

Calibrating Parameters of Sierra Nevada SORTIE-ND model with USGS and FIA Data

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August 18, 2015

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 081815b-X.xml. The tree maps in 081815b-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 0.9-1.1 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 0.9-1.1 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.

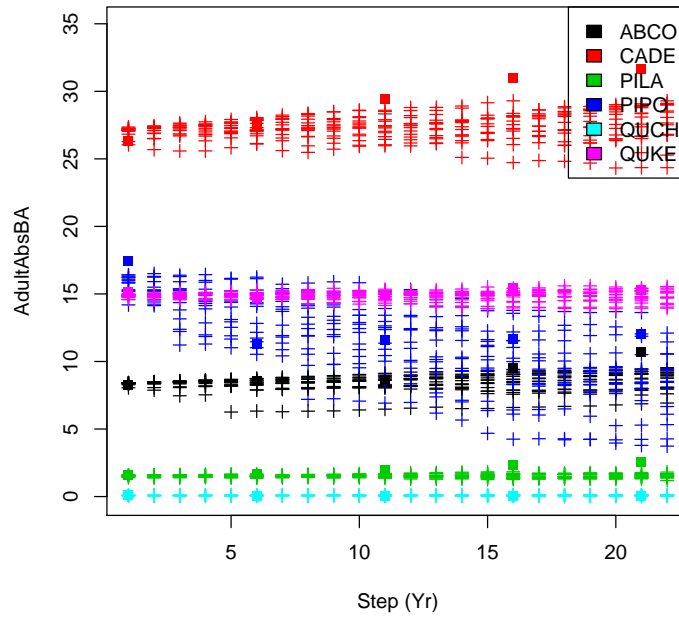
3 Results

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/b", 0,
+                       charactername="AdultAbsBA",
+                       writefile="outfiles/b/means/BBBPIPO-AdultAbsBA.csv",
+                       numsubplots = 3, subplotid=1))
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	8.225156	8.356612	8.760073e-05	Sig
2	6	ABCO	8.558442	8.275485	9.024780e-02	NS
3	11	ABCO	8.602290	8.418540	2.885252e-01	NS
4	16	ABCO	9.553299	8.422240	4.167163e-05	Sig
5	21	ABCO	10.693378	8.537665	3.954507e-08	Sig
6	1	CADE	26.306953	27.025364	3.158378e-06	Sig

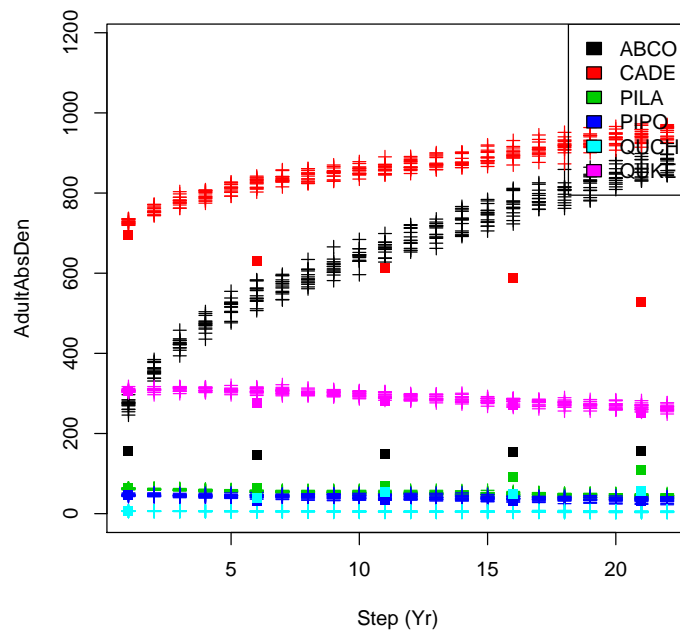


```

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

```

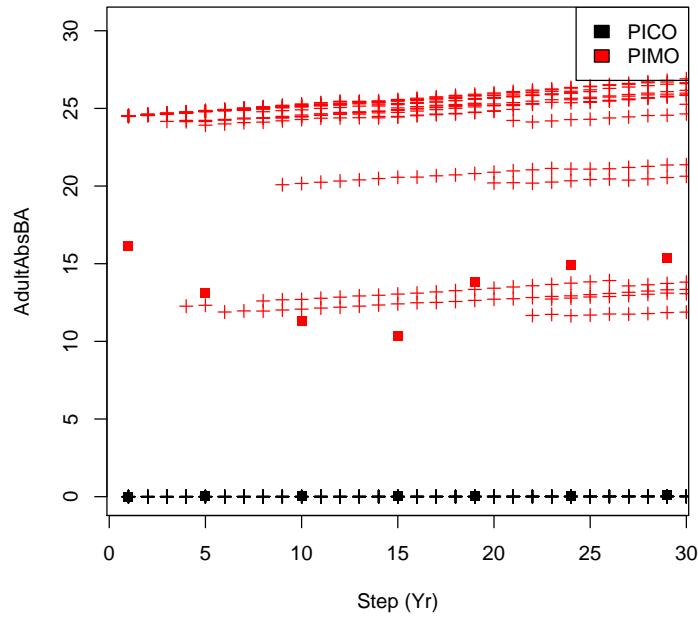
	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	157	272.0044	5.351445e-15	Sig
2	6	ABCO	147	548.0153	1.043808e-18	Sig
3	11	ABCO	148	661.1194	1.703467e-21	Sig
4	16	ABCO	155	768.9226	9.948389e-21	Sig
5	21	ABCO	157	858.4813	1.922510e-22	Sig
6	1	CADE	695	727.9338	2.310503e-12	Sig



3.2 EMRIDGE: Adult Basal Area and Density

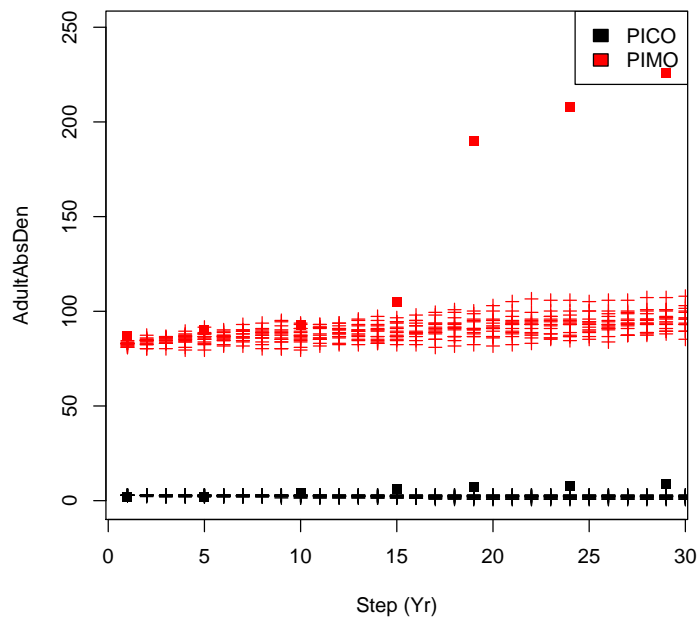
```
> head(processTestPlot("EMRIDGE", "outfiles/b", 0,
+                      charactername="AdultAbsBA",
+                      writefile="outfiles/b/means/EMRIDGE-AdultAbsBA.csv",
+                      numsubplots = 3, subplotid=1))
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	PICO	0.005724781	0.004391130	1.000000e+00	NS
2	5	PICO	0.011388300	0.005216017	1.502738e-11	Sig
3	10	PICO	0.019037311	0.006091980	6.409793e-12	Sig
4	15	PICO	0.022427097	0.007640869	6.455906e-12	Sig
5	19	PICO	0.035197701	0.008938212	8.655643e-14	Sig
6	24	PICO	0.051995836	0.011130739	2.576951e-15	Sig



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

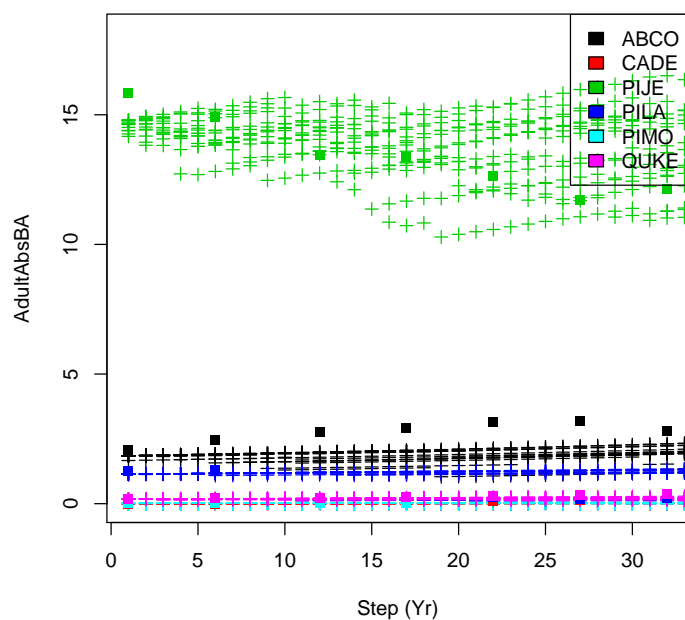
	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	PICO	2	2.840910	1.000000e+00	NS
2	5	PICO	2	2.651515	1.943905e-06	Sig
3	10	PICO	4	2.462121	2.052555e-08	Sig
4	15	PICO	6	2.225377	1.255616e-13	Sig
5	19	PICO	7	2.035984	3.833447e-13	Sig
6	24	PICO	8	2.035984	3.063222e-14	Sig



3.3 FRPIJE: Adult Basal Area and Density

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

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	2.053798	1.832747	3.192128e-11	Sig
2	6	ABCO	2.453112	1.852472	1.476722e-12	Sig
3	12	ABCO	2.764404	1.768817	9.740766e-11	Sig
4	17	ABCO	2.916810	1.823764	2.617219e-11	Sig
5	22	ABCO	3.169380	1.831291	2.907220e-11	Sig
6	27	ABCO	3.181021	1.866572	1.589845e-10	Sig

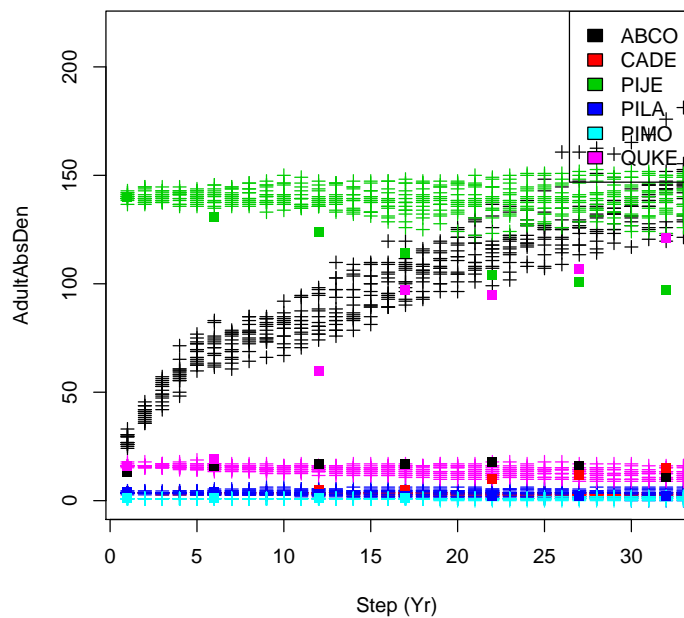


```

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

```

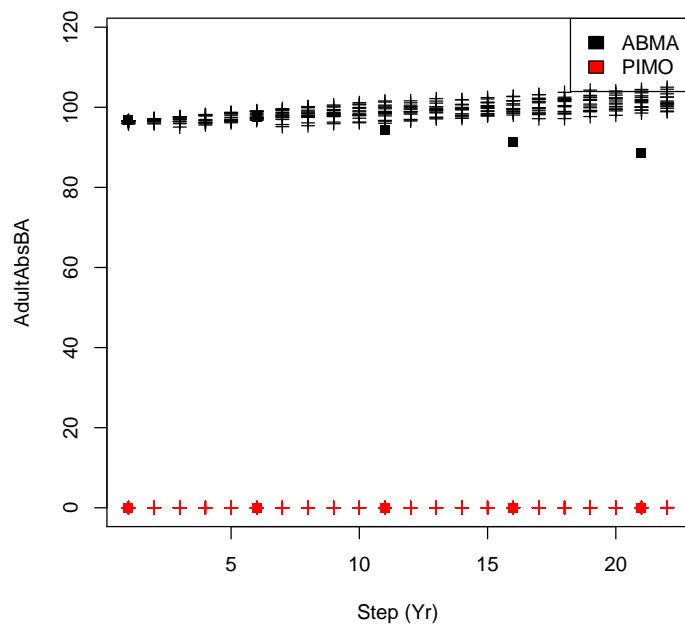
	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	13	27.97620	1.773236e-12	Sig
2	6	ABCO	16	71.13095	1.037557e-14	Sig
3	12	ABCO	17	85.05953	1.329616e-14	Sig
4	17	ABCO	17	102.85714	7.282946e-16	Sig
5	22	ABCO	18	118.03571	3.713129e-15	Sig
6	27	ABCO	16	128.86905	2.304922e-15	Sig



3.4 PGABMA: Adult Basal Area and Density

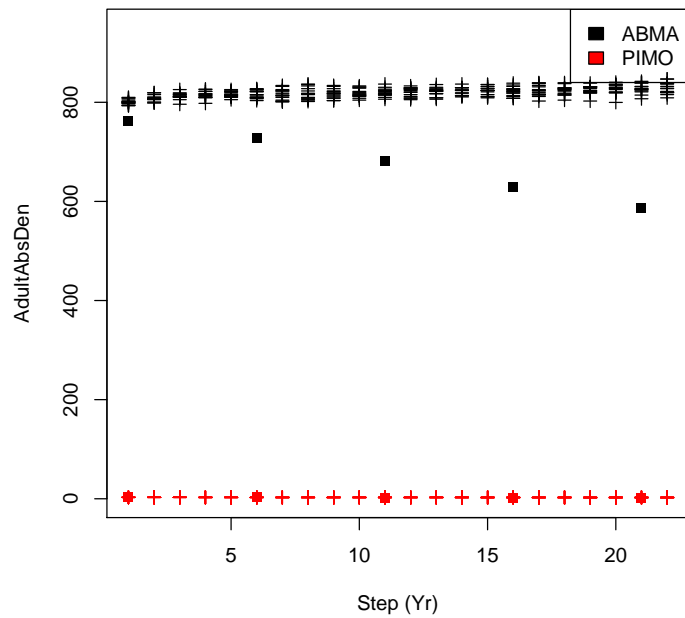
```
> head(processTestPlot("PGABMA", "outfiles/b", 0,
+                       charactername="AdultAbsBA",
+                       writefile="outfiles/b/means/PGABMA-AdultAbsBA.csv",
+                       numsubplots = 3, subplotid=1))
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	96.84838877	96.4346400	6.398665e-05	Sig
2	6	ABMA	97.52063023	97.9088280	9.480337e-02	NS
3	11	ABMA	94.43564576	98.9058060	6.525362e-08	Sig
4	16	ABMA	91.25577994	100.2608587	1.850349e-12	Sig
5	21	ABMA	88.46650645	101.4025287	1.595018e-13	Sig
7	1	PIMO	0.02068744	0.0199037	1.000000e+00	NS



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

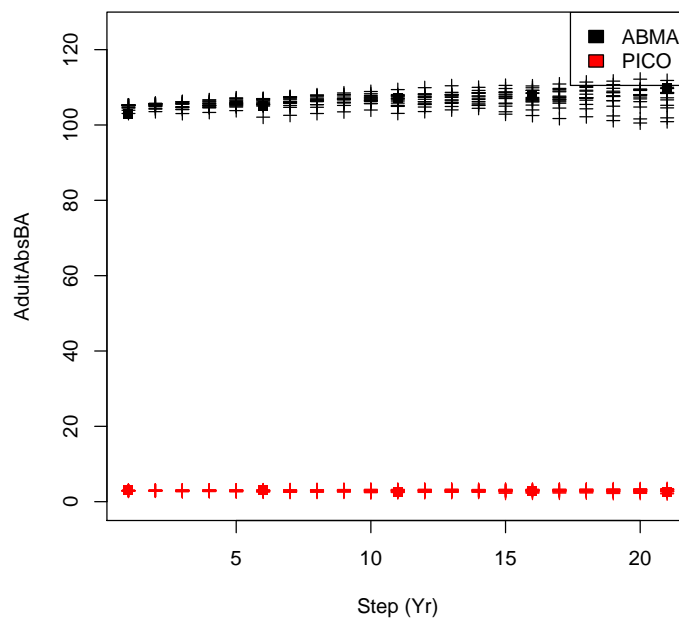
	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	762	800.54198	9.336238e-14	Sig
2	6	ABMA	727	816.56805	2.708323e-16	Sig
3	11	ABMA	682	819.77299	4.687219e-19	Sig
4	16	ABMA	630	822.05367	4.569513e-20	Sig
5	21	ABMA	587	828.09426	4.157436e-21	Sig
7	1	PIMO	3	2.77367	1.000000e+00	NS



3.5 POFLABMA: Adult Basal Area and Density

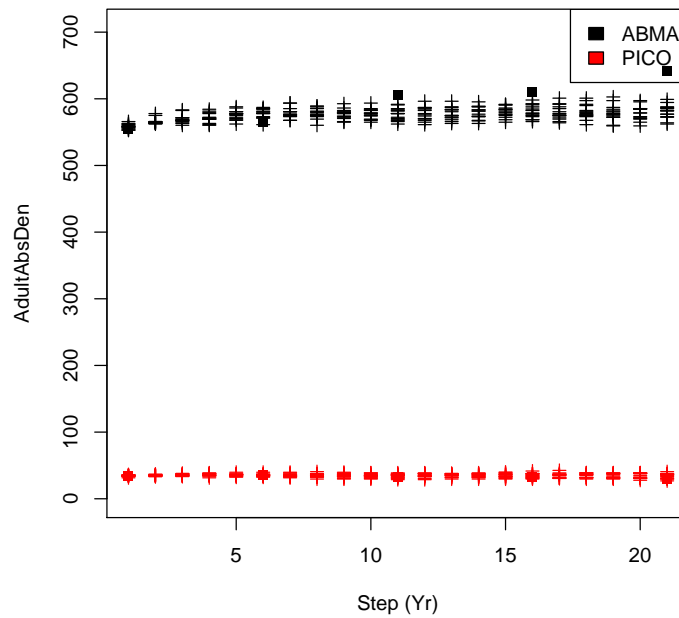
```
> head(processTestPlot("POFLABMA", "outfiles/b", 0,
+                       charactername="AdultAbsBA",
+                       writefile="outfiles/b/means/POFLABMA-AdultAbsBA.csv",
+                       numsubplots = 3, subplotid=1))
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	102.873900	104.907159	8.350155e-09	Sig
2	6	ABMA	105.098894	105.757877	5.441039e-02	NS
3	11	ABMA	107.131277	106.614039	2.265813e-01	NS
4	16	ABMA	107.930403	107.165042	1.967842e-01	NS
7	21	ABMA	109.695510	107.345884	9.667561e-03	Sig
8	1	PICO	3.081969	2.933476	8.452554e-08	Sig



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

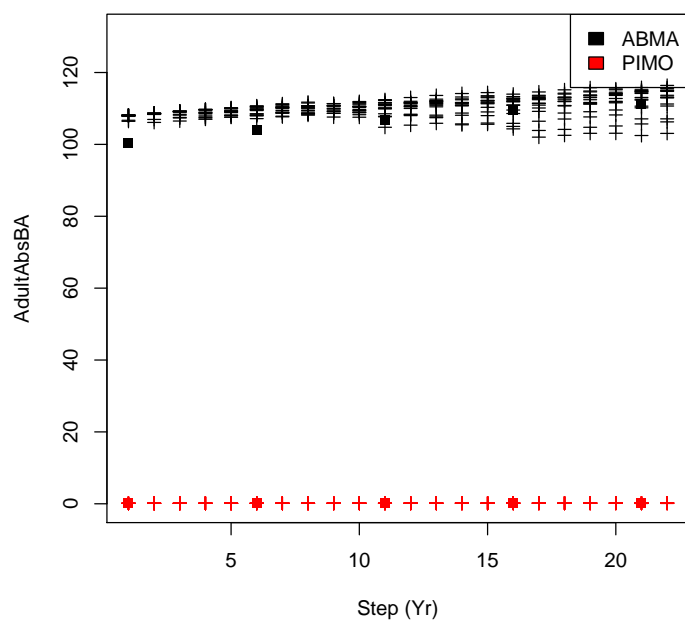
	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	555	558.30883	3.890511e-03	Sig
2	6	ABMA	565	577.72467	5.748914e-06	Sig
3	11	ABMA	606	577.10817	6.457894e-09	Sig
4	16	ABMA	610	580.49799	1.160132e-08	Sig
7	21	ABMA	642	580.80627	1.421047e-12	Sig
8	1	PICO	34	34.45514	1.412592e-01	NS



3.6 SFTRABMA: Adult Basal Area and Density

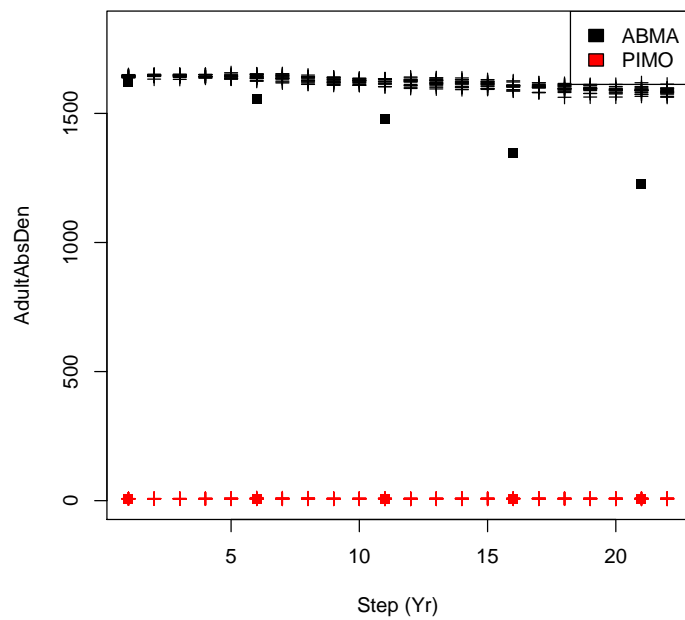
```
> head(processTestPlot("SFTRABMA", "outfiles/b", 0,
+                       charactername="AdultAbsBA",
+                       writefile="outfiles/b/means/SFTRABMA-AdultAbsBA.csv",
+                       numsubplots = 3, subplotid=1))
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	100.5079451	107.844441	1.432249e-17	Sig
2	6	ABMA	104.0460566	109.270361	4.618241e-11	Sig
5	11	ABMA	106.7590529	110.041885	2.463131e-05	Sig
7	16	ABMA	109.5121569	110.438563	2.697802e-01	NS
8	21	ABMA	111.2301741	111.874508	5.396454e-01	NS
10	1	PIMO	0.1356692	0.132683	1.000000e+00	NS



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

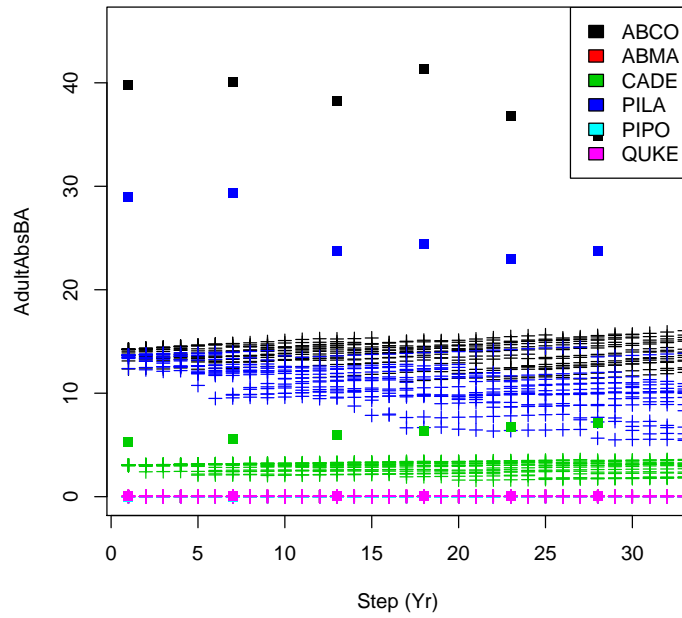
	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	1623	1643.737872	2.405601e-12	Sig
2	6	ABMA	1554	1641.765233	2.052909e-15	Sig
5	11	ABMA	1477	1623.027753	1.420864e-17	Sig
7	16	ABMA	1348	1605.338380	7.157469e-21	Sig
8	21	ABMA	1228	1589.497887	7.197514e-22	Sig
10	1	PIMO	7	7.458083	3.192993e-06	Sig



3.7 SUPILA: Adult Basal Area and Density

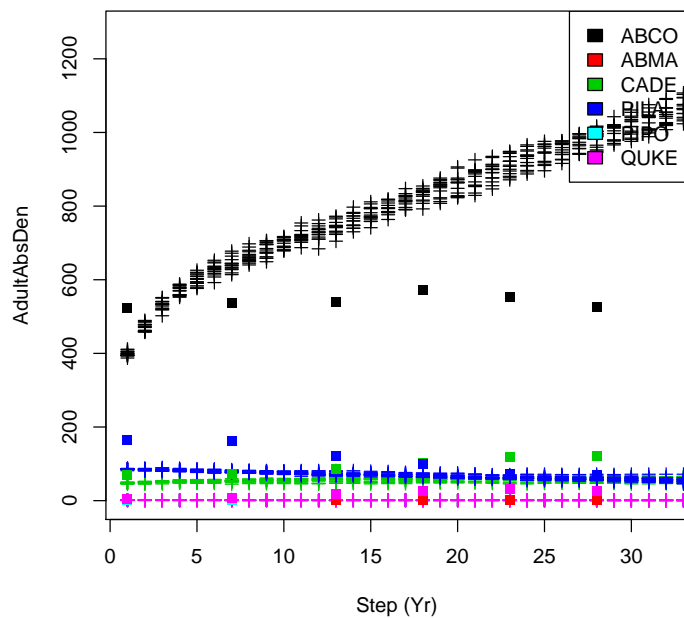
```
> head(processTestPlot("SUPILA", "outfiles/b", 0,
+                      charactername="AdultAbsBA",
+                      writefile="outfiles/b/means/SUPILA-AdultAbsBA.csv",
+                      numsubplots = 3, subplotid=1))
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	39.81285	13.91487	6.046467e-25	Sig
2	7	ABCO	40.09227	13.84779	1.812546e-23	Sig
3	13	ABCO	38.26280	13.92572	2.628109e-21	Sig
4	18	ABCO	41.36284	13.84776	1.526987e-21	Sig
5	23	ABCO	36.77110	13.66553	5.406886e-19	Sig
6	28	ABCO	34.84711	13.80881	2.009959e-18	Sig



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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	522	398.9156	2.630527e-19	Sig
2	7	ABCO	538	642.6445	2.501407e-12	Sig
3	13	ABCO	539	743.5159	2.751422e-16	Sig
4	18	ABCO	571	830.8886	2.870883e-18	Sig
5	23	ABCO	553	911.2990	1.093321e-17	Sig
6	28	ABCO	525	985.2788	1.414485e-19	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/b/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$Species),
+                                     FUN=mean, na.rm=T)[,3]
> ## Adjusting column names and writing file for later
> colnames(AllAbsBAmeans) <- c("Step", "Species", "SimAbsBA", "ExpAbsBA")
> write.csv(AllAbsBAmeans, file="outfiles/b/081815-adultba.csv", row.names=F)
> ## make the plot
> plot(AllAbsBAmeans[, "SimAbsBA"], AllAbsBAmeans[, "ExpAbsBA"],
+      col=as.factor(AllAbsBA$Species),
+      xlab="Simulated Means", ylab="Expected Means",
+      main="Group Adult Absolute 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
	-24.1954	0.1530	0.7945	1.2403	14.2258

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
--	----------	------------	---------	----------

```

(Intercept) -0.80691    0.69111   -1.168    0.246
ExpAbsBA    0.93925    0.02842   33.044   <2e-16 ***

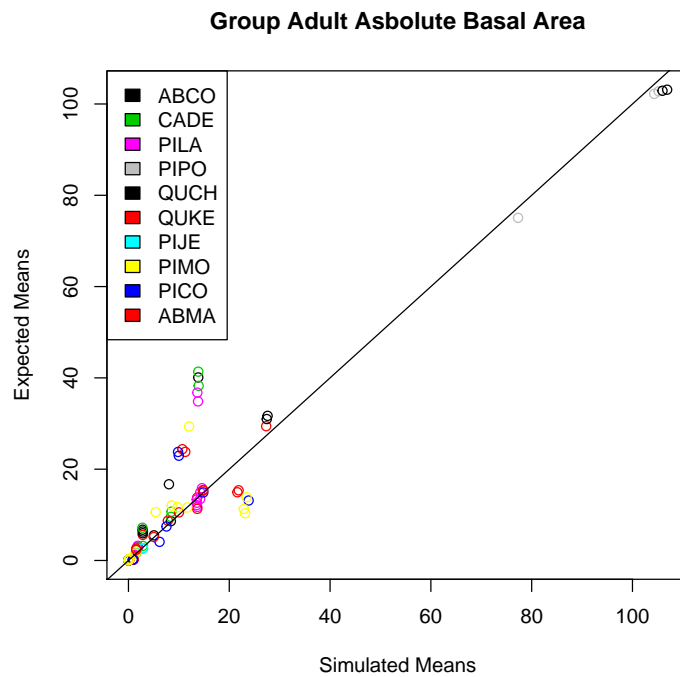
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Residual standard error: 6.364 on 110 degrees of freedom
Multiple R-squared:  0.9085,    Adjusted R-squared:  0.9076
F-statistic: 1092 on 1 and 110 DF,  p-value: < 2.2e-16

```



```

> ## 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$Species),
+                                FUN=mean, na.rm=T)[,3]
> colnames(AllAbsDen) <- c("Step", "Species", "SimAbsDen", "ExpAbsDen")
> write.csv(AllAbsDen, file="outfiles/b/081815-adultdensity.csv", row.names=F)
> plot(AllAbsDen[, "SimAbsDen"], AllAbsDen[, "ExpAbsDen"],
+      col=as.factor(AllAbsDen$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
	-189.87	-50.05	-7.25	0.27	660.32

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-0.5814	14.1330	-0.041	0.967
ExpAbsDen	1.2659	0.0557	22.725	<2e-16 ***

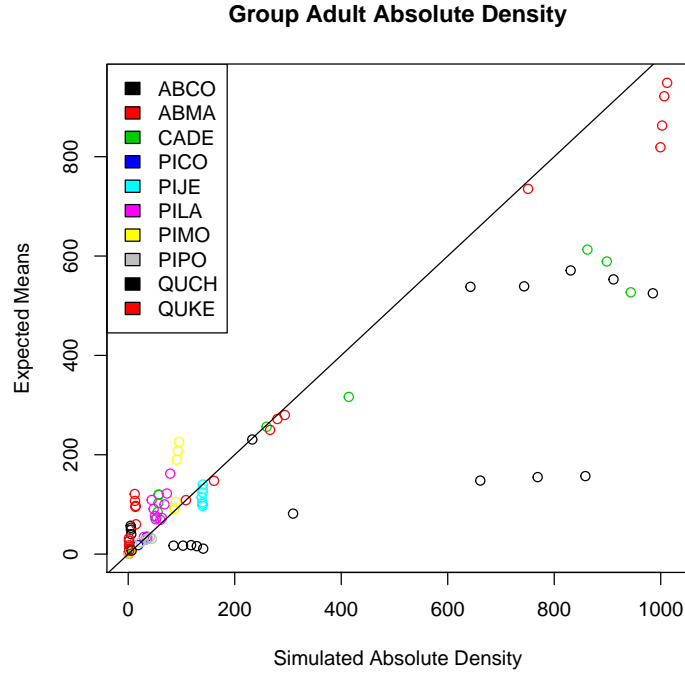
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 125 on 110 degrees of freedom

Multiple R-squared: 0.8244, Adjusted R-squared: 0.8228

F-statistic: 516.4 on 1 and 110 DF, p-value: < 2.2e-16

>



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.