

Adding Seedling Allometry Values

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1 Summary

This run is the first run in November. I kept the reduction of seed/ling mortality from the 103015 run, and added in a different allometric parameter for seedlings. The parameter is the slope of the relationship between diam10 and seedling height. The default parameter that the original program set was 0.03, when I ran ours, I actually found a value of about 0.22 across species. It didn't vary enough (plus or minus 0.02) for me to think that the differences were appreciable. That is the only change in this run.

2 Seedling Absolute Density

Call:

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

Residuals:

Min	1Q	Median	3Q	Max
-1233.87	-84.65	-70.31	-67.50	1133.34

Coefficients:

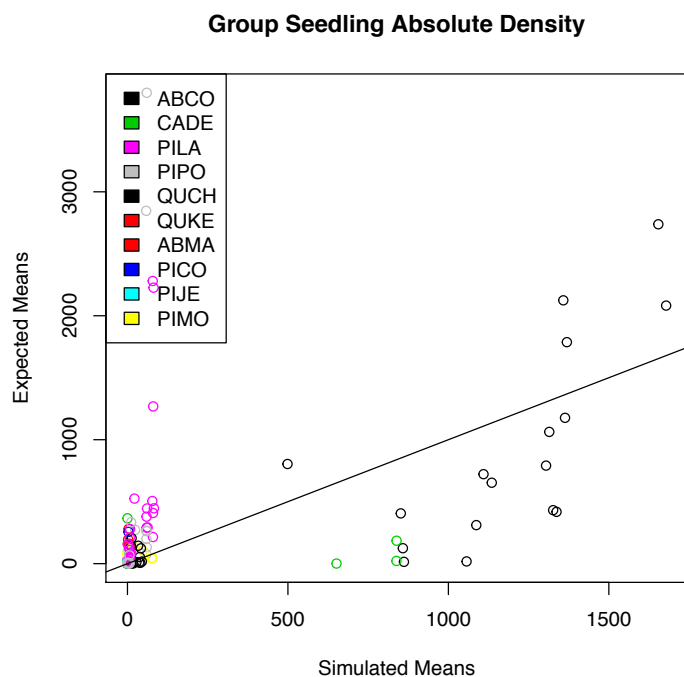
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	68.86711	26.70203	2.579	0.0107 *
ExpAbsDen	0.32247	0.04476	7.204	1.76e-11 ***

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

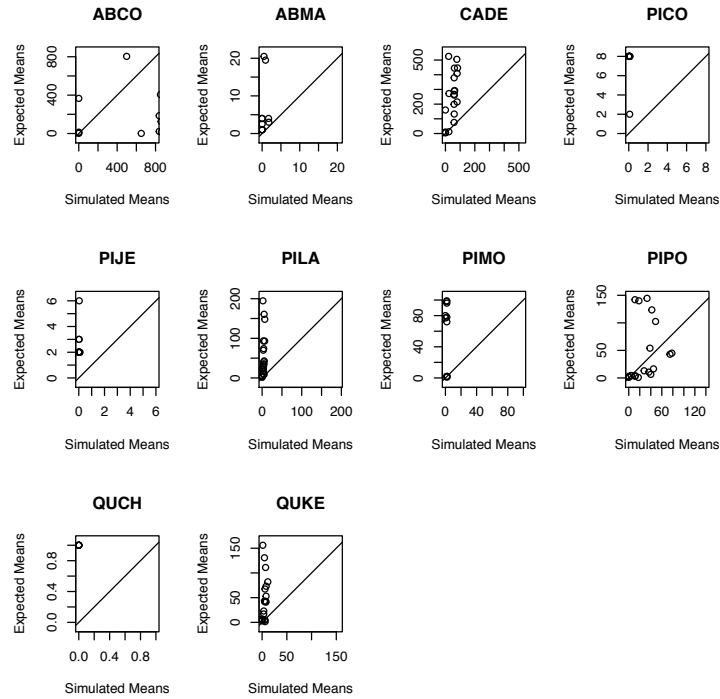
Residual standard error: 326.4 on 172 degrees of freedom

Multiple R-squared: 0.2318, Adjusted R-squared: 0.2273

F-statistic: 51.9 on 1 and 172 DF, p-value: 1.755e-11



Now, how are the individual species doing?



> *sppSlopes*

	species	sdlDen
1	ABCO	1.0146872
2	ABMA	8.2777967
3	CADE	12.8171749
4	PICO	-13.5321395
5	PIJE	1.9136359
6	PILA	12.0836268
7	PIMO	-15.3637140
8	PIPO	0.2800365
9	QUCH	NA
10	QUKE	14.3987423

3 Sapling Density

Call:

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

Residuals:

Min	1Q	Median	3Q	Max
-2993.1	-565.5	-148.4	-121.4	12750.7

Coefficients:

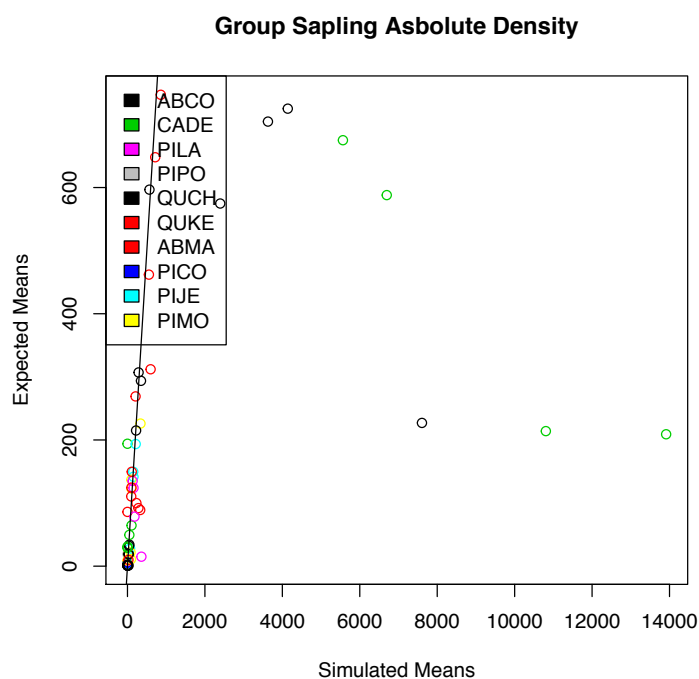
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	116.400	262.053	0.444	0.658
ExpAbsDen	5.002	1.136	4.405	3.1e-05 ***

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

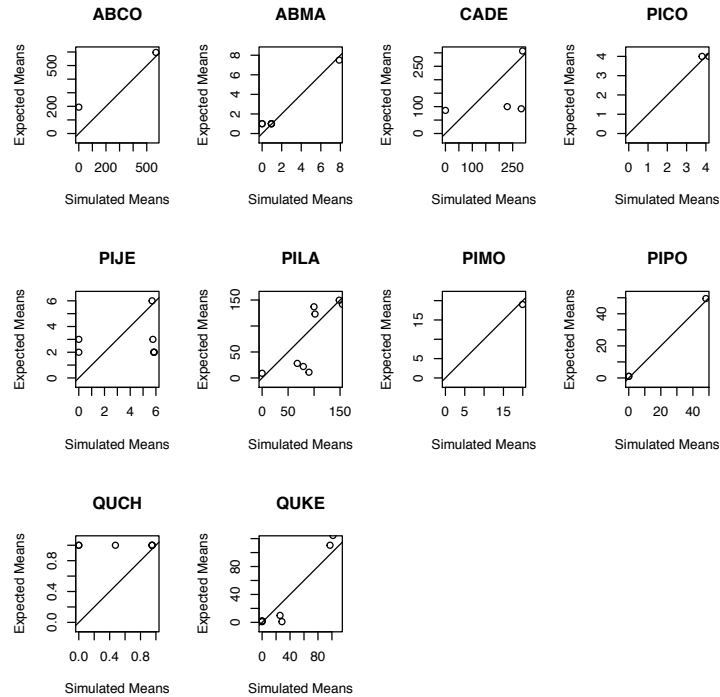
Residual standard error: 2056 on 84 degrees of freedom

Multiple R-squared: 0.1876, Adjusted R-squared: 0.178

F-statistic: 19.4 on 1 and 84 DF, p-value: 3.1e-05



Now, how are the individual species doing?



```
> sppSlopes

species      sdlDen      saplDen
1   ABCO    1.0146872 -2.368110e-02
2   ABMA    8.2777967  5.680939e-01
3   CADE   12.8171749  8.407172e-01
4   PICO  -13.5321395 -7.267092e-02
5   PIJE    1.9136359  7.692643e-02
6   PILA   12.0836268  7.511476e-01
7   PIMO  -15.3637140  2.811277e-02
8   PIPO    0.2800365  8.744458e-02
9   QUCH           NA  1.973967e-16
10  QUKE   14.3987423  1.166009e+00

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

4 Adult Absolute Density

Call:

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

Residuals:

Min	1Q	Median	3Q	Max
-5689.9	-795.8	-607.3	-541.9	13387.3

Coefficients:

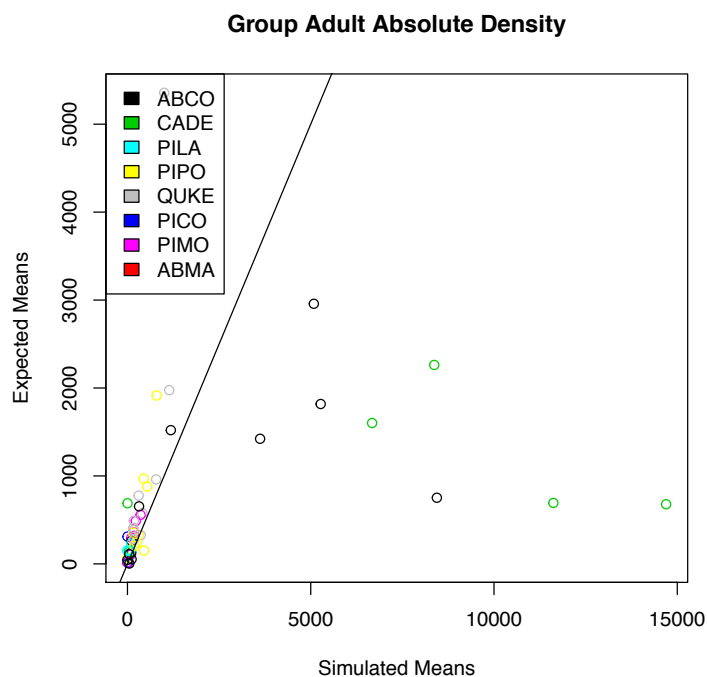
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	529.1146	414.3258	1.277	0.20642
ExpAbsDen	1.1502	0.3967	2.900	0.00519 **

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

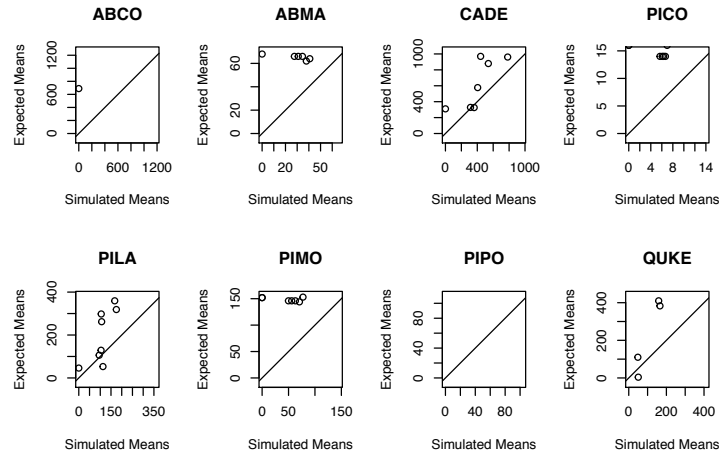
Residual standard error: 2739 on 61 degrees of freedom

Multiple R-squared: 0.1211, Adjusted R-squared: 0.1067

F-statistic: 8.407 on 1 and 61 DF, p-value: 0.005188



Now, how are the individual species doing?



```
> sppSlopes
```

	species	sdlDen	saplDen	AdultDen
1	ABCO	1.0146872	-2.368110e-02	-0.04344119
2	ABMA	8.2777967	5.680939e-01	-0.10842942
3	CADE	12.8171749	8.407172e-01	3.12673632
4	PICO	-13.5321395	-7.267092e-02	-0.22653448
5	PIJE	1.9136359	7.692643e-02	1.63411578
6	PILA	12.0836268	7.511476e-01	-0.05931691
7	PIMO	-15.3637140	2.811277e-02	-0.36350893
8	PIPO	0.2800365	8.744458e-02	2.48287674
9	QUCH	NA	1.973967e-16	NA
10	QUKE	14.3987423	1.166009e+00	NA

5 Adult Absolute Basal Area

Call:

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

Residuals:

	Min	1Q	Median	3Q	Max
	-28.5821	-0.3994	0.4230	1.4020	9.6815

Coefficients:

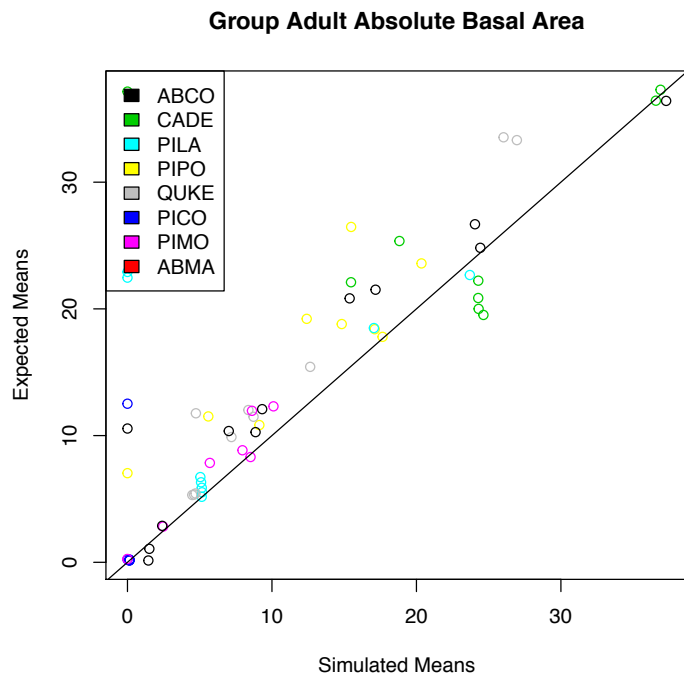
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-0.13665	1.31470	-0.104	0.918
ExpAbsDen	0.77309	0.07434	10.400	3.89e-15 ***

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

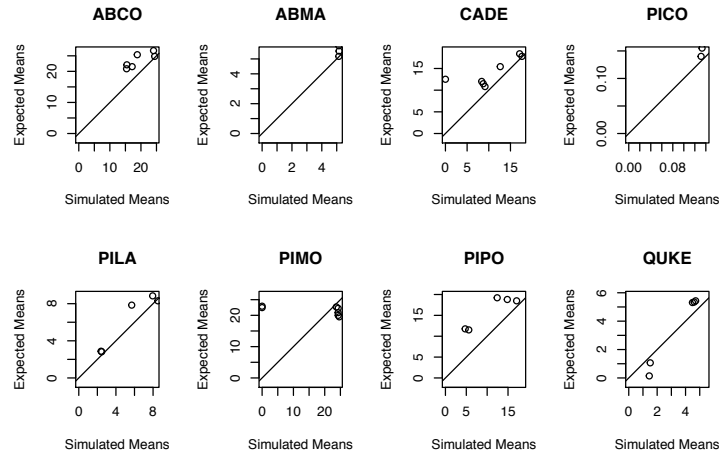
Residual standard error: 6.18 on 61 degrees of freedom

Multiple R-squared: 0.6394, Adjusted R-squared: 0.6335

F-statistic: 108.2 on 1 and 61 DF, p-value: 3.893e-15



Now, how are the individual species doing?



```
> sppSlopes
```

	species	sdlDen	saplDen	AdultDen	adultBA
1	ABCO	1.0146872	-2.368110e-02	-0.04344119	0.23373399
2	ABMA	8.2777967	5.680939e-01	-0.10842942	-0.22194417
3	CADE	12.8171749	8.407172e-01	3.12673632	0.91760256
4	PICO	-13.5321395	-7.267092e-02	-0.22653448	-0.54226454
5	PIJE	1.9136359	7.692643e-02	1.63411578	0.60914395
6	PILA	12.0836268	7.511476e-01	-0.05931691	-0.06922849
7	PIMO	-15.3637140	2.811277e-02	-0.36350893	0.87032822
8	PIPO	0.2800365	8.744458e-02	2.48287674	1.68145733
9	QUCH	NA	1.973967e-16	NA	NA
10	QUKE	14.3987423	1.166009e+00	NA	NA

6 Conclusions

So, in comparing these last two runs, there are some definite differences. The seedling density statistic is back down from where it was, but I think that's because the seedlings changed into saplings rather quickly. So what if we did the new one and dropped the old one? Kept the higher growth but lost the mortality?

We should also do a run to increase STR to actually fix, not hide, the seed problem.