Phenology in R

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## Phenology in R with phenocamr

phenocamr version 1.1.4 is availble on CRAN <https://cran.r-project.org/web/packages/phenocamr/index.html> with a development version availble on GitHUB <https://github.com/khufkens/phenocamr>. A more in-depth tutorial is availble 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 availble 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

## Warning: package 'phenocamr' was built under R version 4.0.5

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")

## Downloading: pace\_DB\_1000\_3day.csv

## -- Flagging outliers!

## -- Smoothing time series!

## -- Estimating transition dates!

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

# load the time series data  
td <- read.table("./data/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: 0x00000000153c25a0>  
## <environment: namespace:stats>

# read in time series data  
df <- read.table("./data/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")

