

# Package: DyMEP (via r-universe)

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**Type** Package

**Title** Dynamic Multi Environment Phenology-Model

**Version** 0.1.2

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**Description** Mechanistically models/predicts the phenology (macro-phases) of 10 crop plants (trained on a big dataset over 80 years derived from the German weather service (DWD) <<https://opendata.dwd.de/>>). Can be applied for remote sensing purposes, dynamically check the best subset of available covariates for the given dataset and crop.

**License** LGPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.3

**Imports** stats, utils

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

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

**RemoteUrl** <https://github.com/ftschurr/dymep>

**RemoteRef** HEAD

**RemoteSha** ec753297a8334ecb9a74777f6ae0202434634d31

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asymptotic\_prediction *DRC function: asymptotic\_prediction*

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## Description

DRC function: asymptotic\_prediction

## Usage

```
asymptotic_prediction(x, params)
```

## Arguments

x	input variable
params	list of input parameter; Asym a numeric parameter representing the horizontal asymptote on the right side (very large values of input). ; lrc a numeric parameter representing the natural logarithm of the rate constant; c0 a numeric parameter representing the x for which the response is zero.

## Value

value with asymptotic response

## Examples

```
asymptotic_prediction(5, list("Asym_value"=0.5,
                             "lrc_value"=0.2,
                             "c0_value"=4))
# visualization
asymptote <- lapply(seq(0, 10, 0.1),
                    asymptotic_prediction,
                    list("Asym_value"=0.5, "lrc_value"=0.2, "c0_value"=4))
plot(seq(0, 10, 0.1), asymptote)
```

---

available\_crops\_and\_phases  
*available\_crops\_and\_phases*

---

**Description**

check what crops and corresponding phenology phases are available at the moment. Chose a crop (crop\_abbrev), phenological phase from the output of this function further usage

**Usage**

```
available_crops_and_phases()
```

**Value**

dataframe with available crops and phenology phases

**Examples**

```
available_crops_and_phases()
```

---

available\_environmental\_covariates  
*available\_environmental\_covariates check what environmental covariates are implemented, use or alter prediction these abbreviations and the corresponding unit*

---

**Description**

available\_environmental\_covariates check what environmental covariates are implemented, use or alter prediction these abbreviations and the corresponding unit

**Usage**

```
available_environmental_covariates()
```

**Value**

dataframe with available environmental covariates

**Examples**

```
available_environmental_covariates()
```

**Description**

Empirically models/predicts the phenology (macro-phases) of 10 crop plants (trained on a big dataset over 80 years derived from the German weather service (DWD)). Can be applied for remote sensing purposes, environmental inputs can be chosen from a range of pre-trained response curves and applied to the trained crops and phenological phases. No retraining is done within the use of this package.

**Examples**

```
available <- available_crops_and_phases()
#what is the best environmental covariates for one or multiple phases?
# check what covairates are implemented in the model
available_covariates <- available_environmental_covariates()

best_DyMEP_model(env_covariates = c("tas", "tasmin", "VPD", "SPI",
  "global_radiation", "tasmax", "RH"),
  pheno_phases = c("sowing-emergence", "jointing-heading"),
  crop_abbrev = "WW")

# create a list of wanted phases and corresponding environmental covariates
phase_covariate_list <- list("sowing-emergence" = c("tasmin", "VPD", "SPI"),
  "emergence-jointing" = c("tas", "tasmin", "VPD", "SPI"),
  "jointing-heading" = c("global_radiation", "tas", "SPI"))

# alternatively you can create this input list directly like this with the
# best available model:
phase_covariate_list <- best_DyMEP_model(env_covariates =
  c("tas", "tasmin", "VPD", "SPI", "global_radiation", "tasmax", "RH"),
  pheno_phases = c("sowing-emergence", "emergence-jointing", "jointing-heading"),
  crop_abbrev = "WW",
  output_list_for_prediction = TRUE)

# create dummy environmental data
environmental_data <- data.frame("DATE" = seq.Date(
  from = as.Date("2021-01-01"), to = as.Date("2023-12-31"), by=1),
  "tas"=runif(1095, min=-10, max=40),
  "RH"=runif(1095, min=0, max=100),
  "tasmin"=runif(1095, min=-10, max=40),
  "tasmax"=runif(1095, min=-5, max=40),
  "VPD" = runif(1095, min=0, max=40),
  "SPI"= runif(1095, min=-1, max=4),
  "global_radiation"= runif(1095, min=0, max=3500))

pheno_phase_prediction(phase_covariate_list = phase_covariate_list,
  environmental_data = environmental_data,
```

```

phase_starting_date =as.Date("2021-01-01"),
crop_abbrev = "WW")

# you can also get a more detailed output, containing detailed predictions
# and the parameters of the used DRC curves:
detailed_output <- pheno_phase_prediction(
  phase_covariate_list = phase_covariate_list,
  environmental_data = environmental_data,
  phase_starting_date =as.Date("2021-01-01"),
  crop_abbrev = "WW",
  output_type = "detailed_information")

# this output can be visualised like:
# get overview plot of the prediction
DyMEP_prediction_visualizer(detailed_output)
# check the DRC curves of the used model
DyMEP_DRC_visualizer(detailed_output)

```

---

DyMEP\_DRC\_visualizer    *DyMEP\_DRC\_visualizer*

---

## Description

Visualizes the Dose-Response Curves (DRC) for each phenological phase and environmental covariate.

## Usage

```
DyMEP_DRC_visualizer(detailed_output)
```

## Arguments

detailed\_output

Output of the `pheno_phase_prediction` function with `output_type = "detailed_information"`.

## Value

Returns plots showing the DRC curves for each phenological phase and environmental covariate. Each row represents a phenology phase.

## Examples

```

phase_covariate_list <- best_DyMEP_model(env_covariates =
c("tas", "tasmin", "VPD", "SPI", "global_radiation", "tasmax", "RH"),
pheno_phases = c("sowing-emergence", "emergence-jointing", "jointing-heading"),
crop_abbrev = "WW",
output_list_for_prediction = TRUE)
# create dummy environmental data
environmental_data<- data.frame("DATE"=seq.Date(from = as.Date("2021-01-01"),

```

```

to = as.Date("2023-12-31"),by=1),
  "tas"=runif(1095,min=-10,max=40),
  "RH"=runif(1095,min=0,max=100),
  "tasmin"=runif(1095,min=-10,max=40),
  "tasmax"=runif(1095,min=0,max=40),
  "VPD" = runif(1095,min=0,max=40),
  "SPI"= runif(1095,min=-1,max=4),
  "global_radiation"= runif(1095,min=0,max=3500))

DyMEP_DRC_visualizer(detailed_output = pheno_phase_prediction(
  phase_covariate_list = phase_covariate_list,
  environmental_data = environmental_data,
  phase_starting_date =as.Date("2021-01-01"),
  crop_abbrev = "WW",
  output_type = "detailed_information")
)

```

---

DyMEP\_prediction\_visualizer

*DyMEP\_prediction\_visualizer*


---

## Description

Visualizes the predictions of the DyMEP model.

## Usage

```
DyMEP_prediction_visualizer(detailed_output)
```

## Arguments

detailed\_output

Output of the pheno\_phase\_prediction function with output\_type = "detailed\_information".

## Value

A plot with one panel per phenology phase, showing the environmental covariate responses, the GLM prediction, and the phase prediction (points).

## Fields

timestamp Description of timestamp column.

## Examples

```

phase_covariate_list <- best_DyMEP_model(env_covariates =
  c("tas", "tasmin", "VPD", "SPI", "global_radiation", "tasmax", "RH"),
  pheno_phases = c("sowing-emergence", "emergence-jointing",
    "jointing-heading"),

```

```

crop_abbrev = "WW",
output_list_for_prediction = TRUE)

# Create dummy environmental data
environmental_data <- data.frame("DATE" =
  seq.Date(from = as.Date("2021-01-01"),
    to = as.Date("2023-12-31"), by = 1),
  "tas" = runif(1095, min = -10, max = 40),
  "RH" = runif(1095, min = 0, max = 100),
  "tasmin" = runif(1095, min = -10, max = 40),
  "tasmax" = runif(1095, min = 0, max = 40),
  "VPD" = runif(1095, min = 0, max = 40),
  "SPI" = runif(1095, min = -1, max = 4),
  "global_radiation" = runif(1095, min = 0, max = 3500))

DyMEP_prediction_visualizer(detailed_output = pheno_phase_prediction(
  phase_covariate_list = phase_covariate_list,
  environmental_data = environmental_data,
  phase_starting_date = as.Date("2021-01-01"),
  crop_abbrev = "WW",
  output_type = "detailed_information"))

```

---

```

envpredutils.pheno_phase_prediction_glm_model
  apply the prediction with glm model

```

---

## Description

apply the prediction with glm model

## Usage

```

envpredutils.pheno_phase_prediction_glm_model(
  env_data_pheno_phase,
  pheno_phase,
  crop_abbrev,
  model,
  output_type = "dates"
)

```

## Arguments

env_data_pheno_phase	environmental data required to predict the phase
pheno_phase	phenological phase
crop_abbrev	abbreviation of the crop
model	the selected model to predict the wanted phenological phase

`output_type` either "dates" or "detailed\_information"; defines what output of the model they user wants to have as return, default is set to "dates". If a user wants to get the response parameters, curves, predictions and model thresholds, it should be chosen "detailed\_information" output = "dates" will return a dataframe with the stages and according dates output = "detailed\_information" will return a list with the dates, but also the corresponding dose response parameters and predictions

### Value

final output, either detailed (if `output_type = "detailed_information"`) as list, or `data.frame` with dates if `output_type = "dates"`

---

`non_linear_prediction` *DRC function: non\_linear\_prediction*

---

### Description

broken stick model according to an env variable

### Usage

```
non_linear_prediction(env_variate, params)
```

### Arguments

`env_variate` value of a environmental covariate  
`params` list of input parameter; `base_value`: minimal value; `slope_value`: slope estimated value, slope of the linear phase

### Value

value with `non_linear` response

### Examples

```
non_linear_prediction(1,list("base_value"=5,"slope_value"=1))

# visualization
non_linear <- lapply(seq(0, 10, 0.1),
  non_linear_prediction,
  list("base_value"=5,"slope_value"=1))
plot(seq(0, 10, 0.1), non_linear)
```



---

 pheno\_phase\_prediction

*function to predict the a phenological phase in winter wheat*


---

## Description

predict one or all phenological phases

## Usage

```
pheno_phase_prediction(
  phase_covariate_list,
  environmental_data,
  phase_starting_date,
  crop_abbrev,
  output_type = "dates",
  external_params_path = NULL
)
```

## Arguments

**phase\_covariate\_list**  
list like: list("sowing-emergence" = c("tas", "VPD", "SPI"), "emergence-jointing" = c("tas")) indicating per phenological phase the covariates to use. List of phenological phases must be consecutive!

**environmental\_data**  
data.frame with the necessary environmental data, one column must be "DATE" (as.Date format), the others with the names of the environmental covariates (e.g. tas, tasmin etc.)

**phase\_starting\_date**  
starting date of the first phase which will be predicted (object of class "Date" (use as.Date()))

**crop\_abbrev**  
abbreviation of the crop to be modeled (valid crop\_abbrevs can be found with available\_crops\_and\_phases())

**output\_type**  
either "dates" or "detailed\_information"; defines what output of the model they user wants to have as return, default is set to "dates". If a user wants to get the response parameters, curves, predictions and model thresholds, it should be chosen "detailed\_information" output = "dates" will return a dataframe with the stages and according dates output = "detailed\_information" will return a list with the dates, but also the corresponding dose response parameters and predictions

**external\_params\_path**  
path where additional crop parameters should be stored if not possible to download in to the regular R repository. The default is NULL, which will use the regular R repository as path

**Value**

returns the end-date of each phase

either return an object of class 'DyMEP', if detailed\_information is selected as output\_type, from a dataframe containing phenology data, or

**Examples**

```
pheno_phase_prediction(phase_covariate_list = list(
  "sowing-emergence" = c("tasmin", "VPD", "SPI", "tasmax", "tas", "RH",
    "global_radiation"),
  "emergence-jointing" = c("tasmin", "VPD", "SPI", "tasmax", "tas", "RH",
    "global_radiation"),
  "jointing-heading" = c("tasmin", "VPD", "SPI", "tasmax", "tas", "RH",
    "global_radiation")),
environmental_data <- data.frame("DATE" = seq.Date(
  from = as.Date("2021-01-01"), to = as.Date("2023-12-31"), by=1),
  "tas"=runif(1095,min=-10,max=40),
  "RH"=runif(1095,min=0,max=100),
  "tasmin"=runif(1095,min=-10,max=40),
  "tasmax"=runif(1095,min=-5,max=40),
  "VPD" = runif(1095,min=0,max=40),
  "SPI"= runif(1095,min=-1,max=4),
  "global_radiation"= runif(1095,min=0,max=3500)),
phase_starting_date =as.Date("2021-01-01"),
crop_abbrev = "WW")
```

---

reg\_linear\_prediction *DRC function: reg\_linear\_prediction*

---

**Description**

linear model according to an env variable

**Usage**

```
reg_linear_prediction(env_variate, params)
```

**Arguments**

env\_variate      value of a environmental covariate  
 params            list of input parameter; intercept estimated value, slope of the linear phase

**Value**

value with reg\_linear response

**Examples**

```
reg_linear_prediction(1,list("intercept_value"=1, "slope_value"=5))
# visualization
reg_linear <- lapply(seq(0, 10, 0.1),
reg_linear_prediction,
list("intercept_value"=-1,"slope_value"=1))
plot(seq(0, 10, 0.1), reg_linear)
```

---

WangEngels\_prediction *DRC function: WangEngels\_prediction*

---

**Description**

DRC function: WangEngels\_prediction

**Usage**

```
WangEngels_prediction(x, params)
```

**Arguments**

x	effective env_variable value
params	list of input parameter; xmin_value represents the minimal env_variable value above which growth response will happen ; xopt_value: optimal growth point, env_variable values here have the highest response; xmax_value represents the maximal env_variable value above which no growth response will happen according to the wang engel model.

**Value**

value with WangEngels response

**Examples**

```
WangEngels_prediction(10, params = list("xmin_value"=1,
                                         "xopt_value"=25,
                                         "xmax_value"=35,
                                         "r_value"=0.5))
# visualization
WangEngels <- lapply(seq(0, 40, 0.1),
WangEngels_prediction,
list("xmin_value"=1,
     "xopt_value"=25,
     "xmax_value"=35,
     "r_value"=0.5))
plot(seq(0, 40, 0.1), WangEngels)
```

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