

04_Main.Rmd

R Markdown Part 4

```
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.0 --
## v ggplot2 3.3.3      v purrr  0.3.4
## v tibble  3.1.0      v dplyr  1.0.5
## v tidyr   1.1.3      v stringr 1.4.0
## v readr   1.4.0      v forcats 0.5.1

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

library(lubridate)

##
## Attaching package: 'lubridate'

## The following objects are masked from 'package:base':
##
##   date, intersect, setdiff, union

## Main script for phenology analysis

## Load required functions
if(file.exists("01_download_phenocam.R")) source("01_download_phenocam.R")
if(file.exists("02_plot_phenocam.R"))     source("02_plot_phenocam.R")
if(file.exists("03_logistic.R"))          source("03_logistic.R")

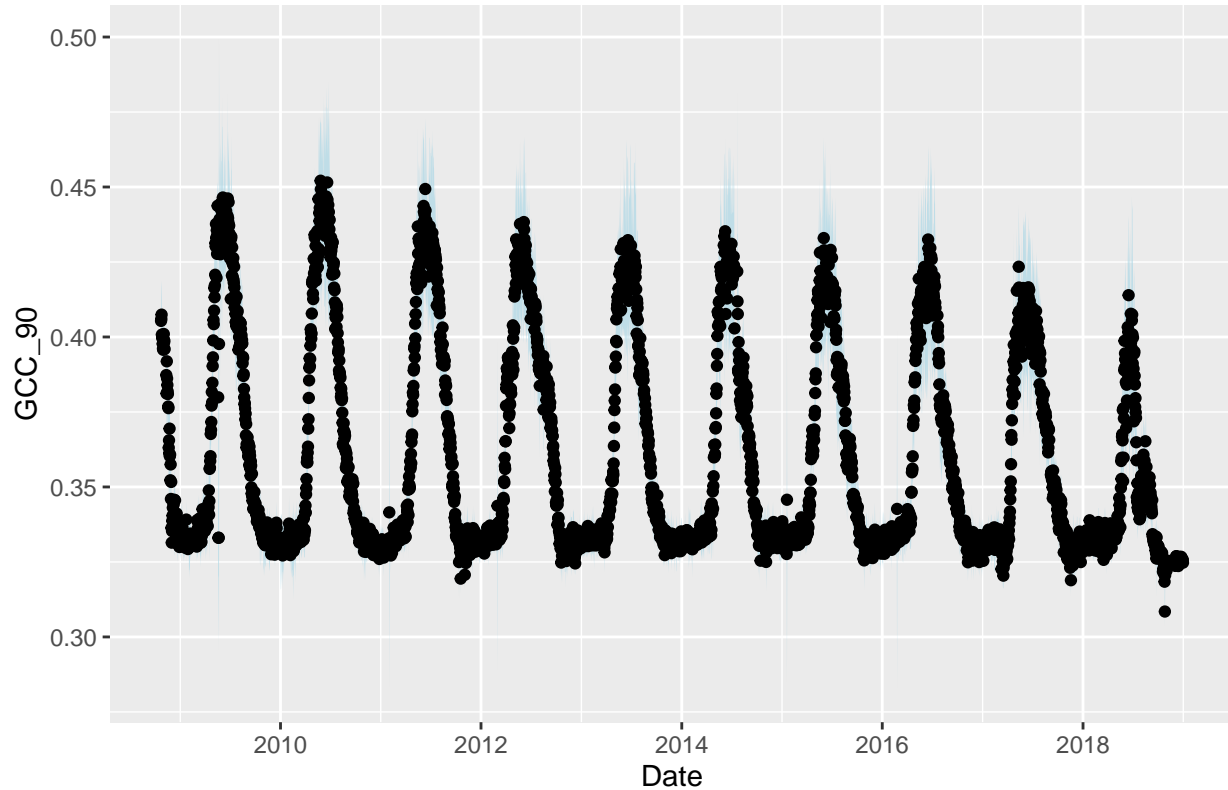
## Download phenology data
URL <- "http://phenocam.sr.unh.edu/data/archive/uiefprairie/ROI/uiefprairie_GR_1000_1day.csv"
prairie_pheno <- download_phenocam(URL)

##
## -- Column specification -----
## cols(
##   .default = col_double(),
##   date = col_date(format = ""),
##   midday_filename = col_character(),
##   snow_flag = col_logical(),
##   outlierflag_gcc_mean = col_logical(),
##   outlierflag_gcc_50 = col_logical(),
##   outlierflag_gcc_75 = col_logical(),
##   outlierflag_gcc_90 = col_logical()
## )
## i Use `spec()` for the full column specifications.
```

```
## Plot overall phenology data
plot_phenocam(prairie_pheno)
```

```
## Warning: Removed 65 rows containing missing values (geom_point).
```

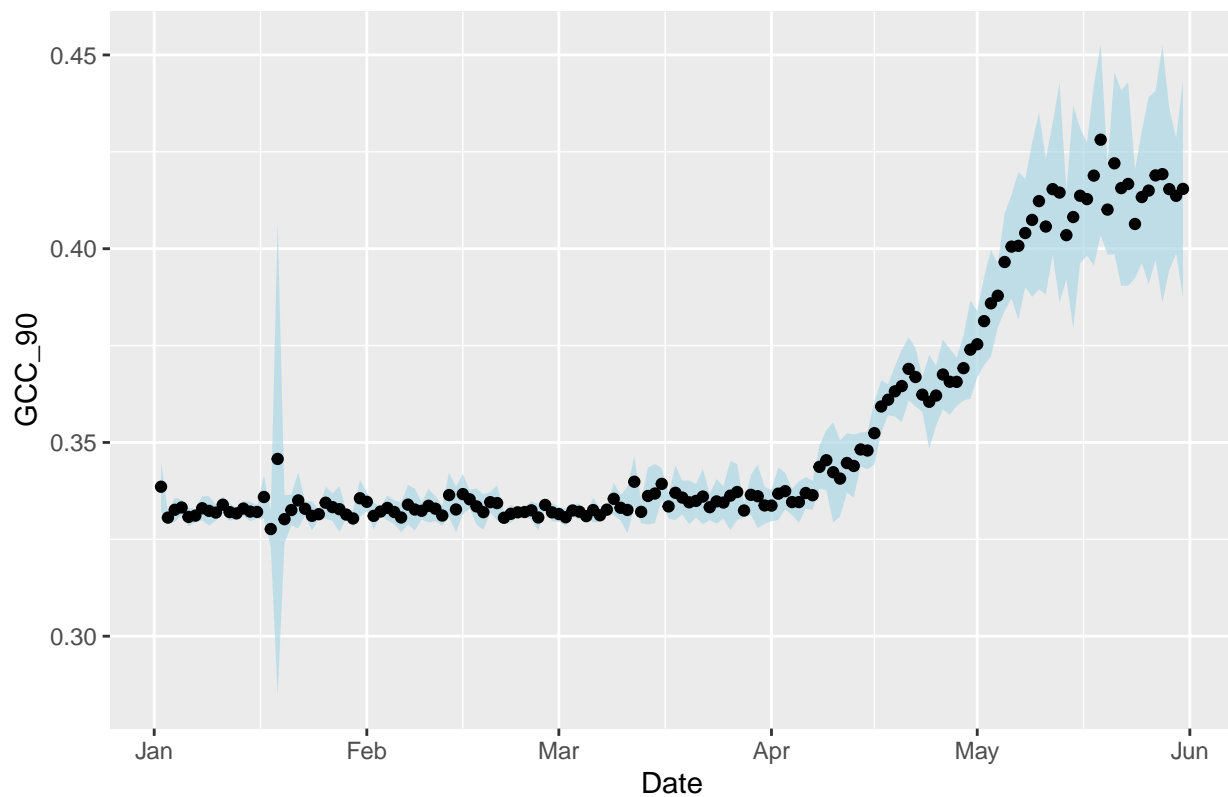
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```
## Create and visualize subset of data for leaf out
spring <- as_date(c("2015-01-01", "2015-06-01"))
dat <- prairie_pheno %>%
  filter(date > spring[1],
         date < spring[2]) %>%
  select(date, gcc_mean, gcc_std)

plot_phenocam(dat)
```

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```
## Fit logistic model
dat <- dat %>%
  mutate(doy = yday(date))
par <- c(0.33, 0.11, -10, 0.1)
fit_pars <- fit_logistic(dat, par)
pred <- tibble(date = dat$date,
               pred = pred_logistic(fit_pars, dat$doy))

## Visualize model and data
plot_phenocam(dat, pred = pred)
```

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