

# Package: phenolocrop (via r-universe)

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**Type** Package

**Title** Time-Series Models to the Crop Phenology

**Version** 0.0.2

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**Description** Fit a time-series model to a crop phenology data, such as time-series rice canopy height. This package returns the model parameters as the summary statistics of crop phenology, and these parameters will be useful to characterize the growth pattern of each cultivar and predict manually-measured traits, such as days to heading and biomass. Please see Taniguchi et al. (2022) <[doi:10.3389/fpls.2022.998803](https://doi.org/10.3389/fpls.2022.998803)> for detail. This package has been designed for scientific use. Use for commercial purposes shall not be allowed.

**Imports** purrr

**Suggests** dplyr, knitr, testthat (>= 3.0.0)

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**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.1

**Depends** R (>= 4.2.0)

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** <https://taniguchinaro.r-universe.dev>

**RemoteUrl** <https://github.com/cran/phenolocrop>

**RemoteRef** HEAD

**RemoteSha** d8a68ed3f41fc578692b08e5c261193d13b72c9a

## Contents

logisLateDicr . . . . .	2
phenololine . . . . .	3
riceCH_eg . . . . .	4
<b>Index</b>	<b>5</b>

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logisLateDicr	<i>Three-parameter logistic with the decrease in the late growth phase</i>
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### Description

Apply a time-series model, three-parameter logistic with the decrease in the late growth phase, to the time-series trait data. This function was originally developed for the time-series data of rice canopy height. Fitting the time-series model is done by the "two-step procedure". For more information, see Taniguchi et al. (2022).

### Usage

```
logisLateDicr(
  dat,
  x,
  y,
  returnModels = FALSE,
  start = c(d0 = 50, r = 0.05, a = 1e-04),
  upper = c(d0 = 200, r = Inf, a = 1),
  lower = c(d0 = 0, r = 0, a = 0)
)
```

### Arguments

dat	data.frame including date and trait (e.g. canopy height).
x	Column name (character) for the date after sowing or plantingl.
y	Column name (character) for the trait.
returnModels	Logical value whether to return the time-series model object. Default is F.
start	Start values to estimate 'd0', 'r' and 'a'. Default is 'c(d0 = 50, r = 0.05, a = 0.0001)'.
upper	Upper bounds to estimate 'd0', 'r' and 'a'. Default is 'c(d0 = 200, r = Inf, a = 1)'.
lower	Lower bounds to estimate 'd0', 'r' and 'a'. Default is 'c(d0 = 0, r = 0, a = 0)'.

### Value

logisLateDicr function returns the vector of estimated parameter values. If returnModels = TRUE, this function also returns the cubic polynomial regression object and logistic with the decrease in the late growth phase regression object.

## References

S. Taniguchi et al., (2022) Prediction of heading date, culm length, and biomass from canopy-height-related parameters derived from time-series UAV observations of rice. *Frontiers in Plant Science*, 13:998803.

## Examples

```
library(phenolocrop)
riceCH_eg |>
  logisLateDicr("x", "height")
```

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phenololine	<i>Return time-series curve given the time-series model and parameter values</i>
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## Description

phenololine function returns the predicted values given the model name and model parameters.

## Usage

```
phenololine(param, x, method)
```

## Arguments

param	Vector of model parameter values.
x	Vector of time (e.g. vector of dates).
method	Character name of the time-series model. At present, only "logisLateDicr" is accepted.

## Details

If method = "logisLateDicr", param should be the vector of c(K, d0, r, a, d1).

## Value

phenololine function returns the trait values given x.

## Examples

```
library(phenolocrop)
y <- riceCH_eg |>
  logisLateDicr("x", "height") |>
  phenololine(x = 1:160, method = "logisLateDicr")
plot(1:160, y, type = "l")
```

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`riceCH_eg`*Rice canopy height example data*

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**Description**

This data was a simulated rice CH data to show the usage of this package.

**Usage**`riceCH_eg`**Format**

**date** Date of observation

**height** CH

**id** Cultivar ID

**x** Dayes after sowing

# Index

## \* datasets

riceCH\_eg, 4

logisLateDicr, 2

phenololine, 3

riceCH\_eg, 4