Package: LactCurveModels (via r-universe)

May 29, 2026

Title Lactation Curve Model Fitting for Dairy Animals

Version 0.1.5

Suggests knitr, rmarkdown, spelling

VignetteBuilder knitr

Config/Needs/check spelling

Description Fits up to 20 nonlinear lactation curve models to dairy animal milk yield data. Models fitted include exponential, polynomial, mixed logarithmic, inverse polynomial, and sigmoid families published between 1923 and 2000. Supports batch processing of multiple animals from a single CSV file, with flexible selection of animals and models. Produces per-animal parameter tables, goodness-of-fit metrics including R-squared (R2), Root Mean Square Error (RMSE), Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), and a serial autocorrelation statistic, 15 diagnostic figures, and combined cross-animal comparison outputs. References: <doi:10.1085/jgp.5.4.441>, <doi:10.1038/216164a0>, <doi:10.1016/0301-6226(87)90003-0>, <doi:10.4141/cjas87-067>, <doi:10.3168/jds.S0022-0302(00)75136-8>.

License GPL-3

Encoding UTF-8

Language en-GB

RoxygenNote 7.3.3

Imports stats, utils, grDevices, graphics

URL `https://github.com/venkatesanraja/LactCurveModels`

BugReports `https://github.com/venkatesanraja/LactCurveModels/issues`

NeedsCompilation no

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Repository https://venkatesanraja.r-universe.dev

Date/Publication 2026-03-29 19:05:37 UTC

RemoteUrl https://github.com/cran/LactCurveModels

RemoteRef HEAD

RemoteSha 26c548e324d96c55beb89e8545c4bb044b7bd980

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LactCurveModels: Lactation Curve Model Fitting for Dairy Animals

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Description

Fits up to 20 nonlinear lactation curve models to daily milk yield data from one or more dairy animals. For each animal the package produces:

- Four CSV tables (parameter estimates, actual vs predicted values, residuals, and a goodness-of-fit summary).
- Fifteen diagnostic figures (model overlays, ranked panels, residual diagnostics, bubble charts, bar charts for R-squared (R2), Root Mean Square Error (RMSE), Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), Durbin-Watson (DW) statistic, correlation heatmap, and peak-yield charts).

When multiple animals are analysed, three additional combined cross-animal outputs are produced: an R2 comparison figure, an RMSE comparison figure, and a best-model overlay figure, plus combined CSV tables.

Quick start

Note: `out_dir` must always be supplied — choose any folder on your system where you want results saved.

```
library(LactCurveModels)

# All animals, all 20 models
results <- run_lactation_analysis(
  input_csv_path = "path/to/mydata.csv",
  out_dir        = "path/to/results"
)
```

```
# Selected animals and models
results <- run_lactation_analysis(
  input_csv_path   = "path/to/mydata.csv",
  selected_models  = c("Wood_1967", "Wilmink_k005", "Ali_Schaeffer"),
  selected_animals = c("Animal_A", "Animal_B"),
  out_dir          = "path/to/results"
)
```

Input CSV format

The CSV file must contain exactly three columns:

`animal_id` Character identifier for each animal.

`dim` Integer fortnightly time index (1 to 20).

`dmy` Numeric daily milk yield (kg/day).

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See Also

Useful links:

- `https://github.com/venkatesanraja/LactCurveModels`
- Report bugs at `https://github.com/venkatesanraja/LactCurveModels/issues`

`fit_lactation_models` *Fit lactation curve models to a single animal's data*

Description

Attempts to fit up to 20 nonlinear lactation curve models using `nls()` with the `"port"` algorithm. Models that fail to converge are silently skipped.

Usage

```
fit_lactation_models(data, selected_models = "all")
```

Arguments

`data`	A data frame with columns `x` (time index), `y` (milk yield kg/day), and `z` (x/365, for Morant-Gnanasakthy). Create it with `make_animal_df()`.
`selected_models`	Either `"all"` (default) to fit all 20 models, or a character vector of model names to fit a subset. Valid names: `"Brody_1923"`, `"Brody_1924"`, `"Parabolic_Exp_Sikka"`, `"Wood_1967"`, `"Wood_Dhanoa"`, `"Cobby_LeDu"`, `"Quadratic_Dave"`, `"Mixed_Log_GS"`, `"Khandekar"`, `"Wilmink_k005"`, `"Wilmink_k_estimated"`, `"Ali_Schaeffer"`, `"Cappio_Borlino"`, `"Papajcsik_Bodero1"`, `"Papajcsik_Bodero2"`, `"Papajcsik_Bodero3"`, `"Inverse_Poly_Nelder"`, `"Log_Quadratic_Adediran"`, `"Morant_Gnanasakthy"`, `"Pollott_Multiplicative"`.

Value

A named list. Each element corresponds to one successfully fitted model and contains: `model` (nls object), `metrics` (list of fit statistics), `predictions` (fitted values), `std_errors` (parameter SEs).

Examples

```
# Minimal toy example (auto-tested)
toy <- data.frame(
  x = 1:10,
  y = c(8, 11, 13, 12, 11, 10, 9, 8, 7, 6),
  z = (1:10) / 365
)
fits <- fit_lactation_models(toy, selected_models = "Wood_1967")


# Full run with all 20 models (takes longer)
fits_all <- fit_lactation_models(toy)

# Selected models only
fits_sub <- fit_lactation_models(toy,
              selected_models = c("Wood_1967", "Wilmink_k005"))
```

`run_lactation_analysis` *Run lactation curve analysis for one or more dairy animals*

Description

Reads a CSV file containing milk yield records, fits up to 20 nonlinear lactation curve models for each animal (or a selected subset of animals and/or models), saves per-animal diagnostic figures and CSV tables, and produces combined cross-animal summary outputs.

Usage

```
run_lactation_analysis(
  input_csv_path,
  selected_models = "all",
  selected_animals = "all",
  out_dir
)
```

Arguments

`input_csv_path` Character. Full path to the input CSV file. The file must contain exactly these three columns (any column order):

- **animal_id** Character or factor identifying each animal.
- **dim** Integer or numeric time index (days-in-milk fortnightly index, i.e. 1, 2, ..., 20).
- **dmy** Numeric daily milk yield (kg/day).

`selected_models` Either `"all"` (default) to fit all 20 lactation curve models, or a character vector of model names. Valid names: `"Brody_1923"`, `"Brody_1924"`, `"Parabolic_Exp_Sikka"`, `"Wood_1967"`, `"Wood_Dhanoa"`, `"Cobby_LeDu"`, `"Quadratic_Dave"`, `"Mixed_Log_GS"`, `"Khandekar"`, `"Wilmink_k005"`, `"Wilmink_k_estimated"`, `"Ali_Schaeffer"`, `"Cappio_Borlino"`, `"Papajcsik_Bodero1"`, `"Papajcsik_Bodero2"`, `"Papajcsik_Bodero3"`, `"Inverse_Poly_Nelder"`, `"Log_Quadratic_Adediran"`, `"Morant_Gnanasakthy"`, `"Pollott_Multiplicative"`.

`selected_animals` Either `"all"` (default) to analyse every animal present in the CSV, or a character vector of animal IDs that match entries in the `animal_id` column exactly.

`out_dir` Character. Base output directory. A sub-folder is created for each animal. Must be supplied explicitly — there is no default. The directory is created automatically if it does not already exist. Example: `out_dir = "D:/lactation_results"`.

Value

A named list (one element per animal) each containing:

- **id** Animal ID string.
- **model_fits** Named list of fitted model objects and metrics.
- **param_table** Parameter estimates data frame.
- **pred_table** Actual vs predicted data frame.
- **resid_table** Residuals data frame.
- **metrics_df** Per-model goodness-of-fit metrics, sorted by R2.
- **summary_metrics** Wide summary metrics data frame.

Returned invisibly so large objects are not auto-printed.

Examples

```
# Build a small example CSV in a temporary directory
tmp_csv <- file.path(tempdir(), "example_animals.csv")
example_data <- data.frame(
  animal_id = rep(c("Animal_A", "Animal_B"), each = 20),
  dim       = rep(1:20, times = 2),
  dmy       = c(
    8.1, 11.2, 13.0, 12.5, 11.8, 11.0, 10.4, 9.8, 9.3, 8.8,
    8.3, 7.9, 7.5, 7.1, 6.8, 6.5, 6.2, 5.9, 5.7, 5.4,
    7.5, 10.1, 11.8, 11.3, 10.7, 10.0, 9.4, 8.9, 8.4, 7.9,
    7.5, 7.1, 6.8, 6.4, 6.1, 5.8, 5.6, 5.3, 5.1, 4.9
  )
)
write.csv(example_data, tmp_csv, row.names = FALSE)

# Analyse all animals with two selected models
results <- run_lactation_analysis(
  input_csv_path  = tmp_csv,
  selected_models = c("Wood_1967", "Wilmink_k005"),
  out_dir         = tempdir()
)

# Analyse one animal only
results2 <- run_lactation_analysis(
  input_csv_path   = tmp_csv,
  selected_models  = c("Wood_1967", "Ali_Schaeffer"),
  selected_animals = "Animal_A",
  out_dir          = tempdir()
)
```

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