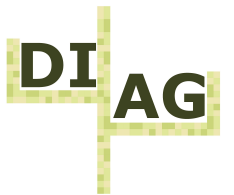


Making Data Analysis Accessible to Everyone

Kristina Riemer

Digital Agriculture Group (DIAG), Data Science Institute



Challenges for sharing results

1. Collaborator understanding



2. Reproducibility



Rmarkdown file

markdown file

text

code

```
biocro_opt_darpa.Rmd
1 ---
2 title: "How to Optimize Biomass Estimation for DARPA Data Using BioCro Model"
3 author: "Kristina Riemer, University of Arizona"
4 output: github_document
5 urlcolor: blue
6 ---
7
8 ### Walkthrough for optimizing using `DEoptim`
9
10 Optimizing biomass coefficients so that biomass estimates from BioCro as
11 closely as possible match the measured biomass values. Parameters of interest
12 are phenoParms, with thermal times and rhizome coefficients being fixed and
13 leaf, stem, root, and grain coefficients being optimized across. This returns
14 values of biomass for each stage and plant part, but the value being minimized
15 is the difference between measured biomass values and biomass estimated by
16 BioCro. It seems like we can optimized across all stages at once within our
17 objective function.
18
19 First read in all the necessary input data:
20
21 * BioCro config file
22 * weather file created for biomass partitioning in
23 [biocro_biomass_darpa.Rmd](https://github.com/az-digitalag/model-vignettes/blob/master/BioCro/DARPA/biocro_biomass_darpa.md)
24 * biomass file from Setaria experiments in
25 [biocro_biomass_darpa.Rmd](https://github.com/az-digitalag/model-vignettes/blob/master/BioCro/DARPA/biocro_biomass_darpa.md)
26
27 ```{r, message=FALSE}
28 library(dplyr)
29
30 rundir <- getwd()
31
32 OpBioGro_weather <- read.csv("biocro_opt_darpa_files/OpBioGro_weather.csv")
33 colnames(OpBioGro_weather) <- c("year", "doy", "hour", "Solar", "Temp", "RH",
34 "WS", "precip")
35 readr::write_csv(OpBioGro_weather, path = file.path(rundir,
36 'SA-median.2019.csv'))
37 WetDat <- OpBioGro_weather
38
39 confia <- PEcAn.BIOcRO::read.biocro.confia(file.path(rundir,
40
41:42:31 Chunk 1 R Markdown
```



```
az-digitalag / model-vignettes
Unwatch 4 Star 0 Fork 1
Code Issues Pull requests 2 ZenHub Actions Projects 0 Wiki Security Insights
Settings
Branch: master model-vignettes / BioCro / DARPA / biocro_opt_darpa.md Find file Copy path
KristinaRiemer Remove LAI from optimization f3d6857 4 days ago
1 contributor
268 lines (233 sloc) 11.4 KB Raw Blame History
How to Optimize Biomass Estimation for DARPA Data Using BioCro Model
Kristina Riemer, University of Arizona
Walkthrough for optimizing using DEoptim
Optimizing biomass coefficients so that biomass estimates from BioCro as closely as possible match the measured biomass values. Parameters of interest are phenoParms, with thermal times and rhizome coefficients being fixed and leaf, stem, root, and grain coefficients being optimized across. This returns values of biomass for each stage and plant part, but the value being minimized is the difference between measured biomass values and biomass estimated by BioCro. It seems like we can optimized across all stages at once within our objective function.
First read in all the necessary input data:
• BioCro config file
• weather file created for biomass partitioning in biocro_biomass_darpa.Rmd
• biomass file from Setaria experiments in biocro_biomass_darpa.Rmd
library(dplyr)
rundir <- getwd()
OpBioGro_weather <- read.csv("biocro_opt_darpa_files/OpBioGro_weather.csv")
colnames(OpBioGro_weather) <- c("year", "doy", "hour", "Solar", "Temp", "RH", "WS", "precip")
readr::write_csv(OpBioGro_weather, path = file.path(rundir, 'SA-median.2019.csv'))
WetDat <- OpBioGro_weather
```

github.com/az-digitalag/model-vignettes



Reviews via pull requests

The screenshot shows a GitHub pull request interface for the repository 'az-digitalag / model-vignettes'. The pull request is titled 'Improve BioCro regional runs of Setaria #16' and is in a 'Merged' state. It was merged by KristinaRiemer on Feb 18, merging 3 commits from the branch 'KristinaRiemer:fix_regional_runs' into the 'az-digitalag:master' branch. The interface includes tabs for Code, Issues, Pull requests, ZenHub, Actions, Projects, Wiki, Security, Insights, and Settings. Below the title, there are statistics for Conversation (3), Commits (3), Checks (0), and Files changed (3). A green bar indicates a net change of +125 lines and -22 lines. The main content area shows a diff for the file 'BioCro/DARPA/biocro_regional_darpa.Rmd'. The diff shows changes to the 'end_date' calculation and the 'biocro_met' variable. The left side of the diff shows the original code, and the right side shows the proposed changes. The changes include adding a new variable 'biocro_met_locations' and updating the 'biocro_met' variable to use 'cf2biocro' on 'met_hourly'.

```
@@ -54,20 +54,59 @@ end_date <- as.Date(time_origin2) + time_vec[length(time_vec)] - 1
54  dir.create("biocro_regional_darpa_files/biocro_met_by_location/")
55  met_nc <- ncd4::nc_open(metfile)
56  point <- 1
57  for(point in 1:nrow(latlon)){
58    met <- load.cfmet(met_nc, lat = latlon$lat[point], lon =
    latlon$lon[point],
59    start.date = start_date, end.date = end_date)
60 - biocro_met <- cf2biocro(met)
61
62    biocro_met <- biocro_met %>%
63    mutate(RH = case_when(RH >= 1 ~ 0.9999999999999999,
64    RH < 1 ~ RH))
65
66 + biocro_met_locations <- c()
67 + for(point in 1:nrow(latlon)){
68 +   met <- load.cfmet(met_nc, lat = latlon$lat[point], lon =
69 +   latlon$lon[point],
70 +   start.date = start_date, end.date = end_date)
71 +   met_hourly <- cfmet.downscale.time(met, output.dt = 1)
72 +   biocro_met <- cf2biocro(met_hourly)
73 +   biocro_met <- biocro_met %>%
74 +   mutate(RH = case_when(RH >= 1 ~ 0.9999999999999999,
75 +   RH < 1 ~ RH))
76 +   biocro_met_location <- biocro_met %>%
```

The screenshot shows the comments section of the pull request. The first comment is from 'tarinzin' (Collaborator) dated Feb 18, stating 'Done! It ran all well. I think instructions are pretty clear. There were a couple of troubles to set up some libraries such as nc.tools, after that everything ran smoothly. This text will be useful to write our deliverable.' and has 1 thumbs up. The second comment is from 'KristinaRiemer' (Author) dated Feb 18, responding 'Thanks so much for taking the time to review this @tarinzin! I'm going to merge this now because all of the code works. I've moved the items in the TODO list above to a new issue to be dealt with after merging the other standing PRs in this repo.' Below the comments, a message indicates that KristinaRiemer merged commit 'e7c2970' into 'az-digitalag:master' on Feb 18, with a 'Revert' button.

Contact me!

kristinariemer@arizona.edu

  @KristinaRiemer



WOMEN IN DATA SCIENCE
TUCSON