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      0  2.5138889 0.9395434 1.945417      0
## 2 2004   1    1      0  1.2424834 0.9528131 1.676811      0
## 3 2004   1    2      0  0.2668996 0.9611548 1.470702      0
## 4 2004   1    3      0 -0.3463780 0.9640000 1.341137      0
## 5 2004   1    4      0 -0.5555556 0.9611548 1.296944      0
## 6 2004   1    5      0 -0.3463780 0.9528131 1.341137      0
```

```
cmi04_results <- BioGro(cmi04)
```

```
## [1] 6
```

```
names(cmi04_results)
```

```
##  [1] "DayofYear"        "Hour"             "CanopyAssim"
##  [4] "CanopyTrans"      "Leaf"             "Stem"
##  [7] "Root"             "Rhizome"          "Grain"
## [10] "LAI"              "ThermalT"         "SoilWatCont"
## [13] "StomatalCondCoefs" "LeafReductionCoefs" "LeafNitrogen"
## [16] "AboveLitter"      "BelowLitter"      "VmaxVec"
## [19] "AlphaVec"         "SpVec"            "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)
```
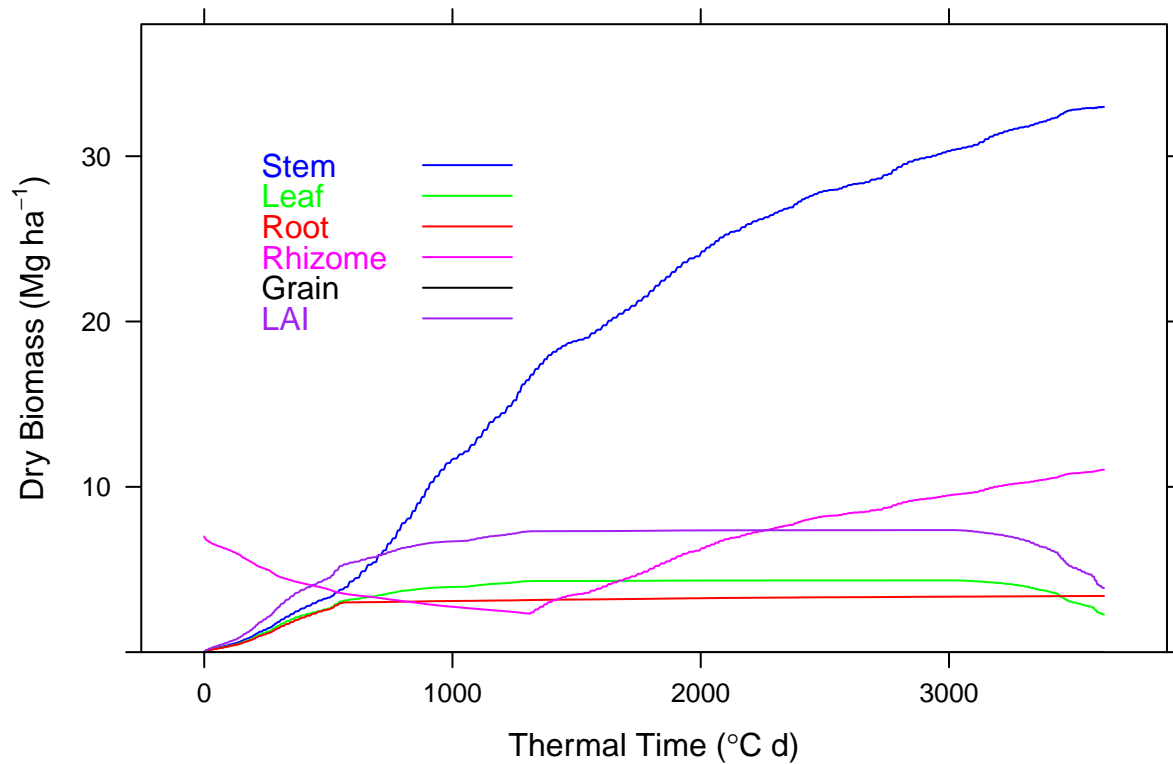


```
plot(cmi04_results, plot.kind = "cumET")
```
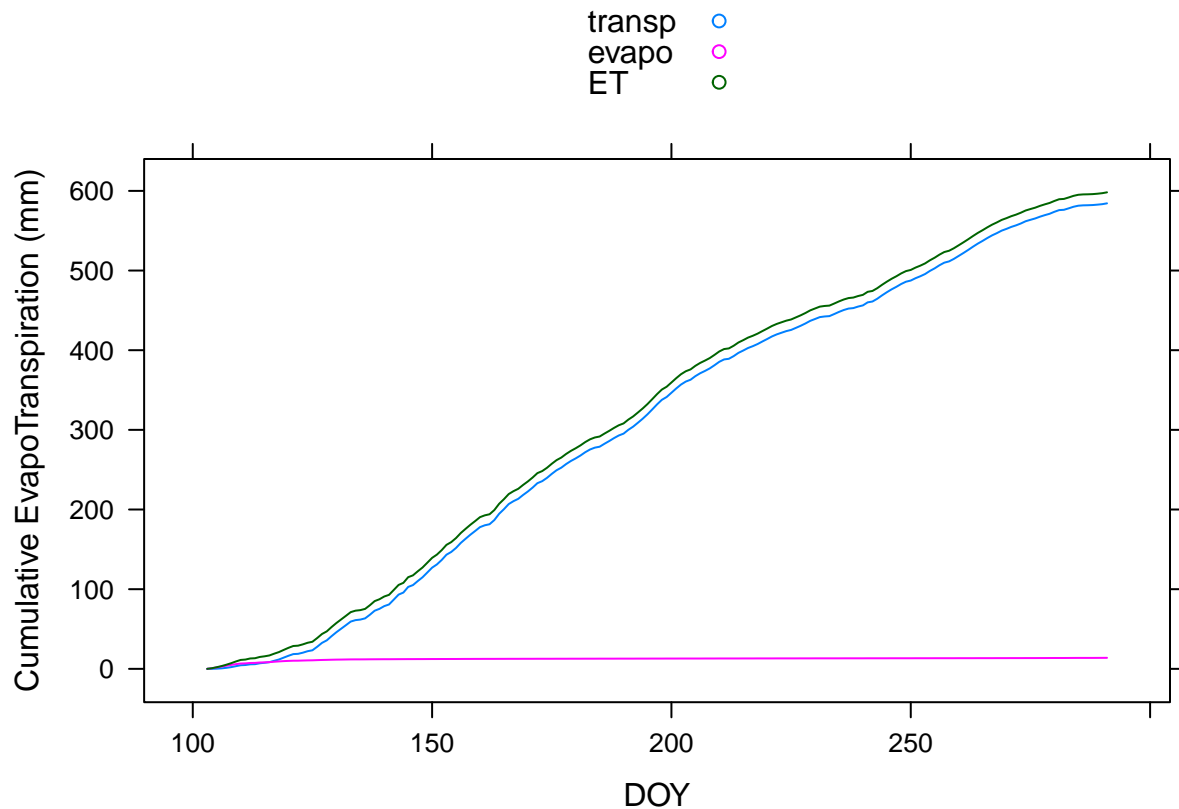
Many other model parameters can be specified. For example, information about soil properties can be added. The model outputs are plotted for low and high values for the effect of water stress on leaf growth. There is not a built-in way to plot

```r
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)
```
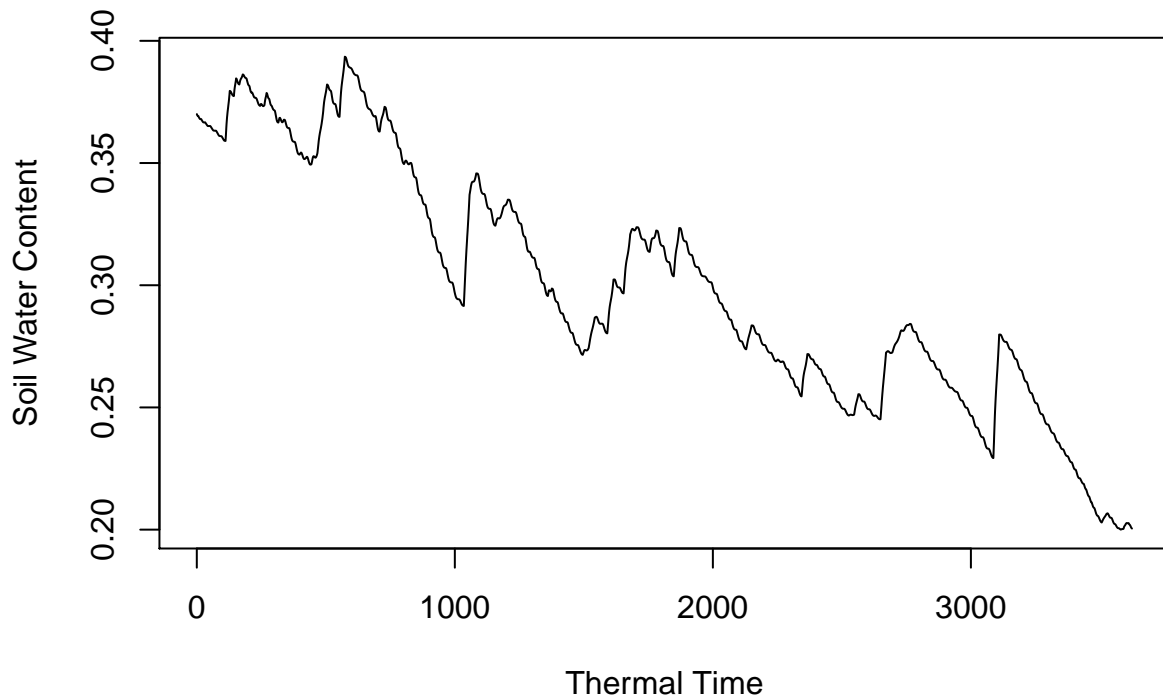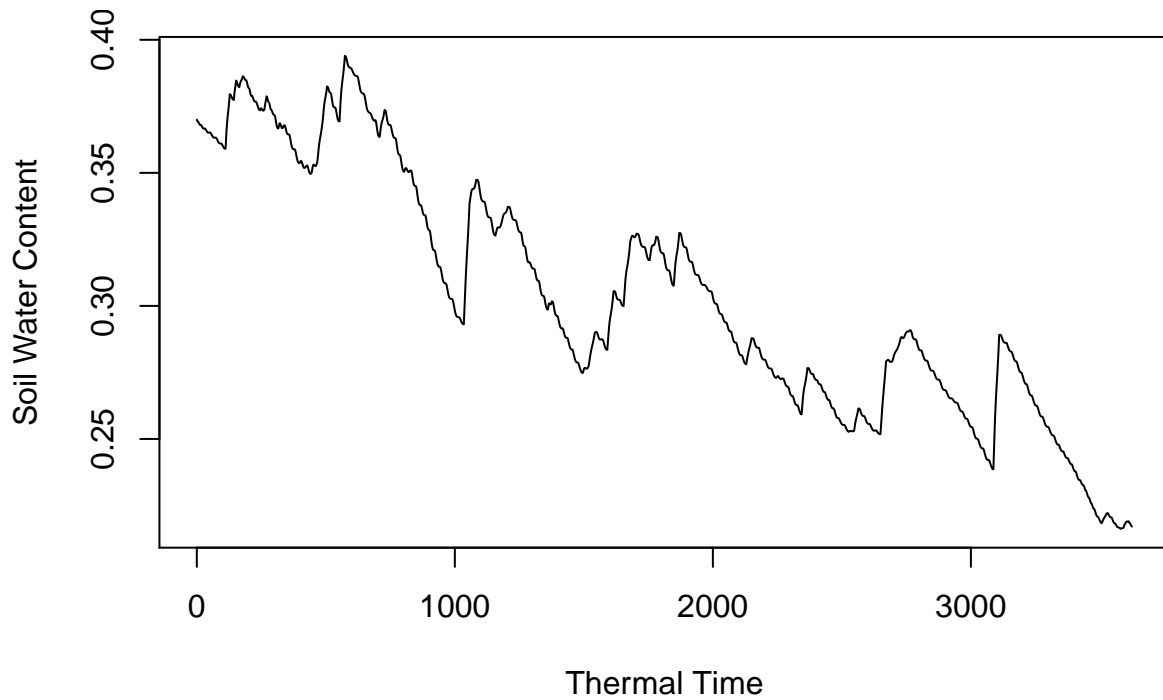
```
## [1] 6
```

```r
cmi04_results_highphi <- BioGro(cmi04, soilControl = high_phi)
```

```
## [1] 6
```

```r
plot(cmi04_results_lowphi, plot.kind = "SW")
```

```
plot(cmi04_results_highphi, plot.kind = "SW")
```


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.

```r
photosynthesis_c4 <- c4photo(Qp = 1500, Tl = 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 CO_2 varies.

```r
photosynthesis_c4_lowco2 <- c4photo(Qp = 1250, Tl = 35, RH = 0.7, Catm = 350)
photosynthesis_c4_highco2 <- c4photo(Qp = 1250, Tl = 35, RH = 0.7, Catm = 400)

photosynthesis_c4_lowco2$Assim
```

```
## [1] 34.39333
```

```r
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.

```r
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.

```r
aq_observations_priors <- Opc4photo(aq_observations)
aq_observations_priors$bestVmax
```

```
## [1] 19.09404
```

```r
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.

```
canopy_fewlayers <- CanA(lai = 3, doy = 200, hr = 12, solar = 1500, temp = 25,
                         rh = 0.7, windspeed = 2)
canopy_morelayers <- CanA(lai = 3, doy = 200, hr = 12, solar = 1500, temp = 25,
                          rh = 0.7, windspeed = 2, nlayers = 14)

canopy_fewlayers$CanopyAssim
```

```
## [1] 0.003663916
```

```
canopy_morelayers$CanopyAssim
```

```
## [1] 0.00371193
```

```
canopy_fewlayers$CanopyTrans
```

```
## [1] 0.360428
```

```
canopy_morelayers$CanopyTrans
```

```
## [1] 0.3807981
```

Determine biomass partitioning

The function `OpBioGro` is used to estimate the proportion of biomass in each of five parts of the plant throughout six phenological stages. The first input this function requires is weather data, including solar radiation, temperature, relative humidity, wind speed, and precipitation, at hourly time steps. We use here a built-in dataset from the `BioCro` package. The second input is the biomass of the different plant parts across thermal temperature; an example dataset is generated below.

```
data(weather05)
weather_data <- weather05
biomass_data = data.frame(
    ThermalT = c(0.21088112958955, 431.522425672787, 1005.62149992847,
                 1644.3961341225, 2293.29763493264, 2877.88197263589,
                 3414.94836181958, 3746.93356347913),
        Stem = c(0.007329, 1.04151488848428, 5.11942776350724,
                 7.81286730821308, 11.0907005177492, 13.2507662405245,
                 14.4052150630531, 14.7401303915464),
        Leaf = c(0.001036, 0.842484261465219, 1.39383059411517,
                 1.46256196044261, 1.47410120058506, 1.47948442902015,
                 1.07906869265829, 0.450513028403679),
        Root = c(0.007035, 0.112702867880121, 1.20666362376652, 1.928688377409,
                 2.62366412192997, 3.08821592657137, 3.3414401199094,
                 3.52726574823008),
     Rhizome = c(6.9993, 6.58508401628827, 6.1953811812003, 6.44908010432176,
                 8.05287028398554, 9.12491291008107, 9.70927643316885,
                 10.1381048062166),
       Grain = c(0, 0, 0, 0, 0, 0, 0, 0),
         LAI = c(0.00119, 1.43168584789548, 2.3693645451772, 2.48635533275244,
                 2.5059720409946, 2.51512352933425, 1.83441677751909,
                 0.765872148286255)
)
```

The input biomass data is then used to create initial guesses at what the biomass coefficients for each part of

the plant at each phenological stage will be. This is done using `idbp`, and the results are checked for errors using `valid_dpb`, which are both `BioCro` functions.

```
approx_biomass_coefs <- valid_dbp(idbp(biomass_data))
```

These initial coefficients, along with the weather and biomass data, are put into `OpBioGro`, which uses both the `BioGro` and `optim` functions. The `phen` argument is set as zero to return values optimized for all six stages. Otherwise, a particular stage to optimize can be specified.

```
biomass_coefs <- OpBioGro(phen = 0, WetDat = weather_data, data = biomass_data,
                          iCoef = approx_biomass_coefs)
```

The "Optimized coefficients" table in `biomass_coefs` contains the proportions of biomass allocated to each part of the plant in each of the phenological stages.

```
biomass_coefs
```

```
##
##  Optimization for stage: 1 2 3 4 5 6
##
##  Optimized coefficients
##            Leaf         Stem        Root      Rhizome         Grain
## 1 4.699050e-01 0.480609978 0.04948498 -1.004819e-04 0.000000e+00
## 2 6.501908e-01 0.139569458 0.21023973 -9.944771e-05 0.000000e+00
## 3 5.606136e-01 0.009623840 0.13020890  2.995536e-01 0.000000e+00
## 4 5.579495e-01 0.011222947 0.12925090  3.015766e-01 0.000000e+00
## 5 5.664778e-01 0.006169053 0.13258745  2.947657e-01 0.000000e+00
## 6 3.110866e-07 0.078591426 0.37649696  5.449107e-01 6.392513e-07
##
##  Residual Sum of Squares: 3.267388
##
##  Convergence
##    stage:  1 YES
##    stage:  2 YES
##    stage:  3 YES
##    stage:  4 YES
##    stage:  5 YES
##    stage:  6 YES
```