

Package ‘ezmmek’

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Title Easy Michaelis-Menten Enzyme Kinetics

Version 0.2.4

Description Serves as a platform for published fluorometric enzyme assay protocols. 'ezmmek' calibrates, calculates, and plots enzyme activities as they relate to the transformation of synthetic substrates. At present, 'ezmmek' implements two common protocols found in the literature, and is modular to accommodate additional protocols. Here, these protocols are referred to as the In-Sample Calibration (Hoppe, 1983; <[doi:10.3354/meps011299](https://doi.org/10.3354/meps011299)>) and In-Buffer Calibration (German et al., 2011; <[doi:10.1016/j.soilbio.2011.03.017](https://doi.org/10.1016/j.soilbio.2011.03.017)>). protocols. By containing multiple protocols, 'ezmmek' aims to stimulate discussion about how to best optimize fluorometric enzyme assays. A standardized approach would make studies more comparable and reproducible.

License AGPL-3

Encoding UTF-8

Language en-US

LazyData true

RoxygenNote 7.1.1

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

Imports magrittr, assertable, ggplot2, purrr, dplyr, nls2, rlang, tidyr

NeedsCompilation no

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ezmmek_calc_mm_fit	<i>ezmmek_calc_mm_fit</i>
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Description

Calculate Michaelis-Menten fit

Usage

```
ezmmek_calc_mm_fit(df, km, vmax)
```

Arguments

df	Dataframe of class 'new_ezmmek_calibrate'
km	Starting value to estimate km. Default value is median of 'sub.conc' values
vmax	Starting value to estimate vmax. Default value is max activity calculated

ezmmek_calc_std_lm_buffer	<i>ezmmek_calc_std_lm_homo</i>
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Description

Calculate linear model for standard curve in homogenate

Usage

```
ezmmek_calc_std_lm_buffer(df)
```

Arguments

df	Standard curve dataframe
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ezmmek_calc_std_lm_homo
ezmmek_calc_std_lm_homo

Description

Calculate linear model for standard curve in homogenate

Usage

`ezmmek_calc_std_lm_homo(df)`

Arguments

`df` Standard curve dataframe

ezmmek_calc_std_lm_homo_buffer
ezmmek_calc_std_lm_homo_buffer

Description

Calculate linear model for standard curve in homogenate-buffer solution

Usage

`ezmmek_calc_std_lm_homo_buffer(df)`

Arguments

`df` Standard curve dataframe

```
ezmmek_calibrate_activities
      ezmmek_calibrate_activities
```

Description

Calibrates enzyme activity data by standard curve

Usage

```
ezmmek_calibrate_activities(df, method, columns)
```

Arguments

df	Joined dataframes of class 'new_ezmmek_std_group' and 'new_ezmmek_act_group'
method	Enzyme assay protocol. Must define method as 'isc' or 'ibc'
columns	Column names carried from parent functions

```
ezmmek_std_lm      ezmmek_std_lm
```

Description

Creates dataframe of standard curve models as determined by grouping of user-defined columns

Usage

```
ezmmek_std_lm(df, method = method, columns = NULL)
```

Arguments

df	Standard curve dataframe
method	Enzyme assay protocol. Defined in parent function
columns	Column names carried over from parent functions if parent functions used

```
new_ezmmek_act_calibrate  
  new_ezmmek_act_calibrate
```

Description

Creates dataframe containing calibrated enzyme activity data of class 'new_ezmmek_calibrate'

Usage

```
new_ezmmek_act_calibrate(  
  std.data.fn,  
  act.data.fn,  
  ...,  
  method = NA,  
  columns = NULL  
)
```

Arguments

std.data.fn	Standard data file as character string
act.data.fn	Activity data file as character string
...	User defined column names to join std.data.fn and act.data.fn
method	Enzyme assay protocol. Must define method as 'isc' or 'ibc'
columns	Column names carried over from parent functions if parent functions used

Examples

```
## Not run: new_obj <- new_ezmmek_act_calibrate("data/tyson_std_04172020.csv",  
  "data/tyson_sat_steen_04172020.csv",  
  site_name,  
  std_type,  
  method = "isc",  
  columns = NULL)  
new_obj <- new_ezmmek_act_calibrate("data/tyson_std_04172020.csv",  
  "data/tyson_sat_german_04172020.csv",  
  site_name,  
  std_type,  
  method = "ibc",  
  columns = NULL)  
## End(Not run)
```

new_ezmmek_act_group *new_ezmmek_act_group*

Description

Groups raw activity data by user-defined columns

Usage

```
new_ezmmek_act_group(act.data.fn, ..., method = NA, columns = NULL)
```

Arguments

act.data.fn	Activity data file as character string
...	User defined column names to join std.data.fn and act.data.fn
method	Enzyme assay protocol. Must define method as 'isc' or 'ibc'
columns	Column names carried over from parent functions if parent functions used

Examples

```
## Not run: new_obj <- new_ezmmek_act_group("data/tyson_sat_steen_04172020.csv,
  site_name,
  std_type,
  method = "isc",
  columns = NULL)
new_obj <- new_ezmmek_act_group("data/tyson_sat_german_04172020.csv,
  site_name,
  std_type,
  method = "ibc",
  columns = NULL)
## End(Not run)
```

new_ezmmek_sat_fit *new_ezmmek_sat_fit*

Description

Creates dataframe containing calibrated enzyme activity data and Michaelis-Menton fit of class 'new_ezmmek_sat_fit'

Usage

```
new_ezmmek_sat_fit(
  std.data.fn,
  act.data.fn,
  ...,
  km = NULL,
  vmax = NULL,
  method = NA
)
```

Arguments

std.data.fn	Standard data file as character string
act.data.fn	Activity data file as character string
...	User defined column names to join and group std.data.fn and act.data.fn
km	Starting value to estimate km. Default value is median of 'sub.conc' values
vmax	Starting value to estimate vmax. Default value is max activity calculated
method	Enzyme assay protocol. Must define method as 'isc' or 'ibc'

Examples

```
## Not run: new_obj <- new_ezmmek_sat_fit("data/tyson_std_04172020.csv",
  "data/tyson_sat_steen_04172020.csv",
  site_name,
  std_type,
  km = NULL,
  vmax = NULL,
  method = "isc")
new_obj <- new_ezmmek_sat_fit("data/tyson_std_04172020.csv",
  "data/tyson_sat_german_04172020.csv",
  site_name,
  std_type,
  km = NULL,
  vmax = NULL,
  method = "ibc")
## End(Not run)
```

new_ezmmek_std_group *new_ezmmek_std_group*

Description

Groups standard curve data by user-defined columns

Usage

```
new_ezmmek_std_group(std.data.fn, ..., method = NA, columns = NULL)
```

Arguments

std.data.fn	Standard data file as character string
...	User defined column names to group std.data.fn
method	Enzyme assay protocol. Must define method as 'isc' or 'ibc'
columns	Column names carried over from parent functions if parent functions used

Examples

```
## Not run: new_obj <- new_ezmmek_std_group("data/tyson_std_04172020.csv",
  site_name,
  std_type,
  method = "isc",
  columns = NULL)
new_obj <- new_ezmmek_std_group("data/tyson_std_04172020.csv",
  site_name,
  std_type,
  method = "ibc",
  columns = NULL)
## End(Not run)
```

```
plot.new_ezmmek_act_group
      plot_new_ezmmek_act_group
```

Description

Plots new_ezmmek_act_group object and facets by specified column names

Usage

```
## S3 method for class 'new_ezmmek_act_group'
plot(x, ...)
```

Arguments

x	data.frame object of class new_ezmmek_act_group
...	User defined column names by which to facet plot

Examples

```
## Not run: plot.new_ezmmek_act_group(new_ezmmek_act_group_obj,
  site_name,
  std_type)
## End(Not run)
```

```
plot.new_ezmmek_calibrate  
  plot_new_ezmmek_calibrate
```

Description

Plots new_ezmmek_calibrate object and facets by specified column names

Usage

```
## S3 method for class 'new_ezmmek_calibrate'  
plot(x, ...)
```

Arguments

x	data.frame object of class new_ezmmek_calibrate
...	User defined column names by which to facet plot

Examples

```
## Not run: plot.new_ezmmek_calibrate(new_ezmmek_calibrate_obj,  
  site_name,  
  std_type)  
## End(Not run)
```

```
plot.new_ezmmek_sat_fit  
  plot_new_ezmmek_sat_fit
```

Description

Plots new_ezmmek_sat_fit object and facets by specified column names

Usage

```
## S3 method for class 'new_ezmmek_sat_fit'  
plot(x, ...)
```

Arguments

x	data.frame object of class new_ezmmek_sat_fit
...	User defined column names by which to facet plot

Examples

```
## Not run: plot.new_ezmmek_act_group(new_ezmmek_sat_fit_obj,  
site_name,  
stdy_type)  
## End(Not run)
```

```
plot.new_ezmmek_std_group  
plot_new_ezmmek_std_group
```

Description

Plots `new_ezmmek_std_group` object and facets by specified column names

Usage

```
## S3 method for class 'new_ezmmek_std_group'  
plot(x, ...)
```

Arguments

<code>x</code>	data.frame object of class <code>new_ezmmek_std_group</code>
<code>...</code>	User defined column names by which to facet plot

Examples

```
## Not run: plot.new_ezmmek_std_group(new_ezmmek_std_group_obj,  
site_name,  
std_type)  
## End(Not run)
```

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