

Phenology in R

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Phenology in R with phenocamr

`phenocamr` version 1.1.4 is available on CRAN <https://cran.r-project.org/web/packages/phenocamr/index.html> with a development version available on GitHub <https://github.com/khufkens/phenocamr>. A more in-depth tutorial is available via the National Ecological Observatory Network's (NEON) Data Tutorial Series <https://www.neonscience.org/phenocam-phenor-modeling>. Note, this tutorial also includes information on additional data packages, including some not available currently on CRAN.

Here we show how to analyze phenocam data, taken from the PhenoCAM network <https://phenocam.sr.unh.edu/webcam/> for the Pace site, a mixed-temperate site located in the central Virginia Piedmont of the US.

Installation of phenocamr

```
# install the package if not already installed and call it via library()  
if(!require(phenocamr)){install.packages("phenocamr")}
```

```
## Loading required package: phenocamr
```

```
library(phenocamr)
```

Working with `phenocamr` is fairly straight-forward. Data from a site can be imported using the `download_phenocam` function which asks for: - `site` - `veg_type` - `frequency` a smoothing window, we are using 3-days, - `phenophase` which when true, creates a separate file that calculates phenological transition dates. - `out_dir` the directory where you want your data saved.

```
download_phenocam(site = "pace",  
                  veg_type = "DB",  
                  frequency = 3,  
                  phenophase = TRUE,  
                  out_dir = "./data/phenology")
```

Data can then be read in via the `read.table` function:

```
# load the time series data  
td <- read.table("../inst/extdata/phenology/pace_DB_1000_3day_transition_dates.csv", header = TRUE, sep = ";")  
df
```

```
## function (x, df1, df2, ncp, log = FALSE)
## {
##   if (missing(ncp))
##     .Call(C_df, x, df1, df2, log)
##   else .Call(C_dnf, x, df1, df2, ncp, log)
## }
## <bytecode: 0x0000000013271268>
## <environment: namespace:stats>
```

```
# read in time series data
df <- read.table("../inst/extdata/phenology/pace_DB_1000_3day.csv",
                 header = TRUE,
                 sep = ",")
```

Plots can then be made in base R with transitional dates overlain:

```
# select the rising (spring dates) for 25% threshold of Gcc 90
td <- td[td$direction == "rising" & td$gcc_value == "gcc_90",]

# create a simple line graph of the smooth Green Chromatic Coordinate (Gcc)
# and add points for transition dates
plot(as.Date(df$date), df$smooth_gcc_90, type = "l", xlab = "Date",
     ylab = "Gcc (90th percentile)")
points(x = as.Date(td$transition_25, origin = "1970-01-01"),
       y = td$threshold_25,
       pch = 19,
       col = "red")
```

