

# Package ‘phenModel’

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**Type** Package

**Title** Insect Phenology Model Evaluation Based on Daily Temperatures

**Version** 1.0

**Date** 2019-08-01

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Rowan Fealy [aut]

**Maintainer** Rafael de Andrade Moral <rafael.deandrademoral@mu.ie>

**Depends** R (>= 3.0.0), ggplot2, dplyr, reshape, grid

**Description** Generates predicted stage change days for an insect, based on daily temperatures and development rate parameters, as developed by Pollard (2014) <[http://mural.maynoothuniversity.ie/view/ethesisauthor/Pollard=3ACiaran\\_P=2E=3A=3A.html](http://mural.maynoothuniversity.ie/view/ethesisauthor/Pollard=3ACiaran_P=2E=3A=3A.html)>. A few example datasets are included and implemented for *P. vulgatissima*, the blue willow beetle, but the approach can be readily applied to other species that display similar behaviour.

**License** GPL (>= 2)

**NeedsCompilation** no

**Repository** CRAN

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phenModel-package	<i>Insect Phenology Model Evaluation Based on Daily Temperatures</i>
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## Description

Generates predicted stage change days for an insect, based on daily temperatures and development rate parameters, as developed by Pollard (2014) <[http://mural.maynoothuniversity.ie/view/ethesisauthor/Pollard=3ACiaran\\_F](http://mural.maynoothuniversity.ie/view/ethesisauthor/Pollard=3ACiaran_F)>  
 A few example datasets are included and implemented for *P. vulgatissima*, the blue willow beetle, but the approach can be readily applied to other species that display similar behaviour.

## Details

The DESCRIPTION file:

```
Package:      phenModel
Type:        Package
Title:       Insect Phenology Model Evaluation Based on Daily Temperatures
Version:     1.0
Date:       2019-08-01
Authors@R:  c(person("Rafael", "de Andrade Moral", role = c("aut", "cre"), email = "rafael.deandrademoral@mu.ie"), person("Rowan Fealy", "Fealy", role = "aut", email = "rowan.fealy@mu.ie"))
Author:     Rafael de Andrade Moral [aut, cre], Rowan Fealy [aut]
Maintainer: Rafael de Andrade Moral <rafael.deandrademoral@mu.ie>
Depends:    R (>= 3.0.0), ggplot2, dplyr, reshape, grid
Description: Generates predicted stage change days for an insect, based on daily temperatures and development rate parameters
License:    GPL (>=2)
```

Index of help topics:

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	Daily Temperatures
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plot_phen_model	Plot Phenology Model Evaluations
pvulg_budburst_parameters	Estimated Parameters for the Exponential Decay Model for Budburst
pvulg_lactin_parameters	Estimated Parameters for the Lactin Model for P. Vulgatissima
pvulg_weibull_parameters	Estimated Parameters for the Weibull Model for P. Vulgatissima
sensitivity	Sensitivity Analysis for Evaluated Phenology Model
valentia	Valentia Data

**Author(s)**

Rafael de Andrade Moral [aut, cre], Rowan Fealy [aut]

Maintainer: Rafael de Andrade Moral <rafael.deandrademoral@mu.ie>

**References**

Pollard C.P., Griffin C.T., Moral R.A., Duffy C., Chuche J., Gaffney M.T., Fealy R. (submitted) phenModel: a temperature-dependent phenology model for the blue willow beetle, *Phratora vulgatissima*.

---

assign\_observed\_data *Observed Data Preparation*

---

**Description**

Prepares observed data for plotting with model evaluation.

**Usage**

```
assign_observed_data(obj, eggs = NA, larvae = NA, pupae = NA, adults)
```

**Arguments**

obj	an object generated from <a href="#">phen_model</a>
eggs	vector of days in which eggs were observed
larvae	vector of days in which larvae were observed
pupae	vector of days in which pupae were observed
adults	vector of days in which adults were observed

**Details**

Reads in the data and returns an object ready to be passed to [plot\\_phen\\_model](#) for plotting. Uses a simple probability checking to determine whether the observations for the adults category belong to the post-diapause, ovipositing or adult emergence stage, based on normal distributions.

**Value**

Returns a `data.frame` with five columns, one for each stage (post-diapause, eggs, larvae, pupae and adults).

**Author(s)**

Rafael de Andrade Moral ([rafael.deandrademoral@mu.ie](mailto:rafael.deandrademoral@mu.ie)) and Rowan Fealy

**See Also**

[phen\\_model](#), [plot\\_phen\\_model](#)

**Examples**

```
data(casement9596)
casement1995 <- data.frame(casement9596,
                          with(casement9596,
                               get_total_info(Tmax, Tmin, Tbase = 7, Lat, day)))

## loading fitted parameters
data(pvulg_budburst_parameters)
data(pvulg_weibull_parameters)
data(pvulg_lactin_parameters)

## evaluating model
quantiles_seq <- seq(.001, .95, .001)

phen95 <- phen_model(Tmean = "Tmean",
                    thermal_units = "thermal_units",
                    chill_days = "chill_days",
                    day_length = "day_length",
                    bud_pars = pvulg_budburst_parameters,
                    weib_pars = pvulg_weibull_parameters,
                    lactin_pars = pvulg_lactin_parameters,
                    max_day_length = 14.92,
                    pop_quantiles = quantiles_seq,
```

```

data = casement1995)

phen95_gen2 <- phen_model_gen2(Tmean = "Tmean",
                             day_length = "day_length",
                             bud_pars = pvulg_budburst_parameters,
                             weib_pars = pvulg_weibull_parameters,
                             lactin_pars = pvulg_lactin_parameters,
                             sex_mat_day = phen95["0.05", "sexual_maturation_day"],
                             pop_quantiles = .05,
                             data = casement1995)

## adding observed points
made_up_data <- assign_observed_data(obj = phen95,
                                    eggs = c(182,184,204,227,233,242),
                                    larvae = c(204,227,233,242,249),
                                    adults = c(204,212,220,221,222,224,227,233,242,269,283,298,
                                               305,310,311,312,313,314,315,316,317,318,
                                               319,320,321,322,323,334,325,326,327,328,
                                               329,330,331,332))

plot_phen_model(obj = phen95, obj_gen2 = phen95_gen2,
                observed_data = made_up_data)

```

---

bivrp-internal

*Internal functions to used to evaluate a phenology model and plot the results*


---

### Description

Internal functions used to evaluate a phenology model and plot the results

### Author(s)

Rafael A. Moral <rafael.deandrademoral@mu.ie> and Rowan Fealy

---

casement9596

*Casement 1995-1996 Data*


---

### Description

Daily minimum and maximum temperature data obtained at the Casement Aerodrome weather station for the period of 1st November 1995 to 31st October 1996.

### Usage

```
data("casement9596")
```



```

      lactin_pars = pvulg_lactin_parameters,
      sex_mat_day = phen95["0.05", "sexual_maturatation_day"],
      pop_quantiles = .05,
      data = casement1995)

plot_phen_model(obj = phen95, obj_gen2 = phen95_gen2)

```

cdl\_check

*Plots for Checking Sensitivity to CDL***Description**

Produces plots based on sensitivity analysis for the critical day length threshold.

**Usage**

```
cdl_check(cdl, quantiles, max_day_length)
```

**Arguments**

`cdl` a vector with the CDL thersholds calculated by [sensitivity](#)  
`quantiles` the quantiles corresponding to each value from `cdl`  
`max_day_length` the maximum day length set when running [sensitivity](#)

**Value**

A ggplot object.

**Author(s)**

Rafael de Andrade Moral (rafael.deandrademoral@mu.ie) and Rowan Fealy

**See Also**

[sensitivity](#)

**Examples**

```

data(casement9596)

casement1995 <- data.frame(casement9596,
                          with(casement9596,
                               get_total_info(Tmax, Tmin, Tbase = 7, Lat, day)))

data(pvulg_budburst_parameters)
data(pvulg_weibull_parameters)
data(pvulg_lactin_parameters)

test_quantiles <- c(.01, .05, .1, .25, .5, .75, .9, .95, .99)

```

```

cdl_thresholds <- NULL
for(q in test_quantiles) {
  sens_casement_cdl <- sensitivity(Tmax = casement9596$Tmax,
                                  Tmin = casement9596$Tmin,
                                  Tbase = 7,
                                  lat = casement9596$Lat,
                                  day = casement9596$day,
                                  bud_pars = pvulg_budburst_parameters,
                                  weib_pars = pvulg_weibull_parameters,
                                  lactin_pars = pvulg_lactin_parameters,
                                  max_day_length = 14.92,
                                  pop_quantile = q,
                                  data = casement9596,
                                  study_type = "cdl",
                                  percent_variation = 1,
                                  resolution = 20) # increase resolution for better visualisation
  cdl_thresholds <- c(cdl_thresholds, summary_sensitivity(sens_casement_cdl)[1])
}

names(cdl_thresholds) <- paste(test_quantiles)
cdl_thresholds

cdl_check(cdl = cdl_thresholds,
          quantiles = test_quantiles,
          max_day_length = 14.92) +
  ggtitle("CDL sensitivity")

```

---

cum\_dev\_rate

*Cumulative Development Rates*

---

### Description

Returns the cumulative development rates calculated when the phenology model is being evaluated.

### Usage

```

cum_dev_rate(Tmean, thermal_units, chill_days, day_length,
             bud_pars, weib_pars, lactin_pars, max_day_length,
             pop_quantiles = 0.5, data)

```

### Arguments

Tmean	name of the column in the data representing the mean temperature
thermal_units	name of the column in the data representing the thermal units
chill_days	name of the column in the data representing the number of chill days
day_length	name of the column in the data representing the day length
bud_pars	vector of parameters for the budburst model
weib_pars	matrix of parameters for the Weibull model for each developmental stage



lactin\_pars      matrix of parameters for the lactin model for each developmental stage  
max\_day\_length    critical day length threshold  
pop\_quantiles    quantile of the population to be evaluated by the phenology model  
data              a data.frame

**Value**

Returns the data with an appended column representing the cumulative development rates evaluated by the model.

**Author(s)**

Rafael de Andrade Moral (rafael.deandrademoral@mu.ie) and Rowan Fealy

**See Also**

[phen\\_model](#)

**Examples**

```
data(casement9596)

casement1995 <- data.frame(casement9596,
                          with(casement9596,
                               get_total_info(Tmax, Tmin, Tbase = 7, Lat, day)))

## loading fitted parameters
data(pvulg_budburst_parameters)
data(pvulg_weibull_parameters)
data(pvulg_lactin_parameters)

casement1995 <- cum_dev_rate(Tmean = "Tmean",
                             thermal_units = "thermal_units",
                             chill_days = "chill_days",
                             day_length = "day_length",
                             bud_pars = pvulg_budburst_parameters,
                             weib_pars = pvulg_weibull_parameters,
                             lactin_pars = pvulg_lactin_parameters,
                             max_day_length = 14.92,
                             data = casement1995)
```

---

get\_cycle

*Obtain Yearly Cycles*

---

**Description**

Given a data.frame with columns representing days and months, returns a vector of indices representing which cycle each row corresponds to.

**Usage**

```
get_cycle(data, day, month, day.end, month.end)
```

**Arguments**

data	a data.frame
day	name of the column representing the days
month	name of the column representing the months
day.end	which day determines the end of a cycle?
month.end	which month determines the end of a cycle?

**Value**

A vector of integers.

**Author(s)**

Rafael de Andrade Moral (rafael.deandrademoral@mu.ie) and Rowan Fealy

**Examples**

```
data(valentia)

# cycle ends on 31st of October
valentia$cycle <- get_cycle(data = valentia, day = "day", month = "month",
                           day.end = 31, month.end = 10)
```

---

get_total_info	<i>Compute Day Length, Mean Temperature, Thermal Units, and Cumulative Chill Days</i>
----------------	---

---

**Description**

Computes daily day length, mean temperature, thermal units and cumulative number of chill days for a dataset.

**Usage**

```
get_total_info(Tmax, Tmin, Tbase, lat, day)
```

**Arguments**

Tmax	a vector of daily maximum temperatures
Tmin	a vector of daily minimum temperatures
Tbase	the base temperature used to define a chill day
lat	the latitude
day	day of the year (vector)

**Details**

Implements the method by Forsythe et al. (1995) to calculate the day length, and the single-sine degree-day method to compute the thermal units.

**Value**

Returns a data.frame with the day lengths, mean temperatures, thermal units and cumulative number of chill days.

**Author(s)**

Rafael de Andrade Moral (rafael.denadrademoral@mu.ie) and Rowan Fealy

**References**

Cannell, M.G.R., Smith, R.I. (1983) Thermal time, chill days and prediction of budburst in *Picea sitchensis*. *Journal of Applied Ecology*, 20(3), 951–963.

Forsythe et al. (1995) A model comparison for daylength as a function of latitude and day of the year. *Ecological Modeling* 80:87-95.

**Examples**

```
data(casement9596)

with(casement9596, get_total_info(Tmax, Tmin, Tbase = 7, Lat, day))
```

---

 phen\_model

*Phenology Model Evaluation*


---

**Description**

Evaluates the phenology model for specified population quantiles, based on daily temperatures.

**Usage**

```
phen_model(Tmean, thermal_units, chill_days, day_length,
           bud_pars, weib_pars, lactin_pars, max_day_length,
           pop_quantiles = c(0.05, 0.5, 0.95),
           print.l = FALSE, save.l = FALSE, data)
```

**Arguments**

Tmean	name of the column in the data representing the mean temperature
thermal_units	name of the column in the data representing the thermal units
chill_days	name of the column in the data representing the number of chill days
day_length	name of the column in the data representing the day length

bud_pars	vector of parameters for the budburst model
weib_pars	matrix of parameters for the Weibull model for each developmental stage
lactin_pars	matrix of parameters for the lactin model for each developmental stage
max_day_length	critical day length threshold
pop_quantiles	vector of quantiles of the population to be evaluated by the phenology model
print.l	logical. If TRUE, prints the cumulative development rates as the model iterates.
save.l	logical. If TRUE, returns the cumulative development rates instead of model evaluations.
data	a data.frame

### Details

As inputs, the model requires site latitude and daily minimum and maximum temperatures from the 1st November of the preceding year. Development, quantified by a temperature dependent development rate model defined for each life cycle stage, is initialised in the model following the simulated date of budburst, a biofix dependent on the accumulation of required thermal and chilling days from the 1st November of the preceding year, described below. Once budburst is simulated to have occurred, post-diapause pre-oviposition development commences. Following completion of the post-diapause pre-oviposition stage, the first day of egg-lay is returned for adult females emerging from overwintering. Oviposition period stage advancement occurs when the required development for this life cycle stage has been completed. Egg, larval and pupal development stages are then initiated sequentially. Following completion of the pupal development stage, the emerging adults enter a sexual maturation or post-eclosion pre-oviposition period. This life-cycle stage is hypothesised to be sensitive to a diapause-inducing stimulus - photoperiod (Tauber et al., 1986; Danks, 1987; Dalin, 2011; Hodek 2012; Pollard, 2014) - defined in the model as a critical day length (CDL) threshold. New generation adults that finish sexual maturation after the critical day length (CDL) enter into a state of reproductive diapause. *P. vulgatissima* adults that complete development prior to the CDL threshold can begin ovipositing to initiate subsequent generations.

### Value

A data.frame containing model evaluations for each life cycle (columns) and population quantile (rows).

### Author(s)

Rafael de Andrade Moral (rafael.deandrademoral@mu.ie) and Rowan Fealy

### References

- Dalin P. (2011) Diapause induction and termination in a commonly univoltine leaf beetle (*Phratora vulgatissima*). *Insect Science*, 18, 443–450. doi:10.1111/j.1744-7917.2011.01417.x
- Danks, H.V. (1987) *Insect dormancy: an ecological perspective* 1st ed. H. V. Danks, ed., Biological Survey of Canada (Terrestrial Artropods) (Ottawa).
- Hodek, I. (2012) Adult diapause in Coleoptera. *Psyche*, 2012, 1–10.
- Tauber M.J., Tauber C.A. and Masaki S. (1986) *Seasonal adaptations of insects*. Oxford University Press, New York, USA

Pollard, C. (2014) A Temperature-Dependent Development Model for Willow Beetle Species (Coleoptera: Chrysomelidae) in Ireland: Simulation of Phenology/Voltinism in Response to Climate Change. Unpublished PhD thesis, submitted to the National University of Ireland Maynooth, Maynooth, 1-373.

Pollard C.P., Griffin C.T., Moral R.A., Duffy C., Chucho J., Gaffney M.T., Fealy R. (submitted) phenModel: a temperature-dependent phenology model for the blue willow beetle, *Phratora vulgatissima*.

### See Also

[plot\\_phen\\_model](#)

### Examples

```
data(casement9596)

casement1995 <- data.frame(casement9596,
                          with(casement9596,
                                get_total_info(Tmax, Tmin, Tbase = 7, Lat, day)))

data(pvulg_budburst_parameters)
data(pvulg_weibull_parameters)
data(pvulg_lactin_parameters)

phen_model(Tmean = "Tmean",
           thermal_units = "thermal_units",
           chill_days = "chill_days",
           day_length = "day_length",
           bud_pars = pvulg_budburst_parameters,
           weib_pars = pvulg_weibull_parameters,
           lactin_pars = pvulg_lactin_parameters,
           max_day_length = 14.92,
           data = casement1995)
```

---

phen\_model\_forecast     *Multi-Year Forecast Based on the Phenology Model*

---

### Description

A forecast based on the phenology model for multiple years, based on daily temperatures.

### Usage

```
phen_model_forecast(Tmean, thermal_units, chill_days, day_length,
                   bud_pars, weib_pars, lactin_pars,
                   max_day_length = 14.92, pop_quantile, year, data)
```

**Arguments**

Tmean	name of the column in the data representing the mean temperature
thermal_units	name of the column in the data representing the thermal units
chill_days	name of the column in the data representing the number of chill days
day_length	name of the column in the data representing the day length
bud_pars	vector of parameters for the budburst model
weib_pars	matrix of parameters for the Weibull model for each developmental stage
lactin_pars	matrix of parameters for the lactin model for each developmental stage
max_day_length	critical day length threshold
pop_quantile	quantile of the population to be evaluated by the phenology model
year	a vector of indices representing each yearly cycle (usually the output from <a href="#">get_cycle</a> )
data	a data.frame

**Details**

See [phen\\_model](#)

**Value**

A data.frame with the number of rows equal to the total number of yearly cycles, and each column representing the developmental stage of the insect.

**Author(s)**

Rafael de Andrade Moral (rafael.deandrademoral@mu.ie) and Rowan Fealy

**See Also**

[plot\\_phen\\_forecast](#)

**Examples**

```
data(valentia)

valentia$cycle <- get_cycle(data = valentia, day = "day", month = "month",
                           day.end = 31, month.end = 10)
valentia_split <- split(valentia, valentia$cycle)
valentia_split <- lapply(valentia_split,
                        function(x) data.frame(x,
                                                with(x, get_total_info(Tmax = x$max_temp,
                                                                        Tmin = x$min_temp,
                                                                        Tbase = 7,
                                                                        lat = x$Lat,
                                                                        x$day_of_year))))

valentia <- do.call("rbind", valentia_split)

data(pvulg_budburst_parameters)
```

```

data(pvulg_weibull_parameters)
data(pvulg_lactin_parameters)

phen_forecast <- phen_model_forecast(Tmean = "Tmean",
                                     thermal_units = "thermal_units",
                                     chill_days = "chill_days",
                                     day_length = "day_length",
                                     bud_pars = pvulg_budburst_parameters,
                                     weib_pars = pvulg_weibull_parameters,
                                     lactin_pars = pvulg_lactin_parameters,
                                     pop_quantile = .5,
                                     year = "cycle",
                                     data = valentia)

```

---

phen\_model\_gen2

*Phenology Model Evaluation for Further Generations*


---

### Description

Evaluates the phenology model for specified population quantiles, based on daily temperatures for further generations.

### Usage

```

phen_model_gen2(Tmean, day_length,
                bud_pars, weib_pars, lactin_pars,
                sex_mat_day, pop_quantiles = 0.5,
                max_day_length = 14.92, data)

```

### Arguments

Tmean	name of the column in the data representing the mean temperature
day_length	name of the column in the data representing the day length
bud_pars	vector of parameters for the budburst model
weib_pars	matrix of parameters for the Weibull model for each developmental stage
lactin_pars	matrix of parameters for the lactin model for each developmental stage
sex_mat_day	the day individuals from the first generation reached the sexual maturation stage
pop_quantiles	vector of quantiles of the population to be evaluated by the phenology model
max_day_length	critical day length threshold
data	a data.frame

### Details

See [phen\\_model](#)

**Value**

A data.frame containing model evaluations for each life cycle (columns) and population quantile (rows).

**Author(s)**

Rafael de Andrade Moral (rafael.deandrademoral@mu.ie) and Rowan Fealy

**See Also**

[plot\\_phen\\_model](#)

**Examples**

```
data(casement9596)

casement1995 <- data.frame(casement9596,
                          with(casement9596,
                              get_total_info(Tmax, Tmin, Tbase = 7, Lat, day)))

data(pvulg_budburst_parameters)
data(pvulg_weibull_parameters)
data(pvulg_lactin_parameters)

phen95 <- phen_model(Tmean = "Tmean",
                    thermal_units = "thermal_units",
                    chill_days = "chill_days",
                    day_length = "day_length",
                    bud_pars = pvulg_budburst_parameters,
                    weib_pars = pvulg_weibull_parameters,
                    lactin_pars = pvulg_lactin_parameters,
                    max_day_length = 14.92,
                    data = casement1995)

phen95_gen2 <- phen_model_gen2(Tmean = "Tmean",
                              day_length = "day_length",
                              bud_pars = pvulg_budburst_parameters,
                              weib_pars = pvulg_weibull_parameters,
                              lactin_pars = pvulg_lactin_parameters,
                              sex_mat_day = phen95["0.05", "sexual_maturation_day"],
                              pop_quantiles = .05,
                              data = casement1995)
```

---

plot\_phen\_forecast      *Plot Phenology Model Multi-Year Forecast*

---

**Description**

Produces a plot of the phenology model multi-year forecasting evaluations.



**Usage**

```
plot_phen_forecast(obj, year_from = 1, xlab = "Year",  
                  ylab = "Days from 1st November")
```

**Arguments**

obj	an output from the <a href="#">phen_model_forecast</a> function
year_from	the first year we are forecasting for (e.g. "2015")
xlab	the x-axis label
ylab	the y-axis label

**Value**

A ggplot object.

**Author(s)**

Rafael de Andrade Moral ([rafael.deandrademoral@mu.ie](mailto:rafael.deandrademoral@mu.ie)) and Rowan Fealy

**See Also**

[valentia](#)

---

plot\_phen\_model

*Plot Phenology Model Evaluations*

---

**Description**

Produces a plot of the phenology model evaluations.

**Usage**

```
plot_phen_model(obj, obj_gen2, binwidth = 8, forecast = FALSE,  
               observed_data = NULL, ylab = "Days from 1st November",  
               xlab = "Modelled Life-Cycle Stages",  
               labels = c("Budburst",  
                          "Post-Diapause",  
                          "Ovipositing Period (Eggs)",  
                          "Larvae Emergence",  
                          "Pupae Emergence",  
                          "Adult Emergence",  
                          "Sexual Maturation"))
```

**Arguments**

<code>obj</code>	an output of the <a href="#">phen_model</a> or <a href="#">phen_model_forecast</a> functions
<code>obj_gen2</code>	an output of the <a href="#">phen_model_gen2</a> or <a href="#">phen_model_forecast</a> functions
<code>binwidth</code>	binwidth of the density estimator
<code>forecast</code>	logical. Set to TRUE if you are plotting a multi-year forecast (i.e. if <code>obj</code> and <code>obj_gen2</code> are outputs of <a href="#">phen_model_forecast</a> )
<code>observed_data</code>	an output from the <a href="#">assign_observed_data</a> function
<code>ylab</code>	the y-axis label
<code>xlab</code>	the x-axis label
<code>labels</code>	a vector of strings representing the names of the life-cycle stages

**Details**

Visualisation of days until stage completion for different life cycle stages and generations. Plot can incorporate observed data, where available. All dates are counted from the 1st of November of the previous year. The estimated density is based on a Gaussian kernel whose binwidth can be easily modified using argument `binwidth`. To add observed data points, see [assign\\_observed\\_data](#).

Since this is a `ggplot` object, layers can be easily added by using standard `ggplot` functions.

**Value**

A `ggplot` object.

**Author(s)**

Rafael de Andrade Moral ([rafael.deandrademoral@mu.ie](mailto:rafael.deandrademoral@mu.ie)) and Rowan Fealy

**References**

Pollard C.P., Griffin C.T., Moral R.A., Duffy C., Chuche J., Gaffney M.T., Fealy R. (submitted) `phenModel`: a temperature-dependent phenology model for the blue willow beetle, *Phratora vulgatissima*.

**See Also**

[phen\\_model](#), [phen\\_model\\_gen2](#), [phen\\_model\\_forecast](#)

---

pvulg\_budburst\_parameters

*Estimated Parameters for the Exponential Decay Model for Budburst*

---

## Description

Vector of estimated parameters.

## Usage

```
data("pvulg_budburst_parameters")
```

## Format

The format is: Named num [1:2] 540.196 -0.016 - attr(\*, "names")= chr [1:2] "b" "m"

## Details

The method implied is based on the Alternating Model, which is a degree-day model that accumulates thermal/chilling units above/below a base threshold from a specified date (Cannell and Smith, 1983). The b and m values correspond to the estimates for budburst for *Salix viminalis* (Pollard et al., submitted).

## Source

Chmielewski, F.M., Heider, S., Moryson, S. and Bruns, E. (2013) International phenological observation networks: concept of IPG and GPM. In M. D. Schwartz, ed. Phenology: An integrative environmental science. New York London: Springer, p. 610.

## References

Cannell, M.G.R. and Smith, R.I. (1983) Thermal time, chill days and prediction of budburst in *Picea sitchensis*. *Journal of Applied Ecology*, 20(3), 951–963.

Pollard C.P., Griffin C.T., Moral R.A., Duffy C., Chucho J., Gaffney M.T., Fealy R. (submitted) phenModel: a temperature-dependent phenology model for the blue willow beetle, *Phratora vulgatissima*.

## Examples

```
data(pvulg_budburst_parameters)
```

---

pvulg\_lactin\_parameters

*Estimated Parameters for the Lactin Model for P. Vulgatissima*

---

### Description

Matrix of estimated parameters for each stage of the life-cycle of *P. vulgatissima*

### Usage

```
data("pvulg_lactin_parameters")
```

### Format

The format is: num [1:4, 1:6] 0.00864 28.94449 0.52103 -1.06402 0.002 ... - attr(\*, "dimnames")=List of 2 ..\$ : chr [1:4] "rho" "Tmax" "deltaT" "lambda" ..\$ : chr [1:6] "post\_diapause" "ovipositing" "larva\_emergence" "pupa\_emergence" ...

### Details

The parameters were derived based on constant temperature laboratory experiments (see Pollard, 2014) for different life-cycle stages of *P. vulgatissima*. Development times were converted to rates and subsequently used as input for the Lactin model (Lactin et al., 1995). The model was fitted to the entire temperature range, including where there was no development rate (at the upper temperature threshold).

### Source

Pollard, C. (2014) A Temperature-Dependent Development Model for Willow Beetle Species (Coleoptera: Chrysomelidae) in Ireland: Simulation of Phenology/Voltinism in Response to Climate Change. Unpublished PhD thesis, submitted to the National University of Ireland Maynooth, Maynooth, 1-373.

### References

Lactin D.J., Holliday N.J., Johnson D.L. and Craigen R. (1995) Improved rate model of temperature-dependent development by arthropods. *Environmental Entomology*, 24, 68–75. doi:10.1093/ee/24.1.68

Pollard C.P., Griffin C.T., Moral R.A., Duffy C., Chucho J., Gaffney M.T., Fealy R. (submitted) phenModel: a temperature-dependent phenology model for the blue willow beetle, *Phratora vulgatissima*.

### Examples

```
data(pvulg_lactin_parameters)
```

---

pvulg\_weibull\_parameters

*Estimated Parameters for the Weibull Model for P. Vulgatissima*

---

## Description

Matrix of estimated parameters for each stage of the life-cycle of *P. vulgatissima*

## Usage

```
data("pvulg_weibull_parameters")
```

## Format

The format is: num [1:3, 1:6] 0.7207 0.3517 1.7918 -0.0716 0.5117 ... - attr(\*, "dimnames")=List of 2 ..\$: chr [1:3] "gamma" "eta" "beta" ..\$: chr [1:6] "post\_diapause" "ovipositing" "larva\_emergence" "pupa\_emergence" ...

## Details

The parameters were derived based on constant temperature laboratory experiments (see Pollard, 2014) for different life-cycle stages of *P. vulgatissima*. Development times (or rates) were derived as cumulative frequency distributions at each temperature; development times for each percentile were then divided by the respective median value of the distribution to produce a normalised ("same shape") distribution of development times at each temperature (Wagner et al., 1984; 1991). Based on the "same shape" assumption, a single cumulative distribution representing the normalised distributions for all temperature treatments was produced by averaging all the distributions, weighted by the total frequency of each distribution (Wagner et al., 1984; 1991).

## Source

Pollard, C. (2014) A Temperature-Dependent Development Model for Willow Beetle Species (Coleoptera: Chrysomelidae) in Ireland: Simulation of Phenology/Voltinism in Response to Climate Change. Unpublished PhD thesis, submitted to the National University of Ireland Maynooth, Maynooth, 1-373.

## References

- Wagner T.L., Olson R.L. and Willers J.L. (1991) Modeling arthropod development time. *Journal of Agricultural Entomology*, 8, 251-270.
- Wagner T.L., Wu H.I., Sharpe P.J.H. and Coulson R.N. (1984) Modeling distributions of insect development time: a literature review and application of the Weibull function. *Annals of the Entomological Society of America*, 77, 475-487. doi:10.1093/aesa/77.2.208
- Pollard C.P., Griffin C.T., Moral R.A., Duffy C., Chucho J., Gaffney M.T., Fealy R. (submitted) phenModel: a temperature-dependent phenology model for the blue willow beetle, *Phratora vulgatissima*.

**Examples**

```
data(pvulg_weibull_parameters)
```

---

sensitivity

*Sensitivity Analysis for Evaluated Phenology Model*


---

**Description**

Runs a sensitivity analysis on the evaluated phenology model, by simulating random changes to fitted parameters and/or specifying a range of base temperatures to determine a chill day.

**Usage**

```
sensitivity(Tmax, Tmin, Tbase, lat, day,
            bud_pars, weib_pars, lactin_pars, max_day_length,
            pop_quantile = .5, data,
            study_type = c("Tbase", "lactin", "weibull", "bud_days", "bud_parms", "cd1"),
            percent_variation = .1, resolution = 1000)
```

```
summary_sensitivity(obj)
```

```
boxplot_sensitivity(obj)
```

**Arguments**

obj	an output from a call to the <code>sensitivity</code> function
Tmax	a vector of daily maximum temperatures
Tmin	a vector of daily minimum temperatures
Tbase	the base temperature
lat	the latitude
day	day of the year (vector)
bud_pars	vector of parameters for the budburst model
weib_pars	matrix of parameters for the Weibull model for each developmental stage
lactin_pars	matrix of parameters for the lactin model for each developmental stage
max_day_length	critical day length threshold
pop_quantile	quantile of the population to be evaluated by the phenology model
data	a <code>data.frame</code>
study_type	a character string indicating what type of sensitivity study to be performed. "Tbase" runs a sensitivity study for the temperature threshold that classifies a chill day; "lactin" runs a sensitivity study on variations of the values for the parameters estimated by the lactin model; "weibull" does the same as the latter, but for the Weibull model; "bud_days" changes the budburst day while "bud_parms" randomly changes the parameter estimates for the exponential decay function associated with budburst prediction; "cd1" changes the critical day length threshold

percent\_variation      percentage of variation of the values to be changed for the sensitivity analysis

resolution              number of model evaluations to be performed

**Value**

A list containing the sensitivity analysis results as the first component, and the original model evaluation results as the second component.

**Author(s)**

Rafael de Andrade Moral (rafael.deandrademoral@mu.ie) and Rowan Fealy

**See Also**

[phen\\_model](#)

**Examples**

```
data(casement9596)

casement1995 <- data.frame(casement9596,
                          with(casement9596,
                              get_total_info(Tmax, Tmin, Tbase = 7, Lat, day)))

data(pvulg_budburst_parameters)
data(pvulg_weibull_parameters)
data(pvulg_lactin_parameters)

sens_casement1995 <- sensitivity(Tmax = casement9596$Tmax,
                              Tmin = casement9596$Tmin,
                              Tbase = 7,
                              lat = casement9596$Lat,
                              day = casement9596$day,
                              bud_pars = pvulg_budburst_parameters,
                              weib_pars = pvulg_weibull_parameters,
                              lactin_pars = pvulg_lactin_parameters,
                              max_day_length = 14.92,
                              pop_quantile = .5,
                              data = casement9596,
                              study_type = "lactin",
                              percent_variation = .1,
                              resolution = 100)

summary_sensitivity(sens_casement1995)

boxplot_sensitivity(sens_casement1995)
```

---

 valentia

*Valentia Data*


---

### Description

Daily minimum and maximum temperature data obtained at the Valentia synoptic weather station for the period of 1st November 1939 to 31st October 2000.

### Usage

```
data("valentia")
```

### Format

A data frame with 22281 observations on the following 7 variables.

```
year  a numeric vector
month a numeric vector
day   a numeric vector
Lat   a numeric vector
max_temp a numeric vector
min_temp a numeric vector
day_of_year a numeric vector
```

### Details

The data was obtained from the Irish National Meteorological Agency (Met Éireann).

### Source

<https://www.met.ie/climate/available-data/historical-data>

### Examples

```
data(valentia)

valentia$cycle <- get_cycle(data = valentia, day = "day", month = "month",
                           day.end = 31, month.end = 10)
valentia_split <- split(valentia, valentia$cycle)
valentia_split <- lapply(valentia_split,
                        function(x) data.frame(x,
                                                with(x, get_total_info(Tmax = x$max_temp,
                                                                        Tmin = x$min_temp,
                                                                        Tbase = 7,
                                                                        lat = x$Lat,
                                                                        x$day_of_year))))

valentia <- do.call("rbind", valentia_split)
```



```
data(pvulg_budburst_parameters)
data(pvulg_weibull_parameters)
data(pvulg_lactin_parameters)

phen_forecast <- phen_model_forecast(Tmean = "Tmean",
                                     thermal_units = "thermal_units",
                                     chill_days = "chill_days",
                                     day_length = "day_length",
                                     bud_pars = pvulg_budburst_parameters,
                                     weib_pars = pvulg_weibull_parameters,
                                     lactin_pars = pvulg_lactin_parameters,
                                     pop_quantile = .5,
                                     year = "cycle",
                                     data = valentia)

plot_phen_model(obj = phen_forecast[,1:7], obj_gen2 = phen_forecast[,8:12],
               forecast = TRUE)

plot_phen_forecast(obj = phen_forecast, year_from = 1939)
```

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