

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

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1 Introduction

The eight plots that I chose to use for calibration were: BBBPIPO, EMRIDGE, FRPIJE, PGABMA, POFLABMA, SFTRABMA, and SUPILA. The four plots that I will use for testing are WTABMA, EMSLOPE, SUABCO, and CCRPIPO. This document details the results from the batch files labeled 081715-X.xml. The changes between this and 081315-X.xml are small: The tree maps that I generated now have values ranging between 0.9-1.1 of the original values; the "true" tree map is not present in the plots, just like in 081315.

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.

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 initial run (08/13/15) 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 eight parameter files, one for each calibration plot. Within each, there was a 300m x 300m tree map added. These tree maps had x and y generated by `runif()` in R, and the DBHs were generated by sampling the real data and applying a randomized multiplier between 0.75-1.25. Heights were calculated automatically by SORTIE-ND when the program initiated.

I ran each parameter file thirty 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.

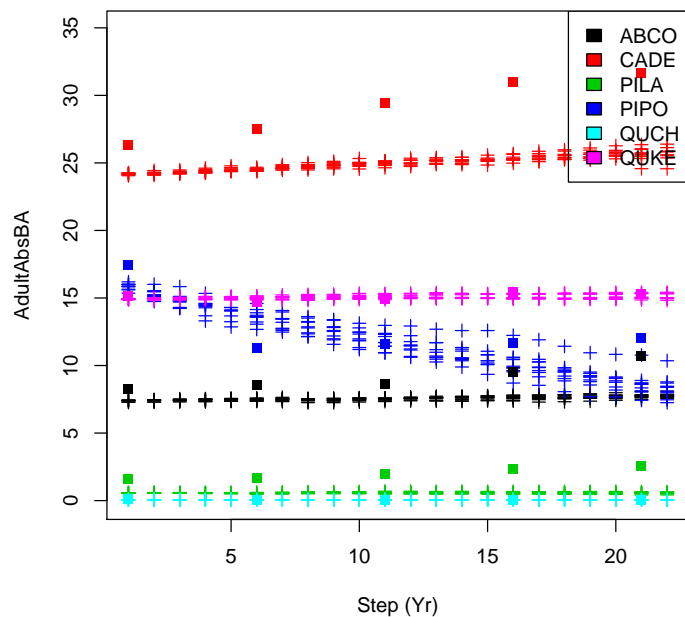
For the first set of figures, by plot, the hashmarks represent a single trial at a single time point, and may be grouped together rather closely. The closed squares of the same color indicate the true means of the real plots. The x-axis is time, and the y-axis is the variable of interest.

3.1 BBBPIPO: Adult Basal Area and Density

```
> library(SortieOutputs)
> processTestPlot("BBBPIPO", "outfiles/orig", 0,
+                 charactername="AdultAbsBA",
+                 writefile="outfiles/orig/means/BBBPIPO-AdultAbsBA.csv")
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	8.22515648	7.38581300	7.144847e-12	Sig

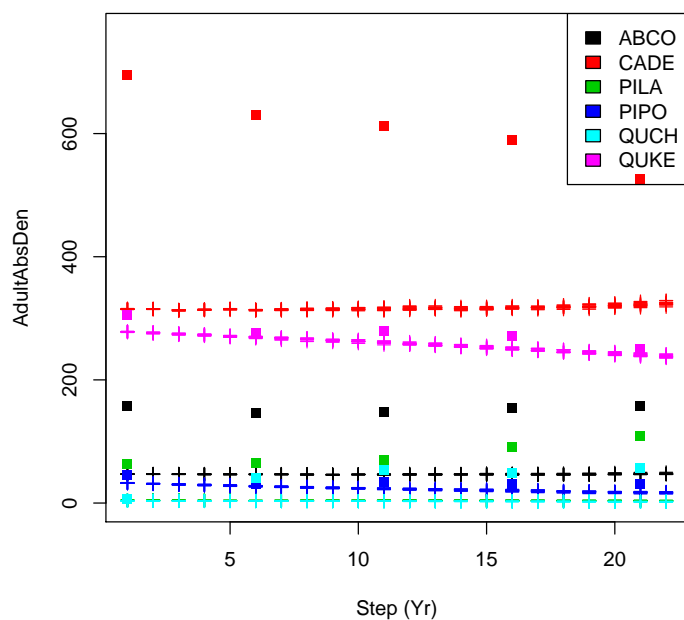
2	6	ABCO	8.55844175	7.47812300	1.750698e-11	Sig
3	11	ABCO	8.60228985	7.51556400	1.179529e-11	Sig
4	16	ABCO	9.55329929	7.62473100	1.649260e-11	Sig
5	21	ABCO	10.69337808	7.74655400	4.614610e-13	Sig
6	1	CADE	26.30695258	24.17692000	6.015804e-15	Sig
7	6	CADE	27.54093222	24.49962000	7.136933e-15	Sig
8	11	CADE	29.41467906	24.97403000	1.949653e-14	Sig
9	16	CADE	30.98351713	25.33973000	1.486561e-14	Sig
10	21	CADE	31.68296924	25.64526000	2.013332e-11	Sig
12	1	PILA	1.56575066	0.56459560	1.068909e-18	Sig
13	6	PILA	1.68034838	0.53978070	1.787176e-14	Sig
14	11	PILA	1.97541059	0.57204070	1.326270e-13	Sig
16	16	PILA	2.30771569	0.57206430	1.795163e-14	Sig
17	21	PILA	2.56894680	0.56171540	1.994525e-14	Sig
19	1	PIPO	17.41989711	15.83825000	7.394378e-09	Sig
20	6	PIPO	11.30799599	13.61222000	3.058243e-07	Sig
21	11	PIPO	11.61260396	11.79439000	4.027048e-01	NS
22	16	PIPO	11.66155637	10.13268400	5.668931e-04	Sig
23	21	PIPO	12.04379013	8.62514900	5.617013e-07	Sig
25	1	QUCH	0.08307961	0.06728268	7.999201e-13	Sig
26	6	QUCH	0.03701669	0.06552883	6.563156e-11	Sig
27	11	QUCH	0.02100788	0.06598225	1.314162e-11	Sig
29	16	QUCH	0.02355851	0.06175042	2.214721e-09	Sig
30	21	QUCH	0.01766050	0.05774202	5.308668e-09	Sig
31	1	QUKE	15.17823670	14.92151000	3.155815e-10	Sig
32	6	QUKE	14.68553643	15.00381000	3.061973e-06	Sig
34	11	QUKE	14.90333257	15.09185000	2.549637e-03	Sig
35	16	QUKE	15.42906912	15.10674000	1.477268e-04	Sig
36	21	QUKE	15.31791852	15.12838000	1.604981e-02	Sig



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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	157	46.977780	2.130903e-25	Sig
2	6	ABCO	147	46.677770	2.409933e-22	Sig
3	11	ABCO	148	46.311110	3.230612e-22	Sig
4	16	ABCO	155	46.633330	1.800032e-20	Sig
5	21	ABCO	157	47.255560	8.818561e-20	Sig
6	1	CADE	695	314.877800	1.659247e-27	Sig
7	6	CADE	630	313.611000	2.238941e-25	Sig
8	11	CADE	613	315.266600	3.595598e-21	Sig
9	16	CADE	589	317.100100	1.130819e-21	Sig
10	21	CADE	527	322.255500	4.436711e-18	Sig
12	1	PILA	63	4.355552	2.366857e-26	Sig
13	6	PILA	65	3.955555	2.475803e-22	Sig
14	11	PILA	70	4.177779	4.191062e-21	Sig
16	16	PILA	91	4.033333	3.840430e-22	Sig
17	21	PILA	109	3.766667	2.687308e-22	Sig
19	1	PIPO	46	32.522220	3.032505e-15	Sig
20	6	PIPO	31	27.222210	5.872435e-08	Sig

21	11	PIPO	34	23.144450	4.848109e-11	Sig
22	16	PIPO	31	20.122220	7.246376e-10	Sig
23	21	PIPO	31	17.111110	1.704447e-11	Sig
25	1	QUCH	7	3.611115	2.209526e-17	Sig
26	6	QUCH	40	3.211109	1.701141e-23	Sig
27	11	QUCH	53	2.977778	3.282145e-23	Sig
29	16	QUCH	49	2.600001	5.286516e-23	Sig
30	21	QUCH	57	2.277777	3.052113e-23	Sig
31	1	QUKE	305	278.122300	4.154492e-17	Sig
32	6	QUKE	276	269.333200	1.830986e-08	Sig
34	11	QUKE	280	260.566800	6.188772e-11	Sig
35	16	QUKE	272	250.677800	2.636673e-11	Sig
36	21	QUKE	250	240.522300	1.960777e-07	Sig

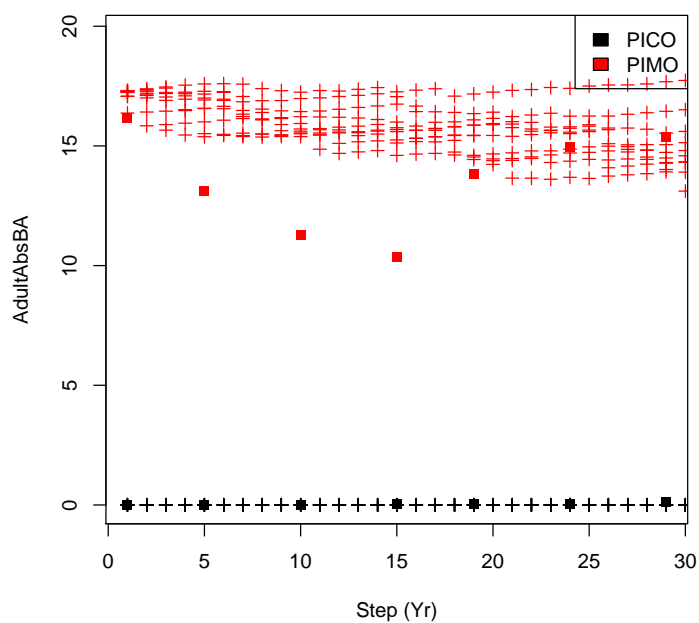


3.2 EMRIDGE: Adult Basal Area and Density

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

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

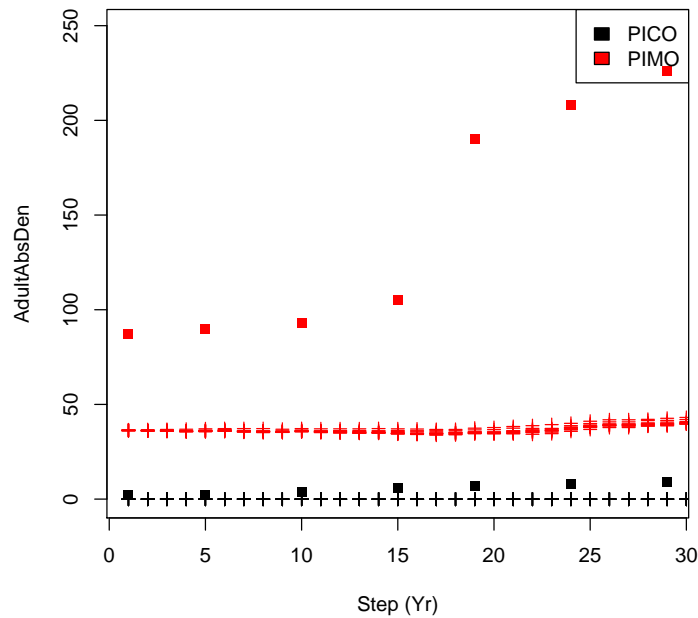
2	5	PICO	0.011388300	0.00000	0.000000e+00	Sig
3	10	PICO	0.019037311	0.00000	0.000000e+00	Sig
4	15	PICO	0.022427097	0.00000	0.000000e+00	Sig
5	19	PICO	0.035197701	0.00000	0.000000e+00	Sig
6	24	PICO	0.051995836	0.00000	0.000000e+00	Sig
7	29	PICO	0.103346859	0.00000	0.000000e+00	Sig
8	1	PIMO	16.164999910	17.14738	1.820166e-06	Sig
9	5	PIMO	13.132768430	16.59960	1.386336e-07	Sig
10	10	PIMO	11.288140290	16.05802	2.346100e-09	Sig
11	15	PIMO	10.351063060	15.90788	8.182710e-09	Sig
12	19	PIMO	13.833822760	15.58053	1.420401e-04	Sig
13	24	PIMO	14.941689150	15.38988	2.078440e-01	NS
14	29	PIMO	15.379181290	15.04529	4.029969e-01	NS



```
> processTestPlot("EMRIDGE", "outfiles/orig", 0,
+                 charactername="AdultAbsDen",
+                 writefile="outfiles/orig/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	36.28887	7.447470e-24	Sig
9	5	PIMO	90	36.08889	2.461572e-20	Sig
10	10	PIMO	93	36.04444	4.527440e-20	Sig
11	15	PIMO	105	35.20001	1.326746e-18	Sig
12	19	PIMO	190	35.46666	1.232509e-21	Sig
13	24	PIMO	208	37.55557	6.674338e-21	Sig
14	29	PIMO	226	40.08891	3.953649e-21	Sig

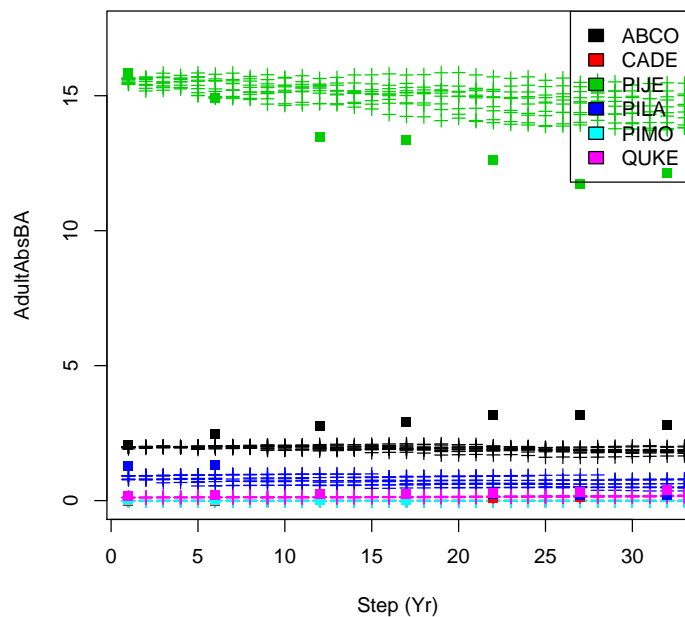


3.3 FRPIJE: Adult Basal Area and Density

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

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	2.053798223	1.9757320	9.319435e-07	Sig
2	6	ABCO	2.453112077	1.9951410	4.574241e-11	Sig

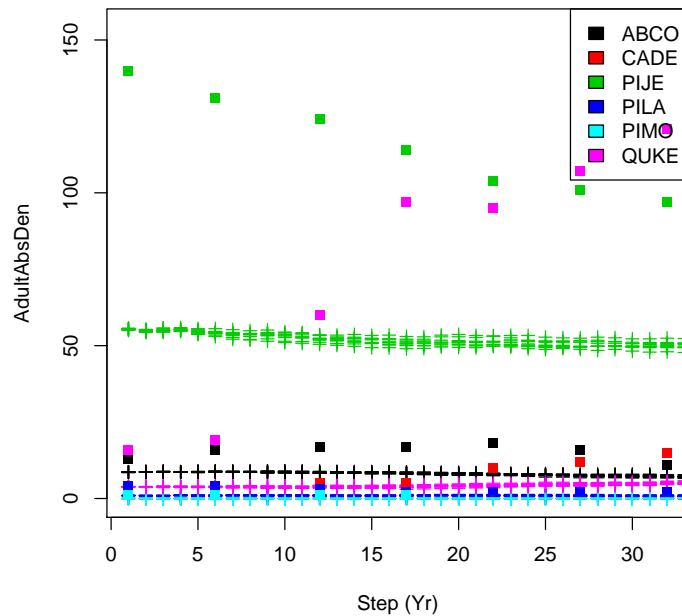
3	12	ABCO	2.764403796	1.9577410	7.155633e-11	Sig
4	17	ABCO	2.916809881	1.9478830	1.234150e-10	Sig
5	22	ABCO	3.169380383	1.9116200	2.384045e-11	Sig
6	27	ABCO	3.181020797	1.8446210	2.432652e-11	Sig
7	32	ABCO	2.799051717	1.8448350	2.725988e-10	Sig
8	1	CADE	0.001053221	0.0000000	0.000000e+00	Sig
9	6	CADE	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	15.5486200	2.968507e-06	Sig
16	6	PIJE	14.924775560	15.3300300	3.548792e-03	Sig
17	12	PIJE	13.464172680	15.2134100	2.053596e-08	Sig
18	17	PIJE	13.358516740	15.0610200	5.235794e-07	Sig
20	22	PIJE	12.633173140	14.8356400	4.122647e-07	Sig
21	27	PIJE	11.725481060	14.7022300	3.159249e-08	Sig
22	32	PIJE	12.124942370	14.5183200	4.572524e-07	Sig
23	1	PILA	1.270279256	0.8802646	1.780930e-08	Sig
24	6	PILA	1.307463234	0.8025502	3.531859e-06	Sig
25	12	PILA	0.179119109	0.7635499	2.406726e-06	Sig
26	17	PILA	0.219019786	0.6997955	3.200823e-06	Sig
27	22	PILA	0.253735251	0.6934673	1.550264e-05	Sig
28	27	PILA	0.194133601	0.6181793	1.315698e-05	Sig
29	32	PILA	0.219090472	0.5909324	2.985777e-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	0.1139598	2.985356e-14	Sig
35	6	QUKE	0.200555032	0.1193534	2.798887e-12	Sig
36	12	QUKE	0.237522239	0.1246985	8.549824e-11	Sig
37	17	QUKE	0.262400569	0.1284628	1.832260e-10	Sig
40	22	QUKE	0.296468865	0.1409234	6.806917e-11	Sig
41	27	QUKE	0.333892240	0.1543424	2.516800e-11	Sig
42	32	QUKE	0.387661659	0.1667527	9.832990e-12	Sig



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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	13	8.6222250	2.808267e-17	Sig
2	6	ABCO	16	8.7888910	3.977855e-17	Sig
3	12	ABCO	17	8.4888890	1.890685e-15	Sig
4	17	ABCO	17	8.2888880	2.781958e-15	Sig
5	22	ABCO	18	7.9333330	1.281247e-15	Sig
6	27	ABCO	16	7.4666660	3.907942e-14	Sig
7	32	ABCO	11	7.2222220	5.358857e-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	55.4111100	9.724318e-25	Sig
16	6	PIJE	131	54.1999900	6.508876e-20	Sig
17	12	PIJE	124	52.2777600	3.437791e-18	Sig

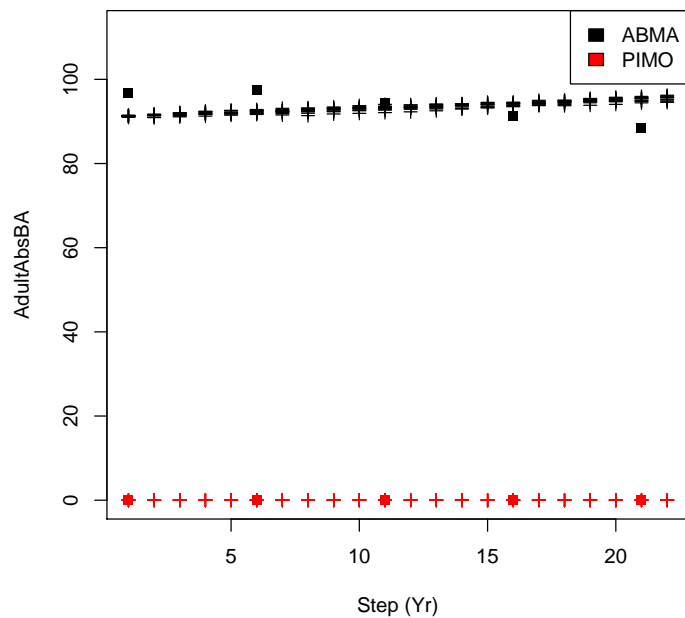
18	17	PIJE	114	50.9888900	4.237659e-17	Sig
20	22	PIJE	104	51.0888700	2.683217e-16	Sig
21	27	PIJE	101	50.3444500	3.214321e-16	Sig
22	32	PIJE	97	50.0444300	6.989892e-16	Sig
23	1	PILA	4	0.9666667	2.733998e-17	Sig
24	6	PILA	4	0.9555553	1.521376e-13	Sig
25	12	PILA	3	0.9444441	1.097204e-10	Sig
26	17	PILA	2	0.9999994	2.078998e-08	Sig
27	22	PILA	2	1.0111105	1.830715e-08	Sig
28	27	PILA	2	0.9111109	9.062381e-09	Sig
29	32	PILA	2	0.8000000	1.133668e-08	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	3.8444460	2.864552e-21	Sig
35	6	QUKE	19	3.7888910	2.685400e-19	Sig
36	12	QUKE	60	3.8555550	8.739596e-22	Sig
37	17	QUKE	97	3.8111120	1.052551e-22	Sig
40	22	QUKE	95	4.1999990	1.403542e-22	Sig
41	27	QUKE	107	4.6222220	2.456740e-23	Sig
42	32	QUKE	121	5.0111130	6.891587e-24	Sig



3.4 PGABMA: Adult Basal Area and Density

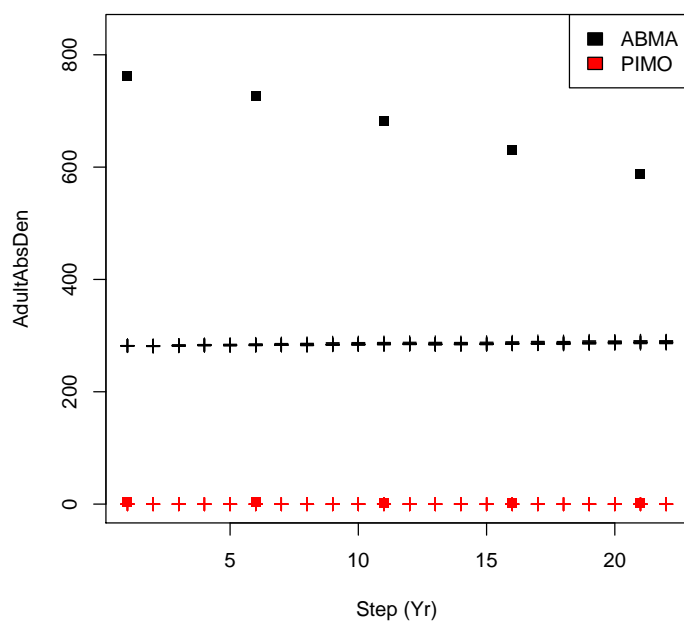
```
> library(SortieOutputs)
> processTestPlot("PGABMA", "outfiles/orig", 0,
+                 charactername="AdultAbsBA",
+                 writefile="outfiles/orig/means/PGABMA-AdultAbsBA.csv")
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	96.84838877	91.27498	1.686859e-15	Sig
2	6	ABMA	97.52063023	92.25418	6.653613e-12	Sig
3	11	ABMA	94.43564576	93.18810	5.006155e-05	Sig
4	16	ABMA	91.25577994	94.09877	1.335774e-09	Sig
5	21	ABMA	88.46650645	95.24969	6.842421e-12	Sig
7	1	PIMO	0.02068744	0.00000	0.000000e+00	Sig
8	6	PIMO	0.02380940	0.00000	0.000000e+00	Sig
9	11	PIMO	0.01586508	0.00000	0.000000e+00	Sig
10	16	PIMO	0.01993031	0.00000	0.000000e+00	Sig
11	21	PIMO	0.02255198	0.00000	0.000000e+00	Sig



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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	762	281.9333	4.924923e-31	Sig
2	6	ABMA	727	283.3556	1.048817e-25	Sig
3	11	ABMA	682	285.1334	2.610747e-24	Sig
4	16	ABMA	630	286.0888	3.138932e-23	Sig
5	21	ABMA	587	288.1780	4.617229e-22	Sig
7	1	PIMO	3	0.0000	0.000000e+00	Sig
8	6	PIMO	3	0.0000	0.000000e+00	Sig
9	11	PIMO	2	0.0000	0.000000e+00	Sig
10	16	PIMO	2	0.0000	0.000000e+00	Sig
11	21	PIMO	2	0.0000	0.000000e+00	Sig

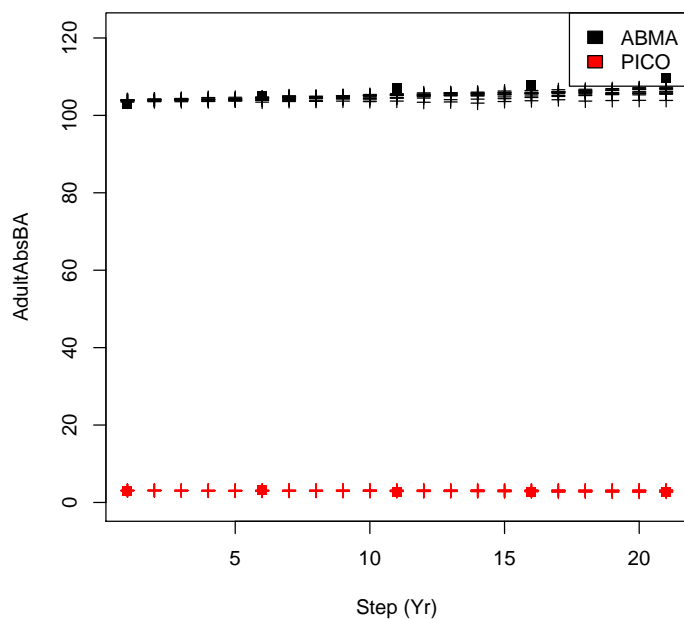


3.5 POFLABMA: Adult Basal Area and Density

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

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	102.873900	103.846700	6.560772e-08	Sig
2	6	ABMA	105.098894	104.270500	1.600896e-04	Sig

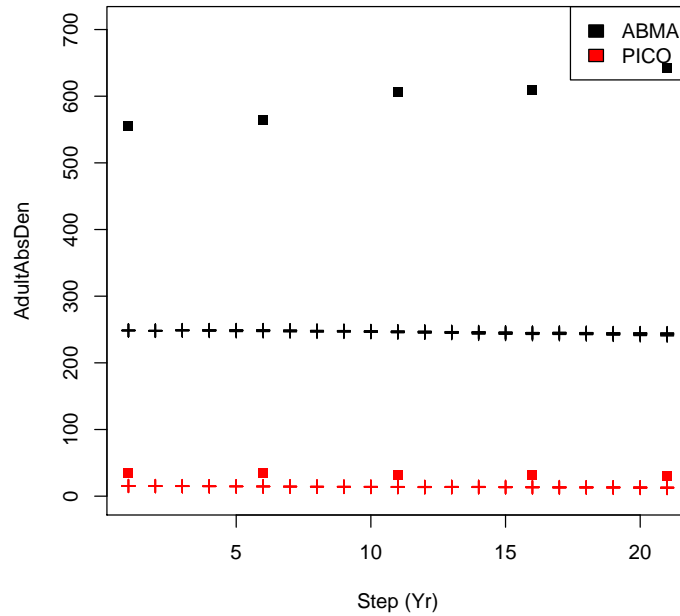
3	11	ABMA	107.131277	104.923000	8.758913e-07	Sig
4	16	ABMA	107.930403	105.425100	2.589137e-06	Sig
7	21	ABMA	109.695510	106.065700	9.242832e-07	Sig
8	1	PICO	3.081969	3.079709	8.231224e-01	NS
9	6	PICO	3.184662	3.037693	3.261071e-04	Sig
10	11	PICO	2.607272	3.005576	2.311430e-06	Sig
11	16	PICO	2.703773	3.000446	1.809966e-04	Sig
12	21	PICO	2.627468	2.963602	2.726954e-04	Sig



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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	555	248.56690	7.026542e-29	Sig
2	6	ABMA	565	248.51100	6.890898e-25	Sig
3	11	ABMA	606	246.48890	3.403005e-25	Sig
4	16	ABMA	610	244.46660	1.284852e-24	Sig
7	21	ABMA	642	242.93330	1.510895e-23	Sig
8	1	PICO	34	15.27775	1.135836e-21	Sig
9	6	PICO	35	14.55557	2.490069e-18	Sig
10	11	PICO	32	13.75557	3.371553e-17	Sig

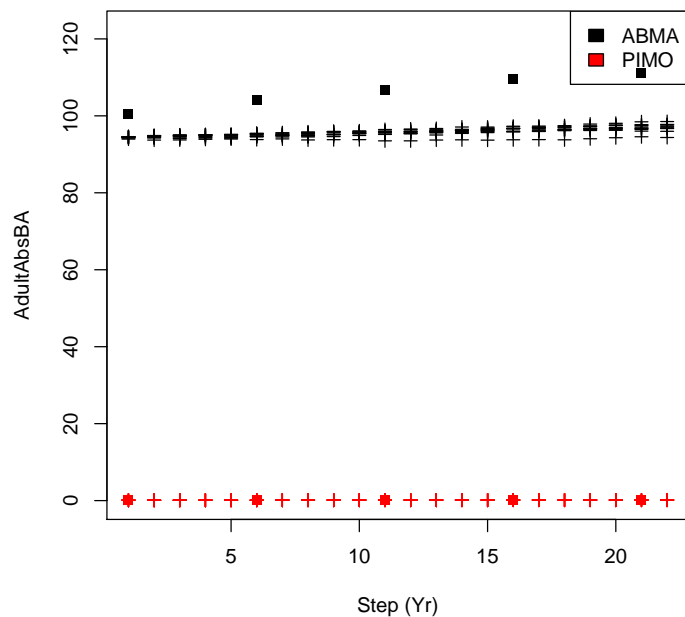
11	16	PICO	32	13.41112	6.987526e-16	Sig
12	21	PICO	30	12.73333	1.610574e-15	Sig



3.6 SFTRABMA: Adult Basal Area and Density

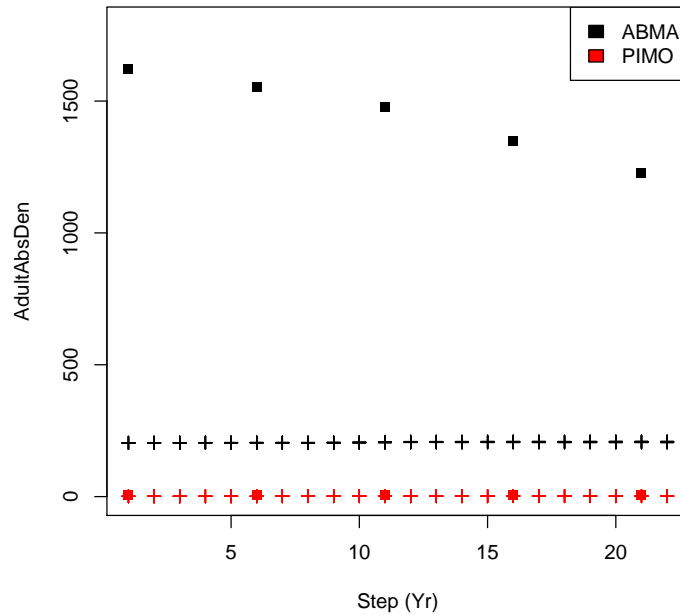
```
> library(SortieOutputs)
> processTestPlot("SFTRABMA", "outfiles/orig", 0,
+                 charactername="AdultAbsBA",
+                 writefile="outfiles/orig/means/SFTRABMA-AdultAbsBA.csv")
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	100.5079451	94.40420000	6.932376e-15	Sig
2	6	ABMA	104.0460566	94.92042000	8.091398e-13	Sig
5	11	ABMA	106.7590529	95.52895000	8.081780e-12	Sig
7	16	ABMA	109.5121569	96.26516000	1.274199e-11	Sig
8	21	ABMA	111.2301741	96.84341000	9.913044e-12	Sig
10	1	PIMO	0.1356692	0.09919984	1.963128e-11	Sig
11	6	PIMO	0.1492166	0.11390145	7.473112e-08	Sig
12	11	PIMO	0.1615780	0.12906120	1.164673e-05	Sig
13	16	PIMO	0.1689607	0.14096290	1.013743e-05	Sig
14	21	PIMO	0.1747664	0.13884180	2.731881e-06	Sig



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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	1623	203.600100	7.145798e-37	Sig
2	6	ABMA	1554	204.555400	8.819750e-33	Sig
5	11	ABMA	1477	205.899900	3.576450e-29	Sig
7	16	ABMA	1348	207.166700	8.205392e-28	Sig
8	21	ABMA	1228	207.266700	7.824918e-27	Sig
10	1	PIMO	7	1.099999	1.516784e-21	Sig
11	6	PIMO	7	1.488890	1.909641e-17	Sig
12	11	PIMO	7	1.900001	1.715968e-15	Sig
13	16	PIMO	7	2.133332	3.204793e-17	Sig
14	21	PIMO	5	2.033333	3.168453e-13	Sig

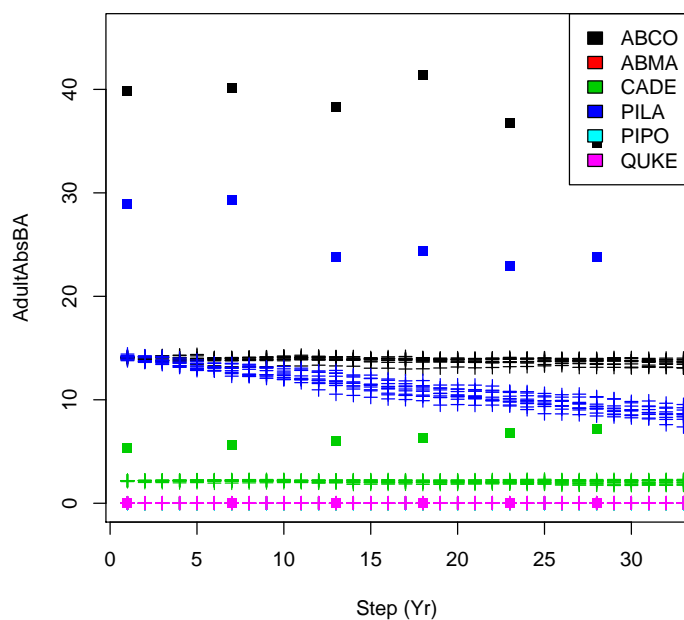


3.7 SUPILA: Adult Basal Area and Density

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

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	39.812853040	14.05519000	1.407565e-23	Sig
2	7	ABCO	40.092266770	13.86023000	1.472764e-19	Sig
3	13	ABCO	38.262802650	13.92017000	3.053828e-19	Sig
4	18	ABCO	41.362842560	13.79955000	5.264471e-19	Sig
5	23	ABCO	36.771096530	13.76919000	6.281817e-19	Sig
6	28	ABCO	34.847107860	13.70339000	1.366244e-18	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	2.16890700	4.159612e-20	Sig
18	7	CADE	5.599432328	2.17054600	1.440253e-15	Sig

19	13	CADE	5.969075285	2.13583900	1.054472e-15	Sig
20	18	CADE	6.342942278	2.08280200	2.608906e-15	Sig
21	23	CADE	6.741611282	2.07053300	3.826336e-15	Sig
22	28	CADE	7.169534110	2.04000400	1.668244e-14	Sig
26	1	PILA	28.925281240	14.12217000	1.640073e-18	Sig
27	7	PILA	29.354349690	12.96121000	4.433436e-16	Sig
28	13	PILA	23.789185860	11.90999000	1.100422e-12	Sig
29	18	PILA	24.377238040	10.84451700	8.633808e-14	Sig
30	23	PILA	22.942010900	10.12532800	4.894098e-14	Sig
32	28	PILA	23.774268490	9.34603300	5.109394e-14	Sig
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	0.02576077	1.013483e-13	Sig
37	7	QUKE	0.050086529	0.02625498	1.935690e-10	Sig
38	13	QUKE	0.060658796	0.02768076	1.976500e-10	Sig
39	18	QUKE	0.038102893	0.02831762	9.161860e-06	Sig
40	23	QUKE	0.041391365	0.02924363	4.612537e-06	Sig
41	28	QUKE	0.047439731	0.02970375	3.536509e-07	Sig

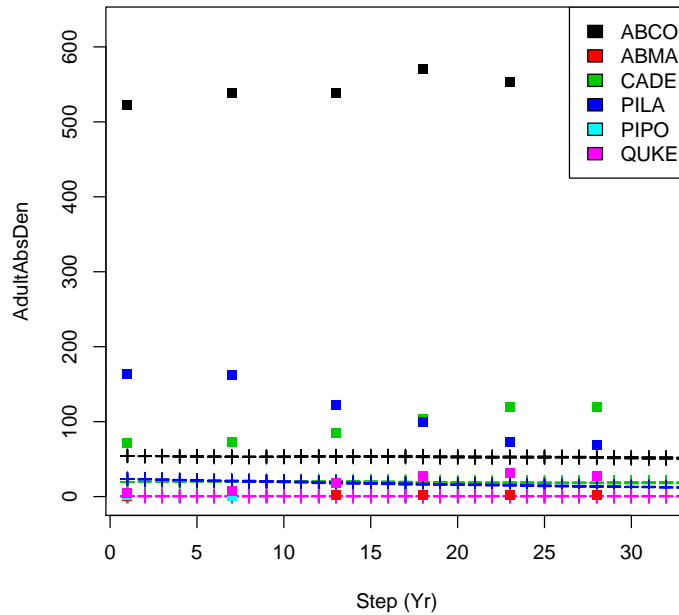


```

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

```

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	522	54.2999900	4.019325e-31	Sig
2	7	ABCO	538	53.2000000	7.013646e-28	Sig
3	13	ABCO	539	53.4333400	1.017101e-27	Sig
4	18	ABCO	571	53.1889000	8.038687e-27	Sig
5	23	ABCO	553	52.7111200	5.167036e-27	Sig
6	28	ABCO	525	52.3333300	8.577310e-27	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	19.7666900	2.908777e-24	Sig
18	7	CADE	73	20.0444400	4.094079e-21	Sig
19	13	CADE	85	20.1444400	3.770314e-20	Sig
20	18	CADE	103	19.1777800	3.620369e-21	Sig
21	23	CADE	119	18.6000000	2.125559e-22	Sig
22	28	CADE	120	18.2666700	1.812867e-21	Sig
26	1	PILA	164	23.6111100	1.360200e-26	Sig
27	7	PILA	162	20.9000000	9.018672e-23	Sig
28	13	PILA	122	18.6000000	1.928705e-20	Sig
29	18	PILA	100	16.6555700	2.246013e-20	Sig
30	23	PILA	73	15.2111100	1.219648e-19	Sig
32	28	PILA	69	13.5555400	3.480835e-19	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	0.8777779	3.822836e-20	Sig
37	7	QUKE	7	0.8222224	1.265863e-18	Sig
38	13	QUKE	18	0.8000002	1.473811e-21	Sig
39	18	QUKE	27	0.7666669	2.136538e-23	Sig
40	23	QUKE	32	0.7444447	9.086831e-24	Sig
41	28	QUKE	27	0.7111114	5.080110e-23	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/orig/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/orig/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
-21.6888	0.2004	0.8575	1.4860	9.5951

Coefficients:

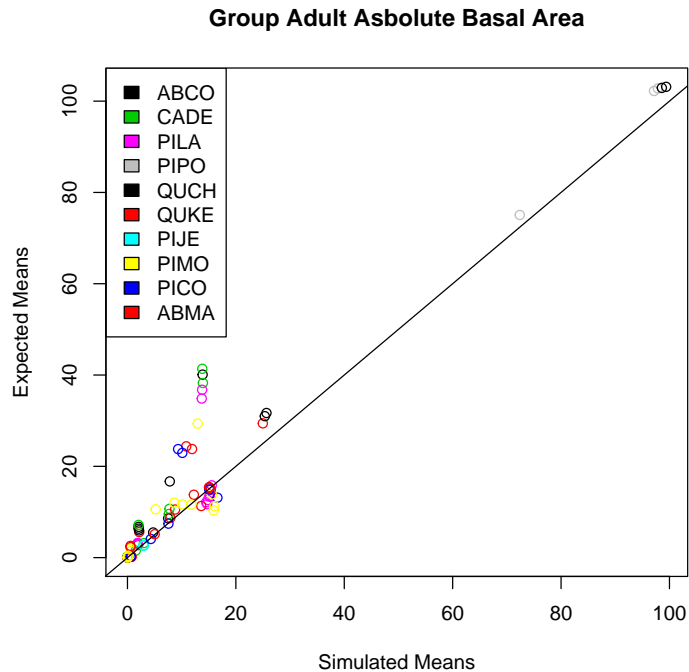
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-0.8755	0.5835	-1.501	0.136
ExpAbsBA	0.8791	0.0240	36.636	<2e-16 ***

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

Residual standard error: 5.373 on 110 degrees of freedom

Multiple R-squared: 0.9243, Adjusted R-squared: 0.9236

F-statistic: 1342 on 1 and 110 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$Species),
+                                     FUN=mean, na.rm=T)[,3]
> colnames(AllAbsDenmeans) <- c("Step", "Species", "SimAbsDen", "ExpAbsDen")
> write.csv(AllAbsDenmeans, file="outfiles/orig/081715-adultdensity.csv", row.names=F)
> AllAbsDen <- AllAbsDenmeans
> plot(AllAbsDen[, "SimAbsDen"], AllAbsDen[, "ExpAbsDen"],
+      col=as.factor(AllAbsDen$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
	-116.389	-14.987	-3.688	1.045	175.829

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.10447	5.35789	0.579	0.563
ExpAbsDen	0.29155	0.02112	13.806	<2e-16 ***

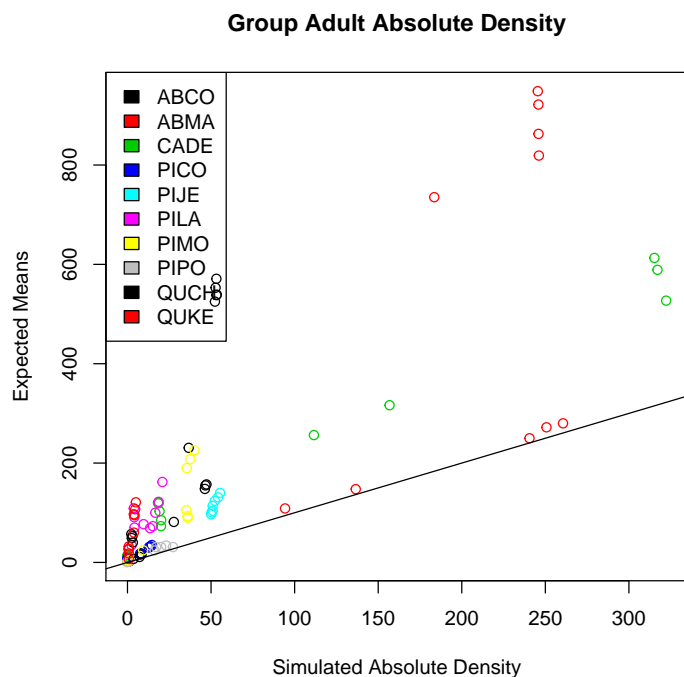
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 47.4 on 110 degrees of freedom

Multiple R-squared: 0.6341, Adjusted R-squared: 0.6307

F-statistic: 190.6 on 1 and 110 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.