Adjusting Individual Parameters

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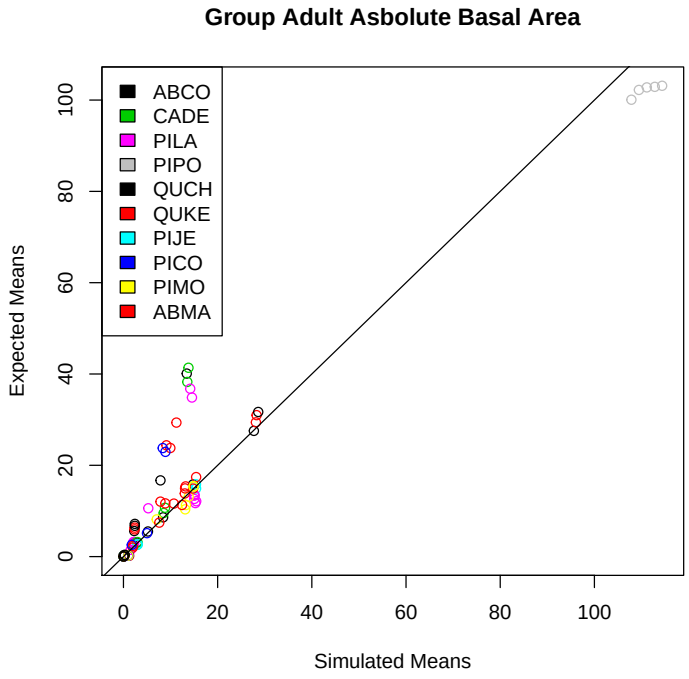
1 Summary

This paper is a first run through of running the model with optimized parameters. I did the adjustment for density graphs post-mortem, so I'll need to re-evaluate and do another run through to get the ideal parameters for both density and basal area as seen in best_matches.R.

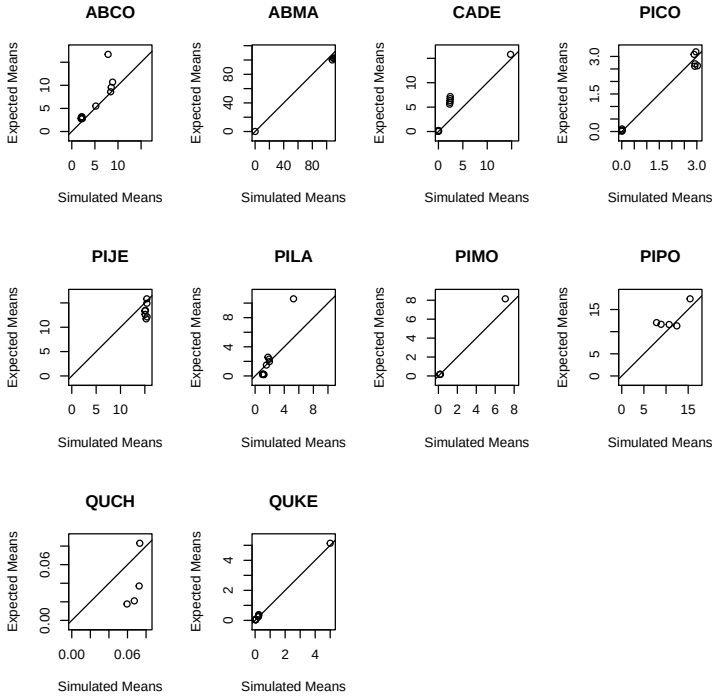
View the Rnw document to view the code; otherwise, I am only printing outputs to save some space and make this document more readable.

2 Basal Area

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

Residuals:
    Min      1Q  Median      3Q     Max
-25.646   0.696   1.863   2.012  13.088

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.95988    0.77860  -2.517   0.0134 *
ExpAbsBA     1.00116    0.02939  34.065   <2e-16 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

Residual standard error: 6.724 on 100 degrees of freedom
Multiple R-squared:  0.9207,        Adjusted R-squared:  0.9199
F-statistic:  1160 on 1 and 100 DF,  p-value: < 2.2e-16
```



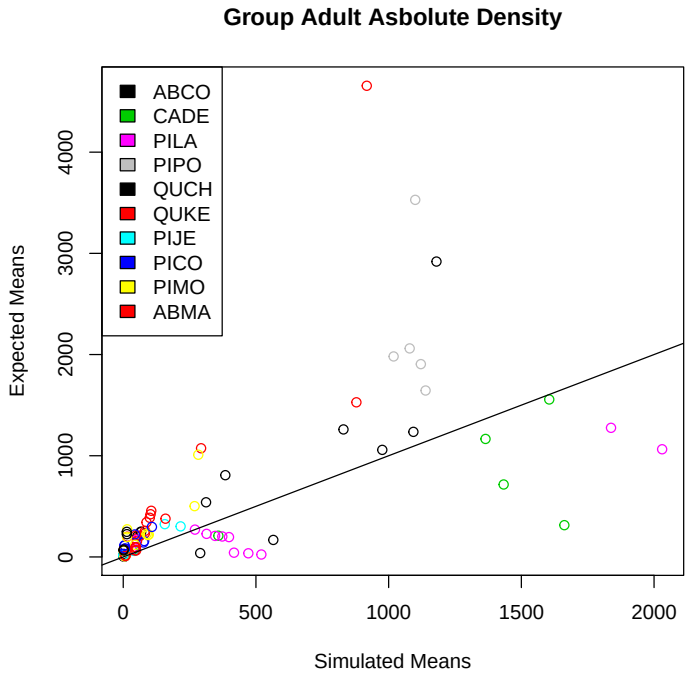
Now, how are the individual species doing?



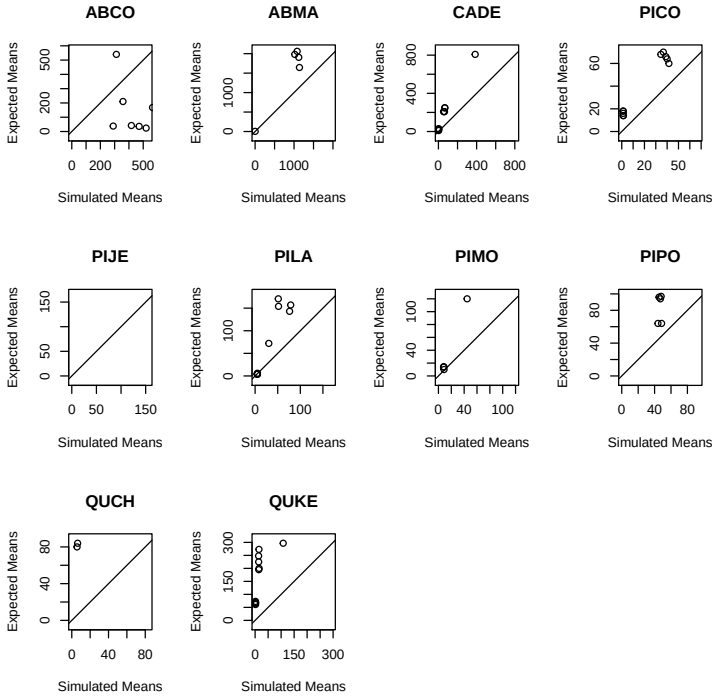

```
>   sppSlopes

   species      ba90
1     ABCO 2.9631043
2     ABMA 0.9183189
3     CADE 0.9886559
4     PICO 0.9506559
5     PIJE 2.4646940
6     PILA 2.9063555
7     PIMO 0.9884627
8     PIPO 0.6494128
9     QUCH 3.4243188
10    QUKE 1.0191361
```

3 Adult Density

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

Residuals:
     Min       1Q   Median       3Q      Max
-1154.65  -135.72  -106.52   -21.09  1472.97

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 108.73065   39.95936   2.721  0.00768 **
ExpAbsDen     0.42171    0.04606   9.156 7.01e-15 ***
---
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: 348.3 on 100 degrees of freedom
Multiple R-squared:  0.456,        Adjusted R-squared:  0.4506
F-statistic: 83.83 on 1 and 100 DF,  p-value: 7.012e-15
```



Now, how are the individual species doing?




```
>   sppSlopes
```

	species	ba90	den90
1	ABCO	2.9631043	0.7325867
2	ABMA	0.9183189	2.0114588
3	CADE	0.9886559	2.3071273
4	PICO	0.9506559	1.3178917
5	PIJE	2.4646940	-0.5837878
6	PILA	2.9063555	3.0308124
7	PIMO	0.9884627	3.6002731
8	PIPO	0.6494128	1.5356896
9	QUCH	3.4243188	-17.4879210
10	QUKE	1.0191361	2.5789914

```
>     write.csv(sppSlopes, file=paste(parName, ".csv", sep=""))
```