

Package ‘agriReg’

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Title Linear and Nonlinear Regression for Agricultural Data

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Description Fit, compare, and visualise linear and nonlinear regression models tailored to field-trial and dose-response agricultural data. Provides S3 classes for mixed-effects models (via 'lme4'), nonlinear growth curves (logistic, 'Gompertz', asymptotic, linear-plateau, quadratic), and four/five-parameter log-logistic dose-response models (via 'drc'). Includes automated starting-value heuristics, goodness-of-fit statistics, residual diagnostics, and 'ggplot2'-based visualisation. Methods are based on Bates and Watts (1988, ISBN:9780471816430), Ritz and others (2015) <[doi:10.1371/journal.pone.0146021](https://doi.org/10.1371/journal.pone.0146021)>, and Bates and others (2015) <[doi:10.18637/jss.v067.i01](https://doi.org/10.18637/jss.v067.i01)>.

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 agriReg-package

agriReg: Linear and Nonlinear Regression for Agricultural Data

Description

agriReg provides a unified interface for fitting, comparing, and visualising regression models commonly used in agricultural research:

- **Linear & mixed-effects models** via `fit_linear()` (wraps `lm` / `lme4::lmer`)
- **Nonlinear growth curves** via `fit_nonlinear()` — logistic, Gompertz, asymptotic, linear-plateau, quadratic
- **Dose-response models** via `fit_dose_response()` — 4/5-parameter log-logistic and Weibull (wraps `drc`)
- **Model comparison** via `compare_models()` — AIC, BIC, RMSE side by side
- **Diagnostics** via `gof_stats()`, `residual_check()`, and `S3 plot()` methods

Typical workflow

```
library(agriReg)

# 1. Clean field trial data
trial <- clean_agri_data(my_data, yield_col = "yield_tha")

# 2. Linear mixed model (treatment + block structure)
lm_fit <- fit_linear(trial,
                    formula = "yield_tha ~ nitrogen + phosphorus",
                    random = "(1|block)")
summary(lm_fit)
plot(lm_fit, type = "residuals")

# 3. Nonlinear growth curve
nl_fit <- fit_nonlinear(trial, x_col = "days", y_col = "biomass",
                       model = "logistic")
plot(nl_fit)

# 4. Dose-response
dr_fit <- fit_dose_response(herb_data,
                           dose_col = "dose_g_ha",
                           resp_col = "weed_control_pct")
ed_estimates(dr_fit, respLev = c(50, 90))

# 5. Compare models
compare_models(linear = lm_fit, nonlinear = nl_fit)
```

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clean_agri_data

Clean and validate agricultural field-trial data

Description

Removes rows with missing yield values, coerces the yield column to numeric, optionally flags IQR-based outliers, and returns an `agriData` object with a concise summary.

Usage

```
clean_agri_data(
  df,
  yield_col = "yield",
  flag_outliers = TRUE,
  na_action = c("remove", "warn")
)
```

Arguments

<code>df</code>	A <code>data.frame</code> containing field trial records.
<code>yield_col</code>	Character. Name of the column that holds the primary response variable (e.g. "yield", "biomass"). Default "yield".
<code>flag_outliers</code>	Logical. When TRUE (default), a logical column <code>.outlier</code> is appended: TRUE marks observations that fall more than 1.5 x IQR below Q1 or above Q3.
<code>na_action</code>	One of "remove" (default) or "warn". "remove" drops rows with NA in <code>yield_col</code> ; "warn" keeps them but issues a warning.

Value

A `data.frame` with additional class "agriData". Attributes `n_removed` (rows dropped) and `n_flagged` (outliers flagged) are attached.

Examples

```
df <- data.frame(
  yield = c(3.1, 4.2, NA, 8.9, 3.8, 100),
  block = c("A", "A", "B", "B", "C", "C")
)
clean_agri_data(df, yield_col = "yield")
```

compare_models

Compare multiple agriReg models side by side

Description

Computes AIC, BIC, RMSE, MAE, and R^2 for a collection of `agriLM`, `agriNLS`, or `agriDRC` objects and returns them in a tidy data frame ranked by AIC.

Usage

```
compare_models(...)
```

Arguments

... Named model objects. Names are used as row identifiers. If unnamed, models are labelled `model1`, `model2`, ...

Value

A `data.frame` with columns `model`, `engine`, `n_par`, `AIC`, `BIC`, `RMSE`, `MAE`, `R2`, and `delta_AIC` (difference from best).

Examples

```

dat <- data.frame(
  nitrogen = rep(c(0, 40, 80, 120, 160), each = 8),
  yield    = c(2.1, 2.8, 3.6, 4.1, 4.3,
              2.0, 2.9, 3.5, 4.2, 4.4,
              2.2, 2.7, 3.7, 4.0, 4.5,
              2.1, 3.0, 3.4, 4.3, 4.2,
              2.3, 2.8, 3.6, 4.1, 4.3,
              2.0, 2.9, 3.5, 4.2, 4.4,
              2.2, 2.7, 3.7, 4.0, 4.5,
              2.1, 3.0, 3.4, 4.3, 4.2)
)
m1 <- fit_linear(dat, "yield ~ nitrogen")
m2 <- fit_nonlinear(dat, "nitrogen", "yield", "quadratic")
compare_models(linear = m1, quadratic = m2)

```

ed_estimates

Compute effective dose (ED) estimates from a dose-response model

Description

Returns the dose required to achieve a specified percentage of the maximum response, with confidence intervals via the delta method.

Usage

```

ed_estimates(
  drc_fit,
  respLev = c(10, 50, 90),
  interval = "delta",
  level = 0.95
)

```

Arguments

drc_fit	An agrIDRC object.
respLev	Numeric vector of response levels (default c(10, 50, 90)). E.g. 50 = ED50 (dose for 50% of maximum effect).
interval	Type of confidence interval: "delta" (default) or "none".
level	Confidence level (default 0.95).

Value

A matrix of ED estimates and confidence bounds (printed and returned invisibly).

fit_dose_response	<i>Fit a log-logistic or Weibull dose-response model</i>
-------------------	--

Description

A wrapper around `drc::drm()` providing the four model families most commonly used in herbicide/pesticide and nutrient-response studies. Returns an `agriDRC` object with `print`, `summary`, and `plot` methods.

Usage

```
fit_dose_response(
  data,
  dose_col,
  resp_col,
  fct = c("LL.4", "LL.5", "W1.4", "W2.4"),
  curveid = NULL,
  ...
)
```

Arguments

<code>data</code>	A data frame containing dose and response columns.
<code>dose_col</code>	Character. Name of the dose/concentration column.
<code>resp_col</code>	Character. Name of the response column (e.g. percentage inhibition, weed biomass reduction, germination rate).
<code>fct</code>	Character. Model function: "LL.4" 4-parameter log-logistic (default). Parameters: b, c, d, e. "LL.5" 5-parameter log-logistic (asymmetry parameter f added). "W1.4" 4-parameter Weibull type-1. "W2.4" 4-parameter Weibull type-2.
<code>curveid</code>	Optional column name for grouping curves (e.g. "species" or "treatment"). Passed directly to <code>drc::drm()</code> .
<code>...</code>	Additional arguments forwarded to <code>drc::drm()</code> .

Value

An object of class "agriDRC" containing:

- fit** The underlying `drc` object.
- fct** The model function name.
- dose_col, resp_col** Column names used.
- data** The data used.
- call** The matched call.

Examples

```
herbicide_trial <- load_example_data("herbicide_trial")
dr <- fit_dose_response(herbicide_trial,
  dose_col = "dose_g_ha",
  resp_col = "weed_control_pct")

summary(dr)
ed_estimates(dr, respLev = c(10, 50, 90))
plot(dr)
```

fit_linear

*Fit a linear or mixed-effects model for agricultural trials***Description**

A wrapper around `stats::lm()` and `lme4::lmer()` that returns an `agriLM` object with consistent `print`, `summary`, `plot`, `coef`, `fitted`, `residuals`, and `predict` S3 methods.

Usage

```
fit_linear(data, formula, random = NULL, weights = NULL, ...)
```

Arguments

<code>data</code>	A data frame or <code>agriData</code> object.
<code>formula</code>	A model formula as a character string or formula object. Example: <code>"yield ~ treatment + block"</code> .
<code>random</code>	Optional character string specifying the random-effects term in <code>lme4</code> syntax, e.g. <code>"(1 block)"</code> or <code>"(1 block) + (1 location)"</code> . When supplied <code>lme4::lmer()</code> is used; otherwise <code>stats::lm()</code> .
<code>weights</code>	Optional numeric vector of observation weights passed to <code>lm()</code> or <code>lmer()</code> .
<code>...</code>	Additional arguments forwarded to <code>lm()</code> or <code>lmer()</code> .

Value

An object of class `"agriLM"` (a named list) containing:

fit The underlying `lm` or `lmerMod` object.

engine Character: `"lm"` or `"lmer"`.

formula The fixed-effects formula.

random The random-effects term (or `NULL`).

data The data used for fitting.

call The matched call.

Examples

```
wheat_trial <- load_example_data("wheat_trial")
# Ordinary least squares
m1 <- fit_linear(wheat_trial, "yield ~ nitrogen + phosphorus")

# Mixed model with block as random effect
m2 <- fit_linear(wheat_trial,
                 "yield ~ nitrogen + phosphorus",
                 random = "(1|block)")
summary(m2)
plot(m2, type = "residuals")
```

fit_nonlinear

Fit a nonlinear growth or response curve to agricultural data

Description

Provides a unified interface for five model families commonly used in agronomic research. Automatic starting-value heuristics are applied when `start` is not supplied, making the function usable without prior knowledge of parameter ranges.

Usage

```
fit_nonlinear(
  data,
  x_col,
  y_col,
  model = c("logistic", "gompertz", "asymptotic", "linear_plateau", "quadratic"),
  start = NULL,
  control = nls.control(maxiter = 500, tol = 1e-06)
)
```

Arguments

<code>data</code>	A data frame (or <code>agriData</code>) with at least <code>x_col</code> and <code>y_col</code> .
<code>x_col</code>	Character. Name of the independent variable column (e.g. "days", "dose", "nitrogen_kg_ha").
<code>y_col</code>	Character. Name of the response column (e.g. "yield", "biomass", "plant_height").
<code>model</code>	One of: "logistic" 3-parameter logistic: $y = Asym / (1 + \exp((x_{mid} - x) / scal))$ "gompertz" 3-parameter Gompertz: $y = Asym \cdot \exp(-\exp(b2(b3 - x)))$ "asymptotic" Asymptotic / Mitscherlich: $y = Asym(1 - \exp(-rate \cdot x))$ "linear_plateau" Linear-plateau (broken-stick): $y = a + b \cdot \min(x, cp)$ "quadratic" Quadratic polynomial: $y = a + b \cdot x + c \cdot x^2$

start	Optional named list of starting parameter values. When NULL (default), heuristic starting values are derived from the data.
control	A list passed to <code>stats::nls.control()</code> . Increase <code>maxiter</code> if convergence fails.

Value

An object of class "agriNLS", a named list containing:

- fit** The nls object.
- model** Character: the model name.
- x_col, y_col** Column names used.
- data** The data used for fitting.
- call** The matched call.

Examples

```
maize_growth <- load_example_data("maize_growth")
nl <- fit_nonlinear(maize_growth, x_col = "days", y_col = "biomass_g",
                   model = "logistic")
summary(nl)
plot(nl)
```

<code>fit_polynomial</code>	<i>Fit a sequence of polynomial linear models and pick the best</i>
-----------------------------	---

Description

Convenience function for testing linear, quadratic, and cubic fits of a single continuous predictor and selecting the best by AIC.

Usage

```
fit_polynomial(data, x_col, y_col, max_degree = 3)
```

Arguments

- `data` A data frame.
- `x_col` Predictor column name.
- `y_col` Response column name.
- `max_degree` Maximum polynomial degree to test (default 3).

Value

An agriLM object for the best-fitting model. A comparison table is printed as a side-effect.

Examples

```
wheat_trial <- load_example_data("wheat_trial")
best <- fit_polynomial(wheat_trial, x_col = "nitrogen", y_col = "yield")
plot(best)
```

gof_stats

Compute goodness-of-fit statistics for a model

Description

Extracts R^2 , adjusted- R^2 , RMSE, MAE, AIC, and BIC from an `agriLM`, `agriNLS`, or `agriDRC` object (or any object with `fitted()`, `residuals()`, and `AIC()` methods).

Usage

```
gof_stats(model)
```

Arguments

`model` An `agriLM`, `agriNLS`, `agriDRC`, or compatible model object.

Value

A named list with elements `R2`, `adj_R2`, `RMSE`, `MAE`, `AIC`, and `BIC`.

herbicide_trial

Simulated herbicide dose-response dataset

Description

Weed control percentage measured across seven herbicide doses for two weed species.

Format

A data frame with 84 rows and 4 variables:

species Weed species (Amaranth, Ryegrass).

dose_g_ha Herbicide dose (g active ingredient per hectare).

weed_control_pct Weed control percentage (0–100).

rep Replicate number (1–6).

Source

Simulated for package demonstration.

load_example_data	<i>Load a bundled agriReg example dataset</i>
-------------------	---

Description

Reads one of the three example datasets shipped with the package from `inst/extdata`. Under normal installation the datasets are available directly via `data(wheat_trial)` etc; this function is a fallback that works even when `.rda` files have not been compiled.

Usage

```
load_example_data(name = c("wheat_trial", "maize_growth", "herbicide_trial"))
```

Arguments

`name` One of "wheat_trial", "maize_growth", or "herbicide_trial".

Value

A `data.frame`.

Examples

```
wheat <- load_example_data("wheat_trial")
head(wheat)
```

maize_growth	<i>Simulated maize growth time-series</i>
--------------	---

Description

Daily above-ground biomass measurements from 10 maize plants tracked from emergence to physiological maturity under well-watered conditions.

Format

A data frame with 200 rows and 4 variables:

plant_id Plant identifier (1–10).

days Days after emergence.

biomass_g Dry biomass (g/plant).

treatment Water treatment (WW = well-watered, DS = drought-stressed).

Source

Simulated for package demonstration.

model_summary	<i>Comprehensive model summary with fit statistics</i>
---------------	--

Description

Prints a formatted block with coefficient table, goodness-of-fit statistics, and (for `agriLM`) an ANOVA table.

Usage

```
model_summary(model, anova = TRUE)
```

Arguments

model	An <code>agriLM</code> or <code>agriNLS</code> object.
anova	Logical. Include ANOVA table for <code>agriLM</code> models (default TRUE).

Value

Invisibly returns the model object (called for its side effect of printing a formatted summary block containing coefficients, goodness-of-fit statistics, and, for `agriLM` models fitted with `engine = "lm"`, an ANOVA table).

optimum_dose	<i>Find the optimal x value (e.g. economic optimum dose)</i>
--------------	--

Description

For quadratic and linear-plateau models, computes the x value that maximises the predicted response.

Usage

```
optimum_dose(nls_fit)
```

Arguments

nls_fit	An <code>agriNLS</code> object fitted with <code>model = "quadratic"</code> or <code>"linear_plateau"</code> .
---------	--

Value

A named numeric vector with `x_opt` (optimum x) and `y_max` (predicted maximum y).

outlier_flag	<i>Flag outliers using multiple methods</i>
--------------	---

Description

A standalone outlier-detection function supporting IQR, Z-score, and modified Z-score (Iglewicz-Hoaglin) methods.

Usage

```
outlier_flag(df, col, method = c("iqr", "zscore", "modz"), threshold = NULL)
```

Arguments

df	A data frame.
col	Column name to test.
method	One of "iqr" (default), "zscore", "modz".
threshold	Numeric threshold: for "iqr" the IQR multiplier (default 1.5); for "zscore" the SD multiplier (default 3); for "modz" the modified Z-score cutoff (default 3.5).

Value

df with a logical column <col>_outlier.

plot.agriDRC	<i>Plot a fitted dose-response curve</i>
--------------	--

Description

Plot a fitted dose-response curve

Usage

```
## S3 method for class 'agriDRC'
plot(x, log_dose = TRUE, n_points = 200, ...)
```

Arguments

x	An agriDRC object.
log_dose	Logical. Plot dose on a log10 scale (default TRUE).
n_points	Integer. Points on the smooth curve (default 200).
...	Ignored.

Value

A ggplot object (printed invisibly).

plot.agriLM *Plot diagnostics for an agriLM model*

Description

Plot diagnostics for an agriLM model

Usage

```
## S3 method for class 'agriLM'
plot(x, type = c("fit", "residuals", "qq", "scale"), ...)
```

Arguments

x	An agriLM object.
type	One of "fit" (observed vs fitted), "residuals" (residuals vs fitted), "qq" (normal Q-Q), or "scale" (sqrt(residuals) vs fitted). Default "fit".
...	Ignored.

Value

A ggplot object (printed invisibly).

plot.agriNLS *Plot a fitted nonlinear curve over observed data*

Description

Plot a fitted nonlinear curve over observed data

Usage

```
## S3 method for class 'agriNLS'
plot(x, n_points = 300, show_residuals = FALSE, ...)
```

Arguments

x	An agriNLS object.
n_points	Integer. Number of points on the fitted curve (default 300).
show_residuals	Logical. When TRUE, adds vertical line segments from observed points to the curve. Default FALSE.
...	Ignored.

Value

A ggplot object (printed invisibly).

plot_fit	<i>A convenience wrapper for ggplot2 visualisation of model fit</i>
----------	---

Description

Dispatches to `plot.agriLM`, `plot.agriNLS`, or `plot.agriDRC` depending on model class. Useful in pipeline contexts.

Usage

```
plot_fit(model, ...)
```

Arguments

model	An <code>agriLM</code> , <code>agriNLS</code> , or <code>agriDRC</code> object.
...	Arguments passed to the underlying plot method.

Value

A `ggplot` object, returned invisibly. Called primarily for the side effect of printing the plot. The exact structure of the returned object depends on the class of `model`: `plot.agriLM`, `plot.agriNLS`, or `plot.agriDRC` is dispatched accordingly.

residual_check	<i>Residual diagnostic plot panel</i>
----------------	---------------------------------------

Description

Generates a 2x2 panel of residual diagnostics: residuals vs fitted, normal Q-Q, scale-location, and a histogram of residuals.

Usage

```
residual_check(model, ncol = 2)
```

Arguments

model	An <code>agriLM</code> or <code>agriNLS</code> object.
ncol	Integer. Number of plot columns (default 2).

Value

Invisibly returns the list of four `ggplot` objects.

wheat_trial	<i>Simulated wheat nitrogen-response trial</i>
-------------	--

Description

A simulated dataset from a randomised complete block design (RCBD) testing four nitrogen rates across three blocks and two phosphorus levels.

Format

A data frame with 72 rows and 6 variables:

block Block identifier (A, B, C).

nitrogen Nitrogen application rate (kg/ha).

phosphorus Phosphorus level (low, high).

variety Crop variety (V1, V2).

yield Grain yield (t/ha).

biomass Above-ground dry biomass (t/ha).

Source

Simulated for package demonstration.

yield_normalize	<i>Normalise yield values within groups</i>
-----------------	---

Description

Z-score or min-max normalises a numeric column, optionally within groups (e.g. per trial site or year).

Usage

```
yield_normalize(
  df,
  yield_col = "yield",
  method = c("zscore", "minmax"),
  group_by = NULL
)
```

Arguments

df	A data frame.
yield_col	Character. Column to normalise.
method	"zscore" (default) or "minmax".
group_by	Character vector of grouping column names, or NULL for global normalisation.

Value

df with a new column <yield_col>_norm.

Examples

```
df <- data.frame(yield = c(3, 4, 5, 6), site = c("A", "A", "B", "B"))
yield_normalize(df, group_by = "site")
```

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