

Package: ezmtt (via r-universe)

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Title Easy MTT Assay Tidying and Plotting

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Description This package automates the analysis and plotting of standard MTT workflows.

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Encoding UTF-8

Language en

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Imports cli, drc, ggplot2, ggrepel, gplate, rlang, stats

Remotes KaiAragaki/gplate, KaiAragaki/mop

Depends R (>= 4.1.0)

LazyData true

URL <https://kaiaragaki.github.io/ezmtt/>

Suggests knitr, rmarkdown, dplyr, mop, readr, ggsci

VignetteBuilder knitr

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

RemoteUrl <https://github.com/KaiAragaki/ezmtt>

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GeomMtt	<i>Plot MTT data</i>
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Description

Plot MTT data

Usage

GeomMtt

```
geom_mtt(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  n = 1000,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

Arguments

mapping	Set of aesthetic mappings created by aes() . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to ggplot().</p> <p>A <code>data.frame</code>, 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.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).</p>
stat	<p>The statistical transformation to use on the data for this layer. When using a <code>geom_*()</code> function to construct a layer, the <code>stat</code> argument can be used to override the default coupling between geoms and stats. The <code>stat</code> argument accepts the following:</p> <ul style="list-style-type: none"> • A Stat ggproto subclass, for example <code>StatCount</code>. • A string naming the stat. To give the stat as a string, strip the function name of the <code>stat_</code> prefix. For example, to use <code>stat_count()</code>, give the stat as <code>"count"</code>.

	<ul style="list-style-type: none"> For more information and other ways to specify the stat, see the layer stat documentation.
position	<p>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:</p> <ul style="list-style-type: none"> The result of calling a position function, such as <code>position_jitter()</code>. 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 <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as "jitter". For more information and other ways to specify the position, see the layer position documentation.
n	How many line segments should be used to draw an MTT curve?
na.rm	Remove NA values?
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.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .
...	Additional arguments passed to <code>ggplot2::layer</code> params

Format

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

mtt	<i>Example data from an MTT</i>
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Description

A dataset including absorbance data at 562nm and 660nm

Usage

```
mtt
```

Format

A `spectramax` object

data a `gp` object containing absorbance values

Details

There are four conditions on this plate. The plate is divided into quadrants. Concentrations of drug increase from left to right (0, 1nM, 10nM, 100nM, 1uM, 10uM).

mtt_calc *Calculate normalized ODs without fitting*

Description

It can be useful to calculate normalized ODs without fitting, particularly if you would like to use `geom_mtt`, or need to manipulate your data downstream.

Usage

```
mtt_calc(  
  data,  
  signal = "nm562",  
  background = "nm660",  
  dose = "dose",  
  out = "div",  
  .by = NULL  
)
```

Arguments

<code>data</code>	A <code>data.frame</code> of absorbances, containing at least the <code>signal</code> , <code>background</code> , and <code>dose</code> columns (see below)
<code>signal</code>	The name of the column that contains the signal absorbances
<code>background</code>	The name of the column that contains the background absorbances. If <code>NULL</code> , will just use <code>signal</code> .
<code>dose</code>	The name of the column containing the concentrations of the drug. Will use the lowest concentration as the baseline.
<code>out</code>	The name of the output column
<code>.by</code>	Character vector of columns to summarize by. Other columns will be dropped

mtt_fit *Fit an curve through MTT data*

Description

Fit an curve through MTT data

Usage

```
mtt_fit(x, model, ...)  
  
## Default S3 method:  
mtt_fit(x, model = NULL, ...)  
  
## S3 method for class 'gp'  
mtt_fit(x, model = NULL, ...)  
  
## S3 method for class 'data.frame'  
mtt_fit(x, model = NULL, ...)  
  
## S3 method for class 'spectramax'  
mtt_fit(x, conditions, model = NULL, ...)
```

Arguments

x	An object of class <code>gplate::gp</code> , <code>data.frame</code> , or <code>mop::spectramax</code> . See details.
model	A character vector of models that should be used to fit the data. If <code>NULL</code> , will start with a 4-parameter log-logistic model and fall back using a linear model. Options for supplying a vector include <code>NA</code> , <code>"lm"</code> , and <code>"ll"</code> . See details.
...	Unused
conditions	A named list of numerics of length 4. Contains doses per quadrant. Names are the drug. If quadrant should be omitted, supply <code>NA</code> . Quadrants go from left to right, top to bottom. Identical names are allowed.

Details

If a `data.frame` or `gplate::gp` is supplied, it should have columns `condition`, `dose`, `nm562` and `nm660`

This function will first attempt to fit the data using a 4-parameter log-logistic model, then use a linear model as a fallback if fitting fails.

The `model` argument can be used to specify a model manually by supplying a character vector with length equal to the number of *unique* conditions. Valid values for the character vector include:

- `NA`: Fitting will start with log-logistic, fallback on linear
- `"ll"`: Only (try to) fit with log-logistic
- `"lm"`: Only fit with `lm`

mtt_plot	<i>Plot MTT fits</i>
----------	----------------------

Description

Plot MTT fits

Usage

```
mtt_plot(fits, ic_pct = NULL, ...)
```

Arguments

fits	a list of fits, usually the output from <code>mtt_fit</code>
ic_pct	Numeric. If NULL, no IC will be plotted. Otherwise, will plot <code>ic_pct%</code> IC the <code>% IC</code> supplied.
...	Arguments passed to <code>drc::ED</code>

Value

a `ggplot`

mtt_tidy	<i>Tidy mtt data</i>
----------	----------------------

Description

A convenience function for tidying mtt data. For data that do not follow the standard format of 'one condition per quadrant', consider tidying the data using `gplate`. See the "Using `ezmtt`" vignette for more information.

Usage

```
mtt_tidy(x, ...)
```

Arguments

x	Object to be tidied
...	Additional arguments passed to appropriate methods
conditions	A named list of length 4, where the name is the name of the condition, and the values are the doses. If a quadrant of the plate was not used, use NA.

`stat_ic_mtt`*Plot MTT data*

Description

Plot MTT data

Usage

```
stat_ic_mtt(  
  mapping = NULL,  
  data = NULL,  
  geom = "point",  
  position = "identity",  
  ...,  
  ic = 50,  
  show.legend = NA,  
  inherit.aes = TRUE  
)
```

Arguments

- | | |
|----------------------|---|
| <code>mapping</code> | Set of aesthetic mappings created by aes() . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply <code>mapping</code> if there is no plot mapping. |
| <code>data</code> | <p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to ggplot().</p> <p>A <code>data.frame</code>, 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.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).</p> |
| <code>geom</code> | <p>The geometric object to use to display the data for this layer. When using a <code>stat_*()</code> function to construct a layer, the <code>geom</code> argument can be used to override the default coupling between stats and geoms. The <code>geom</code> argument accepts the following:</p> <ul style="list-style-type: none">• A <code>Geom</code> ggproto subclass, for example <code>GeomPoint</code>.• A string naming the geom. To give the geom as a string, strip the function name of the <code>geom_</code> prefix. For example, to use <code>geom_point()</code>, give the geom as "point".• For more information and other ways to specify the geom, see the layer geom documentation. |

<code>position</code>	<p>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 <code>position</code> argument accepts the following:</p> <ul style="list-style-type: none">• The result of calling a position function, such as <code>position_jitter()</code>. 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 <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as "jitter".• For more information and other ways to specify the position, see the layer position documentation.
<code>...</code>	Additional arguments passed to <code>ggplot2::layer</code> params
<code>ic</code>	The IC percentage that should be calculated
<code>show.legend</code>	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.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .

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