

Package ‘phenocamr’

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Title Facilitates 'PhenoCam' Data Access and Time Series
Post-Processing

Version 1.1.3

Description Programmatic interface to the 'PhenoCam' web services (<<http://phenocam.sr.unh.edu>>).
Allows for easy downloading of 'PhenoCam' data directly to your R workspace
or your computer and provides post-processing routines for consistent and easy
timeseries outlier detection, smoothing and estimation of phenological transition dates.
Methods for this package are described in detail in Hufkens et. al (2018) <[doi:10.1111/2041-210X.12970](https://doi.org/10.1111/2041-210X.12970)>.

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contract_phenocam	<i>Contracts the file from 1-day to a 3-day time step</i>
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Description

Reverts the ‘expand_phenocam()’ function in order to save space and generate files as outlined in the cited data paper. This routine is used as a post-production measure.

Usage

```
contract_phenocam(data, internal = TRUE, no_padding = FALSE,
  out_dir = tempdir())
```

Arguments

data	a phenocam data file with a 1 or 3 day time step
internal	return a data structure if given a file on disk (TRUE / FALSE = default)
no_padding	allow for padding to REMAIN or not (TRUE / FALSE = default)
out_dir	output directory where to store data (default = tempdir())

Value

A contracted PhenoCam 3-day time series to its original 3-day time step (if provided at a 1-day interval), also removes padding introduced by processing for 1-day data.

Examples

```
# download demo data
download_phenocam(site = "harvard$",
                 veg_type = "DB",
                 roi_id = "1000",
                 frequency = "3")

# Overwrites the original file, increasing
# it's file size.
expand_phenocam(file.path(tempdir(), "harvard_DB_1000_3day.csv"))

# Contracts the file to it's original size, skipping
# two days.
contract_phenocam(file.path(tempdir(), "harvard_DB_1000_3day.csv"))
```

daylength

Calculates day length (in hours) and the solar elevation

Description

This routine uses Forsythe et al. 1995.

Usage

```
daylength(doy, latitude)
```

Arguments

doy	a vector with doy values 1 - 365(6)
latitude	a given latitude

Value

nested list with daylength (daylength) and solar elevation (solar_elev) elements

Examples

```
# calculate the hours of sunlight and solar elevation on day of year 1
# and latitude 51
ephem <- daylength(1, 51)
print(ephem)
```

detect_outliers *Detect outliers in PhenoCam time series*

Description

The function fills in the existing column to hold outlier flags, and either overwrites the original file or outputs a data structure.

Usage

```
detect_outliers(data, iterations = 20, sigma = 2, grvi = FALSE,
  snowflag = FALSE, plot = FALSE, internal = TRUE,
  out_dir = tempdir())
```

Arguments

data	PhenoCam data structure or filename
iterations	number of iterations in order to detect outliers ()
sigma	number of deviations to exclude outliers at
grvi	reverse the direction of the screening intervals to accommodate for GRVI outliers
snowflag	integrate snow flags?
plot	visualize the process, mostly for debugging (TRUE / FALSE = default)
internal	return a data structure if given a file on disk (TRUE / FALSE = default) to accommodate for GRVI outliers
out_dir	output directory where to store data

Examples

```
# download demo data (do not detect outliers)
download_phenocam(site = "harvard$",
  veg_type = "DB",
  roi_id = "1000",
  frequency = "3",
  outlier_detection = FALSE)

# detect outliers in the downloaded file
detect_outliers(file.path(tempdir(), "harvard_DB_1000_3day.csv"))
```

download_phenocam *Function to download and post-process PhenoCam time series*

Description

This is a wrapper around most of all the other functions. It downloads a time series and extract relevant phenological transition dates or phenophases.

Usage

```
download_phenocam(site = "harvard$", veg_type = NULL,
  frequency = "3", roi_id = NULL, outlier_detection = TRUE,
  smooth = TRUE, contract = FALSE, daymet = FALSE,
  trim_daymet = TRUE, trim = NULL, phenophase = FALSE,
  out_dir = tempdir(), internal = FALSE)
```

Arguments

site	the site name, as mentioned on the PhenoCam web page expressed as a regular expression ("harvard\$" == exact match)
veg_type	vegetation type (DB, EN, ... default = ALL)
frequency	frequency of the time series product (1, 3, "roistats")
roi_id	the id of the ROI to download (default = ALL)
outlier_detection	TRUE or FALSE, detect outliers
smooth	smooth data (logical, default is TRUE)
contract	contract 3-day data (logical, default is TRUE)
daymet	TRUE or FALSE, merges the daymet data
trim_daymet	TRUE or FALSE, trims data to match PhenoCam data
trim	year (numeric) to which to constrain the output (default = NULL)
phenophase	logical, calculate transition dates (default = FALSE)
out_dir	output directory where to store downloaded data (default = tempdir())
internal	allow for the data element to be returned to the workspace

Value

Downloaded files in out_dir of requested time series products, as well as derived phenophase estimates based upon these time series.

Examples

```
# download the first ROI time series for the Harvard PhenoCam site
# at an aggregation frequency of 3-days.
download_phenocam(site = "harvard$",
                  veg_type = "DB",
                  roi_id = "1000",
                  frequency = "3")

# read phenocam data into phenocamr data structure
df <- read_phenocam(file.path(tempdir(), "harvard_DB_1000_3day.csv"))
```

 expand_phenocam

Expand a PhenoCam time series from 3-day to a 1-day time step

Description

Necessary step to guarantee consistent data processing between 1 and 3-day data products. Should rarely be used independent of ‘download_phenocam()’.

Usage

```
expand_phenocam(data, truncate = NULL, internal = TRUE,
                out_dir = tempdir())
```

Arguments

data	a PhenoCam file
truncate	year (numerical), limit the time series to a particular year (default = NULL)
internal	return a data structure if given a file on disk (TRUE / FALSE = default)
out_dir	output directory where to store data (default = tempdir())

Value

Expanded PhenoCam data structure or file, including 90 day padding if requested.

Examples

```
# download demo data
download_phenocam(site = "harvard$",
                  veg_type = "DB",
                  roi_id = "1000",
                  frequency = "3")
```

```
# Overwrites the original file, increasing
# it's file size.
expand_phenocam(file.path(tempdir(), "harvard_DB_1000_3day.csv"))

# Contracts the file to it's original size, skipping
# two days.
contract_phenocam(file.path(tempdir(), "harvard_DB_1000_3day.csv"))
```

grvi

Calculate green-red vegetation index (GRVI)

Description

The GRVI is defined as the normalized ratio between the red and green channel of a RGB image or digital number triplet. However, the blue channel can be used as well using a weighting factor. As such a paramter vector is provided so different channels / DN can be weighted separately.

Usage

```
grvi(data, par = c(1, 1, 1), internal = TRUE, out_dir = tempdir())
```

Arguments

data	a PhenoCam data file or data frame (when using a file provide a full path if not in the current working directory)
par	grvi parameters (digital number weights)
internal	return a data structure if given a file on disk (TRUE / FALSE = default)
out_dir	output directory where to store data

Value

Inserts a GRVI data column into the provided PhenoCam data structure or file.

Examples

```
# with defaults, outputting a data frame
# with smoothed values, overwriting the original

# download demo data
download_phenocam(site = "harvard$",
                  veg_type = "DB",
                  roi_id = "1000",
                  frequency = "3")
```

```
# calculate and append the GRVI for a file (overwrites the original)
grvi(file.path(tempdir(),"harvard_DB_1000_3day.csv"))

# as all functions this also works on a PhenoCam data structure
df <- read_phenocam(file.path(tempdir(),"harvard_DB_1000_3day.csv"))
df <- grvi(df, par = c(1, 1, 0))
```

list_rois	<i>Function to list all site regions-of-interest (ROIs)</i>
-----------	---

Description

The ROI list can be helpful in determining which time series to download using ‘download_phenocam()’.

Usage

```
list_rois(out_dir = tempdir(), internal = TRUE)
```

Arguments

out_dir	output directory (default = tempdir())
internal	TRUE or FALSE (default = TRUE)

Value

A data frame with ROIs for all available cameras

Examples

```
# download the site meta-data
df <- list_rois()
```

list_sites	<i>Function to list all site meta-data</i>
------------	--

Description

The site list can be helpful in determining which time series to download using ‘download_phenocam()’. The site list also includes meta-data concerning plant functional types, general climatological conditions such as mean annual temperature or geographic location.

Usage

```
list_sites(out_dir = tempdir(), internal = TRUE)
```

Arguments

```
out_dir      output directory (default = tempdir())
internal     TRUE or FALSE (default = TRUE)
```

Value

A data frame with meta-data for all available sites.

Examples

```
# download the site meta-data
df <- list_sites()
```

merge_daymet

Merge Daymet data with a PhenoCam time series

Description

Combine PhenoCam time series with matching climatological variables from Daymet.

Usage

```
merge_daymet(data, trim = FALSE, internal = TRUE,
             out_dir = tempdir())
```

Arguments

```
data          a PhenoCam data file or data structure
trim          logical, trim the daymet data to the length of the PhenoCam time series or include the whole Daymet time series (1980-current). (default = FALSE)
internal      return a data structure if given a file on disk (TRUE / FALSE = default)
out_dir       output directory where to store data (default = tempdir())
```

Value

A PhenoCam data structure or file which combines PhenoCam time series data with Daymet based climate values (columns will be added).

Examples

```
# download demo data
download_phenocam(site = "harvard$",
                 veg_type = "DB",
                 roi_id = "1000",
                 frequency = "3")

# merge data with daymet data
merge_daymet(file.path(tempdir(), "harvard_DB_1000_3day.csv"))
```

normalize_ts

Normalize PhenoCam time series

Description

Normalize PhenoCam data between 0-1 to to standardize further processing, independent of the relative amplitude of the time series (works on vectors not data frames). For internal use only.

Usage

```
normalize_ts(df, percentile = 90)
```

Arguments

df	a PhenoCam data frame
percentile	percentile value to interpret

Value

A normalized PhenoCam time series.

Examples

```
# Internal function only, should not be used stand-alone.
# As such no documentation is provided.
```

optimal_span	<i>Calculates the optimal span for a loess spline</i>
--------------	---

Description

The optimal span is calculated based upon the bayesian information criterion (BIC).

Usage

```
optimal_span(y, x = NULL, weights = NULL, step = 0.01,
            label = NULL, plot = FALSE)
```

Arguments

y	a vector with measurement values to smooth
x	a vector with dates / time steps
weights	optional values to weigh the loess fit with
step	span increment size
label	title to be used when plotting function output
plot	plot visual output of the optimization routine

Value

Returns an optimal span to smooth a provided vector using the 'loess()' smoother.

Examples

```
# Internal function only, should not be used stand-alone.
l <- sin(seq(1,10,0.01))
l <- l + runif(length(l))
optimal_span(l, plot = TRUE)
```

phenocam_explorer	<i>Starts the phenocamr shiny interface</i>
-------------------	---

Description

The GUI allows you to interactively download data and visualize time series.

Usage

```
phenocam_explorer()
```

Examples

```
## Not run:
# Starts the PhenoCam explorer GUI in a browser
phenocam_explorer()

## End(Not run)
```

phenophases

Calculates phenophases, for rising and falling parts of a time series

Description

This routine combines a forward and backward run of `transition_dates` function to calculate the phenophases in both rising and falling parts of a PhenoCam time series.

Usage

```
phenophases(data, mat = NULL, internal = TRUE, out_dir = tempdir(),
  ...)
```

Arguments

<code>data</code>	a PhenoCam data file (or data frame)
<code>mat</code>	mean annual temperature
<code>internal</code>	return PhenoCam data file or data frame
<code>out_dir</code>	output directory
<code>...</code>	pass parameters to the <code>transition_dates()</code> function

Value

Estimates of transition dates for both rising and falling parts of a PhenoCam time series. All time series are evaluated (`gcc_90`, `gcc_75`, etc). The function returns a nested list with UNIX time based values including uncertainties on these estimates and their associated thresholds. When written to disk UNIX dates are converted to YYYY-MM-DD. The nested list has named locations rising and falling, or location 1 and 2 in the list respectively.

Examples

```
# downloads a time series
download_phenocam(site = "harvard$",
  veg_type = "DB",
  roi_id = "1000",
  frequency = "3")
```

```
# read in data as data frame and calculate phenophases
df <- read_phenocam(file.path(tempdir(), "harvard_DB_1000_3day.csv"))
my_dates <- phenophases(df, internal = TRUE)

# print results
print(my_dates)
```

read_phenocam	<i>Read PhenoCam time series data</i>
---------------	---------------------------------------

Description

Reads PhenoCam data into a nested list, preserving header data and critical file name information.

Usage

```
read_phenocam(filename)
```

Arguments

filename a PhenoCam data file

Value

A nested data structure including site meta-data, the full header and the data as a 'data.frame()'.

Examples

```
# download demo data (do not smooth)
download_phenocam(site = "harvard$",
                  veg_type = "DB",
                  roi_id = "1000",
                  frequency = "3",
                  smooth = FALSE)

# read the phenocamo data file
df = read_phenocam(file.path(tempdir(), "harvard_DB_1000_3day.csv"))

# print data structure
print(summary(df))

# write the phenocamo data file
write_phenocam(df, out_dir = tempdir())
```

smooth_ts *Smooths a PhenoCam time series*

Description

Smooths time series iteratively using a bayesian information criterion (BIC) to find an optimal smoothing parameter and curve.

Usage

```
smooth_ts(data, metrics = c("gcc_mean", "gcc_50", "gcc_75", "gcc_90",
  "rcc_mean", "rcc_50", "rcc_75", "rcc_90"), force = TRUE,
  internal = TRUE, out_dir = tempdir())
```

Arguments

data	a PhenoCam data file or data structure
metrics	which metrics to process, normally all default ones
force	TRUE / FALSE, force reprocessing?
internal	return a data structure if given a file on disk (TRUE / FALSE = default)
out_dir	output directory where to store data

Value

An PhenoCam data structure or file with optimally smoothed time series objects added to the original file. Smoothing is required for ‘phenophase()’ and ‘transition_dates()’ functions.

Examples

```
# with defaults, outputting a data frame
# with smoothed values, overwriting the original

# download demo data (do not smooth)
download_phenocam(site = "harvard$",
  veg_type = "DB",
  roi_id = "1000",
  frequency = "3",
  smooth = FALSE)

# smooth the downloaded file (and overwrite the original)
smooth_ts(file.path(tempdir(), "harvard_DB_1000_3day.csv"))

# the function also works on a PhenoCam data frame
df <- read_phenocam(file.path(tempdir(), "harvard_DB_1000_3day.csv"))
df <- smooth_ts(df)
```

transition_dates	<i>Calculates transition dates for a PhenoCam time series</i>
------------------	---

Description

Segments of a PhenoCam time series and calculates threshold based transition dates for all segments. This function is rarely called stand alone and 'phenophases()' should be preferred when evaluating PhenoCam time series.

Usage

```
transition_dates(data, lower_thresh = 0.1, middle_thresh = 0.25,
  upper_thresh = 0.5, percentile = 90, penalty = 0.5,
  seg_length = 14, reverse = FALSE, plot = FALSE)
```

Arguments

data	a PhenoCam data file or data structure
lower_thresh	the minimum threshold used (default = 0.1)
middle_thresh	the middle threshold used (default = 0.25)
upper_thresh	the maximum threshold used (default = 0.5)
percentile	time series percentiles to process (mean, 50, 75, 90)
penalty	how sensitive is the algorithm, lower is more sensitive (< 0)
seg_length	minimum length of a segment to be evaluated
reverse	flip the direction of the processing
plot	plot for debugging purposes

Value

Transition date estimates in UNIX time, including uncertainties and the threshold values estimated for each section of a time series.

Examples

```
# download demo data
download_phenocam(site = "harvard$",
  veg_type = "DB",
  roi_id = "1000",
  frequency = "3")

# read the data and calculate transition dates
df <- read_phenocam(file.path(tempdir(), "harvard_DB_1000_3day.csv"))
my_dates <- transition_dates(df,
  lower_thresh = 0.1,
```

```

middle_thresh = 0.25,
upper_thresh = 0.5,
percentile = 90,
reverse = FALSE,
plot = FALSE)

```

truncate_phenocam	<i>Truncate a PhenoCam time series</i>
-------------------	--

Description

The ‘expand_phenocam()’ function provides a similar functionality and is preferred. This function remains as it might serve a purpose to some. Might be deprecated in the future.

Usage

```

truncate_phenocam(data, year = 2015, internal = TRUE,
  out_dir = tempdir())

```

Arguments

data	a PhenoCam file or data frame
year	the last valid year, discard the rest
internal	return a data structure if given a file on disk (TRUE / FALSE = default)
out_dir	output directory where to store data (default = tempdir())

Value

A truncated PhenoCam data structure or file, with data limited to the year specified.

Examples

```

# download demo data
download_phenocam(site = "harvard$",
  veg_type = "DB",
  roi_id = "1000",
  frequency = "3")

# overwrites the original file, increasing
# decreasing the file size, with given year as maximum.
truncate_phenocam(file.paste(tempdir(), "harvard_DB_1000_3day.csv"),
  year = 2015)

```

write_phenocam	<i>Write a phenocamr data structure to file</i>
----------------	---

Description

Writes a nested data structure of class phenocamr to file, reconstructing the original data structure from included headers and data components.

Usage

```
write_phenocam(df = NULL, out_dir = tempdir())
```

Arguments

df	a nested data structure of class phenocamr
out_dir	output directory where to store data

Value

writes PhenoCam data structure to file, retains proper header info and inserts a processing time stamp.

Examples

```
# download demo data (do not smooth)
download_phenocam(site = "harvard$",
  veg_type = "DB",
  roi_id = "1000",
  frequency = "3",
  smooth = FALSE)

# read the phenocamo data file
df = read_phenocam(file.paste(tempdir(), "harvard_DB_1000_3day.csv"))

# print data structure
print(summary(df))

# write the phenocamo data file
write_phenocam(df, out_dir = tempdir())
```

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