arguments

`data`	A data frame.
`left`	A string of the column in data with the concentrations.
`...`	Unused.
`right`	A string of the column in data with the right concentration values.
`weight`	A string of the numeric column in data with positive weights less than or equal to 1,000 or NULL.
`dists`	A character vector of the distribution names.
`nrow`	A positive whole number of the minimum number of non-missing rows.
`rescale`	A flag specifying whether to leave the values unchanged (FALSE) or to rescale concentration values by dividing by the geometric mean of the minimum and maximum positive finite values (TRUE) or a string specifying whether to leave the values unchanged ("no") or to rescale concentration values by dividing by the geometric mean of the minimum and maximum positive finite values ("geomean") or to logistically transform ("odds").

odds_max	A number specifying the upper left value when rescale = "odds". By default left values cannot exceed 0.999.
reweight	A flag specifying whether to reweight weights by dividing by the largest weight.
computable	A flag specifying whether to only return fits with numerically computable standard errors.
at_boundary_ok	A flag specifying whether a model with one or more parameters at the boundary should be considered to have converged (default = TRUE).
all_dists	A flag specifying whether all the named distributions must fit successfully.
min_pmix	A number between 0 and 0.5 specifying the minimum proportion in mixture models.
range_shape1	A numeric vector of length two of the lower and upper bounds for the shape1 parameter.
range_shape2	shape2 parameter.
control	A list of control parameters passed to stats::optim().
silent	A flag indicating whether fits should fail silently.

Details

By default the 'gamma', 'lgumbel', 'llogis', 'lnorm', 'lnorm_lnorm' and 'weibull' distributions are fitted to the data. For a complete list of the distributions that are currently implemented in ssdtools see ssd_dists_all().

If weight specifies a column in the data frame with positive numbers, weighted estimation occurs. However, currently only the resultant parameter estimates are available.

If the right argument is different to the left argument then the data are considered to be censored.

Value

An object of class fitdists.

See Also

ssd_plot_cdf() and ssd_hc()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
fits
ssd_plot_cdf(fits)
ssd_hc(fits)
```

ssd_gof *Goodness of Fit*

Description

Returns a tbl data frame with the following columns

dist The distribution name (chr)

aic Akaike's Information Criterion (dbl)

bic Bayesian Information Criterion (dbl)

at_bound Parameter(s) at boundary (lgl)

computable All parameter have computable standard errors (lgl)

and if the data are non-censored

aicc Akaike's Information Criterion corrected for sample size (dbl)

and if there are 8 or more samples

ad Anderson-Darling statistic (dbl)

ks Kolmogorov-Smirnov statistic (dbl)

cvm Cramer-von Mises statistic (dbl)

In the case of an object of class fitdists the function also returns

delta The Information Criterion differences (dbl)

wt The Information Criterion weights (dbl)

where `delta` and `wt` are based on `aic` for censored data and `aicc` for non-censored data.

Usage

```
ssd_gof(x, ...)

## S3 method for class 'fitdists'
ssd_gof(x, ..., pvalue = FALSE, wt = FALSE)
```

Arguments

`x`	The object.
`...`	Unused.
`pvalue`	A flag specifying whether to return p-values or the statistics (default) for the various tests.
`wt`	A flag specifying whether to return the Akaike weight as "wt" instead of "weight".

Value

A tbl data frame of the gof statistics.

Methods (by class)

- `ssd_gof(fitdists)`: Goodness of Fit

See Also

`glance.fitdists()`

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
ssd_gof(fits, wt = TRUE)
ssd_gof(fits, pvalue = TRUE, wt = TRUE)
```

---

ssd_hc *Hazard Concentrations for Species Sensitivity Distributions*

Description

Calculates concentration(s) with bootstrap confidence intervals that protect specified proportion(s) of species for individual or model-averaged distributions using parametric or non-parametric bootstrapping.

Usage

```
ssd_hc(x, ...)

## S3 method for class 'list'
ssd_hc(x, percent, proportion = 0.05, ...)

## S3 method for class 'fitdists'
ssd_hc(
  x,
  percent = deprecated(),
  proportion = 0.05,
  ...,
  average = TRUE,
  ci = FALSE,
  level = 0.95,
  nboot = 1000,
  min_pboot = 0.8,
  multi_est = deprecated(),
  est_method = "multi",
  ci_method = "weighted_samples",
  parametric = TRUE,
  delta = 9.21,
  samples = FALSE,
  save_to = NULL,
```

```
  control = NULL
)

## S3 method for class 'fitburrlioz'
ssd_hc(
  x,
  percent,
  proportion = 0.05,
  ...,
  ci = FALSE,
  level = 0.95,
  nboot = 1000,
  min_pboot = 0.8,
  parametric = FALSE,
  samples = FALSE,
  save_to = NULL
)
```

Arguments

x	The object.
...	Unused.
percent	A numeric vector of percent values to estimate hazard concentrations for. Deprecated for proportion = 0.05. **[Deprecated]**
proportion	A numeric vector of proportion values to estimate hazard concentrations for.
average	A flag specifying whether to provide model averaged values as opposed to a value for each distribution.
ci	A flag specifying whether to estimate confidence intervals (by bootstrapping).
level	A number between 0 and 1 of the confidence level of the interval.
nboot	A count of the number of bootstrap samples to use to estimate the confidence limits. A value of 10,000 is recommended for official guidelines.
min_pboot	A number between 0 and 1 of the minimum proportion of bootstrap samples that must successfully fit (return a likelihood) to report the confidence intervals.
multi_est	A flag specifying whether to estimate directly from the model-averaged cumulative distribution function (multi_est = TRUE) or to take the arithmetic mean of the estimates from the individual cumulative distribution functions weighted by the AICc derived weights (multi_est = FALSE).
est_method	A string specifying whether to estimate directly from the model-averaged cumulative distribution function (est_method = 'multi') or to take the arithmetic mean of the estimates from the individual cumulative distribution functions weighted by the AICc derived weights (est_method = 'arithmetic') or or to use the geometric mean instead (est_method = 'geometric').
ci_method	A string specifying which method to use for estimating the standard error and confidence limits from the bootstrap samples. The default and recommended value is still ci_method = "weighted_samples" which takes bootstrap samples

from each distribution proportional to its AICc based weights and calculates the confidence limits (and SE) from this single set. `ci_method = "multi_fixed"` and `ci_method = "multi_free"` generate the bootstrap samples using the model-averaged cumulative distribution function but differ in whether the model weights are fixed at the values for the original dataset or re-estimated for each bootstrap sample dataset. The value `ci_method = "MACL"` (was `ci_method = "weighted_arithmetic"`), which is only included for historical reasons, takes the weighted arithmetic mean of the confidence limits while `ci_method = GMACL` which takes the weighted geometric mean of the confidence limits was added for completeness but is also not recommended. Finally `ci_method = "arithmetic_samples"` and `ci_method = "geometric_samples"` take the weighted arithmetic or geometric mean of the values for each bootstrap iteration across all the distributions and then calculate the confidence limits (and SE) from the single set of samples.

`parametric` A flag specifying whether to perform parametric bootstrapping as opposed to non-parametrically resampling the original data with replacement.

`delta` A non-negative number specifying the maximum absolute AIC difference cutoff. Distributions with an absolute AIC difference greater than delta are excluded from the calculations.

`samples` A flag specfying whether to include a numeric vector of the bootstrap samples as a list column in the output.

`save_to` NULL or a string specifying a directory to save where the bootstrap datasets and parameter estimates (when successfully converged) to.

`control` A list of control parameters passed to `stats::optim()`.

Details

Model-averaged estimates and/or confidence intervals (including standard error) can be calculated by treating the distributions as constituting a single mixture distribution versus 'taking the mean'. When calculating the model averaged estimates treating the distributions as constituting a single mixture distribution ensures that `ssd_hc()` is the inverse of `ssd_hp()`.

Distributions with an absolute AIC difference greater than a delta of by default 7 have considerably less support (wt < 0.01) and are excluded prior to calculation of the hazard concentrations to reduce the run time.

Value

A tibble of corresponding hazard concentrations.

Methods (by class)

- `ssd_hc(list)`: Hazard Concentrations for Distributional Estimates
- `ssd_hc(fitdists)`: Hazard Concentrations for fitdists Object
- `ssd_hc(fitburrlioz)`: Hazard Concentrations for fitburrlioz Object

References

Burnham, K.P., and Anderson, D.R. 2002. Model Selection and Multimodel Inference. Springer New York, New York, NY. doi:10.1007/b97636.

See Also

predict.fitdists() and ssd_hp().

Examples

```
ssd_hc(ssd_match_moments())

fits <- ssd_fit_dists(ssddata::ccme_boron)
ssd_hc(fits)

fit <- ssd_fit_burrlioz(ssddata::ccme_boron)
ssd_hc(fit)
```

---

ssd_hc_bcanz *BCANZ Hazard Concentrations*

Description

Gets hazard concentrations with confidence intervals that protect 1, 5, 10 and 20% of species using settings adopted by BC, Canada, Australia and New Zealand for official guidelines. This function can take several minutes to run with recommended 10,000 iterations.

Usage

```
ssd_hc_bcanz(
  x,
  proportion = c(0.01, 0.05, 0.1, 0.2),
  ...,
  average = TRUE,
  ci = FALSE,
  nboot = 10000,
  min_pboot = 0.8
)
```

Arguments

x	The object.
proportion	A numeric vector of proportion values to estimate hazard concentrations for.
...	Unused.
average	A flag specifying whether to provide model averaged values as opposed to a value for each distribution.
ci	A flag specifying whether to estimate confidence intervals (by bootstrapping).
nboot	A count of the number of bootstrap samples to use to estimate the confidence limits. A value of 10,000 is recommended for official guidelines.
min_pboot	A number between 0 and 1 of the minimum proportion of bootstrap samples that must successfully fit (return a likelihood) to report the confidence intervals.

Value

A tibble of corresponding hazard concentrations.

See Also

ssd_hc().

Other BCANZ: ssd_fit_bcanz(), ssd_hp_bcanz()

Examples

```
fits <- ssd_fit_bcanz(ssddata::ccme_boron)
ssd_hc_bcanz(fits, nboot = 100)
```

---

ssd_hp *Hazard Proportion*

Description

Calculates proportion of species affected at specified concentration(s) with quantile based bootstrap confidence intervals for individual or model-averaged distributions using parametric or non-parametric bootstrapping. For more information see the inverse function ssd_hc().

Usage

```
ssd_hp(x, ...)

## S3 method for class 'fitdists'
ssd_hp(
  x,
  conc = 1,
  ...,
  average = TRUE,
  ci = FALSE,
  level = 0.95,
  nboot = 1000,
  min_pboot = 0.8,
  multi_est = deprecated(),
  est_method = "multi",
  ci_method = "weighted_samples",
  parametric = TRUE,
  delta = 9.21,
  proportion = FALSE,
  samples = FALSE,
  save_to = NULL,
  control = NULL
)
```

```
## S3 method for class 'fitburrlioz'
ssd_hp(
  x,
  conc = 1,
  ...,
  ci = FALSE,
  level = 0.95,
  nboot = 1000,
  min_pboot = 0.8,
  parametric = FALSE,
  proportion = FALSE,
  samples = FALSE,
  save_to = NULL
)
```

Arguments

x	The object.
...	Unused.
conc	A numeric vector of concentrations to calculate the hazard proportions for.
average	A flag specifying whether to provide model averaged values as opposed to a value for each distribution.
ci	A flag specifying whether to estimate confidence intervals (by bootstrapping).
level	A number between 0 and 1 of the confidence level of the interval.
nboot	A count of the number of bootstrap samples to use to estimate the confidence limits. A value of 10,000 is recommended for official guidelines.
min_pboot	A number between 0 and 1 of the minimum proportion of bootstrap samples that must successfully fit (return a likelihood) to report the confidence intervals.
multi_est	A flag specifying whether to estimate directly from the model-averaged cumulative distribution function (multi_est = TRUE) or to take the arithmetic mean of the estimates from the individual cumulative distribution functions weighted by the AICc derived weights (multi_est = FALSE).
est_method	A string specifying whether to estimate directly from the model-averaged cumulative distribution function (est_method = 'multi') or to take the arithmetic mean of the estimates from the individual cumulative distribution functions weighted by the AICc derived weights (est_method = 'arithmetic') or or to use the geometric mean instead (est_method = 'geometric').
ci_method	A string specifying which method to use for estimating the standard error and confidence limits from the bootstrap samples. The default and recommended value is still ci_method = "weighted_samples" which takes bootstrap samples from each distribution proportional to its AICc based weights and calculates the confidence limits (and SE) from this single set. ci_method = "multi_fixed" and ci_method = "multi_free" generate the bootstrap samples using the model-averaged cumulative distribution function but differ in whether the model weights are fixed at the values for the original dataset or re-estimated for each bootstrap sample dataset. The value ci_method = "MACL" (was ci_method = "weighted_arithmetic"),

which is only included for historical reasons, takes the weighted arithmetic mean of the confidence limits while ci_method = GMACL which takes the weighted geometric mean of the confidence limits was added for completeness but is also not recommended. Finally ci_method = "arithmetic_samples" and ci_method = "geometric_samples" take the weighted arithmetic or geometric mean of the values for each bootstrap iteration across all the distributions and then calculate the confidence limits (and SE) from the single set of samples.

parametric — A flag specifying whether to perform parametric bootstrapping as opposed to non-parametrically resampling the original data with replacement.

delta — A non-negative number specifying the maximum absolute AIC difference cutoff. Distributions with an absolute AIC difference greater than delta are excluded from the calculations.

proportion — A flag specifying whether to return hazard proportions (proportion = TRUE) or hazard percentages (proportion = FALSE). To not break existing code the default value is FALSE but will be switching the default to TRUE in a future version. The user is recommended to manually set to TRUE now to avoid unexpected changes in future versions.

samples — A flag specfying whether to include a numeric vector of the bootstrap samples as a list column in the output.

save_to — NULL or a string specifying a directory to save where the bootstrap datasets and parameter estimates (when successfully converged) to.

control — A list of control parameters passed to stats::optim().

Value

A tibble of corresponding hazard proportions.

Methods (by class)

- ssd_hp(fitdists): Hazard Proportions for fitdists Object
- ssd_hp(fitburrlioz): Hazard Proportions for fitburrlioz Object

See Also

ssd_hc()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
ssd_hp(fits, conc = 1)

fit <- ssd_fit_burrlioz(ssddata::ccme_boron)
ssd_hp(fit)
```

ssd_hp_bcanz *BCANZ Hazard Proportion*

Description

Gets proportion of species affected at specified concentration(s) using settings adopted by BC, Canada, Australia and New Zealand for official guidelines. This function can take several minutes to run with recommended 10,000 iterations.

Usage

```
ssd_hp_bcanz(
  x,
  conc = 1,
  ...,
  average = TRUE,
  ci = FALSE,
  nboot = 10000,
  min_pboot = 0.8,
  proportion = FALSE
)
```

Arguments

x	The object.
conc	A numeric vector of concentrations to calculate the hazard proportions for.
...	Unused.
average	A flag specifying whether to provide model averaged values as opposed to a value for each distribution.
ci	A flag specifying whether to estimate confidence intervals (by bootstrapping).
nboot	A count of the number of bootstrap samples to use to estimate the confidence limits. A value of 10,000 is recommended for official guidelines.
min_pboot	A number between 0 and 1 of the minimum proportion of bootstrap samples that must successfully fit (return a likelihood) to report the confidence intervals.
proportion	A numeric vector of proportion values to estimate hazard concentrations for.

Value

A tibble of corresponding hazard concentrations.

See Also

ssd_hp().

Other BCANZ: ssd_fit_bcanz(), ssd_hc_bcanz()

Examples

```
fits <- ssd_fit_bcanz(ssddata::ccme_boron)
ssd_hp_bcanz(fits, nboot = 100)
```

`ssd_is_censored` *Is Censored*

Description

Tests if an object has censored data.

Test if a data frame is censored.

Test if a fitdists object is censored.

Usage

```
ssd_is_censored(x, ...)

## S3 method for class 'data.frame'
ssd_is_censored(x, left = "Conc", right = left, ...)

## S3 method for class 'fitdists'
ssd_is_censored(x, ...)
```

Arguments

`x`	The object.
`...`	Unused.
`left`	A string of the column in data with the concentrations.
`right`	A string of the column in data with the right concentration values.

Value

A flag indicating whether an object is censored.

Examples

```
ssd_is_censored(ssddata::ccme_boron)
ssd_is_censored(data.frame(Conc = 1, right = 2), right = "right")

fits <- ssd_fit_dists(ssddata::ccme_boron)
ssd_is_censored(fits)
```

`ssd_label_comma` *Label numbers with significant digits and comma*

Description

Label numbers with significant digits and comma

Usage

```
ssd_label_comma(
  digits = 3,
  ...,
  big.mark = ",",
  decimal.mark = getOption("OutDec", ".")
)
```

Arguments

`digits`	A whole number specifying the number of significant figures.
`...`	Unused.
`big.mark`	A string specifying the thousands separator.
`decimal.mark`	A string specifying the numeric decimal point.

Value

A "labelling" function that takes a vector x and returns a character vector of `length(x)` giving a label for each input value.

See Also

`scales::label_comma()`

Examples

```
ggplot2::ggplot(data = ssddata::anon_e, ggplot2::aes(x = Conc / 10)) +
  geom_ssdpoint() +
  ggplot2::scale_x_log10(labels = ssd_label_comma())
```

`ssd_label_comma_hc` *Label numbers with significant digits and comma. If* `hc_value` *is present in breaks, put on new line and make bold.*

Description

Label numbers with significant digits and comma. If `hc_value` is present in breaks, put on new line and make bold.

Usage

```
ssd_label_comma_hc(
  hc_value,
  digits = 3,
  ...,
  big.mark = ",",
  decimal.mark = getOption("OutDec", ".")
)
```

Arguments

`hc_value`	A number of the hazard concentration value to offset.
`digits`	A whole number specifying the number of significant figures.
`...`	Unused.
`big.mark`	A string specifying the thousands separator.
`decimal.mark`	A string specifying the numeric decimal point.

Value

A "labelling" function that takes a vector x and returns a character vector of `length(x)` giving a label for each input value.

See Also

`scales::label_comma()`

Examples

```
ggplot2::ggplot(data = ssddata::anon_e, ggplot2::aes(x = Conc / 10)) +
  geom_ssdpoint() +
  ggplot2::scale_x_log10(labels = ssd_label_comma_hc(1.26))
```

ssd_licensing_md *Licensing Markdown*

Description

A string of markdown code indicating the licensing of the code and documentation

Usage

```
ssd_licensing_md()
```

Examples

```
ssd_licensing_md()
```

ssd_match_moments *Match Moments*

Description

Gets a named list of the values that produce the moment values (meanlog and sdlog) by distribution and term.

Usage

```
ssd_match_moments(
  dists = ssd_dists_bcanz(),
  meanlog = 1,
  sdlog = 1,
  ...,
  nsim = 1e+05
)
```

Arguments

dists	A character vector of the distribution names.
meanlog	The mean on the log scale.
sdlog	The standard deviation on the log scale.
...	Unused.
nsim	A positive whole number of the number of simulations to generate.

Value

a named list of the values that produce the moment values by distribution and term.

See Also

estimates.fitdists(), ssd_hc() and ssd_plot_cdf()

Examples

```
moments <- ssd_match_moments()
print(moments)
ssd_hc(moments)
ssd_plot_cdf(moments)
```

---

ssd_min_pmix *Calculate Minimum Proportion in Mixture Models*

Description

Calculate Minimum Proportion in Mixture Models

Usage

```
ssd_min_pmix(n)
```

Arguments

n	positive number of observations.

Value

A number between 0 and 0.5 of the minimum proportion in mixture models.

See Also

ssd_fit_dists()

Examples

```
ssd_min_pmix(6)
ssd_min_pmix(50)
```

ssd_pal *Color-blind Palette for SSD Plots*

Description

Color-blind Palette for SSD Plots

Usage

```
ssd_pal()
```

Value

A character vector of a color blind palette with 8 colors.

See Also

Other ggplot: geom_hcintersect(), geom_ssdpoint(), geom_ssdsegment(), geom_xribbon(), scale_colour_ssd()

Examples

```
ssd_pal()
```

ssd_pburrIII3 *Cumulative Distribution Function*

Description

Cumulative Distribution Function

Usage

```
ssd_pburrIII3(
  q,
  shape1 = 1,
  shape2 = 1,
  scale = 1,
  lower.tail = TRUE,
  log.p = FALSE
)

ssd_pgamma(q, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE)

ssd_pgompertz(q, location = 1, shape = 1, lower.tail = TRUE, log.p = FALSE)
```

```
ssd_pinvpareto(q, shape = 3, scale = 1, lower.tail = TRUE, log.p = FALSE)

ssd_plgumbel(
  q,
  locationlog = 0,
  scalelog = 1,
  lower.tail = TRUE,
  log.p = FALSE
)

ssd_pllogis_llogis(
  q,
  locationlog1 = 0,
  scalelog1 = 1,
  locationlog2 = 1,
  scalelog2 = 1,
  pmix = 0.5,
  lower.tail = TRUE,
  log.p = FALSE
)

ssd_pllogis(q, locationlog = 0, scalelog = 1, lower.tail = TRUE, log.p = FALSE)

ssd_plnorm_lnorm(
  q,
  meanlog1 = 0,
  sdlog1 = 1,
  meanlog2 = 1,
  sdlog2 = 1,
  pmix = 0.5,
  lower.tail = TRUE,
  log.p = FALSE
)

ssd_plnorm(q, meanlog = 0, sdlog = 1, lower.tail = TRUE, log.p = FALSE)

ssd_pmulti(
  q,
  burrIII3.weight = 0,
  burrIII3.shape1 = 1,
  burrIII3.shape2 = 1,
  burrIII3.scale = 1,
  gamma.weight = 0,
  gamma.shape = 1,
  gamma.scale = 1,
  gompertz.weight = 0,
  gompertz.location = 1,
  gompertz.shape = 1,
```

```
  lgumbel.weight = 0,
  lgumbel.locationlog = 0,
  lgumbel.scalelog = 1,
  llogis.weight = 0,
  llogis.locationlog = 0,
  llogis.scalelog = 1,
  llogis_llogis.weight = 0,
  llogis_llogis.locationlog1 = 0,
  llogis_llogis.scalelog1 = 1,
  llogis_llogis.locationlog2 = 1,
  llogis_llogis.scalelog2 = 1,
  llogis_llogis.pmix = 0.5,
  lnorm.weight = 0,
  lnorm.meanlog = 0,
  lnorm.sdlog = 1,
  lnorm_lnorm.weight = 0,
  lnorm_lnorm.meanlog1 = 0,
  lnorm_lnorm.sdlog1 = 1,
  lnorm_lnorm.meanlog2 = 1,
  lnorm_lnorm.sdlog2 = 1,
  lnorm_lnorm.pmix = 0.5,
  weibull.weight = 0,
  weibull.shape = 1,
  weibull.scale = 1,
  lower.tail = TRUE,
  log.p = FALSE
)

ssd_pmulti_fitdists(q, fitdists, lower.tail = TRUE, log.p = FALSE)

ssd_pweibull(q, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE)
```

Arguments

q	vector of quantiles.
shape1	shape1 parameter.
shape2	shape2 parameter.
scale	scale parameter.
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x].
log.p	logical; if TRUE, probabilities p are given as log(p).
shape	shape parameter.
location	location parameter.
locationlog	location on the log scale parameter.
scalelog	scale on log scale parameter.
locationlog1	locationlog1 parameter.
scalelog1	scalelog1 parameter.

`locationlog2` locationlog2 parameter.

`scalelog2` scalelog2 parameter.

`pmix` Proportion mixture parameter.

`meanlog1` mean on log scale parameter.

`sdlog1` standard deviation on log scale parameter.

`meanlog2` mean on log scale parameter.

`sdlog2` standard deviation on log scale parameter.

`meanlog` mean on log scale parameter.

`sdlog` standard deviation on log scale parameter.

`burrIII3.weight`
: weight parameter for the Burr III distribution.

`burrIII3.shape1`
: shape1 parameter for the Burr III distribution.

`burrIII3.shape2`
: shape2 parameter for the Burr III distribution.

`burrIII3.scale` scale parameter for the Burr III distribution.

`gamma.weight` weight parameter for the gamma distribution.

`gamma.shape` shape parameter for the gamma distribution.

`gamma.scale` scale parameter for the gamma distribution.

`gompertz.weight`
: weight parameter for the Gompertz distribution.

`gompertz.location`
: location parameter for the Gompertz distribution.

`gompertz.shape` shape parameter for the Gompertz distribution.

`lgumbel.weight` weight parameter for the log-Gumbel distribution.

`lgumbel.locationlog`
: location parameter for the log-Gumbel distribution.

`lgumbel.scalelog`
: scale parameter for the log-Gumbel distribution.

`llogis.weight` weight parameter for the log-logistic distribution.

`llogis.locationlog`
: location parameter for the log-logistic distribution.

`llogis.scalelog`
: scale parameter for the log-logistic distribution.

`llogis_llogis.weight`
: weight parameter for the log-logistic log-logistic mixture distribution.

`llogis_llogis.locationlog1`
: locationlog1 parameter for the log-logistic log-logistic mixture distribution.

`llogis_llogis.scalelog1`
: scalelog1 parameter for the log-logistic log-logistic mixture distribution.

`llogis_llogis.locationlog2`
: locationlog2 parameter for the log-logistic log-logistic mixture distribution.

`llogis_llogis.scalelog2`
: scalelog2 parameter for the log-logistic log-logistic mixture distribution.

`llogis_llogis.pmix`
: pmix parameter for the log-logistic log-logistic mixture distribution.

`lnorm.weight`
: weight parameter for the log-normal distribution.

`lnorm.meanlog`
: meanlog parameter for the log-normal distribution.

`lnorm.sdlog`
: sdlog parameter for the log-normal distribution.

`lnorm_lnorm.weight`
: weight parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.meanlog1`
: meanlog1 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.sdlog1`
: sdlog1 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.meanlog2`
: meanlog2 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.sdlog2`
: sdlog2 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.pmix`
: pmix parameter for the log-normal log-normal mixture distribution.

`weibull.weight`
: weight parameter for the Weibull distribution.

`weibull.shape`
: shape parameter for the Weibull distribution.

`weibull.scale`
: scale parameter for the Weibull distribution.

`fitdists`
: An object of class fitdists.

Functions

- `ssd_pburrIII3()`: Cumulative Distribution Function for BurrIII Distribution
- `ssd_pgamma()`: Cumulative Distribution Function for Gamma Distribution
- `ssd_pgompertz()`: Cumulative Distribution Function for Gompertz Distribution
- `ssd_pinvpareto()`: Cumulative Distribution Function for Inverse Pareto Distribution
- `ssd_plgumbel()`: Cumulative Distribution Function for Log-Gumbel Distribution
- `ssd_pllogis_llogis()`: Cumulative Distribution Function for Log-Logistic/Log-Logistic Mixture Distribution
- `ssd_pllogis()`: Cumulative Distribution Function for Log-Logistic Distribution
- `ssd_plnorm_lnorm()`: Cumulative Distribution Function for Log-Normal/Log-Normal Mixture Distribution
- `ssd_plnorm()`: Cumulative Distribution Function for Log-Normal Distribution
- `ssd_pmulti()`: Cumulative Distribution Function for Multiple Distributions
- `ssd_pmulti_fitdists()`: Cumulative Distribution Function for Multiple Distributions
- `ssd_pweibull()`: Cumulative Distribution Function for Weibull Distribution

See Also

ssd_q and ssd_r

Examples

```
ssd_pburrIII3(1)

ssd_pgamma(1)

ssd_pgompertz(1)

ssd_pinvpareto(1)

ssd_plgumbel(1)

ssd_pllogis_llogis(1)

ssd_pllogis(1)

ssd_plnorm_lnorm(1)

ssd_plnorm(1)

# multi
ssd_pmulti(1, gamma.weight = 0.5, lnorm.weight = 0.5)

# multi fitdists
fit <- ssd_fit_dists(ssddata::ccme_boron)
ssd_pmulti_fitdists(1, fit)

ssd_pweibull(1)
```

---

ssd_plot *Plot Species Sensitivity Data and Distributions*

Description

Plots species sensitivity data and distributions.

Usage

```
ssd_plot(
  data,
  pred,
  left = "Conc",
  right = left,
  ...,
  label = NULL,
  shape = NULL,
```

```
  color = NULL,
  size,
  linetype = NULL,
  linecolor = NULL,
  xlab = "Concentration",
  ylab = "Species Affected",
  ci = TRUE,
  ribbon = TRUE,
  hc = 0.05,
  shift_x = 3,
  add_x = 0,
  bounds = c(left = 1, right = 1),
  big.mark = ",",
  decimal.mark = getOption("OutDec", "."),
  suffix = "%",
  trans = "log10",
  xbreaks = waiver(),
  xlimits = NULL,
  text_size = 11,
  label_size = 2.5,
  theme_classic = FALSE
)
```

Arguments

data	A data frame.
pred	A data frame of the predictions.
left	A string of the column in data with the concentrations.
right	A string of the column in data with the right concentration values.
...	Unused.
label	A string of the column in data with the labels.
shape	A string of the column in data for the shape aesthetic.
color	A string of the column in data for the color aesthetic.
size	A number for the size of the labels. Deprecated for label_size. #' **[Deprecated]**
linetype	A string of the column in pred to use for the linetype.
linecolor	A string of the column in pred to use for the line color.
xlab	A string of the x-axis label.
ylab	A string of the x-axis label.
ci	A flag specifying whether to estimate confidence intervals (by bootstrapping).
ribbon	A flag indicating whether to plot the confidence interval as a grey ribbon as opposed to green solid lines.
hc	A value between 0 and 1 indicating the proportion hazard concentration (or NULL).

shift_x	The value to multiply the label x values by (after adding add_x).
add_x	The value to add to the label x values (before multiplying by shift_x).
bounds	A named non-negative numeric vector of the left and right bounds for uncensored missing (0 and Inf) data in terms of the orders of magnitude relative to the extremes for non-missing values.
big.mark	A string specifying the thousands separator.
decimal.mark	A string specifying the numeric decimal point.
suffix	Additional text to display after the number on the y-axis.
trans	A string of which transformation to use. Accepted values include "log10", "log", and "identity" ("log10" by default).
xbreaks	The x-axis breaks as one of: • NULL for no breaks • waiver() for the default breaks • A numeric vector of positions
xlimits	The x-axis limits as one of: • NULL to use the default scale range • A numeric vector of length two providing the limits. Use NA to refer to the existing minimum or maximum limits.
text_size	A number for the text size.
label_size	A number for the size of the labels.
theme_classic	A flag specifying whether to use the classic theme or the default.

See Also

ssd_plot_cdf() and geom_ssdpoint()

Examples

```
ssd_plot(ssddata::ccme_boron, boron_pred, label = "Species", shape = "Group")
```

---

ssd_plot_cdf *Plot Cumulative Distribution Function (CDF)*

Description

Generic function to plots the cumulative distribution function (CDF).

Usage

```
ssd_plot_cdf(x, ...)

## S3 method for class 'fitdists'
ssd_plot_cdf(x, average = FALSE, est_method = "multi", delta = 9.21, ...)

## S3 method for class 'list'
ssd_plot_cdf(x, ...)
```

Arguments

x	The object.
...	Additional arguments passed to ssd_plot().
average	A flag specifying whether to provide model averaged values as opposed to a value for each distribution or if NA provides model averaged and individual values.
est_method	A string specifying whether to estimate directly from the model-averaged cumulative distribution function (est_method = 'multi') or to take the arithmetic mean of the estimates from the individual cumulative distribution functions weighted by the AICc derived weights (est_method = 'arithmetic') or or to use the geometric mean instead (est_method = 'geometric').
delta	A non-negative number specifying the maximum absolute AIC difference cutoff. Distributions with an absolute AIC difference greater than delta are excluded from the calculations.

Methods (by class)

- ssd_plot_cdf(fitdists): Plot CDF for fitdists object
- ssd_plot_cdf(list): Plot CDF for named list of distributional parameter values

See Also

ssd_plot()

estimates.fitdists() and ssd_match_moments()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
ssd_plot_cdf(fits)
ssd_plot_cdf(fits, average = NA)

ssd_plot_cdf(list(
  llogis = c(locationlog = 2, scalelog = 1),
  lnorm = c(meanlog = 2, sdlog = 2)
))
```

---

ssd_plot_data *Plot Species Sensitivity Data*

Description

Plots species sensitivity data.

Usage

```
ssd_plot_data(
  data,
  left = "Conc",
  right = left,
  ...,
  label = NULL,
  shape = NULL,
  color = NULL,
  size = 2.5,
  xlab = "Concentration",
  ylab = "Species Affected",
  shift_x = 3,
  add_x = 0,
  big.mark = ",",
  decimal.mark = getOption("OutDec", "."),
  suffix = "%",
  bounds = c(left = 1, right = 1),
  trans = "log10",
  xbreaks = waiver()
)
```

Arguments

data	A data frame.
left	A string of the column in data with the concentrations.
right	A string of the column in data with the right concentration values.
...	Unused.
label	A string of the column in data with the labels.
shape	A string of the column in data for the shape aesthetic.
color	A string of the column in data for the color aesthetic.
size	A number for the size of the labels. Deprecated for label_size. #' **[Deprecated]**
xlab	A string of the x-axis label.
ylab	A string of the x-axis label.
shift_x	The value to multiply the label x values by (after adding add_x).
add_x	The value to add to the label x values (before multiplying by shift_x).
big.mark	A string specifying the thousands separator.
decimal.mark	A string specifying the numeric decimal point.
suffix	Additional text to display after the number on the y-axis.
bounds	A named non-negative numeric vector of the left and right bounds for uncensored missing (0 and Inf) data in terms of the orders of magnitude relative to the extremes for non-missing values.

trans — A string of which transformation to use. Accepted values include "log10", "log", and "identity" ("log10" by default).

xbreaks — The x-axis breaks as one of:

- NULL for no breaks
- waiver() for the default breaks
- A numeric vector of positions

See Also

ssd_plot() and geom_ssdpoint()

Examples

```
ssd_plot_data(ssddata::ccme_boron, label = "Species", shape = "Group")
```

---

ssd_qburrIII3 *Quantile Function*

Description

Quantile Function

Usage

```
ssd_qburrIII3(
  p,
  shape1 = 1,
  shape2 = 1,
  scale = 1,
  lower.tail = TRUE,
  log.p = FALSE
)

ssd_qgamma(p, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE)

ssd_qgompertz(p, location = 1, shape = 1, lower.tail = TRUE, log.p = FALSE)

ssd_qinvpareto(p, shape = 3, scale = 1, lower.tail = TRUE, log.p = FALSE)

ssd_qlgumbel(
  p,
  locationlog = 0,
  scalelog = 1,
  lower.tail = TRUE,
  log.p = FALSE
)
```

```
ssd_qllogis_llogis(
  p,
  locationlog1 = 0,
  scalelog1 = 1,
  locationlog2 = 1,
  scalelog2 = 1,
  pmix = 0.5,
  lower.tail = TRUE,
  log.p = FALSE
)

ssd_qllogis(p, locationlog = 0, scalelog = 1, lower.tail = TRUE, log.p = FALSE)

ssd_qlnorm_lnorm(
  p,
  meanlog1 = 0,
  sdlog1 = 1,
  meanlog2 = 1,
  sdlog2 = 1,
  pmix = 0.5,
  lower.tail = TRUE,
  log.p = FALSE
)

ssd_qlnorm(p, meanlog = 0, sdlog = 1, lower.tail = TRUE, log.p = FALSE)

ssd_qmulti(
  p,
  burrIII3.weight = 0,
  burrIII3.shape1 = 1,
  burrIII3.shape2 = 1,
  burrIII3.scale = 1,
  gamma.weight = 0,
  gamma.shape = 1,
  gamma.scale = 1,
  gompertz.weight = 0,
  gompertz.location = 1,
  gompertz.shape = 1,
  lgumbel.weight = 0,
  lgumbel.locationlog = 0,
  lgumbel.scalelog = 1,
  llogis.weight = 0,
  llogis.locationlog = 0,
  llogis.scalelog = 1,
  llogis_llogis.weight = 0,
  llogis_llogis.locationlog1 = 0,
  llogis_llogis.scalelog1 = 1,
  llogis_llogis.locationlog2 = 1,
```

```
  llogis_llogis.scalelog2 = 1,
  llogis_llogis.pmix = 0.5,
  lnorm.weight = 0,
  lnorm.meanlog = 0,
  lnorm.sdlog = 1,
  lnorm_lnorm.weight = 0,
  lnorm_lnorm.meanlog1 = 0,
  lnorm_lnorm.sdlog1 = 1,
  lnorm_lnorm.meanlog2 = 1,
  lnorm_lnorm.sdlog2 = 1,
  lnorm_lnorm.pmix = 0.5,
  weibull.weight = 0,
  weibull.shape = 1,
  weibull.scale = 1,
  lower.tail = TRUE,
  log.p = FALSE
)

ssd_qmulti_fitdists(p, fitdists, lower.tail = TRUE, log.p = FALSE)

ssd_qweibull(p, shape = 1, scale = 1, lower.tail = TRUE, log.p = FALSE)
```

Arguments

p	vector of probabilities.
shape1	shape1 parameter.
shape2	shape2 parameter.
scale	scale parameter.
lower.tail	logical; if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x].
log.p	logical; if TRUE, probabilities p are given as log(p).
shape	shape parameter.
location	location parameter.
locationlog	location on the log scale parameter.
scalelog	scale on log scale parameter.
locationlog1	locationlog1 parameter.
scalelog1	scalelog1 parameter.
locationlog2	locationlog2 parameter.
scalelog2	scalelog2 parameter.
pmix	Proportion mixture parameter.
meanlog1	mean on log scale parameter.
sdlog1	standard deviation on log scale parameter.
meanlog2	mean on log scale parameter.
sdlog2	standard deviation on log scale parameter.

meanlog mean on log scale parameter.

sdlog standard deviation on log scale parameter.

burrIII3.weight
weight parameter for the Burr III distribution.

burrIII3.shape1
shape1 parameter for the Burr III distribution.

burrIII3.shape2
shape2 parameter for the Burr III distribution.

burrIII3.scale scale parameter for the Burr III distribution.

gamma.weight weight parameter for the gamma distribution.

gamma.shape shape parameter for the gamma distribution.

gamma.scale scale parameter for the gamma distribution.

gompertz.weight
weight parameter for the Gompertz distribution.

gompertz.location
location parameter for the Gompertz distribution.

gompertz.shape shape parameter for the Gompertz distribution.

lgumbel.weight weight parameter for the log-Gumbel distribution.

lgumbel.locationlog
location parameter for the log-Gumbel distribution.

lgumbel.scalelog
scale parameter for the log-Gumbel distribution.

llogis.weight weight parameter for the log-logistic distribution.

llogis.locationlog
location parameter for the log-logistic distribution.

llogis.scalelog
scale parameter for the log-logistic distribution.

llogis_llogis.weight
weight parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.locationlog1
locationlog1 parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.scalelog1
scalelog1 parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.locationlog2
locationlog2 parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.scalelog2
scalelog2 parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.pmix
pmix parameter for the log-logistic log-logistic mixture distribution.

lnorm.weight weight parameter for the log-normal distribution.

lnorm.meanlog meanlog parameter for the log-normal distribution.

lnorm.sdlog sdlog parameter for the log-normal distribution.

`lnorm_lnorm.weight`
: weight parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.meanlog1`
: meanlog1 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.sdlog1`
: sdlog1 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.meanlog2`
: meanlog2 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.sdlog2`
: sdlog2 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.pmix`
: pmix parameter for the log-normal log-normal mixture distribution.

`weibull.weight` weight parameter for the Weibull distribution.

`weibull.shape` shape parameter for the Weibull distribution.

`weibull.scale` scale parameter for the Weibull distribution.

`fitdists` An object of class fitdists.

Functions

- `ssd_qburrIII3()`: Quantile Function for BurrIII Distribution
- `ssd_qgamma()`: Quantile Function for Gamma Distribution
- `ssd_qgompertz()`: Quantile Function for Gompertz Distribution
- `ssd_qinvpareto()`: Quantile Function for Inverse Pareto Distribution
- `ssd_qlgumbel()`: Quantile Function for Log-Gumbel Distribution
- `ssd_qllogis_llogis()`: Cumulative Distribution Function for Log-Logistic/Log-Logistic Mixture Distribution
- `ssd_qllogis()`: Cumulative Distribution Function for Log-Logistic Distribution
- `ssd_qlnorm_lnorm()`: Cumulative Distribution Function for Log-Normal/Log-Normal Mixture Distribution
- `ssd_qlnorm()`: Cumulative Distribution Function for Log-Normal Distribution
- `ssd_qmulti()`: Quantile Function for Multiple Distributions
- `ssd_qmulti_fitdists()`: Quantile Function for Multiple Distributions
- `ssd_qweibull()`: Cumulative Distribution Function for Weibull Distribution

See Also

`ssd_p` and `ssd_r`

Examples

```
ssd_qburrIII3(0.5)

ssd_qgamma(0.5)

ssd_qgompertz(0.5)

ssd_qinvpareto(0.5)

ssd_qlgumbel(0.5)

ssd_qllogis_llogis(0.5)

ssd_qllogis(0.5)

ssd_qlnorm_lnorm(0.5)

ssd_qlnorm(0.5)

# multi
ssd_qmulti(0.5, gamma.weight = 0.5, lnorm.weight = 0.5)

# multi fitdists
fit <- ssd_fit_dists(ssddata::ccme_boron)
ssd_qmulti_fitdists(0.5, fit)

ssd_qweibull(0.5)
```

---

ssd_rburrIII3 *Random Number Generation*

Description

Random Number Generation

Usage

```
ssd_rburrIII3(n, shape1 = 1, shape2 = 1, scale = 1, chk = TRUE)

ssd_rgamma(n, shape = 1, scale = 1, chk = TRUE)

ssd_rgompertz(n, location = 1, shape = 1, chk = TRUE)

ssd_rinvpareto(n, shape = 3, scale = 1, chk = TRUE)

ssd_rlgumbel(n, locationlog = 0, scalelog = 1, chk = TRUE)

ssd_rllogis_llogis(
  n,
```

```
  locationlog1 = 0,
  scalelog1 = 1,
  locationlog2 = 1,
  scalelog2 = 1,
  pmix = 0.5,
  chk = TRUE
)

ssd_rllogis(n, locationlog = 0, scalelog = 1, chk = TRUE)

ssd_rlnorm_lnorm(
  n,
  meanlog1 = 0,
  sdlog1 = 1,
  meanlog2 = 1,
  sdlog2 = 1,
  pmix = 0.5,
  chk = TRUE
)

ssd_rlnorm(n, meanlog = 0, sdlog = 1, chk = TRUE)

ssd_rmulti(
  n,
  burrIII3.weight = 0,
  burrIII3.shape1 = 1,
  burrIII3.shape2 = 1,
  burrIII3.scale = 1,
  gamma.weight = 0,
  gamma.shape = 1,
  gamma.scale = 1,
  gompertz.weight = 0,
  gompertz.location = 1,
  gompertz.shape = 1,
  lgumbel.weight = 0,
  lgumbel.locationlog = 0,
  lgumbel.scalelog = 1,
  llogis.weight = 0,
  llogis.locationlog = 0,
  llogis.scalelog = 1,
  llogis_llogis.weight = 0,
  llogis_llogis.locationlog1 = 0,
  llogis_llogis.scalelog1 = 1,
  llogis_llogis.locationlog2 = 1,
  llogis_llogis.scalelog2 = 1,
  llogis_llogis.pmix = 0.5,
  lnorm.weight = 0,
  lnorm.meanlog = 0,
```

```
  lnorm.sdlog = 1,
  lnorm_lnorm.weight = 0,
  lnorm_lnorm.meanlog1 = 0,
  lnorm_lnorm.sdlog1 = 1,
  lnorm_lnorm.meanlog2 = 1,
  lnorm_lnorm.sdlog2 = 1,
  lnorm_lnorm.pmix = 0.5,
  weibull.weight = 0,
  weibull.shape = 1,
  weibull.scale = 1,
  chk = TRUE
)

ssd_rmulti_fitdists(n, fitdists, chk = TRUE)

ssd_rweibull(n, shape = 1, scale = 1, chk = TRUE)
```

Arguments

n	positive number of observations.
shape1	shape1 parameter.
shape2	shape2 parameter.
scale	scale parameter.
chk	A flag specifying whether to check the arguments.
shape	shape parameter.
location	location parameter.
locationlog	location on the log scale parameter.
scalelog	scale on log scale parameter.
locationlog1	locationlog1 parameter.
scalelog1	scalelog1 parameter.
locationlog2	locationlog2 parameter.
scalelog2	scalelog2 parameter.
pmix	Proportion mixture parameter.
meanlog1	mean on log scale parameter.
sdlog1	standard deviation on log scale parameter.
meanlog2	mean on log scale parameter.
sdlog2	standard deviation on log scale parameter.
meanlog	mean on log scale parameter.
sdlog	standard deviation on log scale parameter.
burrIII3.weight	weight parameter for the Burr III distribution.
burrIII3.shape1	shape1 parameter for the Burr III distribution.

burrIII3.shape2
: shape2 parameter for the Burr III distribution.

burrIII3.scale
: scale parameter for the Burr III distribution.

gamma.weight
: weight parameter for the gamma distribution.

gamma.shape
: shape parameter for the gamma distribution.

gamma.scale
: scale parameter for the gamma distribution.

gompertz.weight
: weight parameter for the Gompertz distribution.

gompertz.location
: location parameter for the Gompertz distribution.

gompertz.shape
: shape parameter for the Gompertz distribution.

lgumbel.weight
: weight parameter for the log-Gumbel distribution.

lgumbel.locationlog
: location parameter for the log-Gumbel distribution.

lgumbel.scalelog
: scale parameter for the log-Gumbel distribution.

llogis.weight
: weight parameter for the log-logistic distribution.

llogis.locationlog
: location parameter for the log-logistic distribution.

llogis.scalelog
: scale parameter for the log-logistic distribution.

llogis_llogis.weight
: weight parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.locationlog1
: locationlog1 parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.scalelog1
: scalelog1 parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.locationlog2
: locationlog2 parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.scalelog2
: scalelog2 parameter for the log-logistic log-logistic mixture distribution.

llogis_llogis.pmix
: pmix parameter for the log-logistic log-logistic mixture distribution.

lnorm.weight
: weight parameter for the log-normal distribution.

lnorm.meanlog
: meanlog parameter for the log-normal distribution.

lnorm.sdlog
: sdlog parameter for the log-normal distribution.

lnorm_lnorm.weight
: weight parameter for the log-normal log-normal mixture distribution.

lnorm_lnorm.meanlog1
: meanlog1 parameter for the log-normal log-normal mixture distribution.

lnorm_lnorm.sdlog1
: sdlog1 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.meanlog2`
: meanlog2 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.sdlog2`
: sdlog2 parameter for the log-normal log-normal mixture distribution.

`lnorm_lnorm.pmix`
: pmix parameter for the log-normal log-normal mixture distribution.

`weibull.weight`
: weight parameter for the Weibull distribution.

`weibull.shape`
: shape parameter for the Weibull distribution.

`weibull.scale`
: scale parameter for the Weibull distribution.

`fitdists`
: An object of class fitdists.

Functions

- `ssd_rburrIII3()`: Random Generation for BurrIII Distribution
- `ssd_rgamma()`: Random Generation for Gamma Distribution
- `ssd_rgompertz()`: Random Generation for Gompertz Distribution
- `ssd_rinvpareto()`: Random Generation for Inverse Pareto Distribution
- `ssd_rlgumbel()`: Random Generation for log-Gumbel Distribution
- `ssd_rllogis_llogis()`: Random Generation for Log-Logistic/Log-Logistic Mixture Distribution
- `ssd_rllogis()`: Random Generation for Log-Logistic Distribution
- `ssd_rlnorm_lnorm()`: Random Generation for Log-Normal/Log-Normal Mixture Distribution
- `ssd_rlnorm()`: Random Generation for Log-Normal Distribution
- `ssd_rmulti()`: Random Generation for Multiple Distributions
- `ssd_rmulti_fitdists()`: Random Generation for Multiple Distributions
- `ssd_rweibull()`: Random Generation for Weibull Distribution

See Also

`ssd_p` and `ssd_q`

Examples

```
withr::with_seed(50, {
  x <- ssd_rburrIII3(10000)
})
hist(x, breaks = 1000)

withr::with_seed(50, {
  x <- ssd_rgamma(10000)
})
hist(x, breaks = 1000)

withr::with_seed(50, {
```

```
  x <- ssd_rgompertz(10000)
})
hist(x, breaks = 1000)

withr::with_seed(50, {
  x <- ssd_rinvpareto(10000)
})
hist(x, breaks = 1000)

withr::with_seed(50, {
  x <- ssd_rlgumbel(10000)
})
hist(x, breaks = 1000)

withr::with_seed(50, {
  x <- ssd_rllogis_llogis(10000)
})
hist(x, breaks = 1000)

withr::with_seed(50, {
  x <- ssd_rllogis(10000)
})
hist(x, breaks = 1000)

withr::with_seed(50, {
  x <- ssd_rlnorm_lnorm(10000)
})
hist(x, breaks = 1000)

withr::with_seed(50, {
  x <- ssd_rlnorm(10000)
})
hist(x, breaks = 1000)

withr::with_seed(50, {
  x <- ssd_rmulti(1000, gamma.weight = 0.5, lnorm.weight = 0.5)
})
hist(x, breaks = 100)

# multi fitdists
fit <- ssd_fit_dists(ssddata::ccme_boron)
ssd_rmulti_fitdists(2, fit)

withr::with_seed(50, {
  x <- ssd_rweibull(10000)
})
hist(x, breaks = 1000)
```

---

ssd_sort_data *Sort Species Sensitivity Data*

Description

Sorts Species Sensitivity Data by empirical cumulative density (ECD).

Usage

```
ssd_sort_data(data, left = "Conc", right = left)
```

Arguments

data	A data frame.
left	A string of the column in data with the concentrations.
right	A string of the column in data with the right concentration values.

Details

Useful for sorting data before using geom_ssdpoint() and geom_ssdsegment() to construct plots for censored data with stat = identity to ensure order is the same for the various components.

Value

data sorted by the empirical cumulative density.

See Also

ssd_ecd_data() and ssd_data()

Examples

```
ssd_sort_data(ssddata::ccme_boron)
```

---

subset.fitdists *Subset fitdists Object*

Description

Select a subset of distributions from a fitdists object. The Akaike Information-theoretic Criterion differences are calculated after selecting the distributions named in select.

Usage

```
## S3 method for class 'fitdists'
subset(x, select = names(x), ..., delta = Inf, strict = TRUE)
```

Arguments

x	The object.
select	A character vector of the distributions to select.
...	Unused.
delta	A non-negative number specifying the maximum absolute AIC difference cutoff. Distributions with an absolute AIC difference greater than delta are excluded from the calculations.
strict	A flag indicating whether all elements of select must be present.

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
subset(fits, c("gamma", "lnorm"))
```

---

tidy.fitdists *Turn a fitdists Object into a Tibble*

Description

Turns a fitdists object into a tidy tibble of the estimates (est) and standard errors (se) by the terms (term) and distributions (dist).

Usage

```
## S3 method for class 'fitdists'
tidy(x, all = FALSE, ...)
```

Arguments

x	The object.
all	A flag specifying whether to also return transformed parameters.
...	Unused.

Value

A tidy tibble of the estimates and standard errors.

See Also

coef.fitdists()

Other generics: augment.fitdists(), glance.fitdists()

Examples

```
fits <- ssd_fit_dists(ssddata::ccme_boron)
tidy(fits)
tidy(fits, all = TRUE)
```

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