

Adjusting Individual Parameters

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1 Summary

This run was the only run in October. It was a severe reduction of seedling/sapling mortality to see if we can make the seedling/sapling numbers match more closely without completely screwing up adult growth and reproduction.

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2 Seedling Absolute Density

Call:

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

Residuals:

Min	1Q	Median	3Q	Max
-1237.15	-212.89	-206.09	-95.67	2535.33

Coefficients:

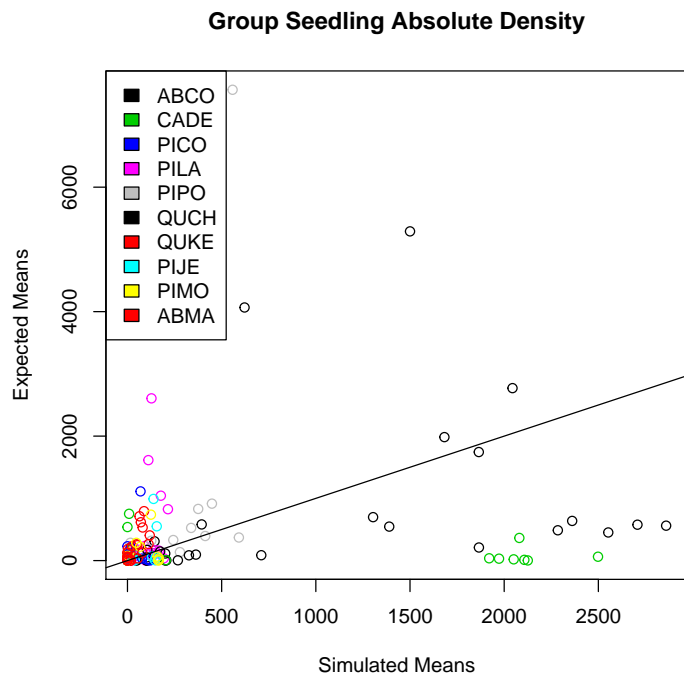
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	206.6497	44.4774	4.646	6.19e-06 ***
ExpAbsDen	0.2100	0.0529	3.970	0.000101 ***

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

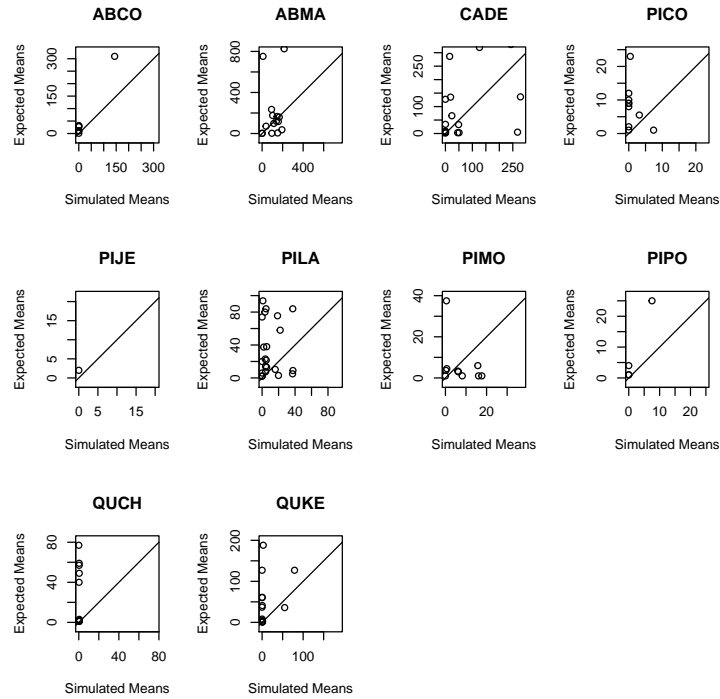
Residual standard error: 590.2 on 196 degrees of freedom

Multiple R-squared: 0.07441, Adjusted R-squared: 0.06969

F-statistic: 15.76 on 1 and 196 DF, p-value: 0.000101



Now, how are the individual species doing?



> sppSlopes

	species	sdlDen
1	ABCO	0.1960952
2	ABMA	1.2459189
3	CADE	4.3204355
4	PICO	2.1647434
5	PIJE	-0.2163740
6	PILA	1.4566700
7	PIMO	2.6091617
8	PIPO	1.0034431
9	QUCH	-151.8999127
10	QUKE	4.4717642

3 Sapling Density

Call:

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

Residuals:

Min	1Q	Median	3Q	Max
-423.02	-25.79	1.34	6.56	565.99

Coefficients:

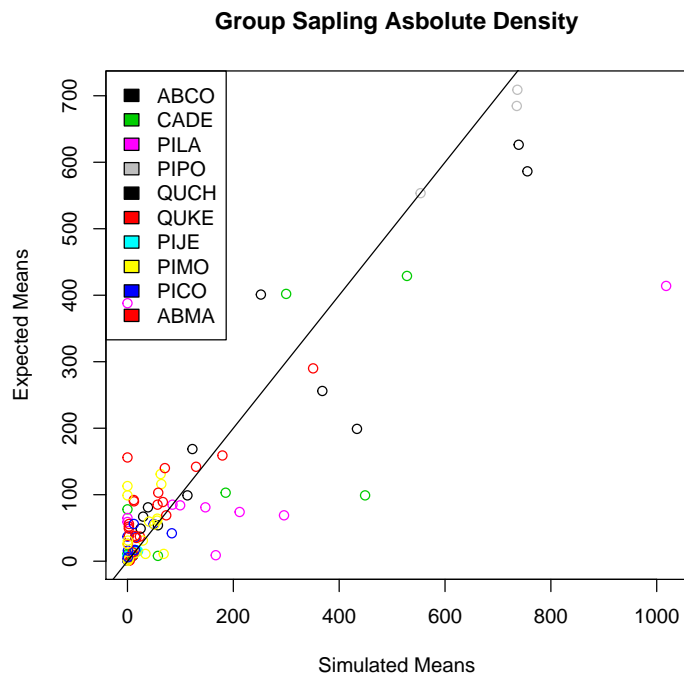
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-6.28107	10.48661	-0.599	0.55
ExpAbsDen	1.10645	0.06031	18.347	<2e-16 ***

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

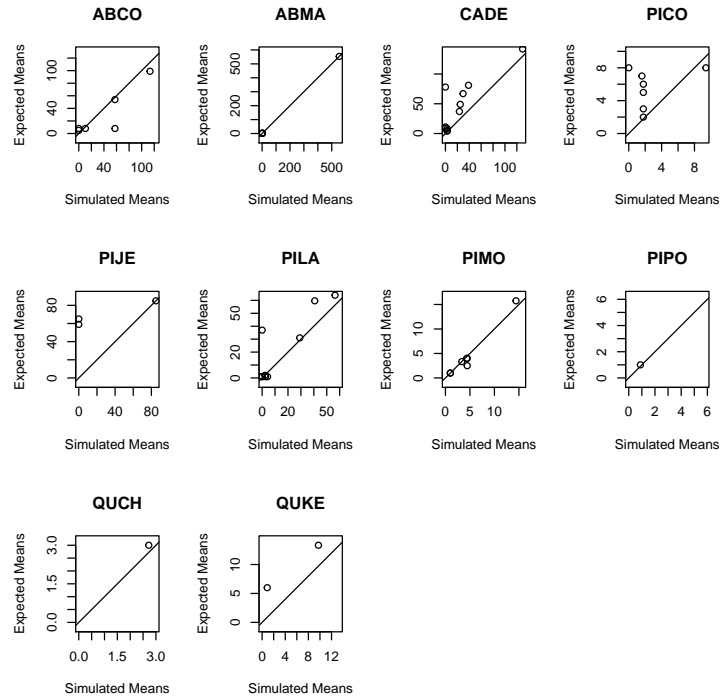
Residual standard error: 95.05 on 110 degrees of freedom

Multiple R-squared: 0.7537, Adjusted R-squared: 0.7515

F-statistic: 336.6 on 1 and 110 DF, p-value: < 2.2e-16



Now, how are the individual species doing?



```
> sppSlopes
```

	species	sdlDen	saplDen
1	ABCO	0.1960952	0.38371483
2	ABMA	1.2459189	0.88649467
3	CADE	4.3204355	0.57013355
4	PICO	2.1647434	0.61904082
5	PIJE	-0.2163740	0.02270199
6	PILA	1.4566700	1.04085803
7	PIMO	2.6091617	1.25069870
8	PIPO	1.0034431	0.09259821
9	QUCH	-151.8999127	226.01237004
10	QUKE	4.4717642	-0.13136261

```
> 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
-1579.0	-210.8	-165.1	-119.1	3617.0

Coefficients:

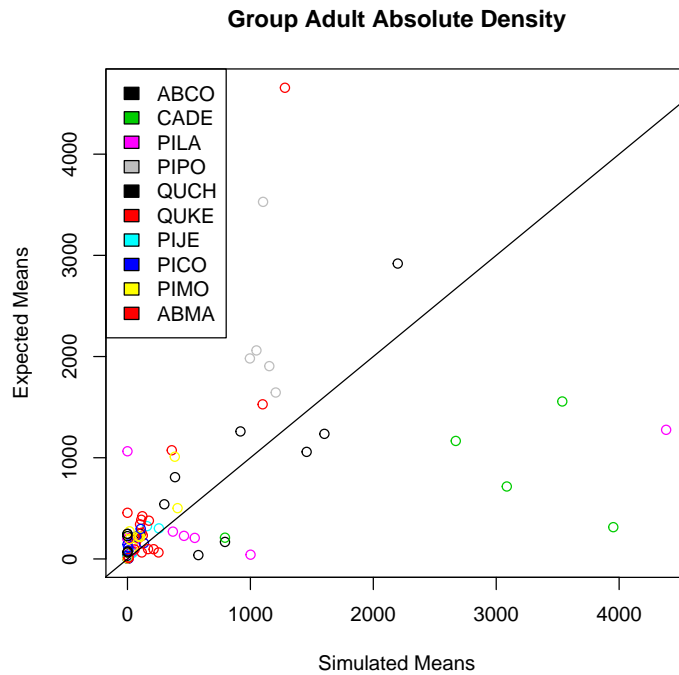
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	152.93603	82.26083	1.859	0.0659 .
ExpAbsDen	0.58143	0.09482	6.132	1.74e-08 ***

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

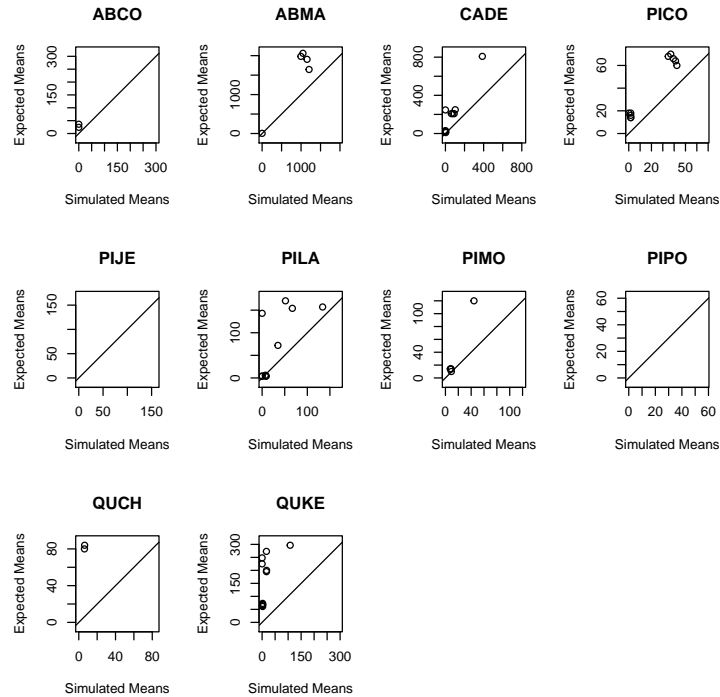
Residual standard error: 717 on 100 degrees of freedom

Multiple R-squared: 0.2733, Adjusted R-squared: 0.266

F-statistic: 37.6 on 1 and 100 DF, p-value: 1.741e-08



Now, how are the individual species doing?



> sppSlopes

	species	sdlDen	saplDen	AdultDen
1	ABCO	0.1960952	0.38371483	0.23875374
2	ABMA	1.2459189	0.88649467	1.92228574
3	CADE	4.3204355	0.57013355	1.71753339
4	PICO	2.1647434	0.61904082	1.29433917
5	PIJE	-0.2163740	0.02270199	0.01596296
6	PILA	1.4566700	1.04085803	1.84091935
7	PIMO	2.6091617	1.25069870	2.01635949
8	PIPO	1.0034431	0.09259821	-0.05328505
9	QUCH	-151.8999127	226.01237004	-33.60559565
10	QUKE	4.4717642	-0.13136261	1.82832250

5 Adult Absolute Basal Area

Call:

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

Residuals:

Min	1Q	Median	3Q	Max
-29.040	0.174	2.041	2.455	13.388

Coefficients:

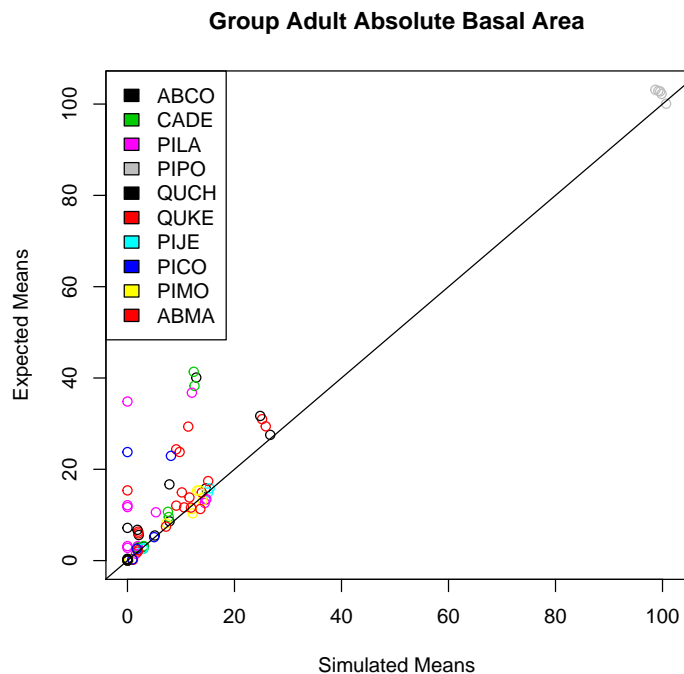
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-2.07609	0.79638	-2.607	0.0105 *
ExpAbsDen	0.89293	0.03006	29.704	<2e-16 ***

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

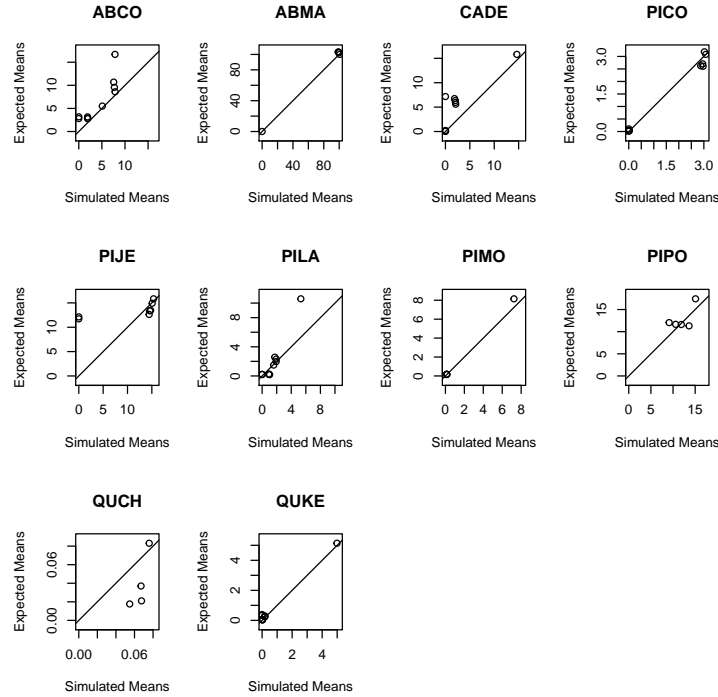
Residual standard error: 6.878 on 100 degrees of freedom

Multiple R-squared: 0.8982, Adjusted R-squared: 0.8972

F-statistic: 882.3 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	0.1960952	0.38371483	0.23875374	2.2992679
2	ABMA	1.2459189	0.88649467	1.92228574	1.0252671
3	CADE	4.3204355	0.57013355	1.71753339	1.0587085
4	PICO	2.1647434	0.61904082	1.29433917	0.9426788
5	PIJE	-0.2163740	0.02270199	0.01596296	0.1486053
6	PILA	1.4566700	1.04085803	1.84091935	2.3562351
7	PIMO	2.6091617	1.25069870	2.01635949	0.7635874
8	PIPO	1.0034431	0.09259821	-0.05328505	0.7028428
9	QUCH	-151.8999127	226.01237004	-33.60559565	2.8492264
10	QUKE	4.4717642	-0.13136261	1.82832250	1.1143598

6 Conclusions

So it seems like reducing / removing mortality rates from seedlings and saplings can "rescue" the lines and make them much, much closer to ideal (1) than otherwise. So in essence, I've answered the question. Dispersal as it is currently modeled is only giving off enough seeds for survivors, with no room for seeds to die off. So, I can simplify like this or try harder to model death and dispersal actually.