

Package ‘seinfitR’

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Title Modeling the Relationship Between Nematode Densities and Plant Growth

Version 1.0.1

Description Implements the Seinhorst model to analyze the relationship between initial nematode densities and plant growth response using nonlinear least squares estimation. The package provides tools for model fitting, prediction, and visualization, facilitating the study of plant-nematode interactions. Model parameters can be estimated or set to predefined values based on Seinhorst (1986) <[doi:10.1007/978-1-4613-2251-1_11](https://doi.org/10.1007/978-1-4613-2251-1_11)>.

License GPL (>= 3)

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Imports minpack.lm

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URL <https://github.com/dslabcena/seinfitR>

BugReports <https://github.com/dslabcena/seinfitR/issues>

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LazyData true

VignetteBuilder knitr

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| coef.seifitR | <i>Extract Coefficients</i> |
|--------------|-----------------------------|

Description

Extract model coefficients from a seifitR object.

Usage

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

Arguments

| | |
|--------|----------------------------|
| object | Object of class 'seifitR'. |
| ... | currently unused. |

Value

A named numeric vector containing the estimated model coefficients.

glasshouse

Glasshouse Experiment Dataset

Description

This dataset originates from a greenhouse experiment that assessed the effect of nematode population density on plant yield. One cultivar was used, and 14 different nematode population densities (p_i), including zero, were tested. Each density was replicated five times. The dataset provides the nematode densities and the corresponding average plant yield.

Usage

```
data(glasshouse, package = "seifitR")
```

Format

A data frame with 14 rows and 2 columns:

- p_i** Nematode population density (initial population).
- y** Average crop yield at the given population density.

References

Schomaker, C., & Been, T. (2013). Plant growth and population dynamics. *Plant Nematology*, 301-330. doi:[10.1079/9781780641515.0301](https://doi.org/10.1079/9781780641515.0301)

jambu

Jambu Dataset

Description

This dataset is based on the results of a pre-modeled raw dataset. The original data was generated using seven repetitions for five initial nematode population densities (p_i): 0, 500, 1000, 2500, and 5000. The model parameters t , m , and z obtained from the raw dataset were then used to predict and extend p_i values across the range from 0 to 5001.

Usage

```
data(jambu, package = "seifitR")
```

Format

A data frame with 5,002 rows and 2 columns:

- p_i** Nematode population density (initial population).
- y** Crop yield, another plant growth parameter, or the ratio of the estimated variable for plant growth at an initial nematode population density.

Details

This dataset is used in the `seinfitR` package to study the relationship between nematode populations and plant growth.

Source

<https://osf.io/pm94t>

References

Silva, M.F., Faccioli, F.C., Honório, A.P. et al. (2024). First report of angular leaf spot in *Acmella oleracea* caused by the foliar nematode *Aphelenchoides pseudobesseyi*. *J Plant Dis Prot*, 131, 1707–1720. doi:[10.1007/s41348024009822](https://doi.org/10.1007/s41348024009822)

plot.seinfitR

Plot SeinfitR

Description

Plot method for `seinfitR` objects

Usage

```
## S3 method for class 'seinfitR'  
plot(x, rel = FALSE, ...)
```

Arguments

| | |
|------------------|--|
| <code>x</code> | An object of class <code>seinfitR</code> (output from <code>seinfitR()</code>). |
| <code>rel</code> | Logical. If <code>TRUE</code> , the observed and fitted values are plotted relative to the maximum fitted value (normalized between 0 and 1). If <code>FALSE</code> , the original observed and fitted values are plotted. |
| <code>...</code> | currently unused. |

Value

A plot showing the observed data (blue points) and the fitted curve (red line).

predict.seifitR *Predict SeifitR*

Description

Predict method for seifitR objects

Usage

```
## S3 method for class 'seifitR'
predict(object, newdata = NULL, ...)
```

Arguments

| | |
|---------|---|
| object | An object of class seifitR (output from seifitR()). |
| newdata | Optional. A data frame containing the independent variable for which predictions should be made. If not provided, predictions are made for the original data. |
| ... | currently unused. |

Details

This function generates predictions based on a fitted Seinhorst model.

Value

A data frame with the independent variable and the corresponding predicted values.

print.seifitR *Print SeifitR*

Description

Print contents of seifitR object.

Usage

```
## S3 method for class 'seifitR'
print(x, digits = max(3L, getOption("digits") - 3L), ...)
```

Arguments

| | |
|--------|---|
| x | Object of class 'seifitR'. |
| digits | minimal number of <i>significant</i> digits |
| ... | currently unused. |

Value

No return value, called for side effects

See Also

[seifitR](#)

| | |
|-----------|------------------------------|
| r_squared | <i>R-squared Calculation</i> |
|-----------|------------------------------|

Description

Compute R-squared for seifitR model.

Usage

```
r_squared(object, ...)
```

Arguments

| | |
|--------|----------------------------|
| object | Object of class 'seifitR'. |
| ... | currently unused. |

Value

A list with the following components:

R2 The coefficient of determination (R-squared).

Adjusted_R2 The adjusted R-squared value.

| | |
|---------|----------------|
| seifitR | <i>SeifitR</i> |
|---------|----------------|

Description

This function fits the Seinhorst equation to experimental data describing the relationship between preplant nematode densities and plant growth using nonlinear least squares fitting. The fitting process is performed using the `nlsLM` function from the `minpack.lm` package.

Usage

```
seifitR(p_i, y, data, start, z_fixed = FALSE, control = seifitR_control())
```

Arguments

| | |
|----------------------|---|
| <code>p_i</code> | A character string specifying the column name in data that contains preplant nematode densities. |
| <code>y</code> | A character string specifying the column name in data that contains the plant growth response. |
| <code>data</code> | A data frame containing the experimental data. It must include at least two columns: one representing the preplant nematode densities (<code>p_i</code>) and another representing the plant growth response (<code>y</code>). |
| <code>start</code> | A list of initial parameter values for <code>m</code> , <code>t</code> , and <code>z</code> (if <code>z_fixed = FALSE</code>). These values are used to initialize the nonlinear least squares fitting process. |
| <code>z_fixed</code> | Logical. If TRUE, the function uses the default value for (z^t) , as described in Seinhorst (1986) doi:10.1007/9781461322511_11 |
| <code>control</code> | A control object created using <code>seifitR_control()</code> , which specifies options for the optimization process. |

Value

A list of class "seifitR" containing:

| | |
|------------------------------|---|
| <code>fit</code> | An object of class <code>nls</code> with the fitted model. |
| <code>summary_seifitR</code> | Summary statistics of the fitted model. |
| <code>cov</code> | The covariance matrix of parameter estimates (if available). |
| <code>data</code> | The original dataset used for fitting. |
| <code>x</code> | The name of the predictor variable used (<code>p_i</code>). |
| <code>y</code> | The name of the response variable used (<code>y</code>). |
| <code>z_fixed</code> | Logical value indicating whether <code>z</code> was fixed. |

Examples

```
# Example: Modeling plant response to nematode densities using "jambu" dataset

# Fit the model using seifitR with specified initial values
model <- seifitR(p_i = "p_i", y = "y", data = jambu,
               start = list(m = 0.103, t = 250, z = 0.991),
               control = seifitR_control(maxiter = 5))

# View model summary
summary(model)
```

seifitR_control *SeifitR Control*

Description

Custom Control Function for the SeifitR Model Fitting

Usage

```
seifitR_control(  
  ftol = sqrt(.Machine$double.eps),  
  ptol = sqrt(.Machine$double.eps),  
  gtol = 0,  
  diag = list(),  
  epsfcn = 0,  
  factor = 100,  
  maxfev = integer(),  
  maxiter = 50,  
  nprint = 0,  
  trace = FALSE  
)
```

Arguments

| | |
|---------|--|
| ftol | Termination condition for relative reduction in the sum of squares. |
| ptol | Termination based on relative error between two consecutive iterations. |
| gtol | Controls the orthogonality between the function vector and the Jacobian. |
| diag | Multiplicative scale factors for the parameters. |
| epsfcn | Step size for forward-difference approximation of the Jacobian. |
| factor | Initial step bound factor. |
| maxfev | Maximum number of function evaluations. |
| maxiter | Maximum number of iterations. |
| nprint | Controls printing of iteration details. |
| trace | A logical value indicating if a trace of the iteration progress should be printed. |

Details

This function returns a list of control parameters for the Levenberg-Marquardt algorithm used by the `nlsLM` function from the `minpack.lm` package. These parameters are specifically designed to control the fitting process in the `seifitR` function.

Value

A list of control parameters to be used in the `nlsLM` function during the fitting of the Seinhorst model using `seifitR`.

summary.seifitR *Summary of seifitR Model*

Description

Display a summary of the seifitR model.

Usage

```
## S3 method for class 'seifitR'  
summary(object, ...)
```

Arguments

| | |
|--------|----------------------------|
| object | Object of class 'seifitR'. |
| ... | currently unused. |

Value

No return value, called for side effects.

See Also

[seifitR](#)

vcov.seifitR *Variance-Covariance Matrix*

Description

Compute variance-covariance matrix for seifitR model.

Usage

```
## S3 method for class 'seifitR'  
vcov(object, ...)
```

Arguments

| | |
|--------|----------------------------|
| object | Object of class 'seifitR'. |
| ... | currently unused. |

Value

A matrix representing the covariance of the estimated coefficients.

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