

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

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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 081715b-X.xml. The tree maps in 081715b-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, if it ever gets fixed.

2 Methods

2.1 Allometry Parameters

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

2.2 Dispersal Parameters

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.

2.3 Growth Parameters

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 eight calibration plots, by species. This run did not use variation in growth rate, but instead used a static increase.

2.4 Mortality Parameters

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 eight calibration plots. Those resulting number of dead and alive per species were combined to estimate mean mortality rate as $\frac{n_{dead}}{n_{dead} + n_{alive}}$.

2.5 Expected Plot Results

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`.

2.6 Simulations

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, if it ever gets fixed.

I ran each parameter file **ten** 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

I'll present all of the individual plots for Basal Area and Density first, then present the plots that were generated by averaging the data from each of the eight plots across species for both expected and simulated data, and plotting them against each other.

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

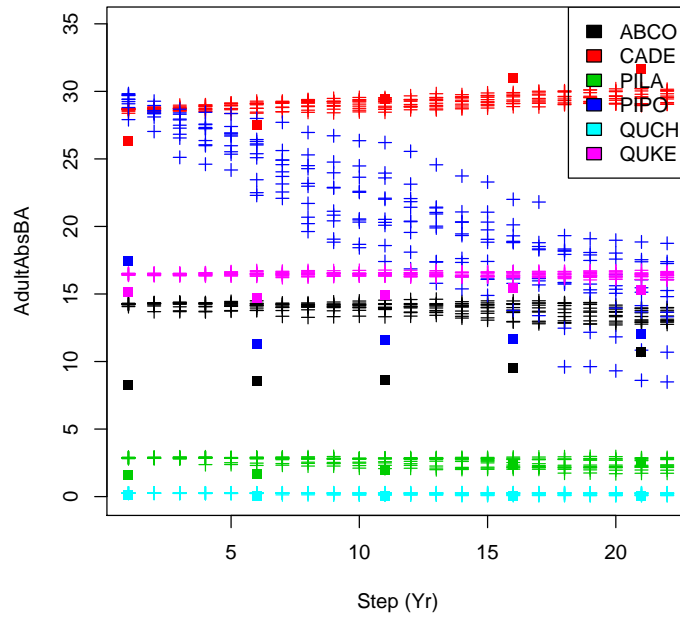
```
> library(SortieOutputs)
> processTestPlot("BBBPIPO", "outfiles/b", 0,
```

```

+           charactername="AdultAbsBA",
+           writefile="outfiles/b/means/BBBPIPO-AdultAbsBA.csv")

```

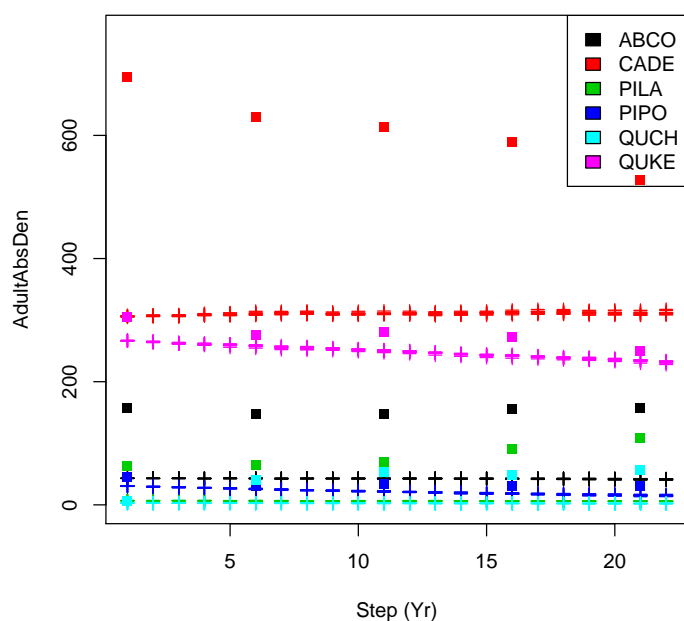
	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	8.22515648	14.2376100	6.549067e-19	Sig
2	6	ABCO	8.55844175	14.1270100	5.260934e-14	Sig
3	11	ABCO	8.60228985	14.0069500	1.469345e-12	Sig
4	16	ABCO	9.55329929	13.8280700	1.279029e-09	Sig
5	21	ABCO	10.69337808	13.3330000	2.064521e-08	Sig
6	1	CADE	26.30695258	28.6357400	1.745088e-13	Sig
7	6	CADE	27.54093222	28.9020200	1.748640e-07	Sig
8	11	CADE	29.41467906	29.0888400	1.998351e-02	Sig
9	16	CADE	30.98351713	29.3798800	1.464073e-07	Sig
10	21	CADE	31.68296924	29.5855700	1.929506e-07	Sig
12	1	PILA	1.56575066	2.8678470	3.043022e-16	Sig
13	6	PILA	1.68034838	2.7693570	4.296869e-08	Sig
14	11	PILA	1.97541059	2.6424910	2.779529e-05	Sig
16	16	PILA	2.30771569	2.4687230	1.622176e-01	NS
17	21	PILA	2.56894680	2.3700080	1.375532e-01	NS
19	1	PIPO	17.41989711	29.2867800	2.731553e-13	Sig
20	6	PIPO	11.30799599	25.1595400	2.037929e-09	Sig
21	11	PIPO	11.61260396	21.4761000	8.854455e-07	Sig
22	16	PIPO	11.66155637	18.0317600	1.576031e-05	Sig
23	21	PIPO	12.04379013	14.7674250	2.256100e-02	Sig
25	1	QUCH	0.08307961	0.2611011	1.511534e-23	Sig
26	6	QUCH	0.03701669	0.2576145	5.508118e-12	Sig
27	11	QUCH	0.02100788	0.2129564	5.037692e-06	Sig
29	16	QUCH	0.02355851	0.2005920	4.972739e-05	Sig
30	21	QUCH	0.01766050	0.1937449	7.361780e-05	Sig
31	1	QUKE	15.17823670	16.4681300	3.157926e-14	Sig
32	6	QUKE	14.68553643	16.4919600	8.715541e-12	Sig
34	11	QUKE	14.90333257	16.4829500	4.490408e-11	Sig
35	16	QUKE	15.42906912	16.4334900	1.506769e-08	Sig
36	21	QUKE	15.31791852	16.3833000	7.654549e-08	Sig



```
> processTestPlot("BBBPIPO", "outfiles/b", 0,
+                 charactername="AdultAbsDen",
+                 writefile="outfiles/b/means/BBBPIPO-AdultAbsDen.csv")
```

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	157	43.088880	3.661824e-26	Sig
2	6	ABCO	147	42.911110	3.820448e-23	Sig
3	11	ABCO	148	42.611100	9.451535e-22	Sig
4	16	ABCO	155	42.466660	7.217887e-22	Sig
5	21	ABCO	157	41.500010	5.904413e-21	Sig
6	1	CADE	695	306.155500	1.166643e-25	Sig
7	6	CADE	630	310.444500	2.052294e-21	Sig
8	11	CADE	613	310.844400	6.462745e-22	Sig
9	16	CADE	589	312.244400	1.910278e-20	Sig
10	21	CADE	527	311.199900	1.841794e-18	Sig
12	1	PILA	63	6.888890	1.215611e-26	Sig
13	6	PILA	65	6.733333	9.124233e-22	Sig
14	11	PILA	70	6.544445	1.809043e-22	Sig
16	16	PILA	91	6.255555	1.222591e-22	Sig
17	21	PILA	109	5.911112	6.430430e-24	Sig
19	1	PIPO	46	30.477780	5.719067e-16	Sig
20	6	PIPO	31	25.700010	1.647632e-09	Sig

21	11	PIPO	34	21.777790	3.422947e-13	Sig
22	16	PIPO	31	18.211110	1.124004e-11	Sig
23	21	PIPO	31	15.288900	6.210238e-12	Sig
25	1	QUCH	7	2.655559	2.383084e-20	Sig
26	6	QUCH	40	2.655557	4.059222e-22	Sig
27	11	QUCH	53	2.477779	1.280650e-22	Sig
29	16	QUCH	49	2.388889	7.834421e-22	Sig
30	21	QUCH	57	2.166665	8.066293e-23	Sig
31	1	QUKE	305	266.611000	1.549538e-19	Sig
32	6	QUKE	276	257.855600	3.054834e-11	Sig
34	11	QUKE	280	250.055600	1.050047e-13	Sig
35	16	QUKE	272	241.833300	5.882108e-13	Sig
36	21	QUKE	250	233.999900	3.180558e-10	Sig

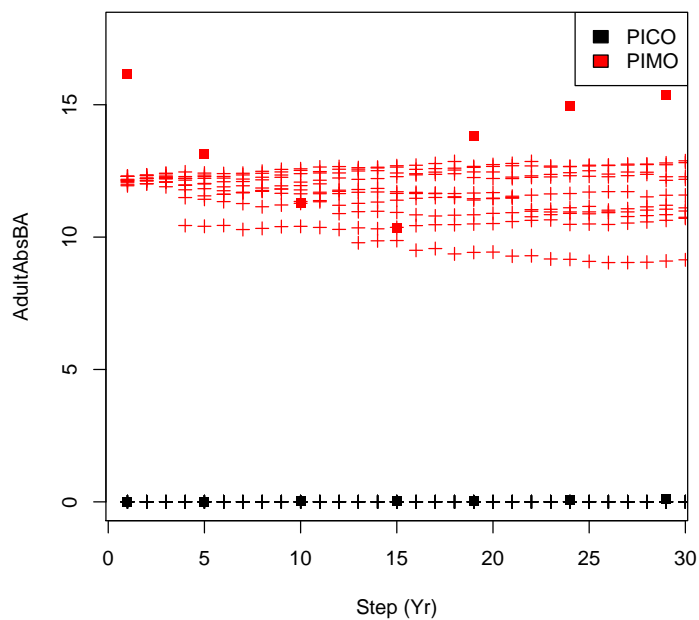


3.2 EMRIDGE: Adult Basal Area and Density

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

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	PICO	0.005724781	0.00000	0.000000e+00	Sig

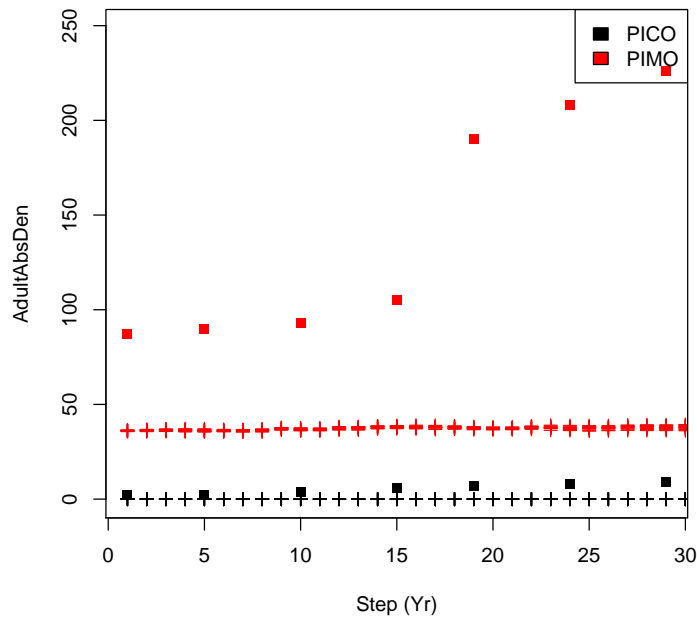
2	5	PICO	0.011388300	0.00000	0.000000e+00	Sig
3	10	PICO	0.019037311	0.00000	0.000000e+00	Sig
4	15	PICO	0.022427097	0.00000	0.000000e+00	Sig
5	19	PICO	0.035197701	0.00000	0.000000e+00	Sig
6	24	PICO	0.051995836	0.00000	0.000000e+00	Sig
7	29	PICO	0.103346859	0.00000	0.000000e+00	Sig
8	1	PIMO	16.164999910	12.14444	6.363873e-15	Sig
9	5	PIMO	13.132768430	11.85243	8.869285e-05	Sig
10	10	PIMO	11.288140290	11.79665	3.967515e-02	Sig
11	15	PIMO	10.351063060	11.59757	2.802075e-03	Sig
12	19	PIMO	13.833822760	11.52935	6.768858e-05	Sig
13	24	PIMO	14.941689150	11.43285	4.268439e-06	Sig
14	29	PIMO	15.379181290	11.43757	1.547444e-06	Sig



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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	PICO	2	0.00000	0.000000e+00	Sig
2	5	PICO	2	0.00000	0.000000e+00	Sig
3	10	PICO	4	0.00000	0.000000e+00	Sig

4	15	PICO	6	0.00000	0.000000e+00	Sig
5	19	PICO	7	0.00000	0.000000e+00	Sig
6	24	PICO	8	0.00000	0.000000e+00	Sig
7	29	PICO	9	0.00000	0.000000e+00	Sig
8	1	PIMO	87	36.12221	3.059778e-22	Sig
9	5	PIMO	90	36.18890	1.265025e-19	Sig
10	10	PIMO	93	36.75555	1.092912e-19	Sig
11	15	PIMO	105	38.03333	1.932500e-20	Sig
12	19	PIMO	190	37.51110	6.407211e-24	Sig
13	24	PIMO	208	37.52223	1.284462e-22	Sig
14	29	PIMO	226	37.75556	5.311171e-22	Sig

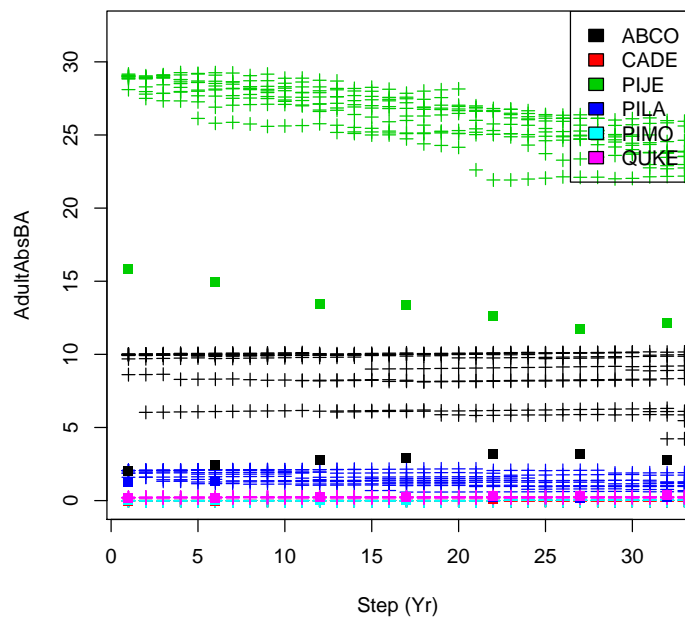


3.3 FRPIJE: Adult Basal Area and Density

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

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	2.053798223	9.8139170	8.384290e-13	Sig
2	6	ABCO	2.453112077	9.3959660	3.388869e-08	Sig
3	12	ABCO	2.764403796	9.2210530	8.275859e-08	Sig

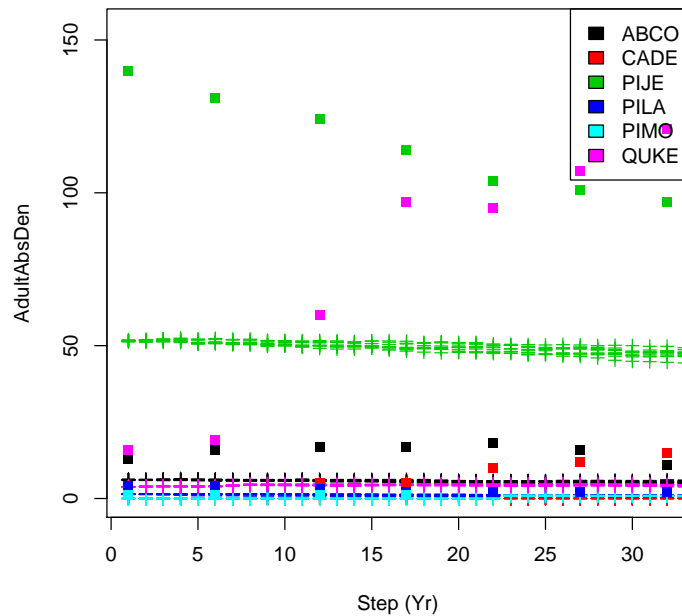
4	17	ABCO	2.916809881	8.7674910	8.924233e-07	Sig
5	22	ABCO	3.169380383	8.7386980	1.838385e-06	Sig
6	27	ABCO	3.181020797	8.7579450	1.536041e-06	Sig
7	32	ABCO	2.799051717	7.8889350	3.056962e-05	Sig
8	1	CADE	0.001053221	0.0000000	0.000000e+00	Sig
9	6	CADE	0.003677243	0.0000000	0.000000e+00	Sig
10	12	CADE	0.017887485	0.0000000	0.000000e+00	Sig
11	17	CADE	0.042952741	0.0000000	0.000000e+00	Sig
12	22	CADE	0.085254385	0.0000000	0.000000e+00	Sig
13	27	CADE	0.148603178	0.0000000	0.000000e+00	Sig
14	32	CADE	0.216574835	0.0000000	0.000000e+00	Sig
15	1	PIJE	15.837382870	28.9059700	2.897116e-16	Sig
16	6	PIJE	14.924775560	28.0468800	1.970255e-11	Sig
17	12	PIJE	13.464172680	27.3857400	2.932512e-12	Sig
18	17	PIJE	13.358516740	26.4185500	4.679986e-11	Sig
20	22	PIJE	12.633173140	25.6428900	5.242682e-10	Sig
21	27	PIJE	11.725481060	24.8286700	1.221649e-10	Sig
22	32	PIJE	12.124942370	23.9042500	2.722270e-10	Sig
23	1	PILA	1.270279256	1.9736180	1.415063e-07	Sig
24	6	PILA	1.307463234	1.7648120	3.251098e-03	Sig
25	12	PILA	0.179119109	1.6016290	1.456812e-06	Sig
26	17	PILA	0.219019786	1.3877765	1.652046e-05	Sig
27	22	PILA	0.253735251	1.3712803	1.992718e-05	Sig
28	27	PILA	0.194133601	1.2228726	4.355853e-05	Sig
29	32	PILA	0.219090472	1.1674026	3.888894e-05	Sig
30	1	PIMO	0.011689894	0.0000000	0.000000e+00	Sig
31	6	PIMO	0.013684810	0.0000000	0.000000e+00	Sig
32	12	PIMO	0.017907905	0.0000000	0.000000e+00	Sig
33	17	PIMO	0.020867293	0.0000000	0.000000e+00	Sig
34	1	QUKE	0.186653452	0.2045581	8.554022e-04	Sig
35	6	QUKE	0.200555032	0.2132743	2.731776e-02	Sig
36	12	QUKE	0.237522239	0.2226585	4.799554e-02	Sig
37	17	QUKE	0.262400569	0.2262897	1.274216e-03	Sig
40	22	QUKE	0.296468865	0.2267675	5.595709e-05	Sig
41	27	QUKE	0.333892240	0.2289142	1.083616e-06	Sig
42	32	QUKE	0.387661659	0.2279645	4.080504e-08	Sig



```
> processTestPlot("FRPIJE", "outfiles/b", 0,
+                 charactername="AdultAbsDen",
+                 writefile="outfiles/b/means/FRPIJE-AdultAbsDen.csv")
```

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	13	6.1222210	2.853894e-17	Sig
2	6	ABCO	16	6.0666660	3.921159e-17	Sig
3	12	ABCO	17	5.8444460	1.333957e-16	Sig
4	17	ABCO	17	5.6666660	7.945104e-16	Sig
5	22	ABCO	18	5.4222230	1.984356e-15	Sig
6	27	ABCO	16	5.3777790	3.257918e-14	Sig
7	32	ABCO	11	5.3666670	1.869652e-11	Sig
8	1	CADE	3	0.0000000	0.000000e+00	Sig
9	6	CADE	3	0.0000000	0.000000e+00	Sig
10	12	CADE	5	0.0000000	0.000000e+00	Sig
11	17	CADE	5	0.0000000	0.000000e+00	Sig
12	22	CADE	10	0.0000000	0.000000e+00	Sig
13	27	CADE	12	0.0000000	0.000000e+00	Sig
14	32	CADE	15	0.0000000	0.000000e+00	Sig
15	1	PIJE	140	51.5889100	1.518012e-25	Sig
16	6	PIJE	131	51.2777800	2.735172e-20	Sig
17	12	PIJE	124	50.4111100	3.333214e-19	Sig

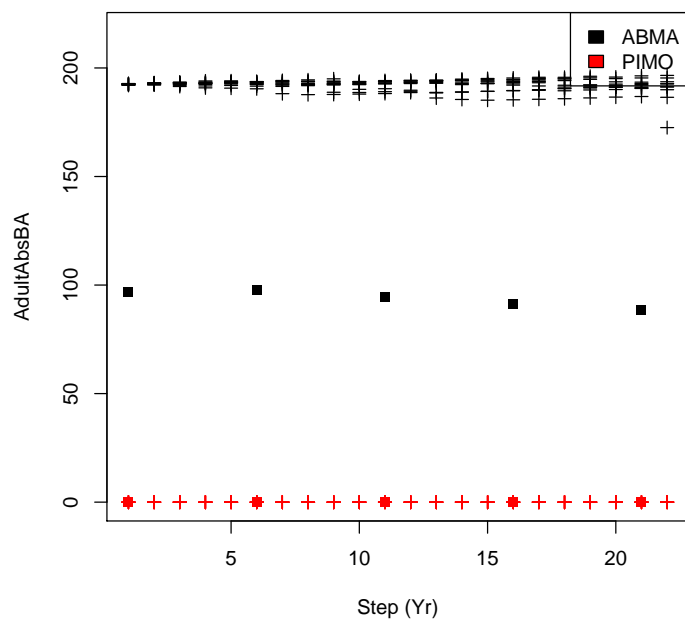
18	17	PIJE	114	49.5555500	1.048471e-17	Sig
20	22	PIJE	104	49.1444400	9.048537e-17	Sig
21	27	PIJE	101	48.2888800	4.753346e-16	Sig
22	32	PIJE	97	47.5222200	1.607235e-15	Sig
23	1	PILA	4	1.4111070	1.137184e-16	Sig
24	6	PILA	4	1.3888889	2.324069e-11	Sig
25	12	PILA	3	1.2111088	1.512224e-09	Sig
26	17	PILA	2	1.0666653	1.143189e-06	Sig
27	22	PILA	2	0.9999992	2.806601e-07	Sig
28	27	PILA	2	0.9999992	2.806601e-07	Sig
29	32	PILA	2	0.8888886	1.128085e-07	Sig
30	1	PIMO	1	0.0000000	0.000000e+00	Sig
31	6	PIMO	1	0.0000000	0.000000e+00	Sig
32	12	PIMO	1	0.0000000	0.000000e+00	Sig
33	17	PIMO	1	0.0000000	0.000000e+00	Sig
34	1	QUKE	16	3.8333350	1.644477e-20	Sig
35	6	QUKE	19	4.0111110	5.497442e-20	Sig
36	12	QUKE	60	4.3666640	6.849448e-24	Sig
37	17	QUKE	97	4.5222220	1.410868e-25	Sig
40	22	QUKE	95	4.4111120	1.179326e-23	Sig
41	27	QUKE	107	4.4444440	3.393232e-25	Sig
42	32	QUKE	121	4.2888890	2.006304e-25	Sig



3.4 PGABMA: Adult Basal Area and Density

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

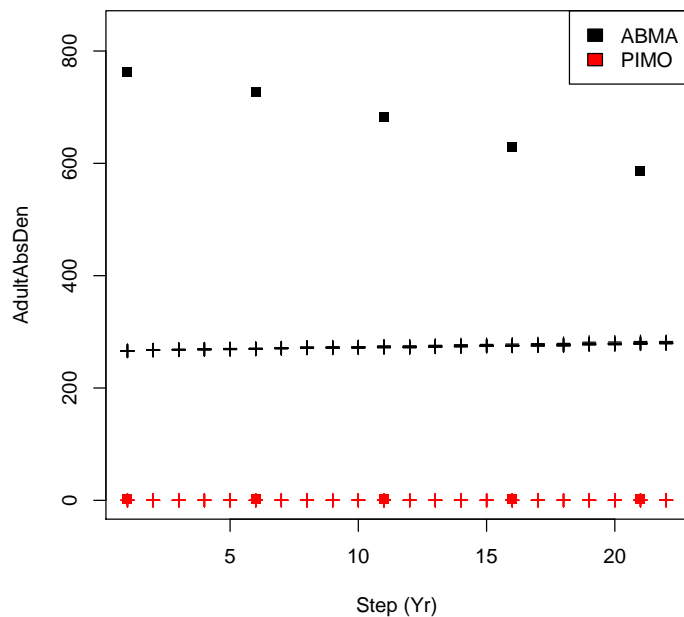
	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	96.84838877	192.45970000	1.858134e-24	Sig
2	6	ABMA	97.52063023	192.71310000	3.809447e-19	Sig
3	11	ABMA	94.43564576	192.12830000	1.663785e-16	Sig
4	16	ABMA	91.25577994	192.07180000	3.783847e-15	Sig
5	21	ABMA	88.46650645	192.13050000	8.389796e-16	Sig
7	1	PIMO	0.02068744	0.00000000	0.000000e+00	Sig
8	6	PIMO	0.02380940	0.00000000	0.000000e+00	Sig
9	11	PIMO	0.01586508	0.00000000	0.000000e+00	Sig
10	16	PIMO	0.01993031	0.00000000	0.000000e+00	Sig
11	21	PIMO	0.02255198	0.00199724	3.863546e-13	Sig



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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	762	266.0444000	6.618134e-30	Sig

2	6	ABMA	727	269.7221000	2.128032e-27	Sig
3	11	ABMA	682	273.1334000	4.637936e-25	Sig
4	16	ABMA	630	275.5000000	4.002188e-24	Sig
5	21	ABMA	587	279.5333000	1.069273e-22	Sig
7	1	PIMO	3	0.0000000	0.000000e+00	Sig
8	6	PIMO	3	0.0000000	0.000000e+00	Sig
9	11	PIMO	2	0.0000000	0.000000e+00	Sig
10	16	PIMO	2	0.0000000	0.000000e+00	Sig
11	21	PIMO	2	0.0888888	5.135689e-16	Sig

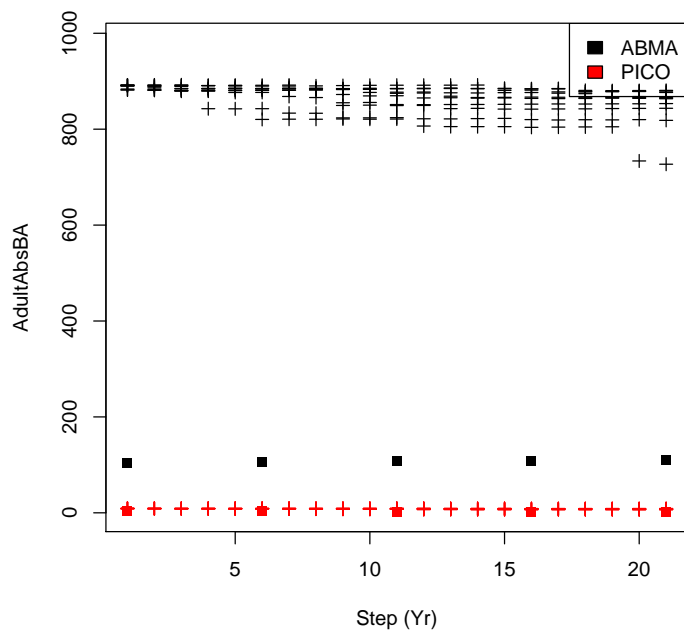


3.5 POFLABMA: Adult Basal Area and Density

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

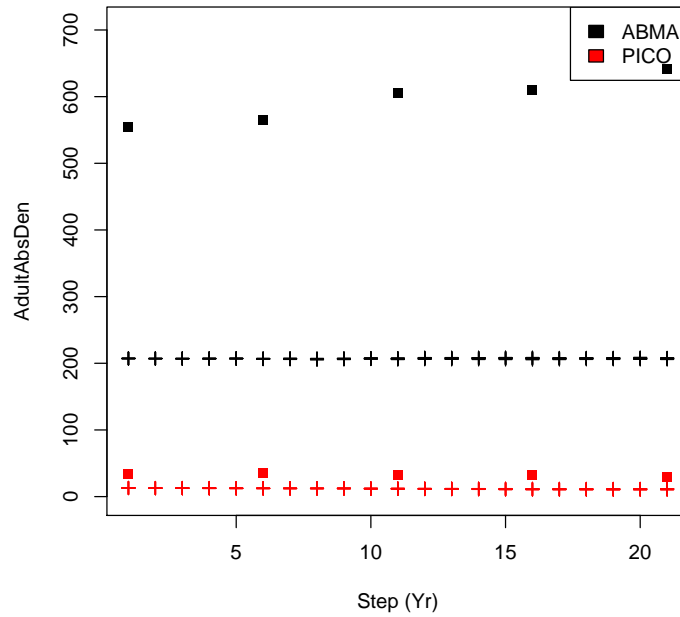
	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	102.873900	888.548500	6.384807e-22	Sig
2	6	ABMA	105.098894	873.762700	3.403526e-15	Sig
3	11	ABMA	107.131277	862.837800	8.312196e-15	Sig
4	16	ABMA	107.930403	857.498300	2.234263e-14	Sig
7	21	ABMA	109.695510	847.303800	2.396903e-12	Sig

8	1	PICO	3.081969	8.946801	1.394859e-12	Sig
9	6	PICO	3.184662	8.654016	2.434823e-11	Sig
10	11	PICO	2.607272	8.360467	1.559134e-09	Sig
11	16	PICO	2.703773	7.797766	1.686918e-08	Sig
12	21	PICO	2.627468	7.608811	2.788722e-08	Sig



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

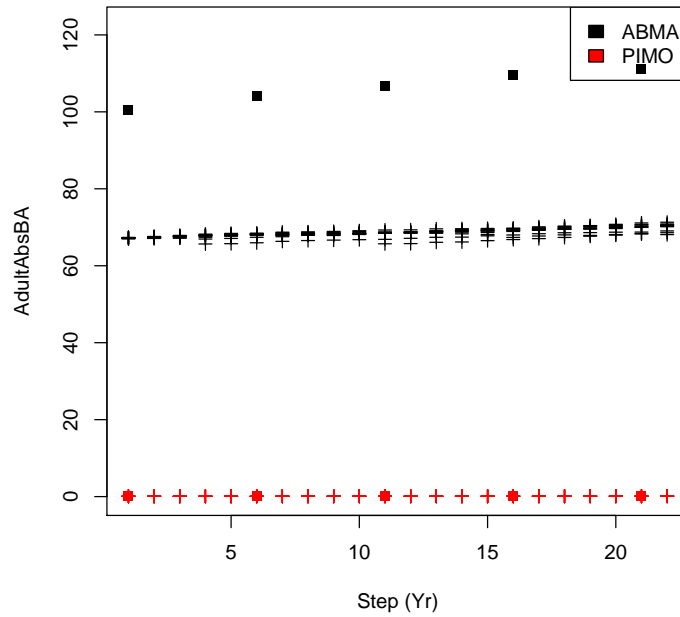
	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	555	207.19990	1.592170e-30	Sig
2	6	ABMA	565	206.69980	5.742661e-28	Sig
3	11	ABMA	606	206.85550	4.491862e-26	Sig
4	16	ABMA	610	207.31120	4.280776e-25	Sig
7	21	ABMA	642	207.10000	4.121634e-26	Sig
8	1	PICO	34	12.91111	3.857769e-20	Sig
9	6	PICO	35	12.34444	2.979468e-19	Sig
10	11	PICO	32	11.83333	3.570099e-17	Sig
11	16	PICO	32	11.10000	5.082695e-16	Sig
12	21	PICO	30	11.18888	5.639482e-15	Sig



3.6 SFTRABMA: Adult Basal Area and Density

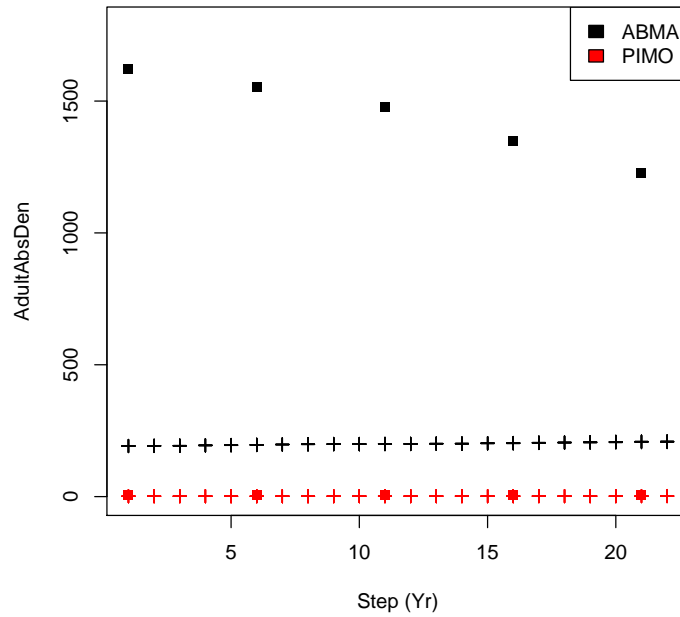
```
> processTestPlot("SFTRABMA", "outfiles/b", 0,
+                 charactername="AdultAbsBA",
+                 writefile="outfiles/b/means/SFTRABMA-AdultAbsBA.csv")
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	100.5079451	67.22695000	1.484019e-23	Sig
2	6	ABMA	104.0460566	67.88141000	9.474889e-17	Sig
5	11	ABMA	106.7590529	68.20008000	1.596829e-15	Sig
7	16	ABMA	109.5121569	68.78436000	6.945375e-16	Sig
8	21	ABMA	111.2301741	69.84181000	5.234643e-16	Sig
10	1	PIMO	0.1356692	0.08338925	1.114136e-11	Sig
11	6	PIMO	0.1492166	0.08894502	1.734278e-09	Sig
12	11	PIMO	0.1615780	0.09560951	8.659941e-09	Sig
13	16	PIMO	0.1689607	0.10370544	2.126092e-07	Sig
14	21	PIMO	0.1747664	0.11513196	1.122958e-06	Sig



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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	1623	191.877900	2.753429e-35	Sig
2	6	ABMA	1554	196.177800	8.668842e-32	Sig
5	11	ABMA	1477	199.533500	1.430765e-31	Sig
7	16	ABMA	1348	202.711100	4.717790e-30	Sig
8	21	ABMA	1228	207.933400	2.988149e-28	Sig
10	1	PIMO	7	1.522224	1.340616e-19	Sig
11	6	PIMO	7	1.544445	2.294943e-16	Sig
12	11	PIMO	7	1.700002	1.720230e-15	Sig
13	16	PIMO	7	1.744445	5.416704e-14	Sig
14	21	PIMO	5	1.966667	4.301949e-12	Sig

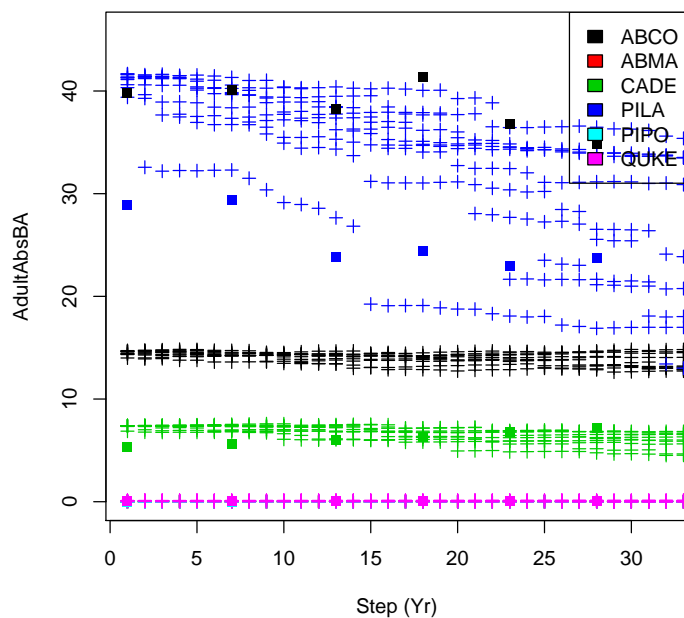


3.7 SUPILA: Adult Basal Area and Density

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

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	39.812853040	14.48480000	4.550964e-20	Sig
2	7	ABCO	40.092266770	14.28624000	5.335641e-19	Sig
3	13	ABCO	38.262802650	14.08113000	2.463042e-17	Sig
4	18	ABCO	41.362842560	13.86747000	3.651678e-17	Sig
5	23	ABCO	36.771096530	13.93506000	3.740904e-16	Sig
6	28	ABCO	34.847107860	13.76590000	9.790880e-15	Sig
11	1	ABMA	0.020612040	0.00000000	0.000000e+00	Sig
12	7	ABMA	0.025165000	0.00000000	0.000000e+00	Sig
13	13	ABMA	0.029637853	0.00000000	0.000000e+00	Sig
14	18	ABMA	0.036583931	0.00000000	0.000000e+00	Sig
15	23	ABMA	0.042594601	0.00000000	0.000000e+00	Sig
16	28	ABMA	0.051377726	0.00000000	0.000000e+00	Sig
17	1	CADE	5.306942349	7.32934800	2.398795e-11	Sig
18	7	CADE	5.599432328	7.21062400	1.763418e-08	Sig
19	13	CADE	5.969075285	6.94024800	2.223218e-04	Sig

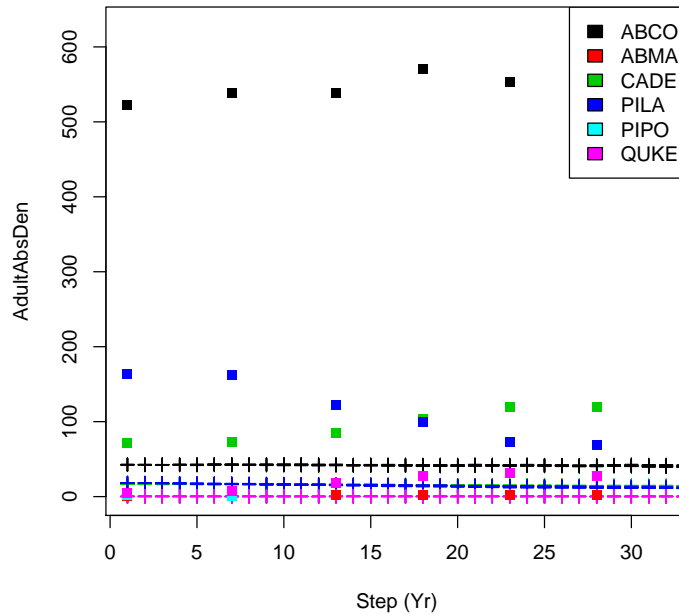
20	18	CADE	6.342942278	6.55248000	1.829355e-01	NS
21	23	CADE	6.741611282	6.23631400	4.132851e-02	Sig
22	28	CADE	7.169534110	6.10554400	1.092983e-03	Sig
26	1	PILA	28.925281240	41.03029000	1.562668e-12	Sig
27	7	PILA	29.354349690	38.61276000	1.508829e-06	Sig
28	13	PILA	23.789185860	36.54077000	1.471381e-06	Sig
29	18	PILA	24.377238040	34.06116000	5.083346e-04	Sig
30	23	PILA	22.942010900	30.49531000	3.872617e-03	Sig
32	28	PILA	23.774268490	28.12268000	7.104609e-02	NS
34	1	PIPO	0.007032471	0.00000000	0.000000e+00	Sig
35	7	PIPO	0.005410621	0.00000000	0.000000e+00	Sig
36	1	QUKE	0.046833400	0.09653662	8.279874e-04	Sig
37	7	QUKE	0.050086529	0.07753737	1.122846e-01	NS
38	13	QUKE	0.060658796	0.07916246	2.695874e-01	NS
39	18	QUKE	0.038102893	0.06953622	1.015443e-01	NS
40	23	QUKE	0.041391365	0.07079680	1.263283e-01	NS
41	28	QUKE	0.047439731	0.06094965	4.865323e-01	NS



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

Step	Species	AdultAbsDen	simMean	pval	signif
------	---------	-------------	---------	------	--------

1	1	ABCO	522	42.6333600	2.054905e-31	Sig
2	7	ABCO	538	42.6111000	2.455661e-28	Sig
3	13	ABCO	539	42.2889000	7.137620e-28	Sig
4	18	ABCO	571	41.4333300	2.465775e-27	Sig
5	23	ABCO	553	41.5222300	3.338511e-27	Sig
6	28	ABCO	525	41.1111000	1.340351e-26	Sig
11	1	ABMA	1	0.0000000	0.000000e+00	Sig
12	7	ABMA	1	0.0000000	0.000000e+00	Sig
13	13	ABMA	2	0.0000000	0.000000e+00	Sig
14	18	ABMA	2	0.0000000	0.000000e+00	Sig
15	23	ABMA	2	0.0000000	0.000000e+00	Sig
16	28	ABMA	2	0.0000000	0.000000e+00	Sig
17	1	CADE	71	16.4777800	3.705764e-25	Sig
18	7	CADE	73	16.3444400	9.565428e-23	Sig
19	13	CADE	85	15.8000100	5.649650e-23	Sig
20	18	CADE	103	15.1777700	2.932964e-22	Sig
21	23	CADE	119	14.6111100	1.205856e-22	Sig
22	28	CADE	120	14.0444400	3.416097e-22	Sig
26	1	PILA	164	18.2444200	1.662028e-28	Sig
27	7	PILA	162	16.9666700	8.910147e-25	Sig
28	13	PILA	122	15.4888900	5.117986e-22	Sig
29	18	PILA	100	14.3444400	2.809862e-20	Sig
30	23	PILA	73	13.2666700	2.060424e-18	Sig
32	28	PILA	69	12.3333400	2.588631e-18	Sig
34	1	PIPO	2	0.0000000	0.000000e+00	Sig
35	7	PIPO	1	0.0000000	0.000000e+00	Sig
36	1	QUKE	5	0.3222219	1.225286e-20	Sig
37	7	QUKE	7	0.2888886	3.928952e-20	Sig
38	13	QUKE	18	0.3444441	1.616249e-22	Sig
39	18	QUKE	27	0.3111108	1.895151e-22	Sig
40	23	QUKE	32	0.3111108	4.040783e-23	Sig
41	28	QUKE	27	0.2888886	1.499647e-21	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 eight 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/081715-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
-35.089	-0.323	-0.034	2.897	12.824

Coefficients:

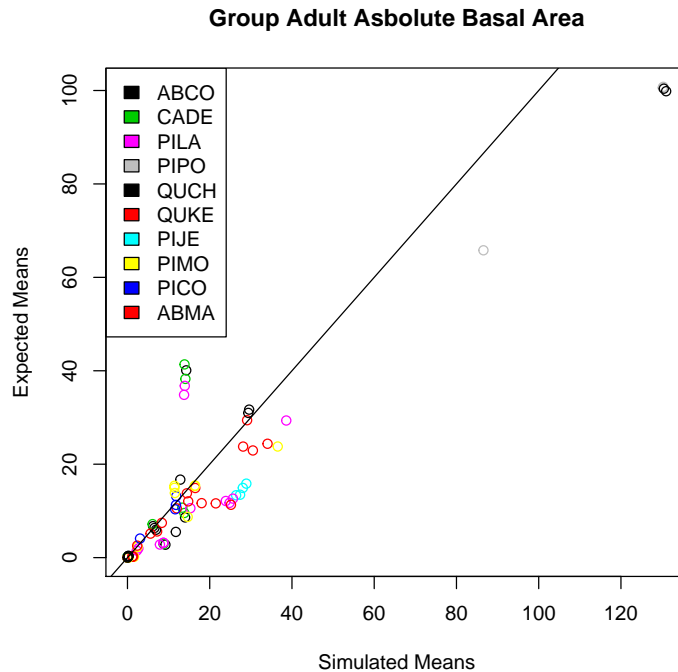
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.01254	0.91985	0.014	0.989
ExpAbsBA	1.18329	0.03810	31.060	<2e-16 ***

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

Residual standard error: 8.263 on 106 degrees of freedom

Multiple R-squared: 0.901, Adjusted R-squared: 0.9001

F-statistic: 964.7 on 1 and 106 DF, p-value: < 2.2e-16



```

> ## And absolute density
> AllAbsDens <- rbind(bbbpipoadultabsden,
+                    frpijeadultabsden,
+                    emridgeadultabsden,
+                    pgabmaadultabsden,
+                    #poflabmaadultabsden,
+                    sftrabmaadultabsden,
+                    supilaadultabsden)
> AllAbsDenmeans <- aggregate(AllAbsDens$simMean,
+                             by=list(AllAbsDens$Step, AllAbsDens$Species),
+                             FUN=mean, na.rm=T)
> AllAbsDenmeans$expmean <- aggregate(AllAbsDens$AdultAbsDen,
+                                     by=list(AllAbsDens$Step, AllAbsDens$Species),
+                                     FUN=mean, na.rm=T)[,3]
> colnames(AllAbsDenmeans) <- c("Step", "Species", "SimAbsDen", "ExpAbsDen")
> write.csv(AllAbsDenmeans, file="outfiles/b/081715-adultdensity.csv", row.names=F)
> AllAbsDen <- AllAbsDenmeans
> plot(AllAbsDen[, "SimAbsDen"], AllAbsDen[, "ExpAbsDen"],
+      col=as.factor(AllAbsDen$Species),
+      xlab="Simulated Absolute Density", ylab="Expected Means",
+      main="Group Adult Absolute Density")
> 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
	-106.244	-15.560	-5.647	-0.621	175.016

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.14728	5.59306	0.92	0.36
ExpAbsDen	0.24961	0.02005	12.45	<2e-16 ***

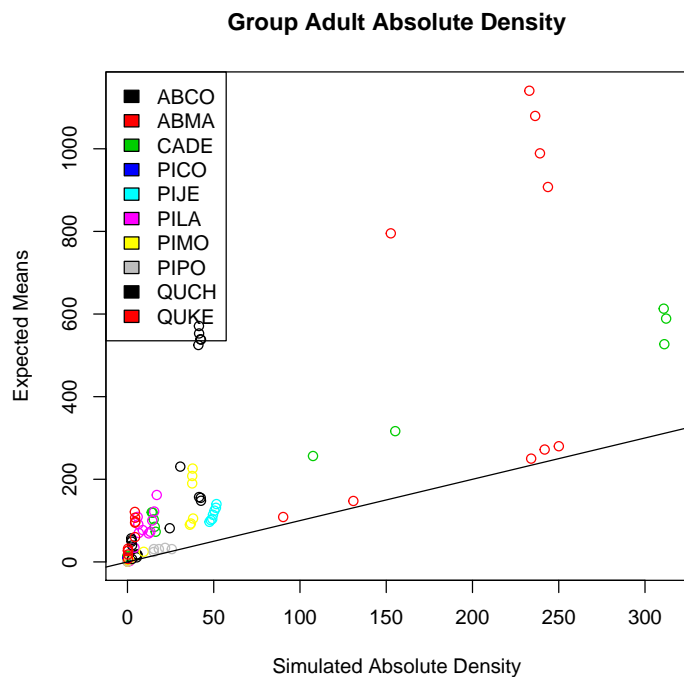
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 49.15 on 106 degrees of freedom

Multiple R-squared: 0.5937, Adjusted R-squared: 0.5899

F-statistic: 154.9 on 1 and 106 DF, p-value: < 2.2e-16

>



4 Next Steps

So it looks like basal area per hectare is straight on, but we're severely underestimating the number of trees in all plots. But the program seems to be right on with basal area, which means that the trees generated by my tree maps are bigger, with fewer total trees being generated than would be expected by the maps.

I think first, I'm going to double check that the number of rows entered into the tree maps, and the number of trees actually counted by SORTIE, are the same. If they are, e.g., they are all being registered and tracked in SORTIE, then I think I'll leave this question for later and move onto evaluating other parameters, like seedling, sapling, and mortality parameters.

I need to revisit the data and calculate seedling and sapling expected parameters, which means figuring out which trees get classified where based on the height equations. Then I can add those values to `expectedPlotOutcomes`, `realPlots`, and take a look at how far away we are.