

# Addding 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
-461.93	-39.34	-37.06	-16.23	568.00

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	36.95024	9.30779	3.970	0.000101 ***
ExpAbsDen	0.07487	0.01107	6.763	1.52e-10 ***

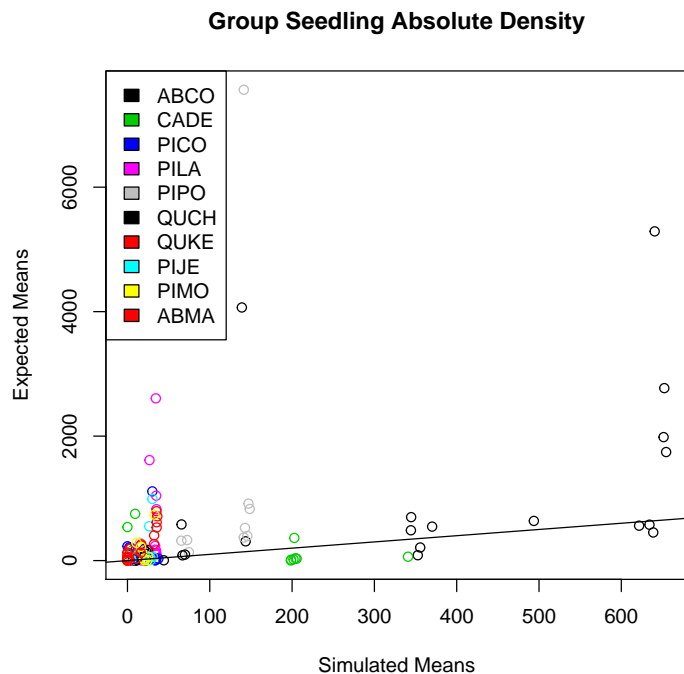
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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

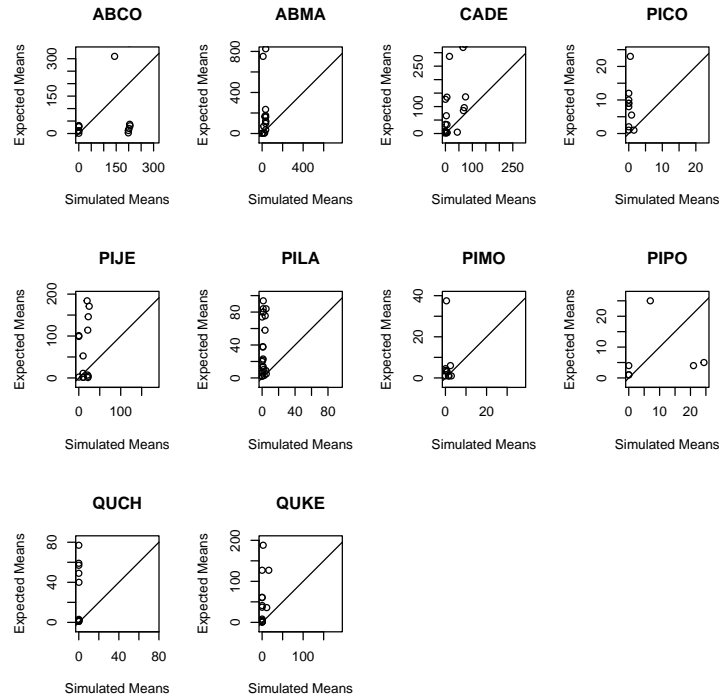
Residual standard error: 123.5 on 196 degrees of freedom

Multiple R-squared: 0.1892, Adjusted R-squared: 0.1851

F-statistic: 45.74 on 1 and 196 DF, p-value: 1.517e-10



Now, how are the individual species doing?



> sppSlopes

	species	sdlDen
1	ABCO	2.859319
2	ABMA	14.887505
3	CADE	13.575579
4	PICO	10.770525
5	PIJE	1.921255
6	PILA	15.121095
7	PIMO	22.632822
8	PIPO	4.323537
9	QUCH	4.314128
10	QUKE	15.792709

### 3 Sapling Density

Call:

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

Residuals:

	Min	1Q	Median	3Q	Max
	-982.90	-178.81	-85.73	-70.45	3012.27

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	69.0936	64.9269	1.064	0.29
ExpAbsDen	2.3552	0.3734	6.308	6.07e-09 ***

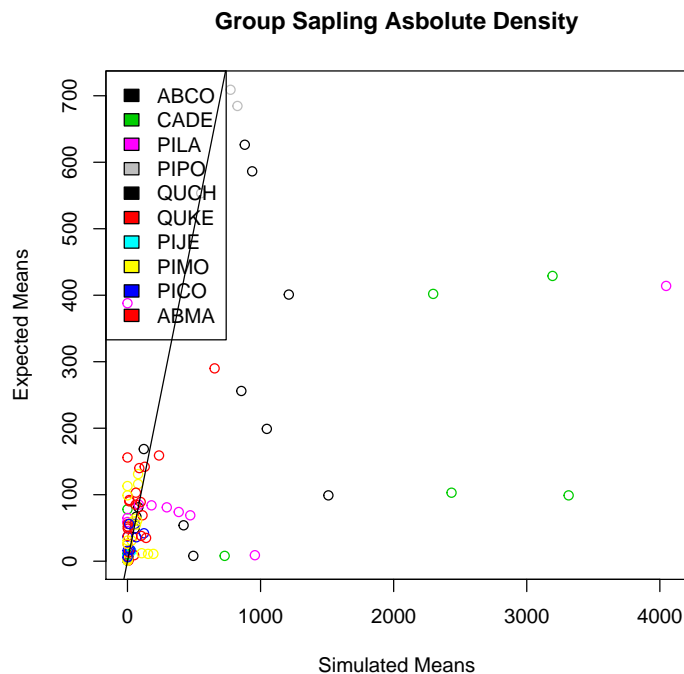
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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

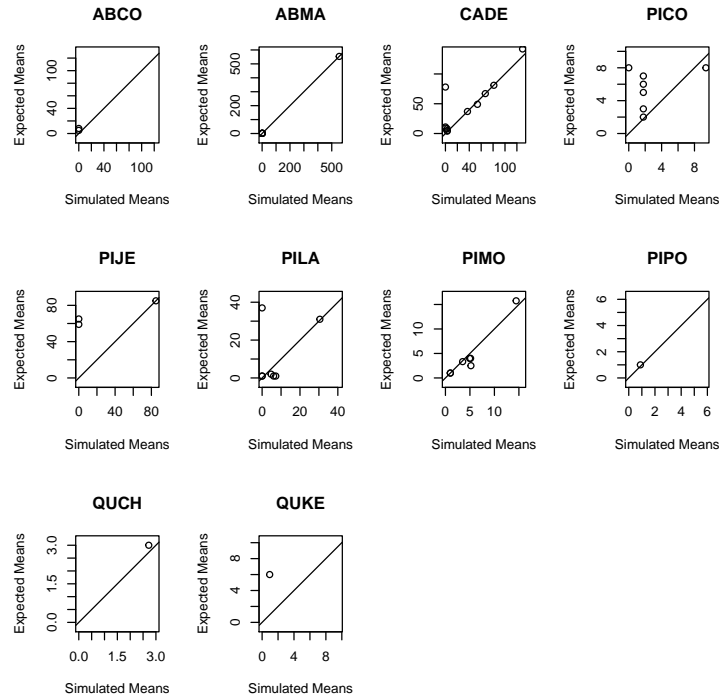
Residual standard error: 588.5 on 110 degrees of freedom

Multiple R-squared: 0.2656, Adjusted R-squared: 0.2589

F-statistic: 39.79 on 1 and 110 DF, p-value: 6.074e-09



Now, how are the individual species doing?



```
> sppSlopes
```

	species	sdlDen	saplDen
1	ABCO	2.859319	0.06437961
2	ABMA	14.887505	0.75972820
3	CADE	13.575579	0.23498495
4	PICO	10.770525	0.44240182
5	PIJE	1.921255	0.01258263
6	PILA	15.121095	0.66695155
7	PIMO	22.632822	1.00199395
8	PIPO	4.323537	0.03938076
9	QUCH	4.314128	203.96238272
10	QUKE	15.792709	-0.10953493

```
> 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
-1580.1	-212.2	-166.4	-119.8	3629.4

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	154.15657	82.80423	1.862	0.0656 .
ExpAbsDen	0.58254	0.09544	6.103	1.98e-08 ***

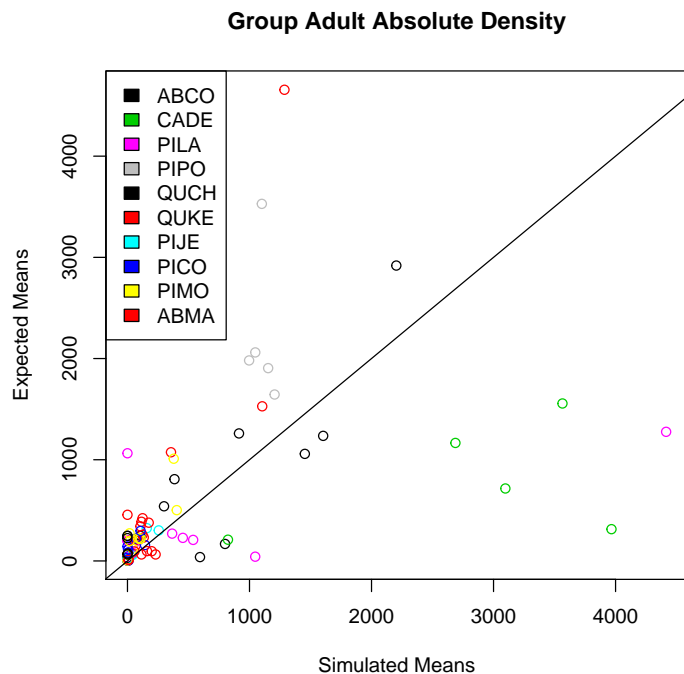
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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

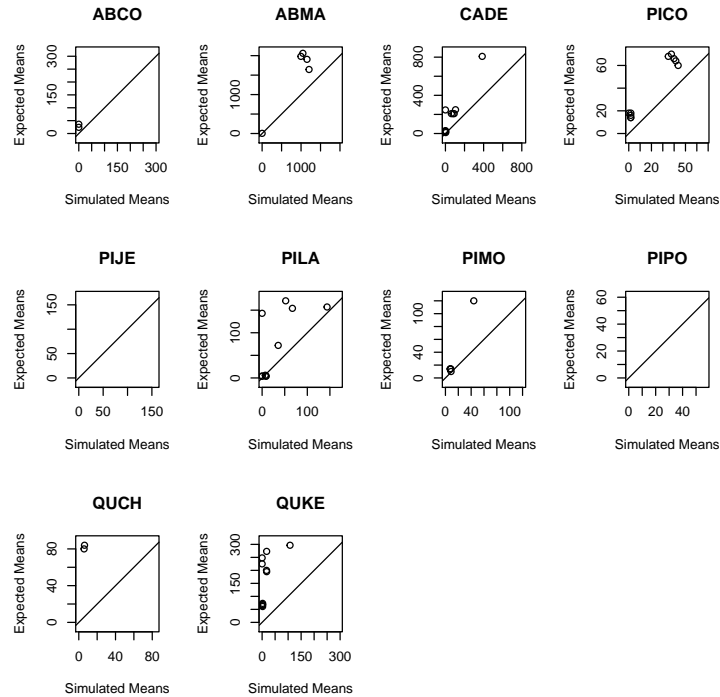
Residual standard error: 721.7 on 100 degrees of freedom

Multiple R-squared: 0.2714, Adjusted R-squared: 0.2641

F-statistic: 37.25 on 1 and 100 DF, p-value: 1.983e-08



Now, how are the individual species doing?



> sppSlopes

	species	sdlDen	saplDen	AdultDen
1	ABCO	2.859319	0.06437961	0.23643434
2	ABMA	14.887505	0.75972820	1.92227693
3	CADE	13.575579	0.23498495	1.72260064
4	PICO	10.770525	0.44240182	1.27385284
5	PIJE	1.921255	0.01258263	0.01778775
6	PILA	15.121095	0.66695155	1.70452350
7	PIMO	22.632822	1.00199395	1.95213715
8	PIPO	4.323537	0.03938076	-0.05898207
9	QUCH	4.314128	203.96238272	-32.01116580
10	QUKE	15.792709	-0.10953493	1.84797263

## 5 Adult Absolute Basal Area

Call:

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

Residuals:

	Min	1Q	Median	3Q	Max
	-29.1015	0.1747	1.9939	2.3118	13.2892

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-2.03582	0.78121	-2.606	0.0106 *
ExpAbsDen	0.89354	0.02949	30.301	<2e-16 ***

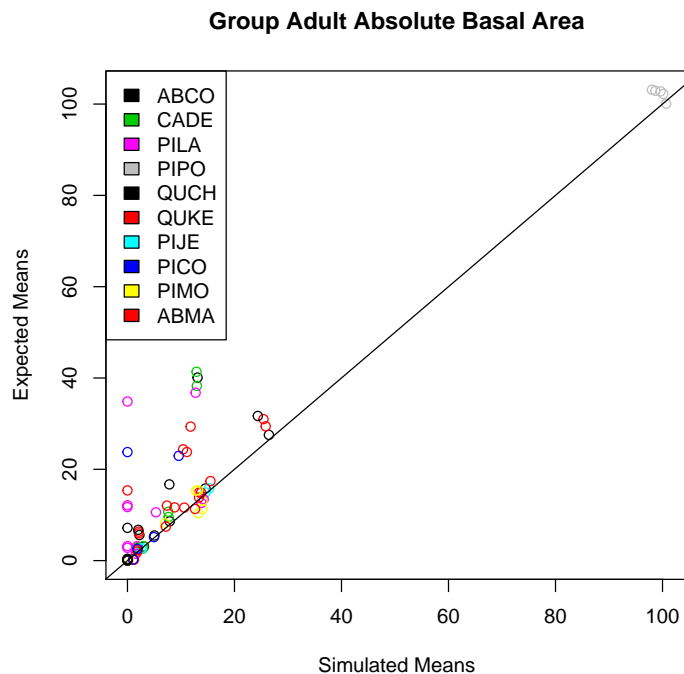
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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.747 on 100 degrees of freedom

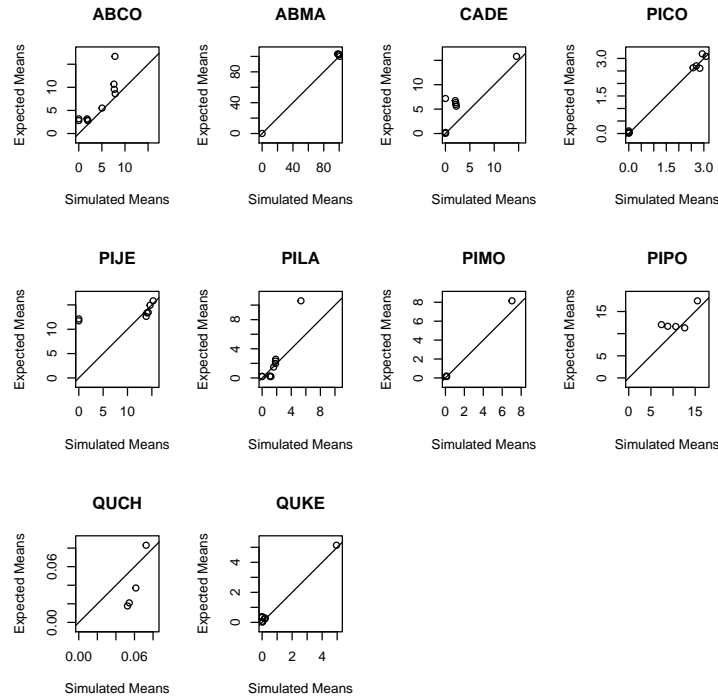
Multiple R-squared: 0.9018, Adjusted R-squared: 0.9008

F-statistic: 918.2 on 1 and 100 DF, p-value: < 2.2e-16



Now, how are the individual species doing?





> sppSlopes

	species	sdlDen	saplDen	AdultDen	adultBA
1	ABCO	2.859319	0.06437961	0.23643434	2.2545039
2	ABMA	14.887505	0.75972820	1.92227693	1.0264083
3	CADE	13.575579	0.23498495	1.72260064	1.0657416
4	PICO	10.770525	0.44240182	1.27385284	0.9911798
5	PIJE	1.921255	0.01258263	0.01778775	0.1562711
6	PILA	15.121095	0.66695155	1.70452350	2.1310951
7	PIMO	22.632822	1.00199395	1.95213715	0.6977826
8	PIPO	4.323537	0.03938076	-0.05898207	0.5859326
9	QUCH	4.314128	203.96238272	-32.01116580	3.2712168
10	QUKE	15.792709	-0.10953493	1.84797263	1.1285892

## 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.