Package 'pam'

May 9, 2026

Type Package

Title Fast and Efficient Processing of PAM Data

Version 2.2.1

URL https://github.com/biotoolbox/pam

BugReports https://github.com/biotoolbox/pam/issues

Description Processing Chlorophyll Fluorescence & P700 Absorbance data. Four models are provided for the regression of Pi curves, which can be compared with each other in order to select the most suitable model for the data set. Control plots ensure the successful verification of each regression. Bundled output of alpha, ETRmax, Ik etc. enables fast and reliable further processing of the data.

License GPL-3

Encoding UTF-8

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

RoxygenNote 7.3.3

Imports rlang, data.table, ggplot2, minpack.lm, cowplot, gridExtra, ggthemes, Metrics

NeedsCompilation no

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Repository CRAN

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Contents

`combo_plot_control` *Combined ETR Plot and Summary Table*

Description

Generates a plot of ETR data with different regression model predictions and a summary table.

Usage

```
combo_plot_control(title, data, model_results, name_list, color_list)
```

Arguments

`title`	Character. Plot title.
`data`	Data frame. ETR and PAR data.
`model_results`	List. Regression data and parameters.
`name_list`	List. Names for models (legend and table).
`color_list`	List. Colors for model lines.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions.

Value

A plot with ETR data, regression results, and a summary table.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

model_results_eilers_peeters <- eilers_peeters_generate_regression_ETR_II(data)
model_results_eilers_peeters_modified <- eilers_peeters_modified(model_results_eilers_peeters)

model_results_platt <- platt_generate_regression_ETR_II(data)
model_results_platt_modified <- platt_modified(model_results_platt)

model_results <- list(model_results_eilers_peeters_modified, model_results_platt_modified)
name_list <- list("Eilers-Peeters", "Platt")
color_list <- list("red", "pink")
plot <- combo_plot_control("test", data, model_results, name_list, color_list)
```

`compare_regression_models_ETR_I`

Compare Regression Models for ETR I

Description

Compares multiple regression models for electron transport rate (ETR) data using predefined performance metrics.

Usage

```
compare_regression_models_ETR_I(data_dir, read_func)
```

Arguments

`data_dir`	A character string specifying the directory containing input data files.
`read_func`	A read function defined in read_pam_data.R depending on the used device.

Details

This function compares the performance of the following models:

- Eilers-Peeters (1988)
- Platt (1980)
- Vollenweider (1965)
- Walsby (1997)

Models are ranked based on the deviation between observed and predicted values. The results guide users in selecting the most appropriate model for their dataset. Start values for parameters cannot be adjusted within this function. A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions

Value

A vector with total points assigned to each regression model based on their performance. Models are ranked as follows:

- 1st place: 3 points
- 2nd place: 2 points
- 3rd place: 1 point
- 4th place: 0 points

If regression is not possible for a model, no points are awarded for any of the models for the respective file.

References

Eilers, P. H. C., & Peeters, J. C. H. (1988). *A model for the relationship between light intensity and the rate of photosynthesis in phytoplankton.* Ecological Modelling, 42(3-4), 199-215. Available at: doi:10.1016/03043800(88)900579

Platt, T., Gallegos, C. L., & Harrison, W. G. (1980). *Photoinhibition of photosynthesis in natural assemblages of marine phytoplankton.* Journal of Marine Research, 38(4). Available at: https://elischolar.library.yale.edu/journal_of_marine_research/1525/.

Romoth, K., Nowak, P., Kempke, D., Dietrich, A., Porsche, C., & Schubert, H. (2019). *Acclimation limits of Fucus evanescens along the salinity gradient of the southwestern Baltic Sea.* Botanica Marina, 62(1), 1-12. Available at: doi:10.1515/bot20180098.

Vollenweider, R. A. (1965). *Calculation models of photosynthesis-depth curves and some implications regarding day rate estimates in primary production measurements.* In C. R. Goldman (Ed.), *Primary Productivity in Aquatic Environments* (pp. 427-457). Mem. Ist. Ital. Idrobiol., 18 Suppl., University of California Press, Berkeley.

Walsby, A. E. (1997). *Numerical integration of phytoplankton photosynthesis through time and depth in a water column.* New Phytologist, 136(2), 189-209. Available at: doi:10.1046/j.1469-8137.1997.00736.x.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"))
points <- compare_regression_models_ETR_I(path, read_dual_pam_data)
```

`compare_regression_models_ETR_II`

Compare Regression Models for ETR II

Description

Compares multiple regression models for electron transport rate (ETR) data using predefined performance metrics.

Usage

```
compare_regression_models_ETR_II(data_dir, read_func)
```

Arguments

`data_dir`	A character string specifying the directory containing input data files.
`read_func`	A read function defined in read_pam_data.R depending on the used device.

Details

This function compares the performance of the following models:

- Eilers-Peeters (1988)
- Platt (1980)
- Vollenweider (1965)
- Walsby (1997)

Models are ranked based on the deviation between observed and predicted values. The results guide users in selecting the most appropriate model for their dataset. Start values for parameters cannot be adjusted within this function. A detailed documentation can be found in the README.

Value

A vector with total points assigned to each regression model based on their performance. Models are ranked as follows:

- 1st place: 3 points
- 2nd place: 2 points
- 3rd place: 1 point
- 4th place: 0 points

If regression is not possible for a model, no points are awarded for any of the models for the respective file.

References

Eilers, P. H. C., & Peeters, J. C. H. (1988). *A model for the relationship between light intensity and the rate of photosynthesis in phytoplankton.* Ecological Modelling, 42(3-4), 199-215. Available at: doi:10.1016/03043800(88)900579

Platt, T., Gallegos, C. L., & Harrison, W. G. (1980). *Photoinhibition of photosynthesis in natural assemblages of marine phytoplankton.* Journal of Marine Research, 38(4). Available at: https://elischolar.library.yale.edu/journal_of_marine_research/1525/.

Romoth, K., Nowak, P., Kempke, D., Dietrich, A., Porsche, C., & Schubert, H. (2019). *Acclimation limits of Fucus evanescens along the salinity gradient of the southwestern Baltic Sea.* Botanica Marina, 62(1), 1-12. Available at: doi:10.1515/bot20180098.

Vollenweider, R. A. (1965). *Calculation models of photosynthesis-depth curves and some implications regarding day rate estimates in primary production measurements.* In C. R. Goldman (Ed.), *Primary Productivity in Aquatic Environments* (pp. 427-457). Mem. Ist. Ital. Idrobiol., 18 Suppl., University of California Press, Berkeley.

Walsby, A. E. (1997). *Numerical integration of phytoplankton photosynthesis through time and depth in a water column.* New Phytologist, 136(2), 189-209. Available at: doi:10.1046/j.1469-8137.1997.00736.x.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"))
points <- compare_regression_models_ETR_II(path, read_dual_pam_data)
```

---

eilers_peeters_default_start_value_a

Default start value

Description

Default start value

Usage

```
eilers_peeters_default_start_value_a
```

Format

An object of class `numeric` of length 1.

`eilers_peeters_default_start_value_b`
Default start value

Description

Default start value

Usage

```
eilers_peeters_default_start_value_b
```

Format

An object of class `numeric` of length 1.

`eilers_peeters_default_start_value_c`
Default start value

Description

Default start value

Usage

```
eilers_peeters_default_start_value_c
```

Format

An object of class `numeric` of length 1.

`eilers_peeters_generate_regression_ETR_I` *Eilers-Peeters Regression for ETR I*

Description

Fits a regression model for ETR I based on Eilers-Peeters (1988), considering photoinhibition.

Usage

```
eilers_peeters_generate_regression_ETR_I(
  data,
  a_start_value = eilers_peeters_default_start_value_a,
  b_start_value = eilers_peeters_default_start_value_b,
  c_start_value = eilers_peeters_default_start_value_c
)
```

Arguments

`data`	A `data.table` from read function (e.g.`read_dual_pam_data`).
`a_start_value`	Numeric. Starting value for a. Default: `a_start_values_eilers_peeters_default`.
`b_start_value`	Numeric. Starting value for b. Default: `b_start_values_eilers_peeters_default`.
`c_start_value`	Numeric. Starting value for c. Default: `c_start_values_eilers_peeters_default`.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions.

Value

A list containing:

- `etr_regression_data`: Predicted ETR values.
- `residual_sum_of_squares`: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- `root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- `relative_root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- `a`, `b`, `c`: Fitted parameters.
- `pm`: Maximum ETR (p_m).
- `s`: Initial slope (s).
- `ik`: Transition point from light limitation to light saturation (I_k).
- `im`: PAR at maximum ETR (I_m).
- `w`: Peak sharpness (w).

References

Eilers, P. H. C., & Peeters, J. C. H. (1988). *A model for the relationship between light intensity and the rate of photosynthesis in phytoplankton.* Ecological Modelling, 42(3-4), 199-215. Available at: doi:10.1016/03043800(88)900579

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- eilers_peeters_generate_regression_ETR_I(data)
```

---

eilers_peeters_generate_regression_ETR_II

Eilers-Peeters Regression for ETR II

Description

Fits a regression model for ETR II based on Eilers-Peeters (1988), considering photoinhibition.

Usage

```
eilers_peeters_generate_regression_ETR_II(
  data,
  a_start_value = eilers_peeters_default_start_value_a,
  b_start_value = eilers_peeters_default_start_value_b,
  c_start_value = eilers_peeters_default_start_value_c
)
```

Arguments

`data`	A `data.table` from from read function (e.g.`read_dual_pam_data`).
`a_start_value`	Numeric. Starting value for a. Default: `a_start_values_eilers_peeters_default`.
`b_start_value`	Numeric. Starting value for b. Default: `b_start_values_eilers_peeters_default`.
`c_start_value`	Numeric. Starting value for c. Default: `c_start_values_eilers_peeters_default`.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions.

Value

A list containing:

- `etr_regression_data`: Predicted ETR values.
- `residual_sum_of_squares`: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- `root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- `relative_root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- `a`, `b`, `c`: Fitted parameters.
- `pm`: Maximum ETR (p_m).
- `s`: Initial slope (s).
- `ik`: Transition point from light limitation to light saturation (I_k).
- `im`: PAR at maximum ETR (I_m).
- `w`: Peak sharpness (w).

References

Eilers, P. H. C., & Peeters, J. C. H. (1988). *A model for the relationship between light intensity and the rate of photosynthesis in phytoplankton.* Ecological Modelling, 42(3-4), 199-215. Available at: doi:10.1016/03043800(88)900579

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- eilers_peeters_generate_regression_ETR_II(data)
```

`eilers_peeters_modified`

Eilers & Peeters Model Modification

Description

This function enhances the Eilers and Peeters (1988) model by adding parameters not originally included in the model, which were introduced by other models. It also renames parameters to a standardized naming convention used across all models.

Usage

```
eilers_peeters_modified(model_result)
```

Arguments

model_result	A list containing the model result (e.g. from eilers_peeters_generate_regression_ETR_II()).

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam?tab=readme-ov-file#eilers_peeters_modified

Value

A modified model result as a list with the following elements:

- etr_type: ETR Type based on the model result.
- etr_regression_data: Regression data with ETR predictions based on the fitted model.
- residual_sum_of_squares: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- root_mean_squared_error: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- relative_root_mean_squared_error: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- a: The obtained parameter a.
- b: The obtained parameter b.
- c: The obtained parameter c.
- d: Not available, set to NA_real_.
- alpha: The initial slope of the light curve, transferred unchanged as s.
- beta: Not available, set to NA_real_.
- etrmax_with_photoinhibition: The maximum electron transport rate with photoinhibition, transferred as pm.
- etrmax_without_photoinhibition: Not available, set to NA_real_.
- ik_with_photoinhibition: PAR where the transition point from light limitation to light saturation is achieved with photoinhibition, transferred as ik.
- ik_without_photoinhibition: Not available, set to NA_real_.
- im_with_photoinhibition: The PAR at which the maximum electron transport rate is achieved with photoinhibition, transferred as im.
- w: The sharpness of the peak, transferred as w.
- ib: Not available, set to NA_real_.
- etrmax_without_with_ratio: Not available, set to NA_real_.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- eilers_peeters_generate_regression_ETR_II(data)
modified_result <- eilers_peeters_modified(result)
```

`platt_default_start_value_alpha` *Default start value*

Description

Default start value

Usage

```
platt_default_start_value_alpha
```

Format

An object of class `numeric` of length 1.

`platt_default_start_value_beta` *Default start value*

Description

Default start value

Usage

```
platt_default_start_value_beta
```

Format

An object of class `numeric` of length 1.

`platt_default_start_value_ps` *Default start value*

Description

Default start value

Usage

```
platt_default_start_value_ps
```

Format

An object of class `numeric` of length 1.

`platt_generate_regression_ETR_I` *Platt Regression for ETR I*

Description

Fits the Platt (1980) regression model using original naming conventions.

Usage

```
platt_generate_regression_ETR_I(
  data,
  alpha_start_value = platt_default_start_value_alpha,
  beta_start_value = platt_default_start_value_beta,
  ps_start_value = platt_default_start_value_ps
)
```

Arguments

`data`	A `data.table` from from read function (e.g.`read_dual_pam_data`).
`alpha_start_value`	Numeric. Initial value for α. Default: `alpha_start_value_platt_default`.
`beta_start_value`	Numeric. Initial value for β. Default: `beta_start_value_platt_default`.
`ps_start_value`	Numeric. Initial value for P_s. Default: `ps_start_value_platt_default`.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions .

Value

A list containing:

- `etr_regression_data`: Predicted ETR values.
- `residual_sum_of_squares`: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- `root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- `relative_root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- `ps`: Maximum electron transport rate without photoinhibition (P_s).
- `alpha`: Initial slope of the light curve (α).
- `beta`: Photoinhibition (β).

- pm: Maximum electron transport rate with photoinhibition (P_m).
- ik: Transition PAR with photoinhibition (I_k).
- is: Transition PAR without photoinhibition (I_s).
- im: PAR at maximum ETR with photoinhibition (I_m).
- ib: (I_b)

References

Platt, T., Gallegos, C. L., & Harrison, W. G. (1980). *Photoinhibition of photosynthesis in natural assemblages of marine phytoplankton. Journal of Marine Research, 38*(4). Retrieved from https://elischolar.library.yale.edu/journal_of_marine_research/1525/.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- platt_generate_regression_ETR_I(data)
```

---

platt_generate_regression_ETR_II

Platt Regression for ETR II

Description

Fits the Platt (1980) regression model using original naming conventions.

Usage

```
platt_generate_regression_ETR_II(
  data,
  alpha_start_value = platt_default_start_value_alpha,
  beta_start_value = platt_default_start_value_beta,
  ps_start_value = platt_default_start_value_ps
)
```

Arguments

data	A data.table from from read function (e.g.read_dual_pam_data).
alpha_start_value	Numeric. Initial value for α. Default: alpha_start_value_platt_default.
beta_start_value	Numeric. Initial value for β. Default: beta_start_value_platt_default.
ps_start_value	Numeric. Initial value for P_s. Default: ps_start_value_platt_default.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions.

Value

A list containing:

- `etr_regression_data`: Predicted ETR values.
- `residual_sum_of_squares`: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- `root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- `relative_root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- `ps`: Maximum electron transport rate without photoinhibition (P_s).
- `alpha`: Initial slope of the light curve (α).
- `beta`: Photoinhibition (β).
- `pm`: Maximum electron transport rate with photoinhibition (P_m).
- `ik`: Transition PAR with photoinhibition (I_k).
- `is`: Transition PAR without photoinhibition (I_s).
- `im`: PAR at maximum ETR with photoinhibition (I_m).
- `ib`: (I_b)

References

Platt, T., Gallegos, C. L., & Harrison, W. G. (1980). *Photoinhibition of photosynthesis in natural assemblages of marine phytoplankton. Journal of Marine Research, 38*(4). Retrieved from https://elischolar.library.yale.edu/journal_of_marine_research/1525/.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- platt_generate_regression_ETR_II(data)
```

platt_modified *Platt Model Modification*

Description

This function enhances the Platt (1980) model by adding parameters not originally included in the model, which were introduced by other models. It also renames parameters to a standardized naming convention used across all models.

Usage

```
platt_modified(model_result)
```

Arguments

model_result	A list containing the model result (e.g. from platt_generate_regression_ETR_II()).

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam?tab=readme-ov-file#platt_modified

Value

A modified model result as a list with the following elements:

- etr_type: ETR Type based on the model result.
- etr_regression_data: Regression data with ETR predictions based on the fitted model.
- residual_sum_of_squares: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- root_mean_squared_error: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- relative_root_mean_squared_error: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- a: Obtained parameter a, equal to etrmax_without_photoinhibition.
- b: Obtained parameter b, equal to alpha.
- c: Obtained parameter c, equal to beta.
- d: Not available, set to NA_real_.
- alpha: The initial slope of the light curve, transferred unchanged as alpha.
- beta: The photoinhibition of the light curve, transferred unchanged as beta.
- etrmax_with_photoinhibition: The maximum electron transport rate with photoinhibition, transferred as pm.
- etrmax_without_photoinhibition: The maximum electron transport rate without photoinhibition, transferred as ps.

- ik_with_photoinhibition: PAR where the transition point from light limitation to light saturation is achieved with photoinhibition, transferred as ik.
- ik_without_photoinhibition: PAR where the transition point from light limitation to light saturation is achieved without photoinhibition, transferred as is.
- im_with_photoinhibition: The PAR at which the maximum electron transport rate is achieved with photoinhibition, transferred as im.
- w: Not available, set to NA_real_.
- ib: Transferred unchanged as ib.
- etrmax_without_with_ratio: Ratio of etrmax_without_photoinhibition / etrmax_with_photoinhibition, and ik_without_photoinhibition / ik_with_photoinhibition.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- platt_generate_regression_ETR_II(data)
modified_result <- platt_modified(result)
```

---

plot_control *Plot Control*

Description

This function creates a control plot for the used model based on the provided data and model results.

Usage

```
plot_control(data, model_result, title, color = "black")
```

Arguments

data	A 'data.table' containing the original ETR and yield data for the plot.
model_result	A list containing the fitting results of the used model and the calculated parameters.
title	A character string that specifies the title of the plot.
color	A color specification for the regression line in the plot.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions

Value

A plot displaying the original ETR and Yield values and the regression data. A table below the plot shows the calculated data.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- eilers_peeters_generate_regression_ETR_I(data)
plot_control(data, result, "Control Plot")
```

---

read_dual_pam_data *Read and Process DualPAM Data*

Description

Reads raw CSV files generated by DualPAM software, calculates electron transport rate (ETR) values, and returns a universal dataset.

Usage

```
read_dual_pam_data(
  csv_path,
  remove_recovery = TRUE,
  etr_factor = 0.84,
  fraction_photosystem_I = 0.5,
  fraction_photosystem_II = 0.5
)
```

Arguments

csv_path	File path to the CSV file.
remove_recovery	Logical. Removes recovery measurements if TRUE. Default is TRUE.
etr_factor	Numeric. Factor for ETR calculation. Default is 0.84.
fraction_photosystem_I	Numeric. Relative distribution of absorbed PAR to photosystem I. Default is 0.5.
fraction_photosystem_II	Numeric. Relative distribution of absorbed PAR to photosystem II. Default is 0.5.

Details

Calculates ETR using:

$$\text{ETR} = \text{PAR} \cdot \text{ETR-Factor} \cdot \text{Fraction of Photosystem (I or II)} \cdot \text{Yield (I or II)}$$

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions

Value

A `data.table` containing:

- `par`: Photosynthetically active radiation.
- `yield_1`: Yield for photosystem I.
- `yield_2`: Yield for photosystem II.
- `etr_1`: Calculated ETR for photosystem I.
- `etr_2`: Calculated ETR for photosystem II.

References

Heinz Walz GmbH. (2024). *DUAL-PAM-100 DUAL-PAM/F MANUAL, 5th Edition, April 2024, Chapter 7 (pp. 162-172).* Heinz Walz GmbH, Effeltrich, Germany. Available at: https://www.walz.com/files/downloads/dualpamed05.pdf

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)
```

---

read_dual_pam_single_channel_fluo_data

Read and Process DualPAM Data Single Chanel Mode Fluo

Description

Reads raw CSV files generated by DualPAM software, calculates electron transport rate (ETR) values for Photosystem II, and returns a universal dataset.

Usage

```
read_dual_pam_single_channel_fluo_data(
  csv_path,
  remove_recovery = TRUE,
  etr_factor = 0.84,
  fraction_photosystem_I = 0.5,
  fraction_photosystem_II = 0.5
)
```

Arguments

`csv_path`	File path to the CSV file.
`remove_recovery`	Logical. Removes recovery measurements if `TRUE`. Default is `TRUE`.
`etr_factor`	Numeric. Factor for ETR calculation. Default is `0.84`.
`fraction_photosystem_I`	Numeric. Relative distribution of absorbed PAR to photosystem I. Default is `0.5`.
`fraction_photosystem_II`	Numeric. Relative distribution of absorbed PAR to photosystem II. Default is `0.5`.

Details

Calculates ETR using:

$$\text{ETR} = \text{PAR} \cdot \text{ETR-Factor} \cdot \text{Fraction of Photosystem (II)} \cdot \text{Yield (II)}$$

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions

Value

A `data.table` containing:

- `par`: Photosynthetically active radiation.
- `yield_1`: NA
- `yield_2`: Yield for photosystem II.
- `etr_1`: NA
- `etr_2`: Calculated ETR for photosystem II.

References

Heinz Walz GmbH. (2024). *DUAL-PAM-100 DUAL-PAM/F MANUAL, 5th Edition, April 2024, Chapter 7 (pp. 162-172).* Heinz Walz GmbH, Effeltrich, Germany. Available at: https://www.walz.com/files/downloads/dualpamed05.pdf

Examples

```
path <- file.path(
  system.file("extdata/dual_pam_single_channel_fluo_data", package = "pam"),
  "20260130_dual_pam_only_fluo.csv"
)
data <- read_dual_pam_single_channel_fluo_data(path)
```

`read_dual_pam_single_channel_p700_data` *Read and Process DualPAM Data Single Chanel Mode P700*

Description

Reads raw CSV files generated by DualPAM software, calculates electron transport rate (ETR) values for Photosystem I, and returns a universal dataset.

Usage

```
read_dual_pam_single_channel_p700_data(
  csv_path,
  remove_recovery = TRUE,
  etr_factor = 0.84,
  fraction_photosystem_I = 0.5,
  fraction_photosystem_II = 0.5
)
```

Arguments

`csv_path`	File path to the CSV file.
`remove_recovery`	Logical. Removes recovery measurements if `TRUE`. Default is `TRUE`.
`etr_factor`	Numeric. Factor for ETR calculation. Default is `0.84`.
`fraction_photosystem_I`	Numeric. Relative distribution of absorbed PAR to photosystem I. Default is `0.5`.
`fraction_photosystem_II`	Numeric. Relative distribution of absorbed PAR to photosystem II. Default is `0.5`.

Details

Calculates ETR using:

$$\text{ETR} = \text{PAR} \cdot \text{ETR-Factor} \cdot \text{Fraction of Photosystem (I)} \cdot \text{Yield (I)}$$

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions

Value

A `data.table` containing:

- `par`: Photosynthetically active radiation.
- `yield_1`: Yield for photosystem I

- yield_2: NA
- etr_1: Calculated ETR for photosystem I
- etr_2: NA

References

Heinz Walz GmbH. (2024). *DUAL-PAM-100 DUAL-PAM/F MANUAL, 5th Edition, April 2024, Chapter 7 (pp. 162-172).* Heinz Walz GmbH, Effeltrich, Germany. Available at: https://www.walz.com/files/downloads/dualpamed05.pdf

Examples

```
path <- file.path(
  system.file("extdata/dual_pam_single_channel_p700_data", package = "pam"),
  "20260130_01_dual_pam_only_p700.csv"
)
data <- read_dual_pam_single_channel_p700_data(path)
```

---

read_junior_pam_data *Read and Process Junior PAM Data*

Description

Reads raw CSV files generated by Junior PAM software, calculates electron transport rate (ETR) values, and returns a cleaned dataset.

Usage

```
read_junior_pam_data(
  csv_path,
  remove_recovery = TRUE,
  etr_factor = 0.84,
  fraction_photosystem_I = 0.5,
  fraction_photosystem_II = 0.5
)
```

Arguments

csv_path	File path to the CSV file.
remove_recovery	Logical. Removes recovery measurements if TRUE. Default is TRUE.
etr_factor	Numeric. Factor for ETR calculation. Default is 0.84.
fraction_photosystem_I	Numeric. Relative distribution of absorbed PAR to photosystem I. Default is 0.5.
fraction_photosystem_II	Numeric. Relative distribution of absorbed PAR to photosystem II. Default is 0.5.

Details

Calculates ETR II using:

$$\text{ETR II} = \text{PAR} \cdot \text{ETR-Factor} \cdot \text{Fraction of Photosystem (II)} \cdot \text{Yield (II)}$$

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions

Value

A `data.table` containing:

- `par`: Photosynthetically active radiation.
- `yield_1`: Yield for photosystem I.
- `yield_2`: Yield for photosystem II.
- `etr_1`: Calculated ETR for photosystem I.
- `etr_2`: Calculated ETR for photosystem II.

References

Heinz Walz GmbH. (2024). *DUAL-PAM-100 DUAL-PAM/F MANUAL, 5th Edition, April 2024, Chapter 7 (pp. 162-172).* Heinz Walz GmbH, Effeltrich, Germany. Available at: https://www.walz.com/files/downloads/dualpamed05.pdf

Examples

```
path <- file.path(
  system.file("extdata/junior_pam_data", package = "pam"),
  "2026_04_22_junior_pam.csv"
)
data <- read_junior_pam_data(path)
```

---

read_pam_2500_data *Read and Process PAM 2500 Data*

Description

Reads raw CSV files generated by PAM 2500 software, calculates electron transport rate (ETR) values, and returns a cleaned dataset.

Usage

```
read_pam_2500_data(
  csv_path,
  remove_recovery = TRUE,
  etr_factor = 0.84,
  fraction_photosystem_I = 0.5,
  fraction_photosystem_II = 0.5
)
```

Arguments

`csv_path`	File path to the CSV file.
`remove_recovery`	Logical. Removes recovery measurements if `TRUE`. Default is `TRUE`.
`etr_factor`	Numeric. Factor for ETR calculation. Default is `0.84`.
`fraction_photosystem_I`	Numeric. Relative distribution of absorbed PAR to photosystem I. Default is `0.5`.
`fraction_photosystem_II`	Numeric. Relative distribution of absorbed PAR to photosystem II. Default is `0.5`.

Details

Calculates ETR II using:

$$\text{ETR II} = \text{PAR} \cdot \text{ETR-Factor} \cdot \text{Fraction of Photosystem (II)} \cdot \text{Yield (II)}$$

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions

Value

A `data.table` containing:

- `par`: Photosynthetically active radiation.
- `yield_1`: Yield for photosystem I.
- `yield_2`: Yield for photosystem II.
- `etr_1`: Calculated ETR for photosystem I.
- `etr_2`: Calculated ETR for photosystem II.

References

Heinz Walz GmbH. (2024). *DUAL-PAM-100 DUAL-PAM/F MANUAL, 5th Edition, April 2024, Chapter 7 (pp. 162-172).* Heinz Walz GmbH, Effeltrich, Germany. Available at: https://www.walz.com/files/downloads/dualpamed05.pdf

Examples

```
path <- file.path(system.file("extdata/pam_2500_data", package = "pam"), "20260422_pam_2500.CSV")
data <- read_pam_2500_data(path)
```

`read_universal_data` *Read and Process Universal PAM Data*

Description

Reads a standardized CSV file containing PAR and yield data for photosystem I and/or II, calculates electron transport rates (ETR), and returns a cleaned and validated dataset. The function is device-agnostic but requires a predefined column structure.

Usage

```
read_universal_data(
  csv_path,
  etr_factor = 0.84,
  fraction_photosystem_I = 0.5,
  fraction_photosystem_II = 0.5
)
```

Arguments

`csv_path`	File path to the CSV file.
`etr_factor`	Numeric. Factor for ETR calculation. Default is `0.84`.
`fraction_photosystem_I`	Numeric. Relative distribution of absorbed PAR to photosystem I. Default is `0.5`.
`fraction_photosystem_II`	Numeric. Relative distribution of absorbed PAR to photosystem II. Default is `0.5`.

Details

Calculates ETR using:

$$\text{ETR} = \text{PAR} \cdot \text{ETR-Factor} \cdot \text{Fraction of Photosystem (I or II)} \cdot \text{Yield (I or II)}$$

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions

Value

A `data.table` containing:

- `par`: Photosynthetically active radiation.
- `yield_1`: Yield for photosystem I.
- `yield_2`: Yield for photosystem II.
- `etr_1`: Calculated ETR for photosystem I.
- `etr_2`: Calculated ETR for photosystem II.

References

Heinz Walz GmbH. (2024). *DUAL-PAM-100 DUAL-PAM/F MANUAL, 5th Edition, April 2024, Chapter 7 (pp. 162-172).* Heinz Walz GmbH, Effeltrich, Germany. Available at: https://www.walz.com/files/downloads/dualpamed05.pdf

Examples

```
path <- file.path(system.file("extdata", package = "pam"), "universal_data", "universal_data.csv")
data <- read_universal_data(path)
```

---

vollenweider_default_start_value_a

Default start value

Description

Default start value

Usage

```
vollenweider_default_start_value_a
```

Format

An object of class `numeric` of length 1.

---

vollenweider_default_start_value_alpha

Default start value

Description

Default start value

Usage

```
vollenweider_default_start_value_alpha
```

Format

An object of class `numeric` of length 1.

`vollenweider_default_start_value_n` *Default start value*

Description

Default start value

Usage

```
vollenweider_default_start_value_n
```

Format

An object of class `numeric` of length 1.

`vollenweider_default_start_value_pmax` *Default start value*

Description

Default start value

Usage

```
vollenweider_default_start_value_pmax
```

Format

An object of class `numeric` of length 1.

vollenweider_generate_regression_ETR_I
Vollenweider Regression for ETR I

Description

Fits the Vollenweider (1965) regression model using original naming conventions from the publication.

Usage

```
vollenweider_generate_regression_ETR_I(
  data,
  pmax_start_value = vollenweider_default_start_value_pmax,
  a_start_value = vollenweider_default_start_value_a,
  alpha_start_value = vollenweider_default_start_value_alpha,
  n_start_value = vollenweider_default_start_value_n
)
```

Arguments

data	A data.table from read function (e.g.read_dual_pam_data).
pmax_start_value	Numeric. Initial value for p_{max}. Default: pmax_start_values_vollenweider_default.
a_start_value	Numeric. Initial value for a. Default: a_start_values_vollenweider_default.
alpha_start_value	Numeric. Initial value for α. Default: alpha_start_values_vollenweider_default.
n_start_value	Numeric. Initial value for n. Default: n_start_values_vollenweider_default.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions.

Value

A list containing:

- etr_regression_data: Predicted ETR values.
- residual_sum_of_squares: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- root_mean_squared_error: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- relative_root_mean_squared_error: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.

- pmax: Maximum electron transport rate without photoinhibition (p_{max}).
- a: Parameter a.
- alpha: Parameter α.
- n: Parameter n.
- popt: Maximum electron transport rate with photoinhibition (p_{opt}).
- ik: Transition point from light limitation to light saturation without photoinhibition (I_k).
- iik: Transition point from light limitation to light saturation with photoinhibition (I'_k).
- pmax_popt_and_ik_iik_ratio: Ratio of p_{max} / p_{opt} and I_k / I'_k.

References

Vollenweider, R. A. (1965). *Calculation models of photosynthesis-depth curves and some implications regarding day rate estimates in primary production measurements*, p. 427-457. In C. R. Goldman [ed.], *Primary Productivity in Aquatic Environments*. Mem. Ist. Ital. Idrobiol., 18 Suppl., University of California Press, Berkeley.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- vollenweider_generate_regression_ETR_I(data)
```

---

vollenweider_generate_regression_ETR_II

Vollenweider Regression for ETR II

Description

Fits the Vollenweider (1965) regression model using original naming conventions from the publication.

Usage

```
vollenweider_generate_regression_ETR_II(
  data,
  pmax_start_value = vollenweider_default_start_value_pmax,
  a_start_value = vollenweider_default_start_value_a,
  alpha_start_value = vollenweider_default_start_value_alpha,
  n_start_value = vollenweider_default_start_value_n
)
```

Arguments

`data`	A `data.table` from read function (e.g.`read_dual_pam_data`).
`pmax_start_value`	Numeric. Initial value for p_{max}. Default: `pmax_start_values_vollenweider_default`.
`a_start_value`	Numeric. Initial value for a. Default: `a_start_values_vollenweider_default`.
`alpha_start_value`	Numeric. Initial value for α. Default: `alpha_start_values_vollenweider_default`.
`n_start_value`	Numeric. Initial value for n. Default: `n_start_values_vollenweider_default`.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions.

Value

A list containing:

- `etr_regression_data`: Predicted ETR values.
- `residual_sum_of_squares`: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- `root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- `relative_root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- `pmax`: Maximum electron transport rate without photoinhibition (p_{max}).
- `a`: Parameter a.
- `alpha`: Parameter α.
- `n`: Parameter n.
- `popt`: Maximum electron transport rate with photoinhibition (p_{opt}).
- `ik`: Transition point from light limitation to light saturation without photoinhibition (I_k).
- `iik`: Transition point from light limitation to light saturation with photoinhibition (I'_k).
- `pmax_popt_and_ik_iik_ratio`: Ratio of p_{max} / p_{opt} and I_k / I'_k.

References

Vollenweider, R. A. (1965). *Calculation models of photosynthesis-depth curves and some implications regarding day rate estimates in primary production measurements*, p. 427-457. In C. R. Goldman [ed.], *Primary Productivity in Aquatic Environments*. Mem. Ist. Ital. Idrobiol., 18 Suppl., University of California Press, Berkeley.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- vollenweider_generate_regression_ETR_II(data)
```

`vollenweider_modified` *Vollenweider Model Modification*

Description

This function adds parameters that were not originally included in the Vollenweider (1965) model, but were introduced by other models, and renames the parameters to a standardized one for all models.

Usage

```
vollenweider_modified(model_result)
```

Arguments

`model_result`	A list containing the model result (e.g. from vollenweider_generate_regression_ETR_II()).

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam?tab=readme-ov-file#vollenweider_modified

Value

A modified model result as a list containing the following elements:

- `etr_type`: ETR Type based on the model result.
- `etr_regression_data`: Regression data with ETR predictions based on the fitted model.
- `residual_sum_of_squares`: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- `root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- `relative_root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- `a`: Obtained parameter `a`, here equal to `etrmax_without_photoinhibition`.
- `b`: Obtained parameter `b`, transferred as `a`.
- `c`: Obtained parameter `c`, here transferred as `alpha`.
- `d`: Obtained parameter `d`, here transferred as `n`.

- alpha: The initial slope of the light curve.
- beta: Not available, here set to NA_real_.
- etrmax_with_photoinhibition: The maximum electron transport rate with photoinhibition, transferred as popt.
- etrmax_without_photoinhibition: The maximum electron transport rate without photoinhibition, transferred as pmax.
- ik_with_photoinhibition: PAR where the transition point from light limitation to light saturation is achieved taking photoinhibition into account, transferred as iik.
- ik_without_photoinhibition: PAR where the transition point from light limitation to light saturation is achieved not taking photoinhibition into account, transferred as ik.
- im_with_photoinhibition: The PAR at which the maximum electron transport rate is achieved by taking photoinhibition into account, determined using the regression data from the model.
- w: Not available, here set to NA_real_.
- ib: Transferred unchanged as ib.
- etrmax_without_with_ratio: Ratio of etrmax_without_photoinhibition / etrmax_with_photoinhibition and ik_without_photoinhibition / ik_with_photoinhibition.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- vollenweider_generate_regression_ETR_II(data)
modified_result <- vollenweider_modified(result)
```

---

walsby_default_start_value_alpha

Default start value

Description

Default start value

Usage

```
walsby_default_start_value_alpha
```

Format

An object of class numeric of length 1.

`walsby_default_start_value_beta` *Default start value*

Description

Default start value

Usage

```
walsby_default_start_value_beta
```

Format

An object of class `numeric` of length 1.

`walsby_default_start_value_etr_max` *Default start value*

Description

Default start value

Usage

```
walsby_default_start_value_etr_max
```

Format

An object of class `numeric` of length 1.

`walsby_generate_regression_ETR_I` *Walsby Regression for ETR I*

Description

Fits a modified Walsby (1997) regression model without the respiration term, using Romoth (2019) naming conventions. Calculates ETR_{max} without accounting for photoinhibition.

Usage

```
walsby_generate_regression_ETR_I(
  data,
  etr_max_start_value = walsby_default_start_value_etr_max,
  alpha_start_value = walsby_default_start_value_alpha,
  beta_start_value = walsby_default_start_value_beta
)
```

Arguments

`data`	A `data.table` from read function (e.g.`read_dual_pam_data`).
`etr_max_start_value`	Numeric. Initial value for ETR_{max}. Default: `etr_max_start_value_walsby_default`.
`alpha_start_value`	Numeric. Initial value for α. Default: `alpha_start_value_walsby_default`.
`beta_start_value`	Numeric. Initial value for β. Default: `beta_start_value_walsby_default`.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions.

Value

A list containing:

- `etr_regression_data`: Predicted ETR values.
- `residual_sum_of_squares`: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- `root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- `relative_root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- `etr_max`: Maximum ETR (ETR_{max}).
- `alpha`: Initial slope (α).
- `beta`: Photoinhibition factor (β).

References

Walsby, A. E. (1997). Numerical integration of phytoplankton photosynthesis through time and depth in a water column. *New Phytologist*, 136(2), 189-209. Available at: doi:10.1046/j.1469-8137.1997.00736.x

Romoth, K., Nowak, P., Kempke, D., Dietrich, A., Porsche, C., & Schubert, H. (2019). Acclimation limits of *Fucus evanescens* along the salinity gradient of the southwestern Baltic Sea. *Botanica Marina*, 62(1), 1-12. Available at: doi:10.1515/bot20180098

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- walsby_generate_regression_ETR_I(data)
```

`walsby_generate_regression_ETR_II`

Walsby Regression for ETR II

Description

Fits a modified Walsby (1997) regression model without the respiration term, using Romoth (2019) naming conventions. Calculates ETR_{max} without accounting for photoinhibition.

Usage

```
walsby_generate_regression_ETR_II(
  data,
  etr_max_start_value = walsby_default_start_value_etr_max,
  alpha_start_value = walsby_default_start_value_alpha,
  beta_start_value = walsby_default_start_value_beta
)
```

Arguments

`data`	A `data.table` from read function (e.g.`read_dual_pam_data`).
`etr_max_start_value`	Numeric. Initial value for ETR_{max}. Default: `etr_max_start_value_walsby_default`.
`alpha_start_value`	Numeric. Initial value for α. Default: `alpha_start_value_walsby_default`.
`beta_start_value`	Numeric. Initial value for β. Default: `beta_start_value_walsby_default`.

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions.

Value

A list containing:

- `etr_regression_data`: Predicted ETR values.
- `residual_sum_of_squares`: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- `root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- `relative_root_mean_squared_error`: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- `etr_max`: Maximum ETR (ETR_{max}).
- `alpha`: Initial slope (α).
- `beta`: Photoinhibition factor (β).

References

Walsby, A. E. (1997). Numerical integration of phytoplankton photosynthesis through time and depth in a water column. *New Phytologist*, 136(2), 189-209. Available at: doi:10.1046/j.1469-8137.1997.00736.x

Romoth, K., Nowak, P., Kempke, D., Dietrich, A., Porsche, C., & Schubert, H. (2019). Acclimation limits of *Fucus evanescens* along the salinity gradient of the southwestern Baltic Sea. *Botanica Marina*, 62(1), 1-12. Available at: doi:10.1515/bot20180098

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- walsby_generate_regression_ETR_II(data)
```

`walsby_modified` *Walsby Model Modification*

Description

Enhances the Walsby (1997) model by adding parameters from other models and standardizing parameter names.

Usage

```
walsby_modified(model_result)
```

Arguments

`model_result`	A list containing the model result (e.g. from walsby_generate_regression_ETR_II()).

Details

A detailed documentation can be found under https://github.com/biotoolbox/pam?tab=readme-ov-file#walsby_modified

Value

A list containing:

- etr_type: ETR Type based on the model result.
- etr_regression_data: Regression data with ETR predictions based on the fitted model.
- residual_sum_of_squares: Difference between observed and predicted ETR values, expressed as the sum of squared residuals.
- root_mean_squared_error: Difference between observed and predicted ETR values, expressed as the root mean squared error.
- relative_root_mean_squared_error: Difference between observed and predicted ETR values, expressed as the relative root mean squared error, normalized by the mean.
- a: Obtained parameter a, equal to etrmax_without_photoinhibition.
- b: Obtained parameter b, equal to alpha.
- c: Obtained parameter c, equal to beta.
- d: Not available, set to NA_real_.
- alpha: The initial slope of the light curve, transferred unchanged as alpha.
- beta: The photoinhibition of the light curve, transferred unchanged as beta.
- etrmax_with_photoinhibition: The maximum electron transport rate with photoinhibition.
- etrmax_without_photoinhibition: The maximum electron transport rate without photoinhibition, transferred as etr_max.
- ik_with_photoinhibition: PAR where the transition point from light limitation to light saturation is achieved with photoinhibition.
- ik_without_photoinhibition: PAR where the transition point from light limitation to light saturation is achieved without photoinhibition.
- im_with_photoinhibition: PAR at the maximum ETR with photoinhibition.
- w: Not available, set to NA_real_.
- ib: Not available, set to NA_real_.
- etrmax_without_with_ratio: Ratio of etrmax_without_photoinhibition / etrmax_with_photoinhibition.

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- walsby_generate_regression_ETR_II(data)
modified_result <- walsby_modified(result)
```

`write_model_result_csv` *Write Model Result CSV*

Description

This function exports the intermediate data table, regression data, and model parameters into separate CSV files for easy access and further analysis.

Usage

```
write_model_result_csv(dest_dir, name, data, model_result)
```

Arguments

`dest_dir`	A character string specifying the directory where the CSV files will be saved.
`name`	A character string specifying the base name for the output files.
`data`	A data.table containing the intermediate data used in the model.
`model_result`	A list containing the model results, including parameter values and regression data.

Details

This function generates three CSV files:

1. **raw_data.csv:** Contains the original raw data used in the model.
2. **regression_data.csv:** Includes the regression data with predicted electron transport rate (ETR) values.
3. **model_result.csv:** Summarizes the parameter values derived from the model results (excluding regression data), such as `alpha` or `beta`.

The ‘name‘ parameter serves as a prefix for each file, ensuring clarity and organization in the output directory. A detailed documentation can be found under https://github.com/biotoolbox/pam/tree/main#functions

Value

No return value, called for side effects

Examples

```
path <- file.path(system.file("extdata/dual_pam_data", package = "pam"), "20240925.csv")
data <- read_dual_pam_data(path)

result <- eilers_peeters_generate_regression_ETR_I(data)
write_model_result_csv(tempdir(), "20240925", data, result)
```

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