Adjusting Individual Parameters

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1 Summary

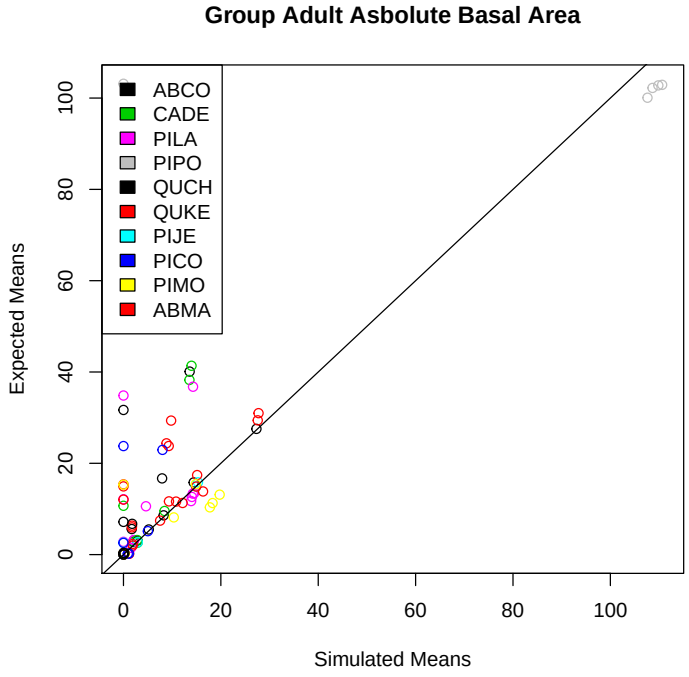
This paper is an upgrade to the 092315 run; specifically, it did 10 years of populating the seed bank before forking into the true runs. That way, I can load with seedlings/saplings already present. Hypothetically.

This one actually did not perform as well as the last one. Not according to the slopes, anyway.

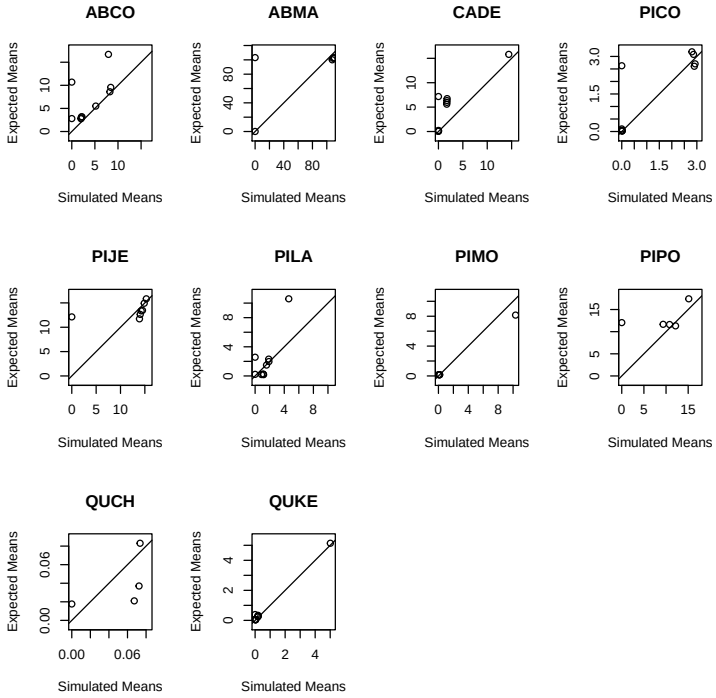
View the Rnw document to view the code; otherwise, I am only printing outputs to save some space and make this document more readable.

2 Basal Area

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

Residuals:
    Min      1Q  Median      3Q     Max
-79.279  -0.796   1.355   2.746  31.532

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.35883    1.38946  -0.978     0.33
ExpAbsBA     0.78190    0.05245  14.908   <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: 12 on 100 degrees of freedom
Multiple R-squared:  0.6897,        Adjusted R-squared:  0.6866
F-statistic: 222.2 on 1 and 100 DF,  p-value: < 2.2e-16
```



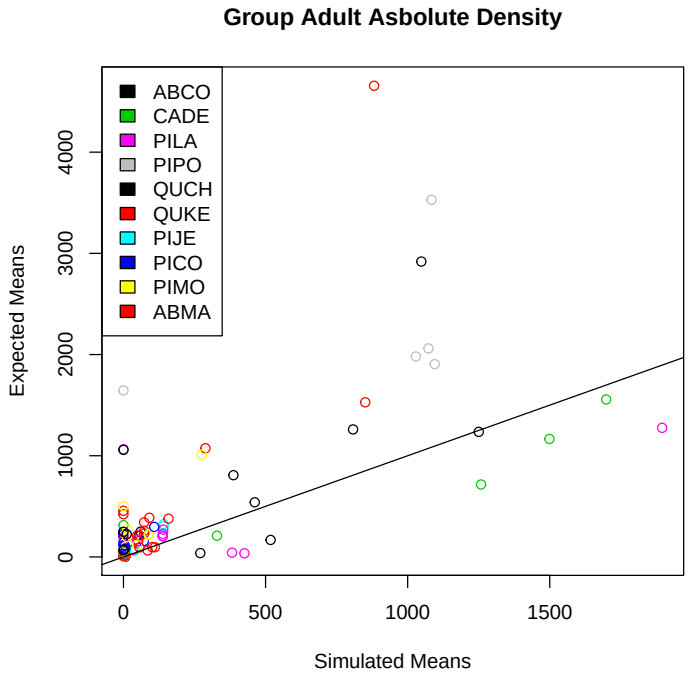
Now, how are the individual species doing?



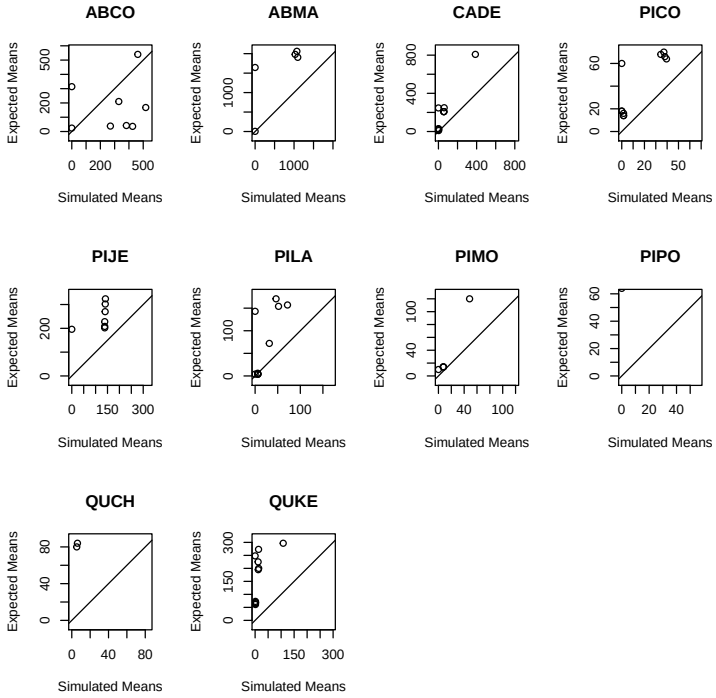

```
>   sppSlopes

   species      ba90
1     ABCO 2.0899943
2     ABMA 0.4617447
3     CADE 0.8400491
4     PICO 0.8397819
5     PIJE 0.1266374
6     PILA 2.5266342
7     PIMO 0.3786069
8     PIPO 0.2133728
9     QUCH 0.4564843
10    QUKE 0.8998571
```

3 Adult Density

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

Residuals:
    Min      1Q  Median      3Q     Max
-906.71  -80.89  -52.13  -27.47 1370.10

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 48.44193   33.82868   1.432    0.155
ExpAbsDen    0.37377    0.03899   9.586 8.02e-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: 294.8 on 100 degrees of freedom
Multiple R-squared:  0.4789,        Adjusted R-squared:  0.4736
F-statistic: 91.88 on 1 and 100 DF,  p-value: 8.023e-16
```



Now, how are the individual species doing?




```
>   sppSlopes
```

	species	ba90	den90
1	ABCO	2.0899943	0.7611341
2	ABMA	0.4617447	1.4537117
3	CADE	0.8400491	2.7527035
4	PICO	0.8397819	1.1758536
5	PIJE	0.1266374	0.4481674
6	PILA	2.5266342	2.6673771
7	PIMO	0.3786069	1.0196469
8	PIPO	0.2133728	0.2341411
9	QUCH	0.4564843	-4.7737627
10	QUKE	0.8998571	2.8567033

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