081815c – Runs with 5mx5m gridded subplots

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1 Summary

The seven plots that I chose to use for calibration were: BBBPIPO, EMRIDGE, FRPIJE, PGABMA, POFLABMA, SFTRABMA, and SUPILA. This document details the results from the batch files labeled 081815c-X.xml. The tree maps in 081815c-X use a mixture of plot generation methods. The real plot data are positioned in the bottom left; the remaining space is filled with points generated between 09-1.1 times a sample of the original data, with replacement. These plots are positioned in the bottom left to facilitate the use of the "subplots" feature in SORTIE-ND. The following data are for the "real" subplot within the larger 300m x 300m space. One weakness is that the subplot boundaries in this run are not exact. 081815c-X will be exact, when I set them up.

One major revision here is that several of the functions have been modified to support subplots. You'll now see extra parameters in "processTestPlot". Finally, these plots are dealing with the initial offset issue that was seen in previous plots. My "real plots" are for all recorded trees, even if they are tiny. SORTIE-ND classifies trees into different size classes as seedlings, saplings, and adults. Although this is useful, I don't feel like reworking "realPlots" quite yet, so I modified testExpSim and plotExpSim to lump the three classes together. As you can see, this brings the numbers for density remarkably closer than where they were.

2 Methods

Allometry parameter calculation is described in the MakeMyForests vignette, which can be accessed on GitHub. Of note, the growth and mortality calculations from that manual are not used in this model run, but are described in more detail below.

Dispersal parameters were calculated using the disperseR package. More details can be found in the disperseR documentation. Dispersal parameters were calculated as a result of species across all seven plots, and not calibrated to individual plots.

For growth rate, I decided to use the NCI growth with auto height sub-model in SORTIE-ND. This sub-model requires a maximum growth rate, and

then a series of modifiers ranging between 0-1 to represent the possible effects of crowding, disturbance, drought, etc. For the base model, I opted to use mean growth rate as calculated from the seven calibration plots, by species. This run did not use variation in growth rate, but instead used a static increase.

Mortality rates were calculated by counting the total number of alive and dead trees for *each year*, and summing those across species for each of the seven calibration plots. Those resulting number of dead and alive per species were combined to estimate mean mortality rate as $\frac{n\,dead}{n\,dead\,+\,n\,alive}$.

Individual "expected" outcomes were calculated from existing plot records. Relevant plot values like "Adult Basal Area Per Hectare" and "Adult Density Per Hectare" were calculated for each timestep in the real plot records. These were saved in a CSV file entitled `expectedPlotOutcomes.csv`, and can also be found in the `SortieOutputs` package in the data.frame `realPlots`.

I generated seven parameter files, one for each calibration plot. Within each, there was a 300m x 300m tree map added. The real plot data are positioned in the bottom left; the remaining space is filled with points generated between 09-1.1 times a sample of the original data, with replacement. These plots are positioned in the bottom left to facilitate the use of the "subplots" feature in SORTIE-ND, and this document shows the results from an approximate subplot containing real plot data only.

I ran each parameter file **fifteen** times in a batch file, and saved summary outputs that calculated Density and Basal Area per hectare for each time step for Adults, Saplings, and Seedlings.

3   Results

For the first set of figures, by plot, the hashmarks represent a single trial at a single time point, and may be grouped together rather closely. The closed squares of the same color indicate the true means of the real plots. The x-axis is time, and the y-axis is the variable of interest.

3.1 BBBPIPO: Adult Basal Area and Density

```
> library(SortieOutputs)
>  head(processTestPlot("BBBPIPO", "outfiles/c", 0,
+                   charactername="AdultAbsBA",
+                   writefile="outfiles/c/means/BBBPIPO-AdultAbsBA.csv",
+                   numsubplots = 3, subplotid=1))
```

```
  Step Species AdultAbsBA   simMean dixonPval    tTestPval dSig tsig
1    1    ABCO   8.225156  8.153867 0.00000000 4.037474e-01  Sig   NS
2    6    ABCO   8.558442  8.291369 0.02302671 4.383621e-02  Sig  Sig
3   11    ABCO   8.602290  8.388129 0.00000000 1.165256e-01  Sig   NS
4   16    ABCO   9.553299  8.386053 0.89710936 1.458374e-05   NS  Sig
5   21    ABCO  10.693378  8.587122 0.16343815 5.609290e-08   NS  Sig
6    1    CADE  26.306953 27.313390 0.00000000 1.898020e-17  Sig  Sig
```
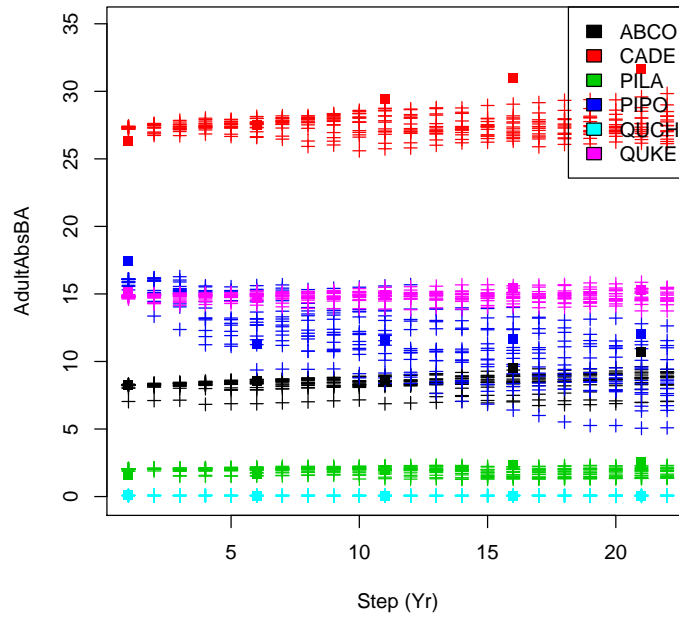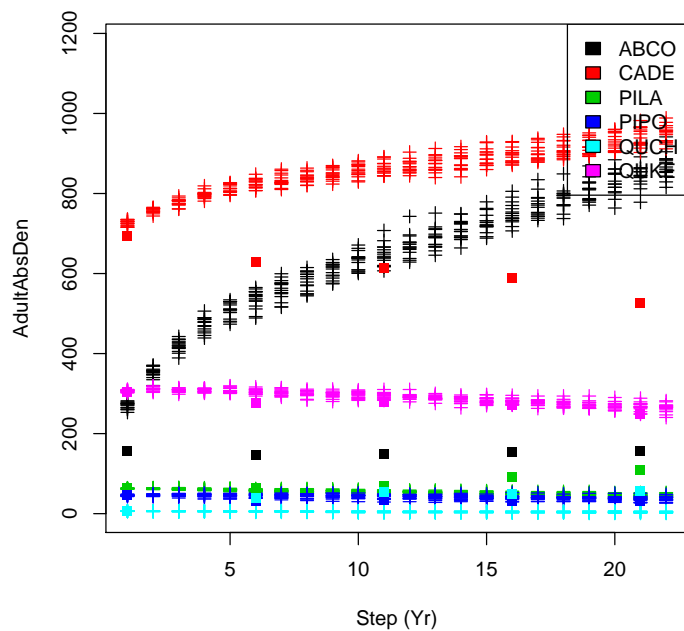

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```
>    head(processTestPlot("BBBPIPO", "outfiles/c", 0,
+                    charactername="AdultAbsDen",
+                    writefile="outfiles/c/means/BBBPIPO-AdultAbsDen.csv",
+                    numsubplots = 3, subplotid=1))

  Step Species AdultAbsDen  simMean   dixonPval    tTestPval dSig tsig
1    1    ABCO         157 269.8115 0.00000000 2.219317e-17  Sig  Sig
2    6    ABCO         147 535.8726 0.00000000 1.189717e-18  Sig  Sig
3   11    ABCO         148 646.5911 0.00000000 2.440662e-19  Sig  Sig
4   16    ABCO         155 750.4157 0.00000000 2.091255e-20  Sig  Sig
5   21    ABCO         157 848.7377 0.00000000 4.881671e-20  Sig  Sig
6    1    CADE         695 726.0468 0.08163664 9.490874e-11   NS  Sig
```
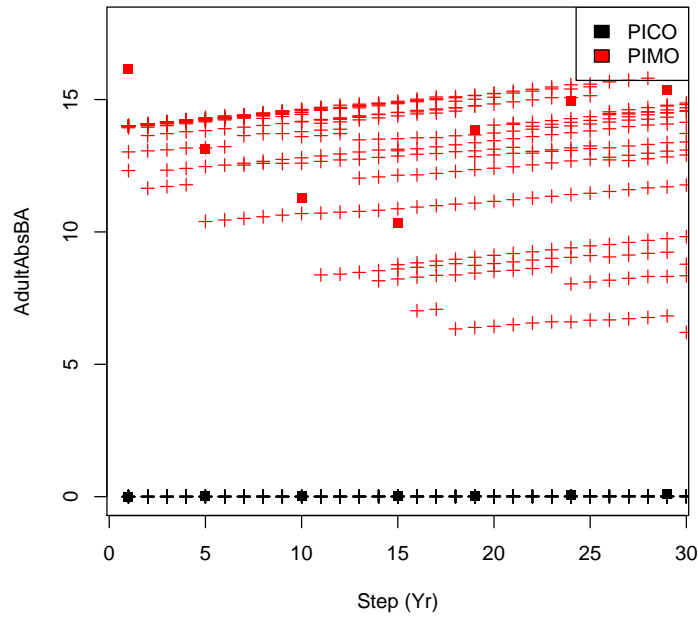
3.2 EMRIDGE: Adult Basal Area and Density
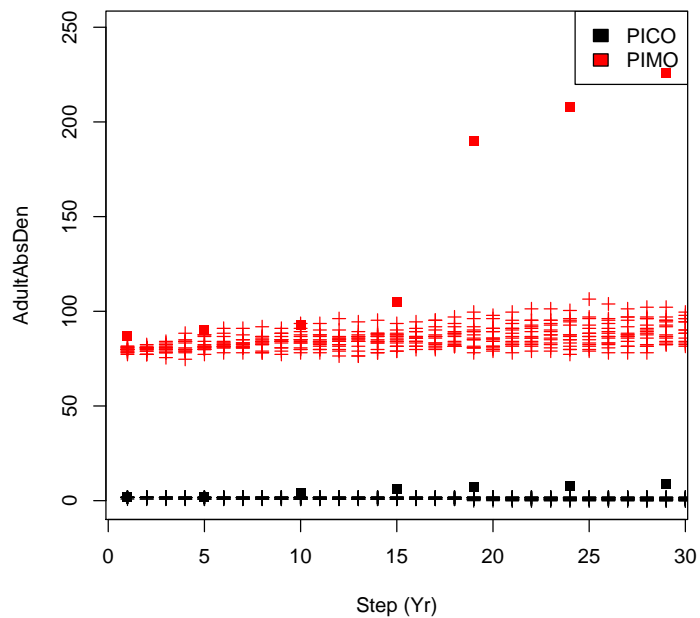
```
> head(processTestPlot("EMRIDGE", "outfiles/c", 0,
+                      charactername="AdultAbsBA",
+                      writefile="outfiles/c/means/EMRIDGE-AdultAbsBA.csv",
+                      numsubplots = 3, subplotid=1))
```

	Step	Species	AdultAbsBA	simMean	dixonPval	tTestPval	dSig	tsig
1	1	PICO	0.005724781	0.004859424	0.00000000	1.826815e-02	Sig	Sig
2	5	PICO	0.011388300	0.005165637	0.17422464	7.752468e-08	NS	Sig
3	10	PICO	0.019037311	0.005640061	0.01469878	3.830119e-10	Sig	Sig
4	15	PICO	0.022427097	0.007079737	0.01917201	6.522405e-10	Sig	Sig
5	19	PICO	0.035197701	0.008088527	0.00000000	2.808294e-12	Sig	Sig
6	24	PICO	0.051995836	0.009193809	0.00000000	5.627467e-14	Sig	Sig

```
>    head(processTestPlot("EMRIDGE", "outfiles/c", 0,
+                      charactername="AdultAbsDen",
+                      writefile="outfiles/c/means/EMRIDGE-AdultAbsDen.csv",
+                      numsubplots = 3, subplotid=1))

  Step Species AdultAbsDen   simMean dixonPval    tTestPval dSig tsig
1    1    PICO           2 1.659515         0 3.547829e-05  Sig  Sig
2    5    PICO           2 1.487841         0 1.778251e-04  Sig  Sig
3   10    PICO           4 1.373392         0 1.289393e-12  Sig  Sig
4   15    PICO           6 1.373392         0 5.211104e-16  Sig  Sig
5   19    PICO           7 1.258942         0 6.586424e-16  Sig  Sig
6   24    PICO           8 1.087268         0 1.867205e-16  Sig  Sig
```
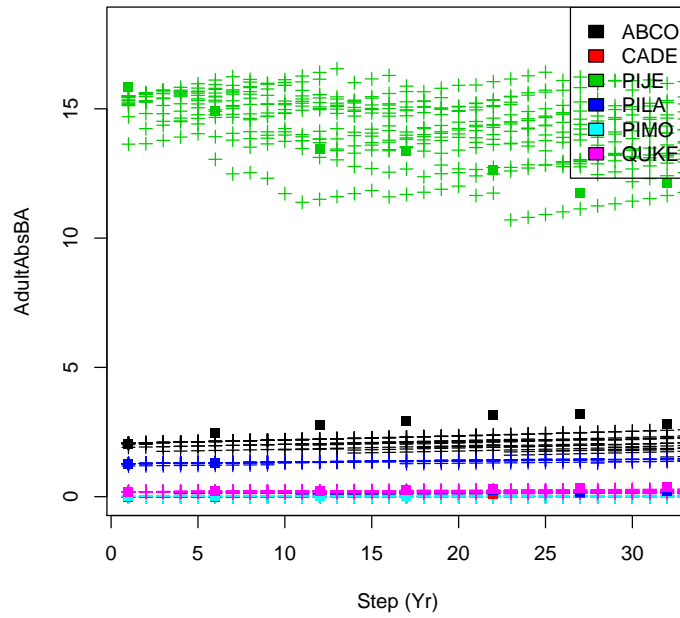
3.3 FRPIJE: Adult Basal Area and Density
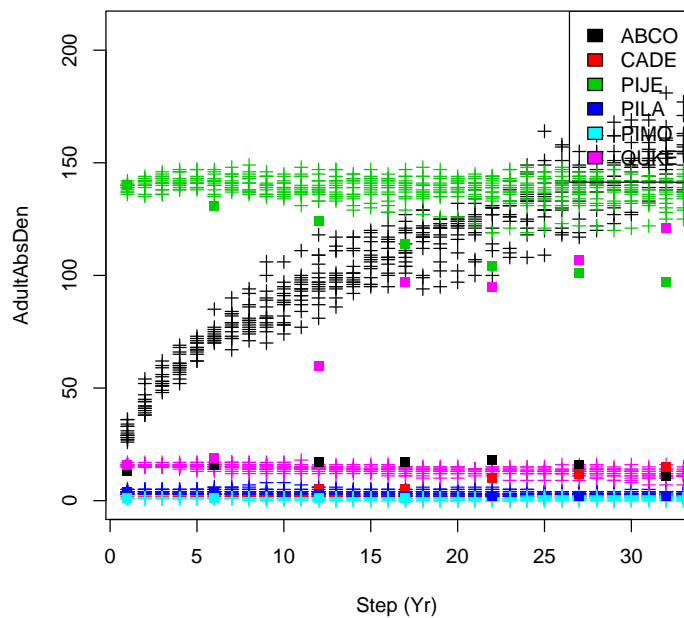
```
> head(processTestPlot("FRPIJE", "outfiles/c", 0,
+                  charactername="AdultAbsBA",
+                  writefile="outfiles/c/means/FRPIJE-AdultAbsBA.csv",
+                  numsubplots = 3, subplotid=1))
```

```
  Step Species AdultAbsBA  simMean    dixonPval     tTestPval dSig tsig
1    1    ABCO   2.053798  2.052920  0.000000000  9.372127e-01  Sig   NS
2    6    ABCO   2.453112  2.090617  0.000000000  1.555867e-09  Sig  Sig
3   12    ABCO   2.764404  2.084247  0.019208461  7.012765e-11  Sig  Sig
4   17    ABCO   2.916810  2.110750  0.010943789  6.422666e-11  Sig  Sig
5   22    ABCO   3.169380  2.110753  0.009261467  2.380757e-12  Sig  Sig
6   27    ABCO   3.181021  2.091651  0.094907221  2.001472e-10   NS  Sig
```

```
>    head(processTestPlot("FRPIJE", "outfiles/c", 0,
+                    charactername="AdultAbsDen",
+                    writefile="outfiles/c/means/FRPIJE-AdultAbsDen.csv",
+                    numsubplots = 3, subplotid=1))

  Step Species AdultAbsDen    simMean dixonPval      tTestPval dSig tsig
1    1    ABCO          13   30.40000         0 7.127515e-12  Sig  Sig
2    6    ABCO          16   73.53333         0 3.477977e-18  Sig  Sig
3   12    ABCO          17   98.06667         0 9.140458e-15  Sig  Sig
4   17    ABCO          17  113.20000         0 1.000122e-16  Sig  Sig
5   22    ABCO          18  125.13333         0 1.252493e-15  Sig  Sig
6   27    ABCO          16  138.13333         0 2.344801e-16  Sig  Sig
```
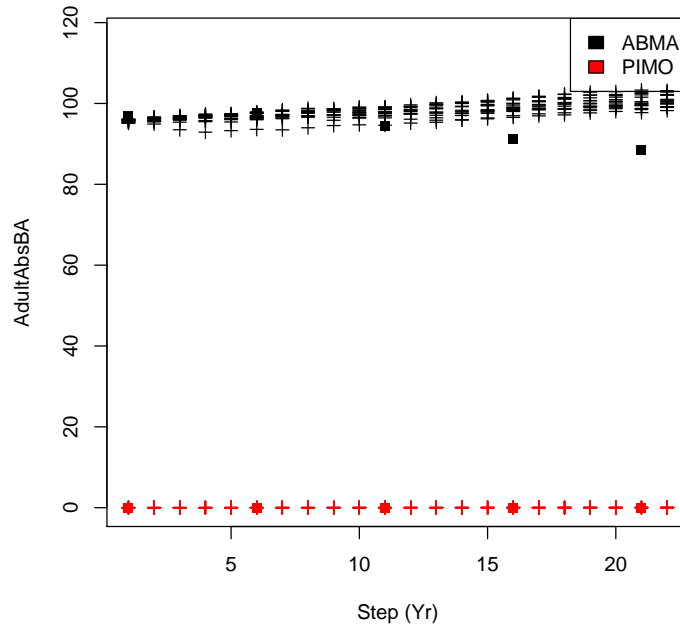
3.4 PGABMA: Adult Basal Area and Density
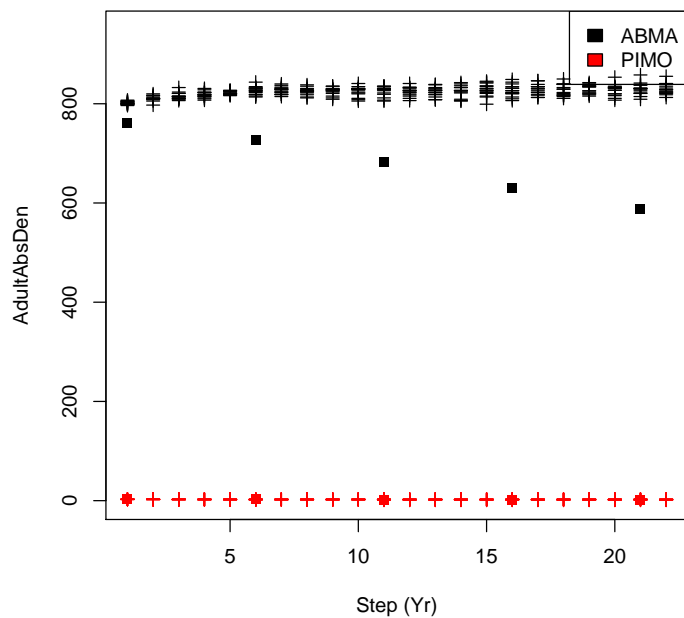
```
> head(processTestPlot("PGABMA", "outfiles/c", 0,
+                 charactername="AdultAbsBA",
+                 writefile="outfiles/c/means/PGABMA-AdultAbsBA.csv",
+                 numsubplots = 3, subplotid=1))
```

	Step	Species	AdultAbsBA	simMean	dixonPval	tTestPval	dSig	tsig
1	1	ABMA	96.84838877	95.72838800	0.15137958	3.383785e-09	NS	Sig
2	6	ABMA	97.52063023	96.70882200	0.01569942	1.088057e-02	Sig	Sig
3	11	ABMA	94.43564576	97.68586400	0.23056193	5.674404e-08	NS	Sig
4	16	ABMA	91.25577994	99.24741933	0.02593032	6.491959e-12	Sig	Sig
5	21	ABMA	88.46650645	100.39435067	0.00000000	1.198504e-13	Sig	Sig
7	1	PIMO	0.02068744	0.01893167	0.00000000	1.050015e-02	Sig	Sig

```
>    head(processTestPlot("PGABMA", "outfiles/c", 0,
+                  charactername="AdultAbsDen",
+                  writefile="outfiles/c/means/PGABMA-AdultAbsDen.csv",
+                  numsubplots = 3, subplotid=1))

  Step Species AdultAbsDen    simMean dixonPval    tTestPval dSig tsig
1    1    ABMA         762 801.632043         0 5.319487e-17  Sig  Sig
2    6    ABMA         727 826.485113         0 5.342942e-17  Sig  Sig
3   11    ABMA         682 825.336253         0 9.437995e-18  Sig  Sig
4   16    ABMA         630 826.485347         0 1.388488e-18  Sig  Sig
5   21    ABMA         587 829.690373         0 5.342463e-20  Sig  Sig
7    1    PIMO           3   2.660621         0 6.403238e-05  Sig  Sig
```
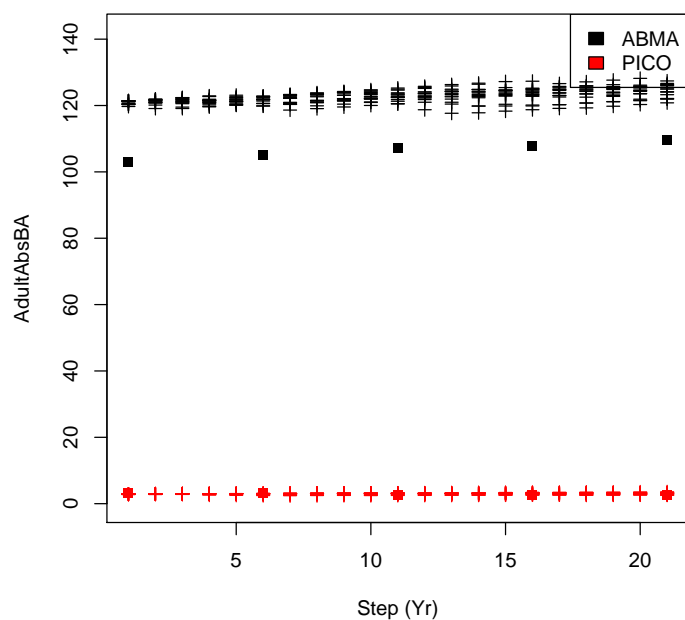
3.5 POFLABMA: Adult Basal Area and Density

```
> head(processTestPlot("POFLABMA", "outfiles/c", 0,
+                      charactername="AdultAbsBA",
+                      writefile="outfiles/c/means/POFLABMA-AdultAbsBA.csv",
+                      numsubplots = 3, subplotid=1))
```
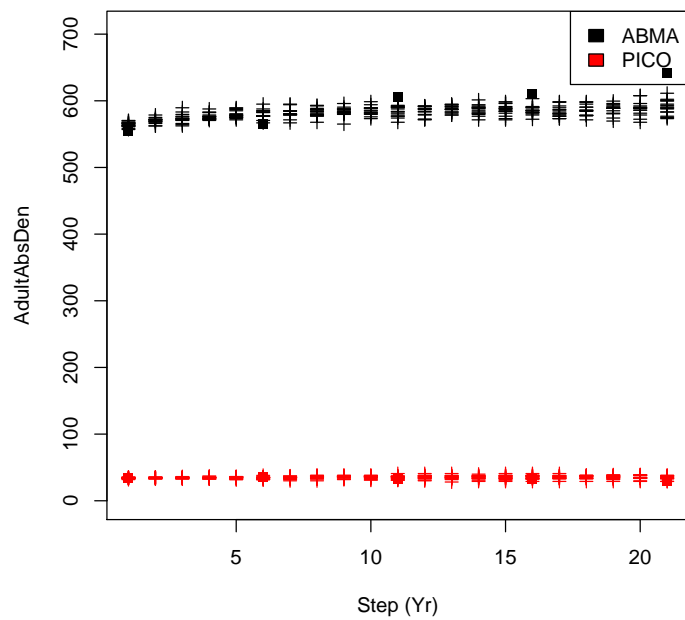
```
  Step Species AdultAbsBA    simMean dixonPval    tTestPval dSig tsig
1    1    ABMA 102.873900 120.913690         0 1.041648e-22  Sig  Sig
2    6    ABMA 105.098894 121.649977         0 1.080873e-18  Sig  Sig
3   11    ABMA 107.131277 122.854124         0 4.521966e-16  Sig  Sig
4   16    ABMA 107.930403 123.423273         0 2.613237e-13  Sig  Sig
7   21    ABMA 109.695510 124.425515         0 9.365773e-14  Sig  Sig
8    1    PICO   3.081969   2.888396         0 1.709365e-10  Sig  Sig
```


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```
>    head(processTestPlot("POFLABMA", "outfiles/c", 0,
+                    charactername="AdultAbsDen",
+                    writefile="outfiles/c/means/POFLABMA-AdultAbsDen.csv",
+                    numsubplots = 3, subplotid=1))

  Step Species AdultAbsDen    simMean    dixonPval     tTestPval dSig tsig
1    1    ABMA         555 564.41421 0.835116353 1.602264e-07   NS  Sig
2    6    ABMA         565 580.13641 0.327265919 7.125496e-07   NS  Sig
3   11    ABMA         606 583.88545 0.163809003 2.522971e-08   NS  Sig
4   16    ABMA         610 585.69947 0.007568299 1.936853e-09  Sig  Sig
7   21    ABMA         642 590.05306 0.014729020 2.631784e-11  Sig  Sig
8    1    PICO          34  33.98337 0.110789543 9.505866e-01   NS   NS
```
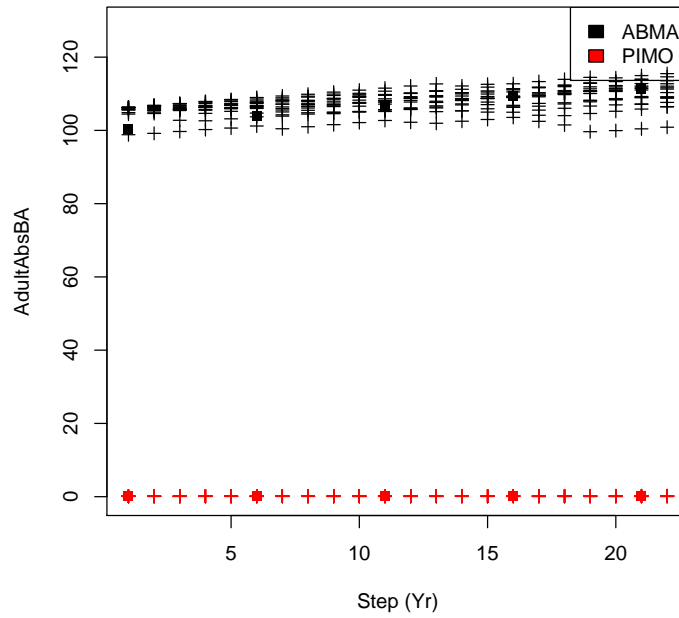
3.6 SFTRABMA: Adult Basal Area and Density
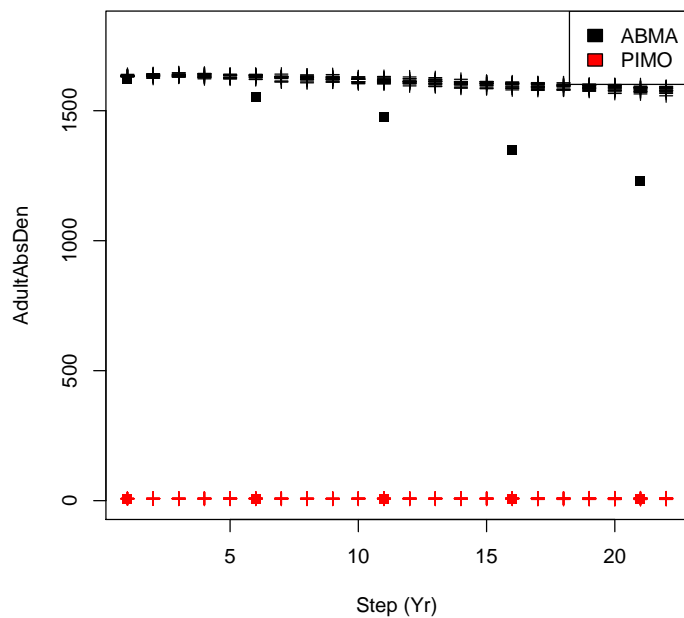
```
> head(processTestPlot("SFTRABMA", "outfiles/c", 0,
+                  charactername="AdultAbsBA",
+                  writefile="outfiles/c/means/SFTRABMA-AdultAbsBA.csv",
+                  numsubplots = 3, subplotid=1))
```

	Step	Species	AdultAbsBA	simMean	dixonPval	tTestPval	dSig	tsig
1	1	ABMA	100.5079451	105.4173007	0.0000000	9.841586e-08	Sig	Sig
2	6	ABMA	104.0460566	106.5648887	0.3526843	3.249788e-04	NS	Sig
5	11	ABMA	106.7590529	107.8781513	0.3235351	8.514254e-02	NS	NS
7	16	ABMA	109.5121569	108.7176167	0.5192317	2.568945e-01	NS	NS
8	21	ABMA	111.2301741	109.9836540	0.1150284	2.246930e-01	NS	NS
10	1	PIMO	0.1356692	0.1248062	0.0000000	9.384759e-02	Sig	NS

```
>    head(processTestPlot("SFTRABMA", "outfiles/c", 0,
+                   charactername="AdultAbsDen",
+                   writefile="outfiles/c/means/SFTRABMA-AdultAbsDen.csv",
+                   numsubplots = 3, subplotid=1))

   Step Species AdultAbsDen     simMean   dixonPval     tTestPval dSig tsig
1     1    ABMA        1623 1633.497998 0.006700698 1.593483e-10  Sig  Sig
2     6    ABMA        1554 1632.047253 0.000000000 5.695210e-17  Sig  Sig
5    11    ABMA        1477 1615.661420 0.000000000 9.174078e-19  Sig  Sig
7    16    ABMA        1348 1598.488353 0.000000000 1.554857e-21  Sig  Sig
8    21    ABMA        1228 1583.310187 0.000000000 1.690689e-23  Sig  Sig
10    1    PIMO           7    7.921395 0.110767656 1.136709e-05   NS  Sig
```
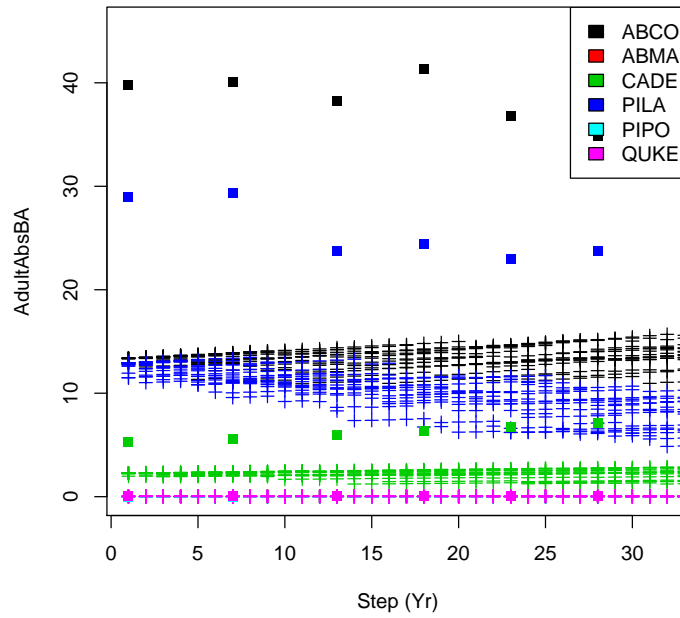
3.7   SUPILA: Adult Basal Area and Density

```
> head(processTestPlot("SUPILA", "outfiles/c", 0,
+                   charactername="AdultAbsBA",
+                   writefile="outfiles/c/means/SUPILA-AdultAbsBA.csv",
+                   numsubplots = 3, subplotid=1))
```

```
  Step Species AdultAbsBA  simMean dixonPval      tTestPval dSig tsig
1    1    ABCO   39.81285 13.32869         0  2.002645e-33  Sig  Sig
2    7    ABCO   40.09227 13.16349         0  2.926223e-23  Sig  Sig
3   13    ABCO   38.26280 13.15554         0  4.011047e-21  Sig  Sig
4   18    ABCO   41.36284 13.34484         0  5.455424e-22  Sig  Sig
5   23    ABCO   36.77110 13.34093         0  3.876539e-20  Sig  Sig
6   28    ABCO   34.84711 13.55376         0  1.989345e-19  Sig  Sig
```

```
>    head(processTestPlot("SUPILA", "outfiles/c", 0,
+                     charactername="AdultAbsDen",
+                     writefile="outfiles/c/means/SUPILA-AdultAbsDen.csv",
+                     numsubplots = 3, subplotid=1))

  Step Species AdultAbsDen    simMean dixonPval    tTestPval dSig tsig
1    1    ABCO         522   407.7040         0 4.152468e-18  Sig  Sig
2    7    ABCO         538   689.7777         0 3.962436e-15  Sig  Sig
3   13    ABCO         539   813.1554         0 3.943891e-18  Sig  Sig
4   18    ABCO         571   900.9776         0 8.995192e-20  Sig  Sig
5   23    ABCO         553   998.9926         0 4.039590e-19  Sig  Sig
6   28    ABCO         525  1085.8076         0 4.159587e-21  Sig  Sig
```
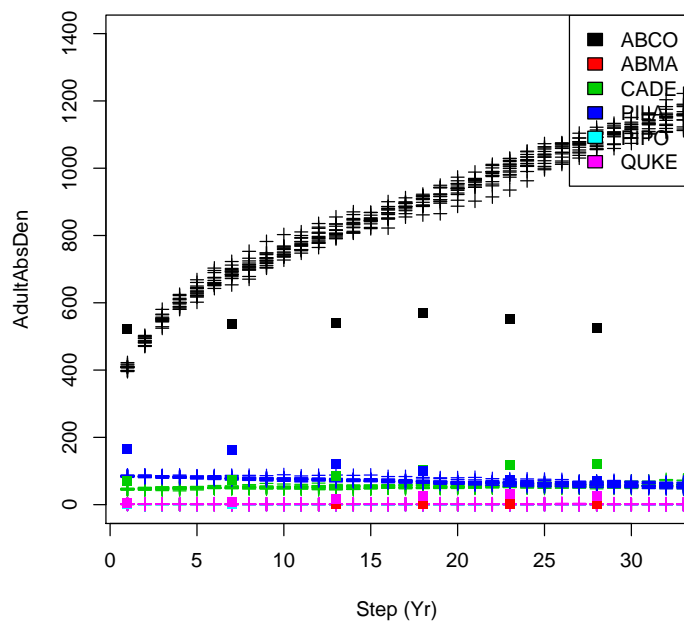
3.8 Averages For All Plots

For time saving and an issue with loading a bunch of files needlessly, I wrote the means, by species, across seven plots, into a separate file for each of the two characters (Basal Area and Density). I will read those files in and plot the simulated against the expected/real plot data. If there is a slope of 1, we can assume that our model did a decent job at predicting that variable.

```
> library(disperseR)
>   store <- readCSVs("outfiles/c/means")
>   eval(parse(text=store))
>   ## Ok, let's look at absolute basal area
>   AllAbsBA <- rbind(bbbpipoadultabsba, frpijeadultabsba, emridgeadultabsba,
+                     pgabmaadultabsba, poflabmaadultabsba, sftrabmaadultabsba,
+                     supilaadultabsba)
>   ## Means of simulated BA by step and species
>   AllAbsBAmeans <- aggregate(AllAbsBA$simMean,
+                              by=list(AllAbsBA$Step, AllAbsBA$Species),
+                              FUN=mean, na.rm=T)
>   ## Means of Expected/Actual BA by step and species
>   AllAbsBAmeans$expmean <- aggregate(AllAbsBA$AdultAbsBA,
+                              by=list(AllAbsBA$Step, AllAbsBA$Species),
+                              FUN=mean, na.rm=T)[,3]
>   ## Adjusting column names and writing file for later
>   colnames(AllAbsBAmeans) <- c("Step", "Species", "SimAbsBA", "ExpAbsBA")
>   write.csv(AllAbsBAmeans, file="outfiles/c/081815-adultba.csv", row.names=F)
>   ## make the plot
> plot(AllAbsBAmeans[,"SimAbsBA"],AllAbsBAmeans[,"ExpAbsBA"],
+      col=as.factor(AllAbsBA$Species),
+      xlab="Simulated Means", ylab="Expected Means",
+      main="Group Adult Asbolute Basal Area")
>   abline(0,1)
>   legend("topleft",
+          legend=as.factor(unique(AllAbsBA$Species)),
+          fill=as.factor(unique(AllAbsBA$Species)))
>   ## get the slope and r2 of the linear model line
>   summary(lm(SimAbsBA ~ ExpAbsBA, data=AllAbsBAmeans))

Call:
lm(formula = SimAbsBA ~ ExpAbsBA, data = AllAbsBAmeans)

Residuals:
    Min      1Q   Median      3Q      Max
-25.2592  0.6817  1.5731  1.6701  12.9618

Coefficients:
          Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept) -1.59862     0.68250  -2.342    0.021 *
ExpAbsBA     0.97195     0.02807  34.626   <2e-16 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

Residual standard error: 6.284 on 110 degrees of freedom
Multiple R-squared:  0.916,         Adjusted R-squared:  0.9152
F-statistic:  1199 on 1 and 110 DF,  p-value: < 2.2e-16
```

Group Adult Asbolute Basal Area

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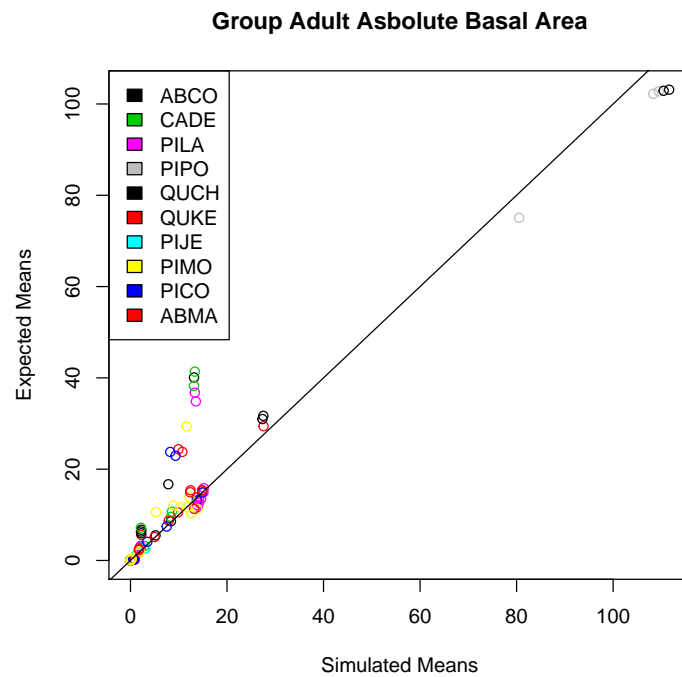
```
>   ## And absolute density
>   AllAbsDenDf <- rbind(bbbpipoadultabsden, frpijeadultabsden, emridgeadultabsden,
+                      pgabmaadultabsden, poflabmaadultabsden, sftrabmaadultabsden,
+                      supilaadultabsden)
>   AllAbsDen <- aggregate(AllAbsDenDf$simMean,
+                             by=list(AllAbsDenDf$Step, AllAbsDenDf$Species),
+                             FUN=mean, na.rm=T)
>   AllAbsDen$expmean <- aggregate(AllAbsDenDf$AdultAbsDen,
+                                   by=list(AllAbsDenDf$Step, AllAbsDenDf$Species),
+                                   FUN=mean, na.rm=T)[,3]
>   colnames(AllAbsDen) <- c("Step", "Species", "SimAbsDen", "ExpAbsDen")
>   write.csv(AllAbsDen, file="outfiles/c/081815-adultdensity.csv", row.names=F)
>   plot(AllAbsDen[,"SimAbsDen"], AllAbsDen[,"ExpAbsDen"],
+        col=as.factor(AllAbsDen$Species), main="Group Adult Absolute Density",
+        xlab="Simulated Absolute Density", ylab="Expected Means")
>   abline(0,1)
>   legend("topleft", legend=unique(as.factor(AllAbsDen$Species)),
+          fill=unique(as.factor(AllAbsDen$Species)))
>   summary(lm(SimAbsDen ~ ExpAbsDen, data=AllAbsDen))

Call:
lm(formula = SimAbsDen ~ ExpAbsDen, data = AllAbsDen)

Residuals:
    Min      1Q  Median      3Q     Max
-214.24  -57.13   -7.16    1.14  647.01

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.62549   14.58254  -0.111    0.911
ExpAbsDen    1.29525    0.05748  22.535   <2e-16 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

Residual standard error: 129 on 110 degrees of freedom
Multiple R-squared:  0.822,      Adjusted R-squared:  0.8203
F-statistic: 507.8 on 1 and 110 DF,  p-value: < 2.2e-16

>
```
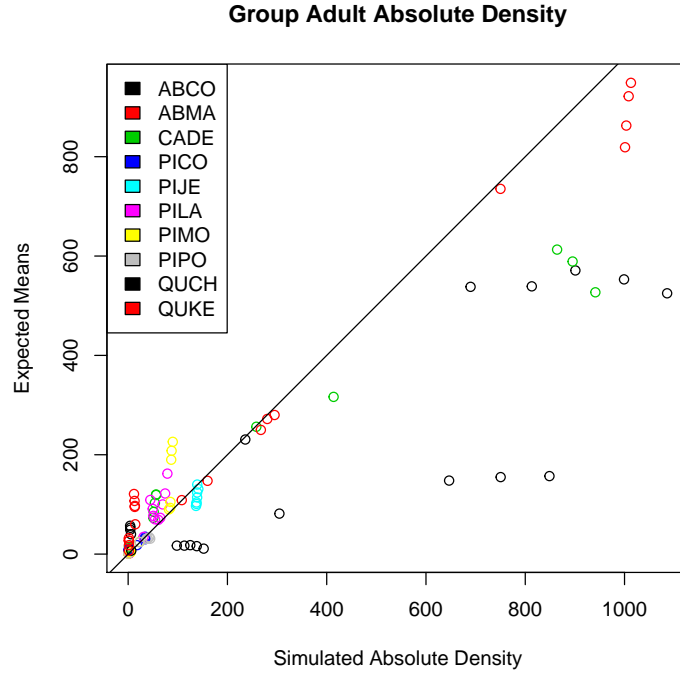
Group Adult Absolute Density

4 Next Steps

The next step is to readjust the subplot boundaries so they match better. Initial subplot grid was set at 8m x 8m, but we should set it to 5m x 5m so we cut out as many simulated trees as possible. We may also need to examine SUPILA, because it seems like the tree map I'm entering doesn't match the real plot data well. It might just be a subplot boundary, or it may have been a programming error that I haven't caught yet.