Introduction to BioCro Model

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Purpose of model

Simulate growth and photosynthesis of plants using weather and plant traits.

Installing package

Run below to install the current stable release of BioCro.

```
devtools::install_github('ebimodeling/biocro')
```

Read in the library.

```
library(BioCro)
```

Estimating biomass for growing season

The function BioGro is used for this. The only required input is a year of hourly weather data. Here we're using such weather data from a site in Illinois.

This returns a list where each element is a variable resulting from the model run. This includes biomass values for different parts of the plants and leaf traits such as stomatal conductance and maximum carboxylation rate.

```
data(cmi04)
head(cmi04)
```

```
##
     year doy hour SolarR
                                  Temp
                                              RH
                                                        WS precip
## 1 2004
            1
                  0
                            2.5138889 0.9395434 1.945417
                                                                 0
## 2 2004
                            1.2424834 0.9528131 1.676811
                                                                 0
            1
                  1
## 3 2004
                  2
                                                                0
                         0 0.2668996 0.9611548 1.470702
            1
                         0 -0.3463780 0.9640000 1.341137
                                                                 0
## 4 2004
            1
                  3
## 5 2004
                         0 -0.5555556 0.9611548 1.296944
                                                                 0
## 6 2004
            1
                  5
                         0 -0.3463780 0.9528131 1.341137
                                                                0
cmi04_results <- BioGro(cmi04)</pre>
```

```
## [1] 6
names(cmi04_results)
```

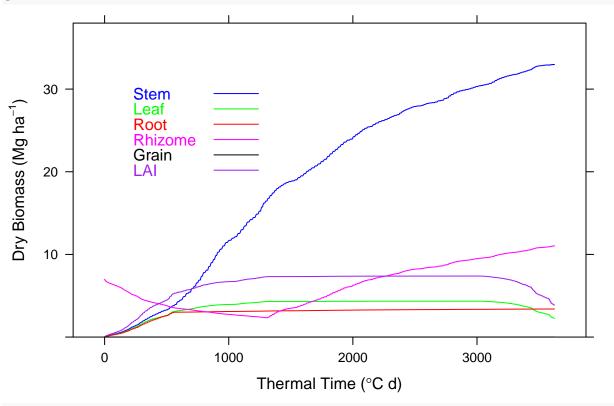
```
[1] "DayofYear"
                                                     "CanopyAssim"
##
                               "Hour"
    [4] "CanopyTrans"
                               "Leaf"
                                                     "Stem"
    [7] "Root"
                               "Rhizome"
                                                     "Grain"
##
   [10] "LAI"
                               "ThermalT"
                                                     "SoilWatCont"
                                                     "LeafNitrogen"
   [13]
        "StomatalCondCoefs"
                               "LeafReductionCoefs"
        "AboveLitter"
                               "BelowLitter"
                                                     "VmaxVec"
                               "SpVec"
  [19]
        "AlphaVec"
                                                      "MinNitroVec"
   [22]
        "RespVec"
                               "SoilEvaporation"
                                                     "cwsMat"
##
   [25]
        "psimMat"
                               "rdMat"
                                                     "SCpools"
## [28] "SNpools"
                               "LeafPsimVec"
```

head(cmi04_results\$Stem)

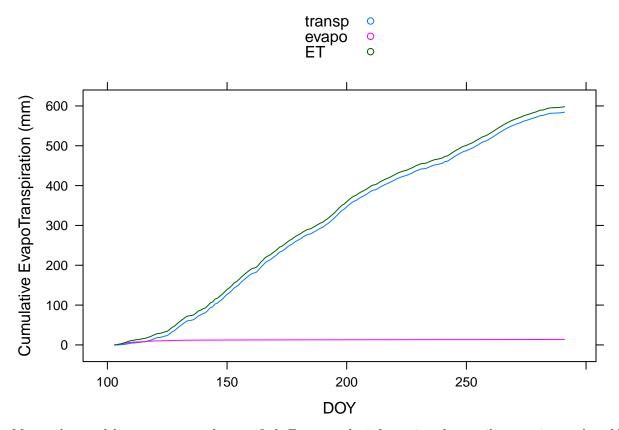
[1] 0.00907200 0.01114234 0.01321103 0.01527806 0.01734344 0.01940716

These results can be visualized using plot, which is a modified version of xyplot from the lattice R package. The default plots the dry biomass of the different plant parts, and other results can be plotted by specifying the plot.kind. The cumulative evapotranspiration plot is shown as an example.

plot(cmi04_results)



plot(cmi04_results, plot.kind = "cumET")



Many other model parameters can be specified. For example, information about soil properties can be added. The model outputs are plotted for low and high values for the effect of water stress on leaf growth. There is not a built-in way to plot

```
low_phi <- soilParms(FieldC = 0.37, WiltP = 0.2, phi2 = 1)
high_phi <- soilParms(FieldC = 0.37, WiltP = 0.2, phi2 = 4)

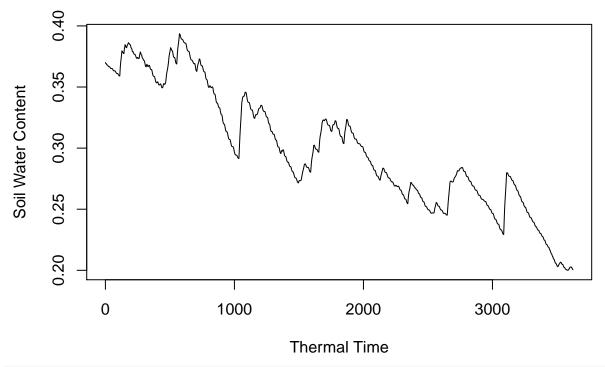
cmi04_results_lowphi <- BioGro(cmi04, soilControl = low_phi)

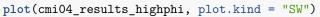
## [1] 6

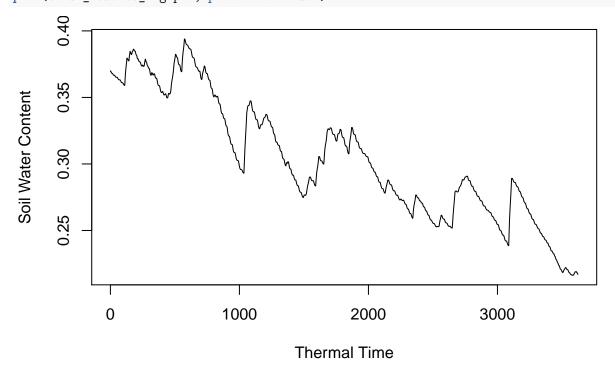
cmi04_results_highphi <- BioGro(cmi04, soilControl = high_phi)

## [1] 6

plot(cmi04_results_lowphi, plot.kind = "SW")</pre>
```







BioGro is built on the c4photo/c3photo and CanA functions. Their use is illustrated below.

Estimating photosynthesis variables at the leaf level

The function c4photo estimates stomatal conductance, net assimilation, intercellular CO_2 , and gross assimilation from photosynthetically active radiation, temperature, and relative humidity. A value for net assimilation is returned below.

```
photosynthesis_c4 <- c4photo(Qp = 1500, T1 = 25, RH = 0.7) photosynthesis_c4^{$Assim}
```

```
## [1] 30.48496
```

This function can take a lot of other parameters, including Vcmax and temperature bounds. The example below shows the difference in output when atmospheric CO₂ varies.

```
photosynthesis_c4_lowco2 <- c4photo(Qp = 1250, T1 = 35, RH = 0.7, Catm = 350)
photosynthesis_c4_highco2 <- c4photo(Qp = 1250, T1 = 35, RH = 0.7, Catm = 400)
photosynthesis_c4_lowco2$Assim</pre>
```

```
## [1] 34.39333
photosynthesis_c4_highco2$Assim
```

```
## [1] 34.45631
```

Observations of net assimilation rate, quantum flux, leaf temperature, and relative humidity can be used to better estimate maximum rate of carboxylation and quantum efficiency to put into c4photo/c3photo. Example observations from a built-in dataset are shown.

```
library(dplyr)
data(aq)
aq_observations <- aq %>%
  filter(ID == 1) %>%
  select(A, PARi, Tleaf, RH_S)
aq_observations
```

```
## A PARI Tleaf RH_S
## 1 16.68 1988.36 26.88 0.47
## 2 17.87 1489.37 26.16 0.47
## 3 18.24 993.60 25.39 0.47
## 4 15.70 493.78 24.66 0.47
## 5 11.10 297.23 24.34 0.47
## 6 7.43 193.86 24.39 0.46
## 7 3.05 96.43 24.42 0.45
## 8 0.46 47.45 24.40 0.44
```

The function Opc4photo takes these observations to produce estimates of Vmax and alpha.

```
aq_observations_priors <- Opc4photo(aq_observations)
aq_observations_priors$bestVmax</pre>
```

```
## [1] 19.09404
aq_observations_priors$bestAlpha
```

```
## [1] 0.05225266
```

These estimates can also be produced for multiple curves at once (mOpc4photo) or with a Bayesian approach (MCMCc4photo).

Simulate canopy carbon assimilation

Estimates at the canopy-level of carbon assimilation and transpiration are done with the function CanA, which is built on c4photo. Required inputs include environmental variables, day and time, and leaf area index.

The number of layers in the canopy can also be specified. While the default is eight layers, an example with more layers is shown. Both carbon assimilation and transpiration outputs are shown.

[1] 0.360428

 $\verb|canopy_morelayers| \$ Canopy Trans|$

canopy_fewlayers\$CanopyTrans

[1] 0.3807981