

# Package: `ssd4mosaic` (via `r-universe`)

October 16, 2024

**Title** Web Application for the SSD Module of the MOSAIC Platform

**Version** 1.0.1

**Description** Web application using 'shiny' for the SSD (Species Sensitivity Distribution) module of the MOSAIC (MOdeling and StAtistical tools for ecotoxICology) platform. It estimates the Hazardous Concentration for x% of the species (HCx) from toxicity values that can be censored and provides various plotting options for a better understanding of the results. See our companion paper Kon Kam King et al. (2014)  [<doi:10.48550/arXiv.1311.5772>](https://doi.org/10.48550/arXiv.1311.5772).

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**URL** <https://gitlab.in2p3.fr/mosaic-software/mosaic-ssd>,  
<https://mosaic.univ-lyon1.fr/>

**BugReports** <https://gitlab.in2p3.fr/mosaic-software/mosaic-ssd/-/issues>

**Depends** R (>= 4.1.0)

**Imports** actuar, config (>= 0.3.1), fitdistrplus (>= 1.1-11), ggplot2, golem (>= 0.3.5), htmltools, htmlwidgets, jsonlite, rhandsontable, rlang, rmarkdown, shiny (>= 1.7.4), shinybusy, shinyjs, stats, utils

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**NeedsCompilation** no

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**Repository** CRAN

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|             |                                                                             |
|-------------|-----------------------------------------------------------------------------|
| add_CI_plot | <i>Add confidence interval(s) to an existing fitted distribution ggplot</i> |
|-------------|-----------------------------------------------------------------------------|

---

### Description

Add confidence interval(s) to an existing fitted distribution ggplot

### Usage

```
add_CI_plot(base_plot, bts, logscale, CI.level = 0.95)
```

**Arguments**

|           |                                                                                      |
|-----------|--------------------------------------------------------------------------------------|
| base_plot | A ggplot object that depicts the fit(s) of the bootstrap(s).                         |
| bts       | A list of bootdist or bootdistcens objects.                                          |
| logscale  | if TRUE, uses a logarithmic scale for the $x$ -axis                                  |
| CI.level  | A strictly positive numeric smaller than 1. The level of the confidence interval(s). |

**Value**

A ggplot object.

---

|          |                                                           |
|----------|-----------------------------------------------------------|
| base_cdf | <i>Graphical representation of fitted distribution(s)</i> |
|----------|-----------------------------------------------------------|

---

**Description**

base\_cdf plots an empirical cdf of the toxicity values against one or several fitted distributions' cdf. It works for both censored and non censored data.

**Usage**

```
base_cdf(fits, unit, logscale, names = NULL, horizontals = TRUE, xlim = NULL)
```

**Arguments**

|             |                                                                                                                                         |
|-------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| fits        | A list of fits of class fitdist or fitdistcens computed from the same toxicity data.                                                    |
| unit        | A character vector, the unit of the toxicity data                                                                                       |
| logscale    | if TRUE, uses a logarithmic scale for the $x$ -axis                                                                                     |
| names       | Label vector for data points (only for non censored data)                                                                               |
| horizontals | If TRUE, draws horizontal lines for the step empirical cumulative distribution function (ecdf). See also <a href="#">plot.stepfun</a> . |
| xlim        | The $x$ -limits of the plot.                                                                                                            |

**Value**

A ggplot object.

---

|              |                                                                            |
|--------------|----------------------------------------------------------------------------|
| bootdist_fun | <i>Determines the appropriate bootstrap function based on a fit object</i> |
|--------------|----------------------------------------------------------------------------|

---

### Description

Determines the appropriate bootstrap function based on a fit object

### Usage

```
bootdist_fun(x, ft, niter = 200)
```

### Arguments

|       |                                                                     |
|-------|---------------------------------------------------------------------|
| x     | Not used                                                            |
| ft    | A fitdist or fitdistcens object                                     |
| niter | An integer. The number of iterations set for the bootstrap function |

### Value

An appropriate bootstrap function.

---

|                 |                                                  |
|-----------------|--------------------------------------------------|
| cens_lines_plot | <i>Graphical representation of censored data</i> |
|-----------------|--------------------------------------------------|

---

### Description

cens\_lines\_plot create a plot representing each interval of toxicity values with a horizontal line, or a point if the bounds of the interval are equal. It is possible to color the lines by a grouping indicator.

### Usage

```
cens_lines_plot(
  data,
  unit,
  logscale,
  fits = NULL,
  leftNA = 0,
  rightNA = Inf,
  color_group = FALSE
)
```

**Arguments**

|             |                                                                                                                                                             |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| data        | A data.frame containing censored toxicity values. It must have columns left, right, and label if color_group = TRUE. Censored values are indicated with NA. |
| unit        | A character vector, the unit of the toxicity data                                                                                                           |
| logscale    | if TRUE, uses a logarithmic scale for the <i>x</i> -axis                                                                                                    |
| fits        | A list of fits of class fitdist or fitdistcens computed from the same toxicity data.                                                                        |
| leftNA      | The value to replace censored left values. Default to 0 because toxicity values are concentrations.                                                         |
| rightNA     | The value to replace censored right values.                                                                                                                 |
| color_group | if TRUE, color the elements of the plot by the group label of the data (column label).                                                                      |

**Value**

A ggplot object.

---

code\_r\_ssd

*Generate a script according to user in-app inputs*


---

**Description**

Generate a script according to user in-app inputs

**Usage**

```
code_r_ssd(
  data,
  distributions,
  censored = FALSE,
  logscale = TRUE,
  unit = "arbitrary unit",
  names = FALSE,
  groups = FALSE,
  CI.level = 0.95
)
```

**Arguments**

|               |                                                                                                                     |
|---------------|---------------------------------------------------------------------------------------------------------------------|
| data          | If censored = TRUE, a data.frame with columns left and right. If censored = FALSE, a data.frame with a column conc. |
| distributions | A list of the names of the distributions to apply (e.g., 'lnorm', 'llogis')                                         |
| censored      | A Boolean, whether the given data is to be interpreted as censored                                                  |

|          |                    |
|----------|--------------------|
| logscale | A logical          |
| unit     | A character string |
| names    | A logical          |
| groups   | A logical          |
| CI.level | A numerical        |

**Value**

A character string containing a R script.

---

|                      |                                                                                        |
|----------------------|----------------------------------------------------------------------------------------|
| combine_boot_samples | <i>Combine several bootstrap samples into a single bootdist or bootdistcens object</i> |
|----------------------|----------------------------------------------------------------------------------------|

---

**Description**

Combine several bootstrap samples into a single bootdist or bootdistcens object

**Usage**

```
combine_boot_samples(bs)
```

**Arguments**

bs                    A list of bootdist or bootdistcens objects obtained from the same fit object.

**Value**

A bootdist or bootdistcens object with a number of samples equal to the sum of number of samples of each bootstrap from the list input.

---

|              |                                                                           |
|--------------|---------------------------------------------------------------------------|
| custom_theme | <i>Custom ggplot theme created for MOSAIC bioacc overwriting theme_bw</i> |
|--------------|---------------------------------------------------------------------------|

---

**Description**

Custom ggplot theme created for MOSAIC bioacc overwriting theme\_bw

**Usage**

```
custom_theme()
```

---

endosulfan

*Summary of 48 to 96-hour acute toxicity values for endosulfan*

---

**Description**

Summary of 48 to 96-hour acute toxicity values (LC50 and EC50 values) for exposure of Australian and Non-Australian taxa to endosulfan.

**Usage**

endosulfan

**Format**

endosulfan

A data frame with 88 rows and 3 columns:

**conc** Lethal or effective concentration in  $\mu\text{g/L}$ .

**name** Specie's name for each concentration.

**group** Classification by geographical origin and type: fish or arthropod.

**Source**

<https://pubmed.ncbi.nlm.nih.gov/15499502/>

---

fluazinam

*48-hour acute toxicity values for fluazinam*

---

**Description**

48-hour acute toxicity values (EC50 values) for exposure of macroinvertebrates and zooplankton to fluazinam.

**Usage**

fluazinam

**Format**

fluazinam

A data frame with 14 rows and 4 columns:

**left, right** Lower & higher bounds of the effective concentration interval in  $\mu\text{g/L}$ .

**name** Specie's name for each effective concentration.

**group** Classification of the specie, not all rows use the same taxonomic rank.

**Source**

<https://pubmed.ncbi.nlm.nih.gov/19837458/>

---

|               |                                                                                      |
|---------------|--------------------------------------------------------------------------------------|
| get_bootstrap | <i>Generate bootstrap sample(s) for a list of fit(s) and check their convergence</i> |
|---------------|--------------------------------------------------------------------------------------|

---

**Description**

Generate bootstrap sample(s) for a list of fit(s) and check their convergence

**Usage**

```
get_bootstrap(fits)
```

**Arguments**

fits                    A list of fitdist or fitdistcens objects

**Value**

A list of two lists. The first list contains the bootstrap sample(s) and the second one the logical value of convergence.

---

|          |                                                          |
|----------|----------------------------------------------------------|
| get_fits | <i>Fit the specified distributions to the given data</i> |
|----------|----------------------------------------------------------|

---

**Description**

Fit the specified distributions to the given data

**Usage**

```
get_fits(data, distributions, censored)
```

**Arguments**

data                    If censored = TRUE, a data.frame with columns left and right. If censored = FALSE, a data.frame with a column conc.

distributions          A list of the names of the distributions to apply (e.g., 'lnorm', 'llogis')

censored                A Boolean, whether the given data is to be interpreted as censored

**Value**

A list containing the fit object(s) of class fitdist or fitdistcens.



---

|               |                                             |
|---------------|---------------------------------------------|
| get_HCx_table | <i>Get HCx values from fit or bootstrap</i> |
|---------------|---------------------------------------------|

---

**Description**

Get HC5, HC10, HC20 and HC50 for each fit provided, with confidence intervals if the corresponding bootstraps were provided.

**Usage**

```
get_HCx_table(fits, distributions, bootstrap = NULL, CI.level = 0.95)
```

**Arguments**

|               |                                                                                                                |
|---------------|----------------------------------------------------------------------------------------------------------------|
| fits          | A list of fits of class <code>fitdist</code> or <code>fitdistcens</code> computed from the same toxicity data. |
| distributions | A list of the names of the distributions to apply (e.g., 'lnorm', 'llogis')                                    |
| bootstrap     | A list of <code>bootdist</code> or <code>bootdistcens</code> objects corresponding to the fits provided.       |
| CI.level      | A numeric, either 0.95 or 0.9. The level of the confidence interval(s).                                        |

**Value**

A data.frame with different HCx as rows and different fits as columns.

---

|                     |                                                               |
|---------------------|---------------------------------------------------------------|
| get_parameters_html | <i>Get fit(s) parameters in HTML format for shiny outputs</i> |
|---------------------|---------------------------------------------------------------|

---

**Description**

Get fit(s) parameters in HTML format for shiny outputs. Should do nothing if the fit is not ready, and should display limited information if the bootstrap is not done.

**Usage**

```
get_parameters_html(fits = NULL, bootstrap = NULL, CI.level = 0.95)
```

**Arguments**

|           |                                                                                                                |
|-----------|----------------------------------------------------------------------------------------------------------------|
| fits      | A list of fits of class <code>fitdist</code> or <code>fitdistcens</code> computed from the same toxicity data. |
| bootstrap | A list of <code>bootdist</code> or <code>bootdistcens</code> objects corresponding to the fits provided.       |
| CI.level  | A numeric, either 0.95 or 0.9. The level of the confidence interval(s).                                        |

**Details**

The output should look like: (once bootstrap is done)

```
**Log normal distribution**
```

```
*(log-likelihood = -161.8)*
```

```
meanlog: 1.1 [ 0.66 ; 1.5 ]
```

```
sdlog: 1.6 [ 1.3 ; 1.9 ]
```

**Value**

A character string with HTML formatting.

---

|          |                                                                            |
|----------|----------------------------------------------------------------------------|
| get_xlab | <i>Create a label for x axis based on concentration unit and log scale</i> |
|----------|----------------------------------------------------------------------------|

---

**Description**

Create a label for x axis based on concentration unit and log scale

**Usage**

```
get_xlab(unit, logscale)
```

**Arguments**

|          |                                                          |
|----------|----------------------------------------------------------|
| unit     | A character vector, the unit of the toxicity data        |
| logscale | if TRUE, uses a logarithmic scale for the <i>x</i> -axis |

**Value**

A character vector.

---

|                    |                                                                   |
|--------------------|-------------------------------------------------------------------|
| group_cdf_censored | <i>Graphical representation of grouped toxicity censored data</i> |
|--------------------|-------------------------------------------------------------------|

---

**Description**

Create an empirical cdf representation colored according to a "group" attribute. The fitted distribution is also represented.

**Usage**

```
group_cdf_censored(fits, unit, logscale, data)
```

**Arguments**

|          |                                                                                                                |
|----------|----------------------------------------------------------------------------------------------------------------|
| fits     | A list of fits of class <code>fitdist</code> or <code>fitdistcens</code> computed from the same toxicity data. |
| unit     | A character vector, the unit of the toxicity data                                                              |
| logscale | if TRUE, uses a logarithmic scale for the $x$ -axis                                                            |
| data     | A <code>data.frame</code> with columns <code>left</code> , <code>right</code> and <code>group</code>           |

**Details**

The plot represents each interval of toxicity values with a horizontal line, or a point if the bounds of the interval are equal, using function `cens_lines_plot()`.

**Value**

A `ggplot` object.

---

group\_cdf\_uncensored *Graphical representation of grouped toxicity uncensored data*

---

**Description**

Add a group coloration to a provided empirical cdf representation according to a "group" column in data.

**Usage**

```
group_cdf_uncensored(data, p)
```

**Arguments**

|      |                                                                                                                      |
|------|----------------------------------------------------------------------------------------------------------------------|
| data | A <code>data.frame</code> with columns <code>conc</code> and <code>group</code> .                                    |
| p    | a <code>ggplot</code> object showing the empirical cumulative distribution function of the uncensored data provided. |

**Value**

A `ggplot` object.

---

my\_CIcdfplot      *Create a pretty confidence interval ggplot*

---

**Description**

Create a pretty confidence interval ggplot

**Usage**

```
my_CIcdfplot(b, logscale, CI.level)
```

**Arguments**

|          |                                                                                      |
|----------|--------------------------------------------------------------------------------------|
| b        | One "bootdist" object.                                                               |
| logscale | if TRUE, uses a logarithmic scale for the <i>x</i> -axis                             |
| CI.level | A strictly positive numeric smaller than 1. The level of the confidence interval(s). |

**Value**

A ggplot with 7 or 8 layers.

**Note**

With a bootdist, the plot created has 8 layers. With a bootdistcens object, the plot created has 7 layers. The ribbon and its delimiting lines are always the last 3 layers.

---

name\_plot\_censored      *Graphical representation of named toxicity censored data*

---

**Description**

Add names to a provided empirical cumulative distribution function ggplot (i.e., species names).

**Usage**

```
name_plot_censored(data, p, leftNA = 0, rightNA = Inf)
```

**Arguments**

|         |                                                                                                                                  |
|---------|----------------------------------------------------------------------------------------------------------------------------------|
| data    | A data.frame with column conc if uncensored data, with left and right if censored data. In any case, must contain a column name. |
| p       | A ggplot object showing the empirical cumulative distribution function of the censored data provided.                            |
| leftNA  | The value to replace censored left values. Default to 0 because toxicity values are concentrations.                              |
| rightNA | The value to replace censored right values.                                                                                      |

**Details**

The positions of the names on the plot are based on the raw data visualization and not the non parametric maximum likelihood estimation (NPMLE) representation, but they can be added to both types of plot.

Compatible with plots colored by group labels.

**Value**

A ggplot object.

---

name\_plot\_uncensored *Graphical representation of named toxicity uncensored data*

---

**Description**

Create an empirical cumulative distribution function ggplot with a name (i.e. species names) associated to each observation.

**Usage**

```
name_plot_uncensored(fits, unit, logscale, data, horizontals = TRUE)
```

**Arguments**

|             |                                                                                                                                                                         |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| fits        | A list of fits of class <code>fitdist</code> or <code>fitdistcens</code> computed from the same toxicity data.                                                          |
| unit        | A character vector, the unit of the toxicity data                                                                                                                       |
| logscale    | if TRUE, uses a logarithmic scale for the <i>x</i> -axis                                                                                                                |
| data        | A data.frame with column <code>conc</code> if uncensored data, with <code>left</code> and <code>right</code> if censored data. In any case, must contain a column name. |
| horizontals | If TRUE, draws horizontal lines for the step empirical cumulative distribution function (ecdf). See also <a href="#">plot.stepfun</a> .                                 |

**Value**

A ggplot object.

---

options\_plot

*Graphical representation of toxicity data with additional elements*


---

### Description

Create an empirical cdf representation with the options to color data according to a group label and to display a name label for each observation.

### Usage

```
options_plot(
  fits,
  unit,
  logscale,
  data,
  use_names = FALSE,
  use_groups = FALSE,
  horizontals = TRUE,
  lines_display = TRUE
)
```

### Arguments

|               |                                                                                                                                                                                                                                                           |
|---------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| fits          | A list of fits of class <code>fitdist</code> or <code>fitdistcens</code> computed from the same toxicity data.                                                                                                                                            |
| unit          | A character vector, the unit of the toxicity data                                                                                                                                                                                                         |
| logscale      | if TRUE, uses a logarithmic scale for the <i>x</i> -axis                                                                                                                                                                                                  |
| data          | A data.frame with column <code>conc</code> if uncensored data, with <code>left</code> and <code>right</code> if censored data, column <code>name</code> if the names are to be displayed and column <code>group</code> if the groups are to be displayed. |
| use_names     | if TRUE, name labels are added to the plot.                                                                                                                                                                                                               |
| use_groups    | if TRUE, data in the plot is colored by group.                                                                                                                                                                                                            |
| horizontals   | A boolean. In case of uncensored data, whether to draw horizontal lines for the step of the cumulative distribution function. Should be set to FALSE when <code>use_group = TRUE</code> for a better visual.                                              |
| lines_display | A boolean. In case of censored data, whether to display the raw data or the non parametric maximum likelihood estimation (NPMLE) representation. Ignored when <code>use_groups = TRUE</code> . Raw data give a better visual with name labels.            |

### Value

A ggplot object.

---

|                 |                                                                                           |
|-----------------|-------------------------------------------------------------------------------------------|
| order_cens_data | <i>Take a data.frame of censored toxicity data and order them like fitdistrplus plots</i> |
|-----------------|-------------------------------------------------------------------------------------------|

---

**Description**

Take a data.frame of censored toxicity data and order them like fitdistrplus plots

**Usage**

```
order_cens_data(data)
```

**Arguments**

data            A data.frame of censored data with columns left and right

**Value**

A data.frame with ordered toxicity values.

**Note**

Left censored data are put in first, based on the value of their right bound, then non censored data are ordered based on their average value. The right censored data are put in last, ordered among themselves by their left bound.

---

|         |                                  |
|---------|----------------------------------|
| run_app | <i>Run the Shiny Application</i> |
|---------|----------------------------------|

---

**Description**

Run the Shiny Application

**Usage**

```
run_app(  
  onStart = NULL,  
  options = list(),  
  enableBookmarking = NULL,  
  uiPattern = "/",  
  ...  
)
```

**Arguments**

|                   |                                                                                                                                                                                                                                                                                                                     |
|-------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| onStart           | A function that will be called before the app is actually run. This is only needed for shinyAppObj, since in the shinyAppDir case, a global .R file can be used for this purpose.                                                                                                                                   |
| options           | Named options that should be passed to the runApp call (these can be any of the following: "port", "launch.browser", "host", "quiet", "display.mode" and "test.mode"). You can also specify width and height parameters which provide a hint to the embedding environment about the ideal height/width for the app. |
| enableBookmarking | Can be one of "url", "server", or "disable". The default value, NULL, will respect the setting from any previous calls to <a href="#">enableBookmarking()</a> . See <a href="#">enableBookmarking()</a> for more information on bookmarking your app.                                                               |
| uiPattern         | A regular expression that will be applied to each GET request to determine whether the ui should be used to handle the request. Note that the entire request path must match the regular expression in order for the match to be considered successful.                                                             |
| ...               | arguments to pass to golem_opts. See ‘?golem::get_golem_options’ for more details.                                                                                                                                                                                                                                  |

**Value**

No return value, called for side effects

---

|                 |                                                                                   |
|-----------------|-----------------------------------------------------------------------------------|
| salinity_family | <i>72-hour acute salinity tolerance of macro-invertebrates grouped by family.</i> |
|-----------------|-----------------------------------------------------------------------------------|

---

**Description**

72-hour acute salinity tolerance (LC50 values) of riverine macro-invertebrates grouped by taxonomic family.

**Usage**

```
salinity_family
```

**Format**

Salinity\_order

A data frame with 108 rows and 3 columns:

**left, right** Lower & higher bounds of the lethal concentration interval in mS/cm<sup>2</sup>.

**group** Family of each tested specie.



**Source**

<https://cdnsiencepub.com/doi/abs/10.1139/f06-080>

---

|                |                                                                                  |
|----------------|----------------------------------------------------------------------------------|
| salinity_order | <i>72-hour acute salinity tolerance of macro-invertebrates grouped by order.</i> |
|----------------|----------------------------------------------------------------------------------|

---

**Description**

72-hour acute salinity tolerance (LC50 values) of riverine macro-invertebrates grouped by taxonomic order.

**Usage**

```
salinity_order
```

**Format**

```
Salinity_order
```

A data frame with 108 rows and 3 columns:

**left, right** Lower & higher bounds of the lethal concentration interval in mS/cm<sup>2</sup>.

**group** Order of each tested specie.

**Source**

<https://cdnsiencepub.com/doi/abs/10.1139/f06-080>

---

|             |                                                |
|-------------|------------------------------------------------|
| switchInput | <i>Custom toggle switch input for shiny UI</i> |
|-------------|------------------------------------------------|

---

**Description**

Custom toggle switch input for shiny UI

**Usage**

```
switchInput(id, aria_label, checked = TRUE)
```

**Arguments**

|            |                                                       |
|------------|-------------------------------------------------------|
| id         | The input slot that will be used to access the value. |
| aria_label | An invisible label for screen readers.                |
| checked    | Whether to create the switch as ON.                   |

**Value**

A toggle switch control that can be added to a UI definition.

---

|           |                                                                                      |
|-----------|--------------------------------------------------------------------------------------|
| test_conv | <i>Test the approximate equality of the quantiles from several bootstrap samples</i> |
|-----------|--------------------------------------------------------------------------------------|

---

**Description**

Test the approximate equality of the quantiles from several bootstrap samples

**Usage**

```
test_conv(bs, probs)
```

**Arguments**

|       |                                                                                                         |
|-------|---------------------------------------------------------------------------------------------------------|
| bs    | A list of <code>bootdist</code> or <code>bootdistcens</code> objects obtained from the same fit object. |
| probs | A numeric vector of probabilities with values in $[0,1]$                                                |

**Value**

A logical.

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