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

Samantha L. Davis

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1   Introduction

The seven 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 081715a-X.xml. The tree maps in 081715a-X use the ainal way of generating tree maps: the real plot data are centered in the middle of the 300m x 300m space; and the surrounding area is calculated from the lognormal distribution estimated by the real plot data.

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. These tree maps had x and y generated by `runif()` in R. DBH was generated by deriving the lognormal means and standard deviations for each plot/species combination, then using those shape parameters to generate trees randomly within that distribution. Heights were calculated automatically by SORTIE-ND when the program initiated.

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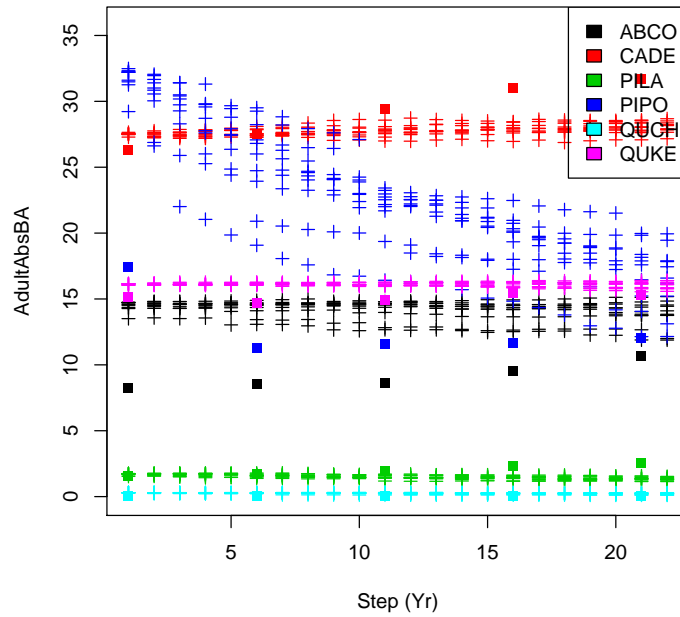
```
> library(SortieOutputs)
>  processTestPlot("BBBPIPO", "outfiles/a", 0,
```

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

   Step Species  AdultAbsBA     simMean         pval signif
1     1    ABCO  8.22515648  14.4874900 1.861492e-12    Sig
2     6    ABCO  8.55844175  14.2882000 1.999045e-10    Sig
3    11    ABCO  8.60228985  14.1845000 3.580143e-09    Sig
4    16    ABCO  9.55329929  14.0081400 3.572729e-08    Sig
5    21    ABCO 10.69337808  13.8726400 2.746388e-06    Sig
6     1    CADE 26.30695258  27.5087700 1.344021e-11    Sig
7     6    CADE 27.54093222  27.5871000 6.026532e-01     NS
8    11    CADE 29.41467906  27.7336100 6.034129e-07    Sig
9    16    CADE 30.98351713  27.8902300 3.056027e-09    Sig
10   21    CADE 31.68296924  28.0236200 1.524051e-09    Sig
12    1    PILA  1.56575066   1.6983490 1.313508e-04    Sig
13    6    PILA  1.68034838   1.5932340 4.600563e-02    Sig
14   11    PILA  1.97541059   1.4827030 3.055049e-06    Sig
16   16    PILA  2.30771569   1.4264630 2.153251e-08    Sig
17   21    PILA  2.56894680   1.3621900 4.502349e-10    Sig
19    1    PIPO 17.41989711  31.7248300 4.802199e-12    Sig
20    6    PIPO 11.30799599  25.5532900 3.788122e-07    Sig
21   11    PIPO 11.61260396  21.6549600 1.392907e-07    Sig
22   16    PIPO 11.66155637  19.4159900 1.365524e-06    Sig
23   21    PIPO 12.04379013  16.9719200 1.594033e-04    Sig
25    1    QUCH  0.08307961   0.2944659 5.912090e-14    Sig
26    6    QUCH  0.03701669   0.2658709 2.943761e-09    Sig
27   11    QUCH  0.02100788   0.2442758 4.695743e-07    Sig
29   16    QUCH  0.02355851   0.2249381 1.063672e-06    Sig
30   21    QUCH  0.01766050   0.2063374 6.026801e-06    Sig
31    1    QUKE 15.17823670  16.1121400 4.583719e-13    Sig
32    6    QUKE 14.68553643  16.1523900 6.682381e-13    Sig
34   11    QUKE 14.90333257  16.1197500 5.228493e-11    Sig
35   16    QUKE 15.42906912  16.1091200 1.289904e-06    Sig
36   21    QUKE 15.31791852  16.0442600 1.799820e-05    Sig
```
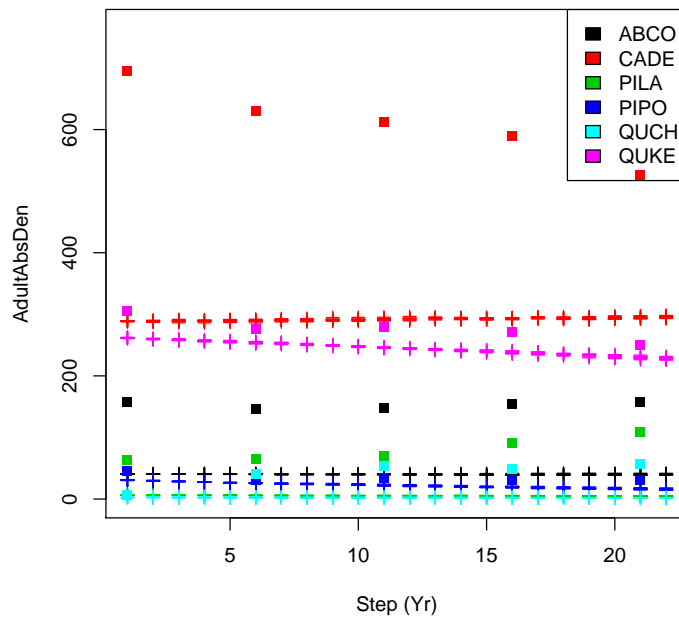
```
>   processTestPlot("BBBPIPO", "outfiles/a", 0,
+                   charactername="AdultAbsDen",
+                   writefile="outfiles/a/means/BBBPIPO-AdultAbsDen.csv")
```

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	157	40.577780	3.015354e-26	Sig
2	6	ABCO	147	40.422220	2.668218e-22	Sig
3	11	ABCO	148	40.122220	2.250402e-22	Sig
4	16	ABCO	155	39.688890	5.281515e-21	Sig
5	21	ABCO	157	39.722220	5.843627e-20	Sig
6	1	CADE	695	289.122200	1.268417e-26	Sig
7	6	CADE	630	289.377800	2.362446e-22	Sig
8	11	CADE	613	292.333300	4.688977e-22	Sig
9	16	CADE	589	293.088900	2.457840e-23	Sig
10	21	CADE	527	294.755500	1.749680e-20	Sig
12	1	PILA	63	6.188887	1.171220e-26	Sig
13	6	PILA	65	5.833335	4.237367e-24	Sig
14	11	PILA	70	5.511111	1.310818e-22	Sig
16	16	PILA	91	5.200000	7.511060e-23	Sig
17	21	PILA	109	4.833334	1.120024e-24	Sig
19	1	PIPO	46	30.711100	2.562904e-15	Sig
20	6	PIPO	31	25.866670	1.149867e-10	Sig

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```
21  11    PIPO            34  22.344450 1.763657e-11    Sig
22  16    PIPO            31  19.377780 1.437717e-11    Sig
23  21    PIPO            31  16.411120 1.332907e-11    Sig
25   1    QUCH             7   2.522224 8.224423e-19    Sig
26   6    QUCH            40   2.422223 2.186880e-21    Sig
27  11    QUCH            53   2.255556 8.219768e-22    Sig
29  16    QUCH            49   2.111111 2.970514e-21    Sig
30  21    QUCH            57   1.811111 1.153632e-21    Sig
31   1    QUKE           305 261.588600 3.844994e-18    Sig
32   6    QUKE           276 254.111200 1.650786e-12    Sig
34  11    QUKE           280 245.822200 6.337974e-16    Sig
35  16    QUKE           272 238.522200 4.906904e-13    Sig
36  21    QUKE           250 230.088800 3.912008e-10    Sig
```
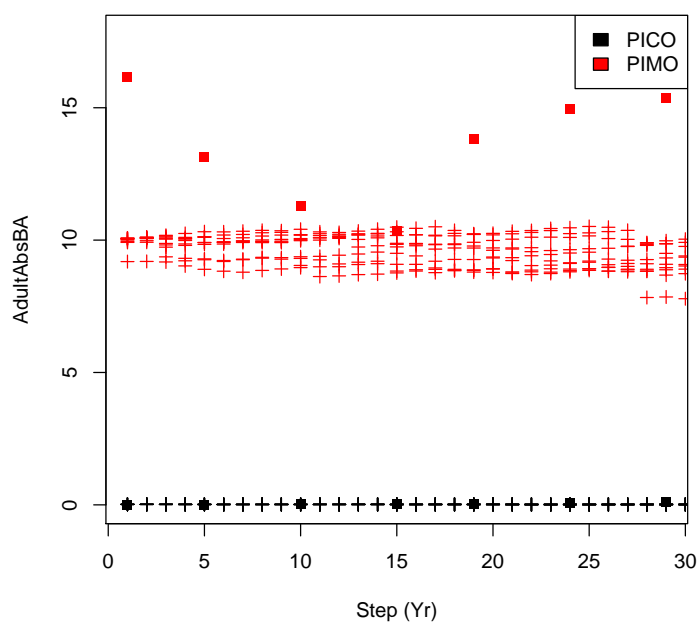

3.2 EMRIDGE: Adult Basal Area and Density

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

   Step Species   AdultAbsBA    simMean         pval signif
1     1    PICO  0.005724781 0.01672320 1.000000e+00     NS
```

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```
2     5   PICO   0.011388300 0.01553262 1.306538e-02    Sig
3    10   PICO   0.019037311 0.01537200 7.129646e-02     NS
4    15   PICO   0.022427097 0.01508054 1.765566e-02    Sig
5    19   PICO   0.035197701 0.01597593 5.152369e-05    Sig
6    24   PICO   0.051995836 0.01387346 1.059849e-06    Sig
7    29   PICO   0.103346859 0.01487849 1.189121e-09    Sig
8     1   PIMO 16.164999910 9.93956100 8.677010e-14    Sig
9     5   PIMO 13.132768430 9.77749700 2.915691e-09    Sig
10   10   PIMO 11.288140290 9.75364500 7.210949e-06    Sig
11   15   PIMO 10.351063060 9.66180900 5.835718e-03    Sig
12   19   PIMO 13.833822760 9.58582900 2.938105e-09    Sig
13   24   PIMO 14.941689150 9.47798800 4.452526e-10    Sig
14   29   PIMO 15.379181290 9.19773700 2.553430e-10    Sig
```



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

  Step Species AdultAbsDen    simMean         pval signif
1    1   PICO           2  0.2222220 1.000000e+00     NS
2    5   PICO           2  0.1888887 2.829241e-15    Sig
3   10   PICO           4  0.1777776 6.227873e-18    Sig
```

```
4     15     PICO            6  0.1666665 2.346973e-18     Sig
5     19     PICO            7  0.1666665 5.651249e-19     Sig
6     24     PICO            8  0.1444443 6.335316e-19     Sig
7     29     PICO            9  0.1444443 2.155085e-19     Sig
8      1     PIMO           87 37.1444300 8.223681e-22     Sig
9      5     PIMO           90 36.7555600 1.572609e-19     Sig
10    10     PIMO           93 36.1555500 2.994313e-19     Sig
11    15     PIMO          105 37.5555500 4.660628e-19     Sig
12    19     PIMO          190 37.7444400 1.775506e-22     Sig
13    24     PIMO          208 37.7777800 6.475015e-22     Sig
14    29     PIMO          226 37.7333400 2.817437e-22     Sig
```
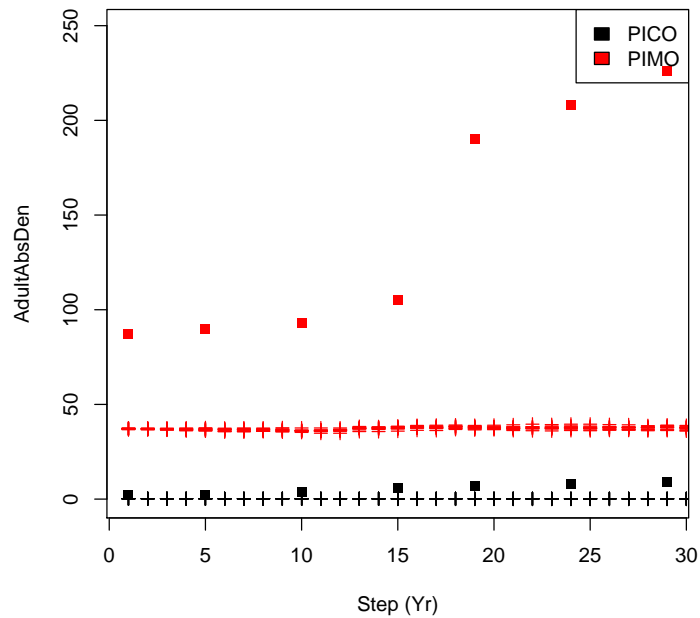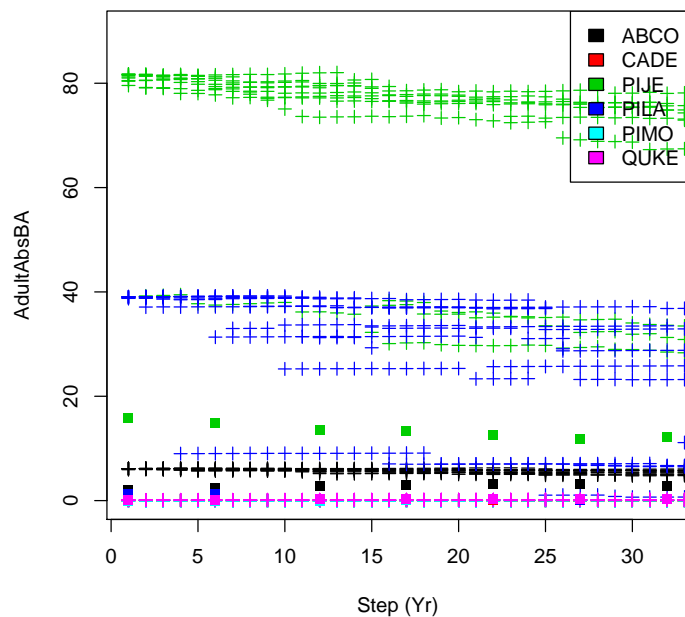

3.3 FRPIJE: Adult Basal Area and Density

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

  Step Species  AdultAbsBA    simMean         pval signif
1    1    ABCO 2.053798223  6.0996910 7.158258e-18    Sig
2    6    ABCO 2.453112077  5.9804620 3.817522e-13    Sig
```
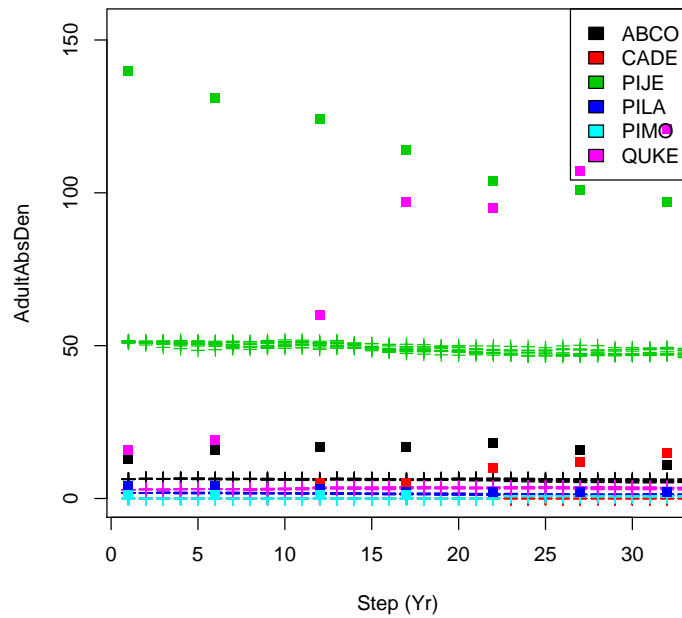
```
3    12    ABCO  2.764403796   5.7902840  2.372572e-10    Sig
4    17    ABCO  2.916809881   5.7023750  6.299497e-10    Sig
5    22    ABCO  3.169380383   5.6240830  8.203032e-09    Sig
6    27    ABCO  3.181020797   5.5224350  8.478692e-09    Sig
7    32    ABCO  2.799051717   5.4307180  1.290497e-08    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  81.0924000  4.415336e-19    Sig
16     6    PIJE 14.924775560  75.6490800  1.749695e-07    Sig
17    12    PIJE 13.464172680  74.2627300  1.842866e-07    Sig
18    17    PIJE 13.358516740  64.2886600  2.206492e-05    Sig
20    22    PIJE 12.633173140  63.5611900  2.860865e-05    Sig
21    27    PIJE 11.725481060  62.1435900  3.266936e-05    Sig
22    32    PIJE 12.124942370  61.3587000  4.176709e-05    Sig
23     1    PILA  1.270279256  38.9702900  4.195644e-24    Sig
24     6    PILA  1.307463234  35.0132110  1.296015e-06    Sig
25    12    PILA  0.179119109  32.1637200  1.692922e-06    Sig
26    17    PILA  0.219019786  28.8962020  2.751562e-05    Sig
27    22    PILA  0.253735251  27.8484990  4.861168e-05    Sig
28    27    PILA  0.194133601  20.2820790  1.083325e-03    Sig
29    32    PILA  0.219090472  20.1580927  1.221165e-03    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   0.1098865  3.518079e-17    Sig
35     6    QUKE  0.200555032   0.1190206  5.920649e-14    Sig
36    12    QUKE  0.237522239   0.1304106  1.778244e-12    Sig
37    17    QUKE  0.262400569   0.1364155  2.793816e-11    Sig
40    22    QUKE  0.296468865   0.1392045  5.966409e-13    Sig
41    27    QUKE  0.333892240   0.1417498  4.393716e-13    Sig
42    32    QUKE  0.387661659   0.1437268  9.013401e-14    Sig
```

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

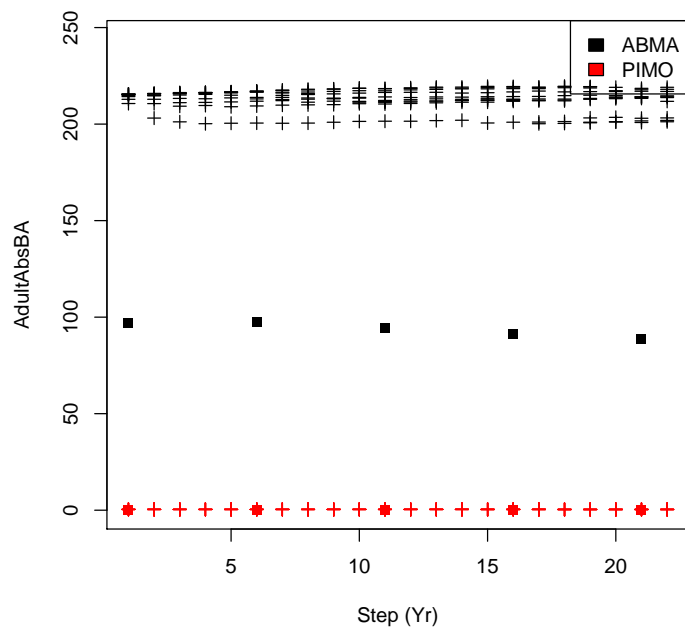|	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABCO	13	6.299997	2.186589e-20	Sig
2	6	ABCO	16	6.388889	2.410483e-17	Sig
3	12	ABCO	17	6.233331	4.067421e-17	Sig
4	17	ABCO	17	6.166665	8.207438e-18	Sig
5	22	ABCO	18	6.266666	5.170175e-16	Sig
6	27	ABCO	16	5.933333	1.387190e-14	Sig
7	32	ABCO	11	5.766667	8.723555e-12	Sig
8	1	CADE	3	0.000000	0.000000e+00	Sig
9	6	CADE	3	0.000000	0.000000e+00	Sig
10	12	CADE	5	0.000000	0.000000e+00	Sig
11	17	CADE	5	0.000000	0.000000e+00	Sig
12	22	CADE	10	0.000000	0.000000e+00	Sig
13	27	CADE	12	0.000000	0.000000e+00	Sig
14	32	CADE	15	0.000000	0.000000e+00	Sig
15	1	PIJE	140	51.266650	1.302739e-24	Sig
16	6	PIJE	131	50.444440	1.475159e-19	Sig
17	12	PIJE	124	50.322220	5.639171e-19	Sig
```

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```
18  17  PIJE       114 48.833330 2.479722e-18    Sig
20  22  PIJE       104 48.055560 7.291644e-18    Sig
21  27  PIJE       101 47.833340 2.076480e-16    Sig
22  32  PIJE        97 48.077760 8.898589e-17    Sig
23   1  PILA         4  1.855557 6.190316e-16    Sig
24   6  PILA         4  1.800002 4.024967e-12    Sig
25  12  PILA         3  1.666668 3.972896e-10    Sig
26  17  PILA         2  1.477777 3.745541e-06    Sig
27  22  PILA         2  1.333331 2.960990e-07    Sig
28  27  PILA         2  1.166665 1.631793e-07    Sig
29  32  PILA         2  1.111111 3.842654e-07    Sig
30   1  PIMO         1  0.000000 0.000000e+00    Sig
31   6  PIMO         1  0.000000 0.000000e+00    Sig
32  12  PIMO         1  0.000000 0.000000e+00    Sig
33  17  PIMO         1  0.000000 0.000000e+00    Sig
34   1  QUKE        16  2.866668 1.505578e-23    Sig
35   6  QUKE        19  3.077777 3.932213e-21    Sig
36  12  QUKE        60  3.455555 6.855223e-24    Sig
37  17  QUKE        97  3.544444 6.949114e-25    Sig
40  22  QUKE        95  3.500001 1.192506e-25    Sig
41  27  QUKE       107  3.466666 3.686231e-25    Sig
42  32  QUKE       121  3.355556 1.428278e-25    Sig
```

3.4 PGABMA: Adult Basal Area and Density

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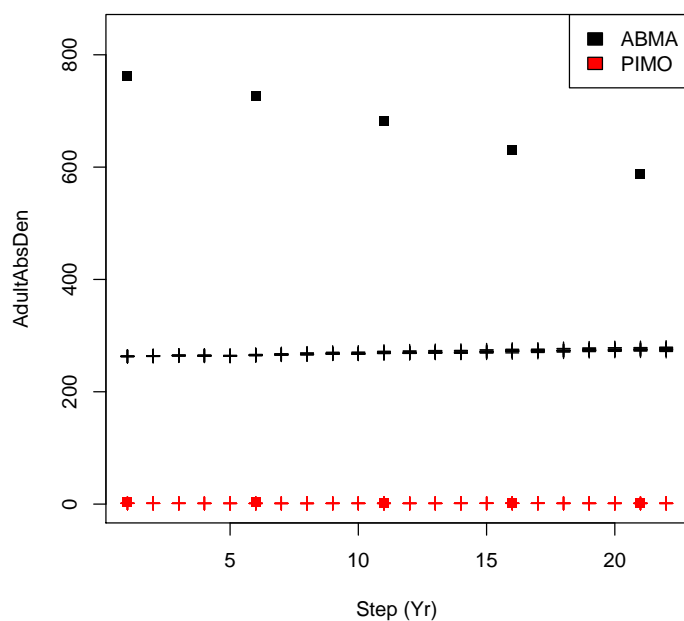> library(SortieOutputs)
> processTestPlot("PGABMA", "outfiles/a", 0,
+                 charactername="AdultAbsBA",
+                 writefile="outfiles/a/means/PGABMA-AdultAbsBA.csv")
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABMA	96.84838877	214.5197000	2.576727e-18	Sig
2	6	ABMA	97.52063023	213.2908000	1.194178e-13	Sig
3	11	ABMA	94.43564576	213.1559000	7.661571e-14	Sig
4	16	ABMA	91.25577994	213.8569000	9.908813e-14	Sig
5	21	ABMA	88.46650645	211.4297000	8.385077e-13	Sig
7	1	PIMO	0.02068744	0.3935558	1.160393e-14	Sig
8	6	PIMO	0.02380940	0.3973471	2.617255e-11	Sig
9	11	PIMO	0.01586508	0.4003728	3.952548e-11	Sig
10	16	PIMO	0.01993031	0.3960619	2.601130e-08	Sig
11	21	PIMO	0.02255198	0.3804513	5.025823e-08	Sig


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

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```
   Step Species AdultAbsDen       simMean          pval signif
1     1    ABMA        762   262.989000  2.987177e-30    Sig
2     6    ABMA        727   265.288900  1.680519e-26    Sig
3    11    ABMA        682   269.422200  1.084329e-23    Sig
4    16    ABMA        630   272.644400  6.152767e-22    Sig
5    21    ABMA        587   275.466600  2.365726e-21    Sig
7     1    PIMO          3     1.299997  4.999245e-15    Sig
8     6    PIMO          3     1.211109  6.060083e-11    Sig
9    11    PIMO          2     1.266664  2.232686e-07    Sig
10   16    PIMO          2     1.399999  1.844340e-06    Sig
11   21    PIMO          2     1.300000  2.289655e-06    Sig
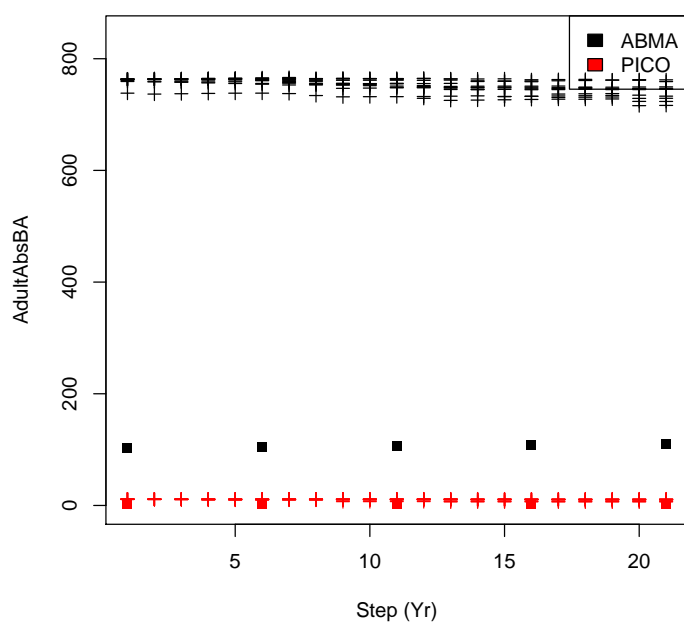```



## 3.5   POFLABMA: Adult Basal Area and Density

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

   Step Species AdultAbsBA   simMean   pval signif
1   1   ABMA 102.873900 760.213800 7.713375e-19   Sig
2   6   ABMA 105.098894 758.979900 1.144077e-18   Sig
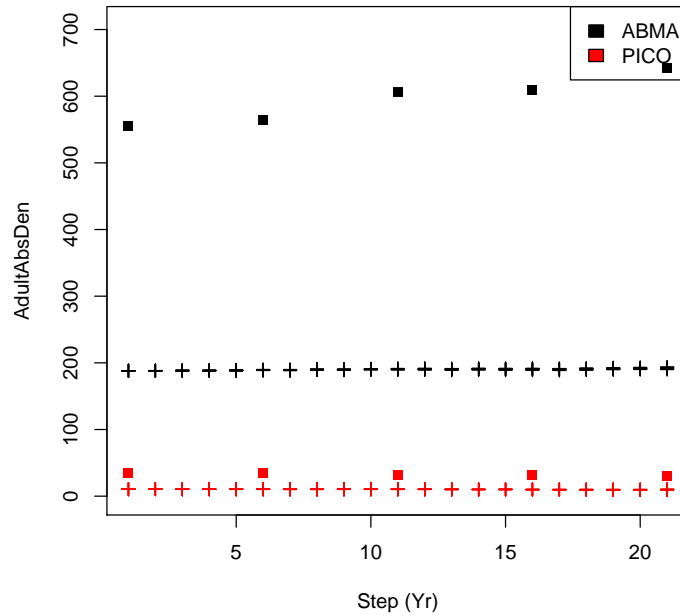```

```
3   11    ABMA 107.131277 754.330100 8.307479e-18    Sig
4   16    ABMA 107.930403 746.443500 6.157926e-17    Sig
7   21    ABMA 109.695510 741.074700 4.044984e-16    Sig
8    1    PICO   3.081969  11.206270 4.038268e-15    Sig
9    6    PICO   3.184662  10.815726 1.207517e-11    Sig
10  11    PICO   2.607272  10.447515 2.284722e-08    Sig
11  16    PICO   2.703773   9.941131 3.699203e-07    Sig
12  21    PICO   2.627468   9.785462 3.198448e-07    Sig
```



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

   Step Species AdultAbsDen     simMean         pval signif
1    1    ABMA         555 188.066600 6.016352e-31    Sig
2    6    ABMA         565 189.133400 1.682323e-27    Sig
3   11    ABMA         606 190.544400 2.088977e-26    Sig
4   16    ABMA         610 190.400100 3.088067e-25    Sig
7   21    ABMA         642 191.989000 1.648561e-24    Sig
8    1    PICO          34  10.555570 3.142422e-23    Sig
9    6    PICO          35  10.466670 3.963694e-19    Sig
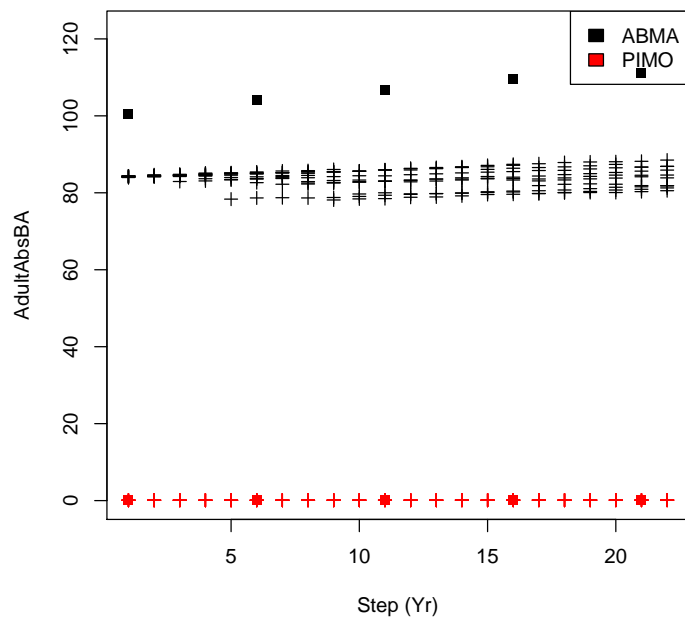10  11    PICO          32  10.422220 3.223146e-19    Sig
```

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```
11    16    PICO           32    9.922220 4.014721e-20    Sig
12    21    PICO           30    9.822214 2.530742e-16    Sig
```


3.6   SFTRABMA: Adult Basal Area and Density

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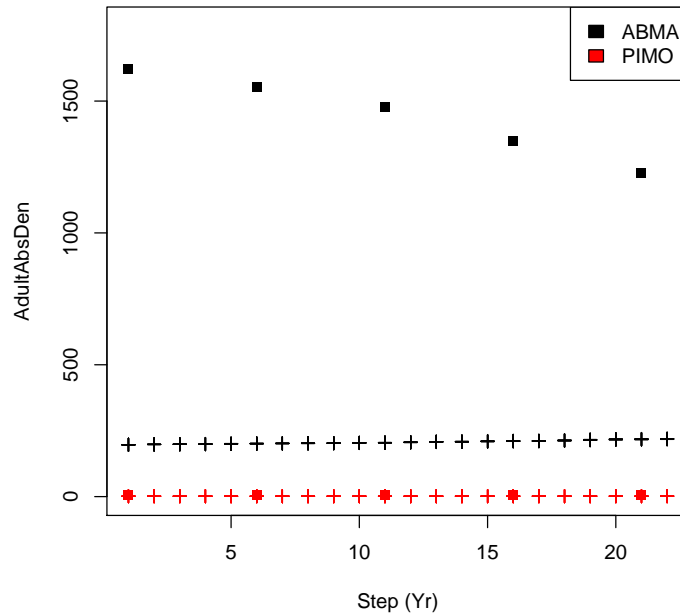> library(SortieOutputs)
> processTestPlot("SFTRABMA", "outfiles/a", 0,
+                 charactername="AdultAbsBA",
+                 writefile="outfiles/a/means/SFTRABMA-AdultAbsBA.csv")

   Step Species  AdultAbsBA     simMean         pval signif
1     1    ABMA 100.5079451 84.2198300 8.705163e-20    Sig
2     6    ABMA 104.0460566 83.8325400 1.561406e-10    Sig
5    11    ABMA 106.7590529 82.9131600 6.391516e-10    Sig
7    16    ABMA 109.5121569 83.7778600 4.482000e-10    Sig
8    21    ABMA 111.2301741 84.0548700 1.780744e-10    Sig
10    1    PIMO   0.1356692  0.1032233 9.285011e-11    Sig
11    6    PIMO   0.1492166  0.1069942 2.437046e-07    Sig
12   11    PIMO   0.1615780  0.1119264 1.149117e-07    Sig
13   16    PIMO   0.1689607  0.1230954 2.034772e-07    Sig
14   21    PIMO   0.1747664  0.1268133 8.932433e-07    Sig
```

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

	Step	Species	AdultAbsDen	simMean	pval	signif
1	1	ABMA	1623	196.589000	6.432820e-35	Sig
2	6	ABMA	1554	201.077800	4.641082e-32	Sig
5	11	ABMA	1477	204.555800	2.489897e-32	Sig
7	16	ABMA	1348	210.466700	6.090492e-30	Sig
8	21	ABMA	1228	217.555600	1.646402e-28	Sig
10	1	PIMO	7	1.544448	3.071753e-21	Sig
11	6	PIMO	7	1.544446	9.220482e-17	Sig
12	11	PIMO	7	1.488889	3.741533e-16	Sig
13	16	PIMO	7	1.622224	4.663174e-16	Sig
14	21	PIMO	5	1.666669	5.936312e-14	Sig

3.7 SUPILA: Adult Basal Area and Density

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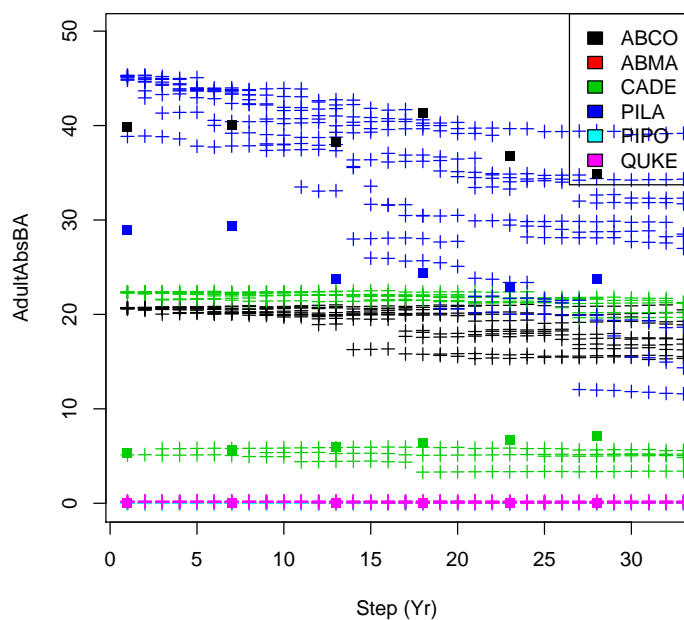> library(SortieOutputs)
> processTestPlot("SUPILA", "outfiles/a", 0,
+                  charactername="AdultAbsBA",
+                  writefile="outfiles/a/means/SUPILA-AdultAbsBA.csv")
```

	Step	Species	AdultAbsBA	simMean	pval	signif
1	1	ABCO	39.812853040	20.6627200	3.342763e-25	Sig
2	7	ABCO	40.092266770	20.3839600	8.165809e-18	Sig
3	13	ABCO	38.262802650	20.1725900	1.492071e-14	Sig
4	18	ABCO	41.362842560	19.2003400	1.331421e-11	Sig
5	23	ABCO	36.771096530	18.3833900	1.656951e-10	Sig
6	28	ABCO	34.847107860	17.9643000	5.217270e-10	Sig
11	1	ABMA	0.020612040	0.0000000	0.000000e+00	Sig
12	7	ABMA	0.025165000	0.0000000	0.000000e+00	Sig
13	13	ABMA	0.029637853	0.0000000	0.000000e+00	Sig
14	18	ABMA	0.036583931	0.0000000	0.000000e+00	Sig
15	23	ABMA	0.042594601	0.0000000	0.000000e+00	Sig
16	28	ABMA	0.051377726	0.0000000	0.000000e+00	Sig
17	1	CADE	5.306942349	20.6135450	9.385409e-06	Sig
18	7	CADE	5.599432328	18.7295400	2.247469e-04	Sig

```
19    13    CADE   5.969075285 17.0101730 2.056544e-03    Sig
20    18    CADE   6.342942278 16.7575420 3.268362e-03    Sig
21    23    CADE   6.741611282 16.5698680 4.183923e-03    Sig
22    28    CADE   7.169534110 14.5306260 2.204218e-02    Sig
26     1    PILA  28.925281240 44.5014400 1.395290e-09    Sig
27     7    PILA  29.354349690 42.1691100 2.004903e-08    Sig
28    13    PILA  23.789185860 39.4168000 3.346707e-08    Sig
29    18    PILA  24.377238040 34.8253100 2.441730e-04    Sig
30    23    PILA  22.942010900 30.0895800 6.805707e-03    Sig
32    28    PILA  23.774268490 27.6253500 1.719359e-01     NS
34     1    PIPO   0.007032471  0.0000000 0.000000e+00    Sig
35     7    PIPO   0.005410621  0.0000000 0.000000e+00    Sig
36     1    QUKE   0.046833400  0.1784625 1.215013e-08    Sig
37     7    QUKE   0.050086529  0.1647955 6.506349e-06    Sig
38    13    QUKE   0.060658796  0.1539636 6.925697e-04    Sig
39    18    QUKE   0.038102893  0.1441848 7.815037e-04    Sig
40    23    QUKE   0.041391365  0.1319654 1.316486e-03    Sig
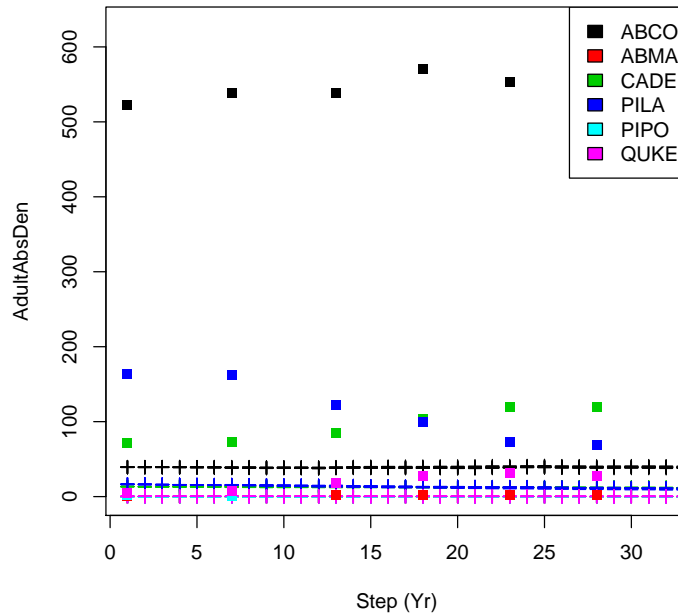41    28    QUKE   0.047439731  0.1333286 2.103347e-03    Sig
```



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

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```
   Step Species AdultAbsDen     simMean         pval signif
1     1    ABCO         522 39.2888800 3.123543e-31    Sig
2     7    ABCO         538 38.7555800 1.119375e-28    Sig
3    13    ABCO         539 38.5555600 5.722771e-28    Sig
4    18    ABCO         571 38.6444500 6.356358e-27    Sig
5    23    ABCO         553 39.2222300 1.617433e-26    Sig
6    28    ABCO         525 39.1777700 1.376625e-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 13.4111000 2.263691e-25    Sig
18    7    CADE          73 13.0222300 7.233364e-21    Sig
19   13    CADE          85 12.6444400 2.106160e-21    Sig
20   18    CADE         103 12.4777700 3.028768e-22    Sig
21   23    CADE         119 12.2222100 8.611722e-25    Sig
22   28    CADE         120 11.9333400 3.128576e-24    Sig
26    1    PILA         164 16.3888800 6.808871e-27    Sig
27    7    PILA         162 15.3777600 9.307546e-26    Sig
28   13    PILA         122 14.0666800 2.630537e-21    Sig
29   18    PILA         100 12.9222200 1.983331e-21    Sig
30   23    PILA          73 12.0444300 1.524280e-18    Sig
32   28    PILA          69 11.2444260 2.934759e-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  0.4222218 1.981859e-19    Sig
37    7    QUKE           7  0.3999996 4.565908e-20    Sig
38   13    QUKE          18  0.3555552 4.059354e-23    Sig
39   18    QUKE          27  0.3333330 3.587192e-23    Sig
40   23    QUKE          32  0.3111108 1.524979e-24    Sig
41   28    QUKE          27  0.2888886 4.401456e-23    Sig
```

3.8 Averages For All Plots

For time saving and an issue with loading a bunch of files needlessy, 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/a/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,
```

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```
+                                          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/a/081715-adultba.csv", row.names=F)
>     ## make the plot
> plot(AllAbsBAmeans[,"SimAbsBA"],AllAbsBAmeans[,"ExpAbsBA"],
+        col=as.factor(AllAbsBA$Species),
+        xlab="Simulated Means", ylab="Expected Means",
+        main="Group Adult Asbolute Basal Area")
>   abline(0,1)
>   legend("topleft",
+         legend=as.factor(unique(AllAbsBA$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
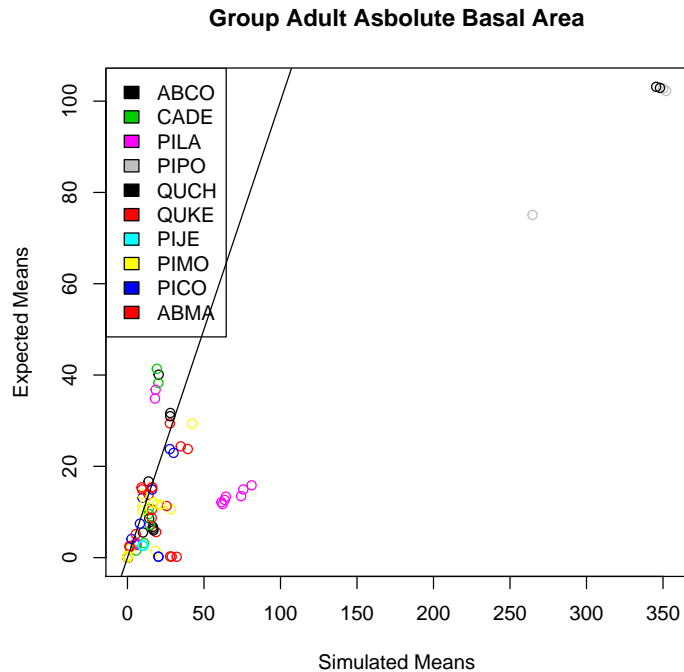-95.416  -7.215   6.589   7.160  58.354

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -7.0839     3.1010  -2.284   0.0243 *
ExpAbsBA      2.9423     0.1275  23.070   <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: 28.55 on 110 degrees of freedom
Multiple R-squared:  0.8287,       Adjusted R-squared:  0.8272
F-statistic: 532.2 on 1 and 110 DF,  p-value: < 2.2e-16
```

Group Adult Asbolute Basal Area


```
>    ## 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$Species),
+                                FUN=mean, na.rm=T)[,3]
>    colnames(AllAbsDenmeans) <- c("Step", "Species", "SimAbsDen", "ExpAbsDen")
>    write.csv(AllAbsDenmeans, file="outfiles/a/081715-adultdensity.csv", row.names=F)
>    AllAbsDen <- AllAbsDenmeans
>     plot(AllAbsDen[,"SimAbsDen"], AllAbsDen[,"ExpAbsDen"],
+          col=as.factor(AllAbsDen$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
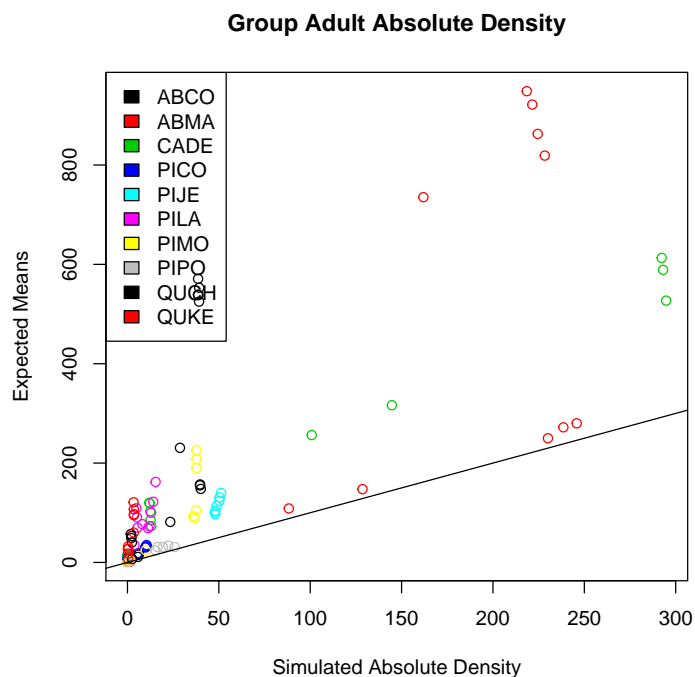-114.277  -14.760   -3.522   -0.762  169.307

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   2.9965     5.1763   0.579    0.564
ExpAbsDen     0.2626     0.0204  12.870   <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: 45.79 on 110 degrees of freedom
Multiple R-squared:  0.6009,        Adjusted R-squared:  0.5973
F-statistic: 165.6 on 1 and 110 DF,  p-value: < 2.2e-16

>
```


Group Adult Absolute Density

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.