

Dispersal Parameter D: Finding Ideal Parameters

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1 Summary

This paper explores the range of values and accuracy of the d (dispersal) parameter in SORTIE-ND for adult trees in our validation plots. For each set of parameters in the 081815c runs, I varied them by 10% to test whether adjusting the parameters would increase the overall model fit. This will also give us an idea of how much swing these parameters have within the simulations.

For each species/step combination, I'll need to evaluate whether the parameters improve or hurt the model fit. I'll be using a general linear model that regresses the expected values (the "realPlots" means) against the simulated values of the model. The model improves as the slope approaches 1. If realPlots data are on the y-axis, then points or lines that fall above the "1" demarkation line are *underpredicting* the true value; and points or lines that fall below the "1" demarkation line are *overpredicting* the true value.

We'll need to view all of the data – data for the 90, 100, and 110 percent values of the parameters – before we can conduct the analysis.

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: At the nintieith percentile

Call:

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

Residuals:

	Min	1Q	Median	3Q	Max
	-26.1942	-0.0346	2.0116	2.2577	13.1676

Coefficients:

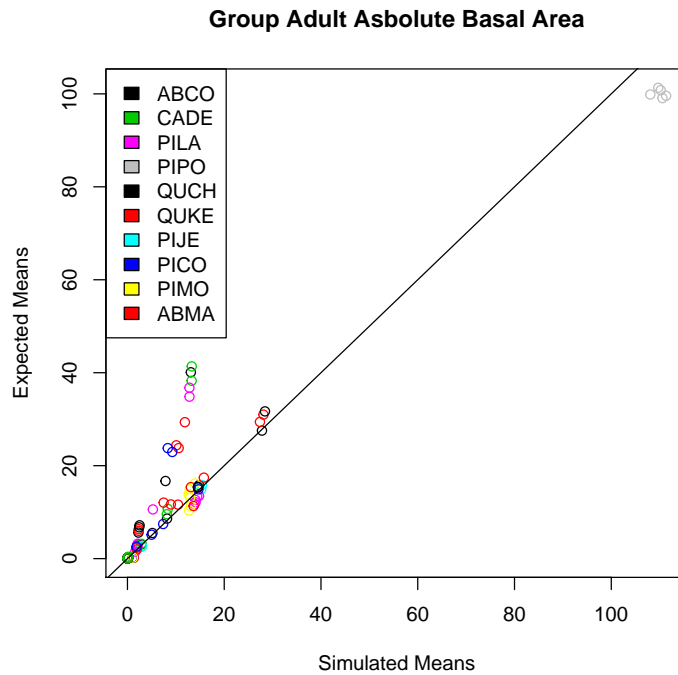
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-2.20785	0.83476	-2.645	0.00955 **
ExpAbsBA	1.00789	0.03131	32.190	< 2e-16 ***

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

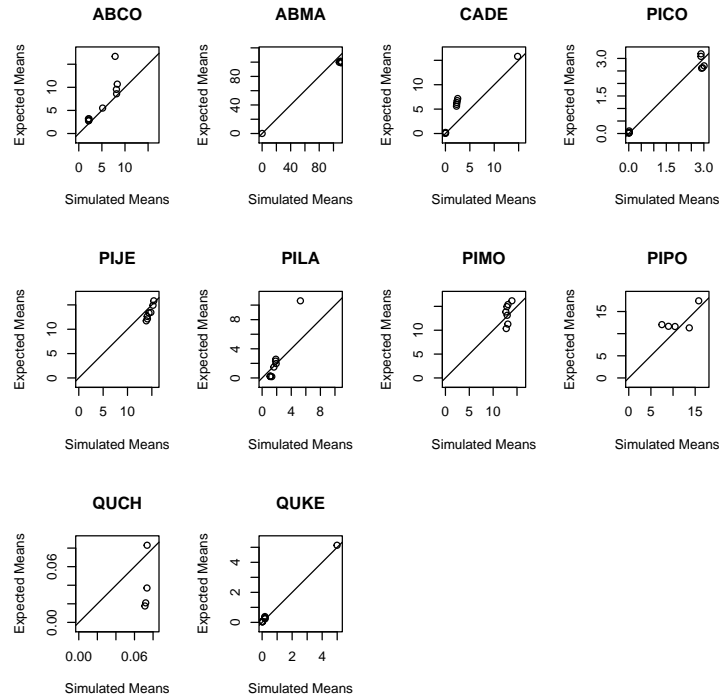
Residual standard error: 6.982 on 96 degrees of freedom

Multiple R-squared: 0.9152, Adjusted R-squared: 0.9143

F-statistic: 1036 on 1 and 96 DF, p-value: < 2.2e-16



Now, how are the individual species doing?



> *sppSlopes*

	species	ba90
1	ABCO	3.2109158
2	ABMA	0.9094796
3	CADE	0.9970746
4	PICO	0.9559808
5	PIJE	2.3726643
6	PILA	2.7357797
7	PIMO	2.8469262
8	PIPO	0.5107506
9	QUCH	21.0878545
10	QUKE	1.0346412

3 At the original parameter designation

Call:

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

Residuals:

	Min	1Q	Median	3Q	Max
	-24.5872	0.6374	1.8231	2.1861	11.1059

Coefficients:

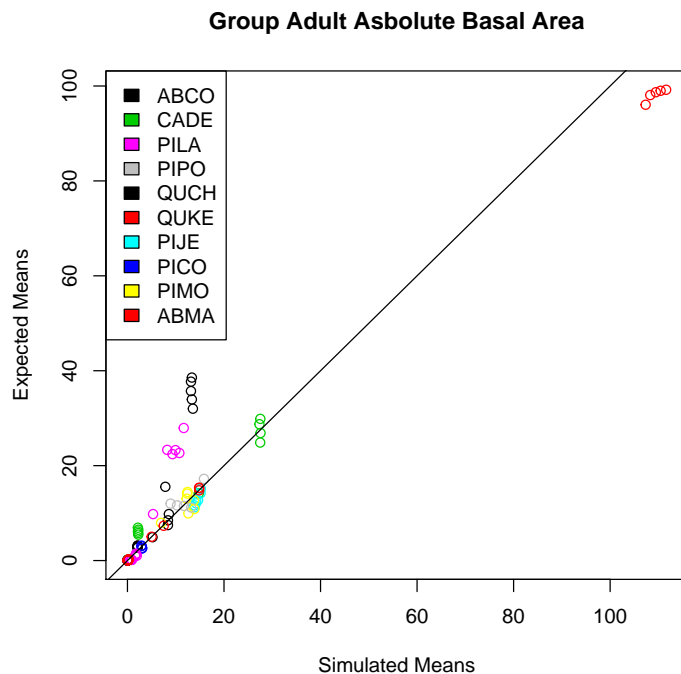
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.8487	0.7418	-2.492	0.0143 *
ExpAbsBA	1.0316	0.0293	35.208	<2e-16 ***

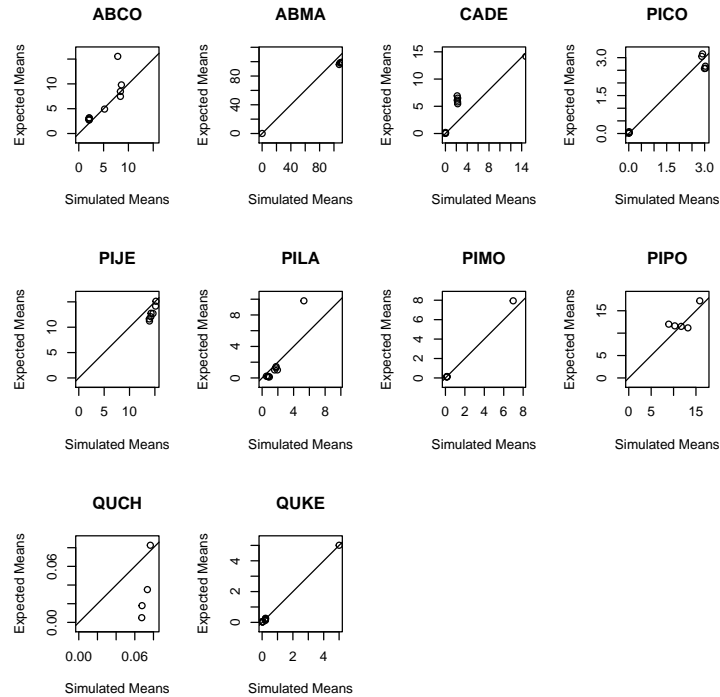
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.421 on 100 degrees of freedom

Multiple R-squared: 0.9254, Adjusted R-squared: 0.9246

F-statistic: 1240 on 1 and 100 DF, p-value: < 2.2e-16





> *sppSlopes*

	species	ba90	ba100
1	ABCO	3.2109158	2.8679859
2	ABMA	0.9094796	0.8968508
3	CADE	0.9970746	0.9240230
4	PICO	0.9559808	0.9295847
5	PIJE	2.3726643	2.4811348
6	PILA	2.7357797	2.5907967
7	PIMO	2.8469262	0.9567542
8	PIPO	0.5107506	0.6919119
9	QUCH	21.0878545	7.0914178
10	QUKE	1.0346412	1.0172449

4 At the one hundred and tenth percentile

Call:

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

Residuals:

	Min	1Q	Median	3Q	Max
	-25.8152	0.8784	1.7711	1.8960	11.4314

Coefficients:

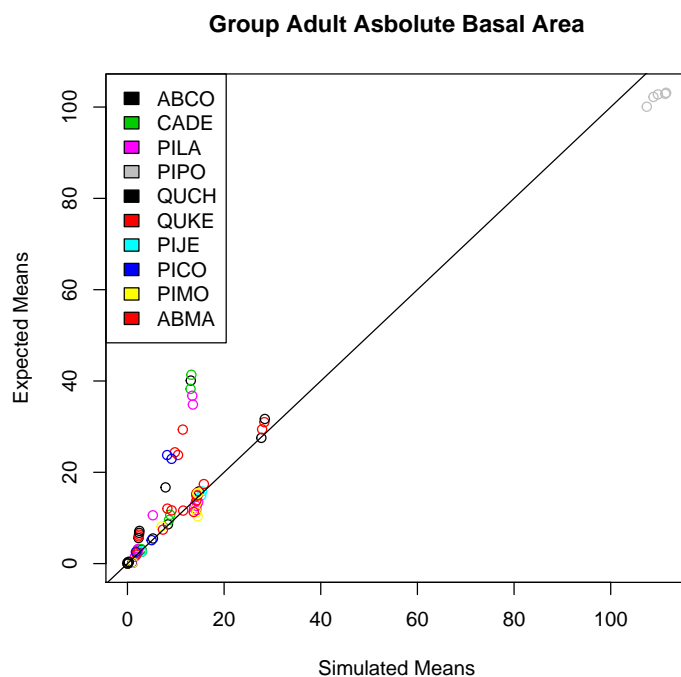
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.84186	0.77383	-2.38	0.0192 *
ExpAbsBA	0.98839	0.02921	33.84	<2e-16 ***

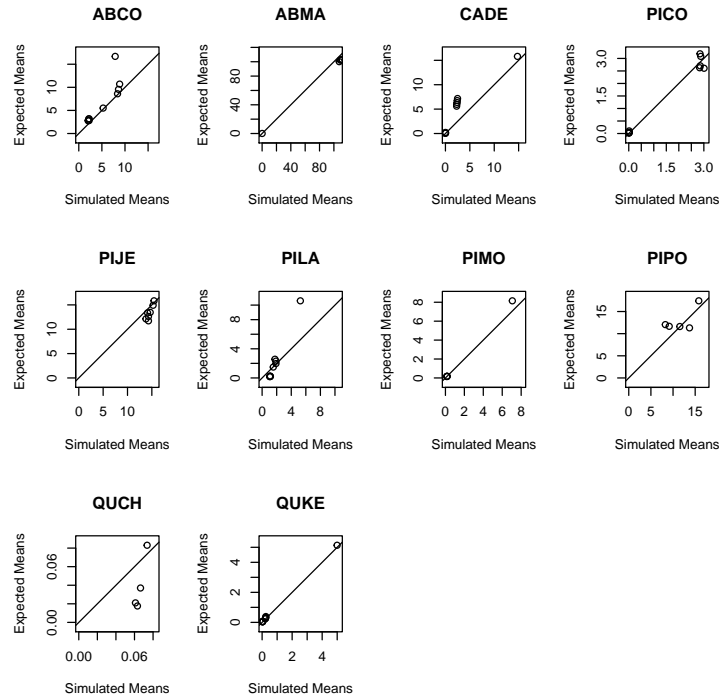
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.683 on 100 degrees of freedom

Multiple R-squared: 0.9197, Adjusted R-squared: 0.9189

F-statistic: 1145 on 1 and 100 DF, p-value: < 2.2e-16





> *sppSlopes*

	species	ba90	ba100	ba110
1	ABCO	3.2109158	2.8679859	3.1087661
2	ABMA	0.9094796	0.8968508	0.9307194
3	CADE	0.9970746	0.9240230	0.9920768
4	PICO	0.9559808	0.9295847	0.9704309
5	PIJE	2.3726643	2.4811348	2.2106834
6	PILA	2.7357797	2.5907967	2.7875110
7	PIMO	2.8469262	0.9567542	0.9114492
8	PIPO	0.5107506	0.6919119	0.5507543
9	QUCH	21.0878545	7.0914178	5.3437429
10	QUKE	1.0346412	1.0172449	1.0437060

5 Adult Density: At the ninetieth percentile

Call:

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

Residuals:

Min	1Q	Median	3Q	Max
-762.49	-73.64	-49.40	-6.59	685.36

Coefficients:

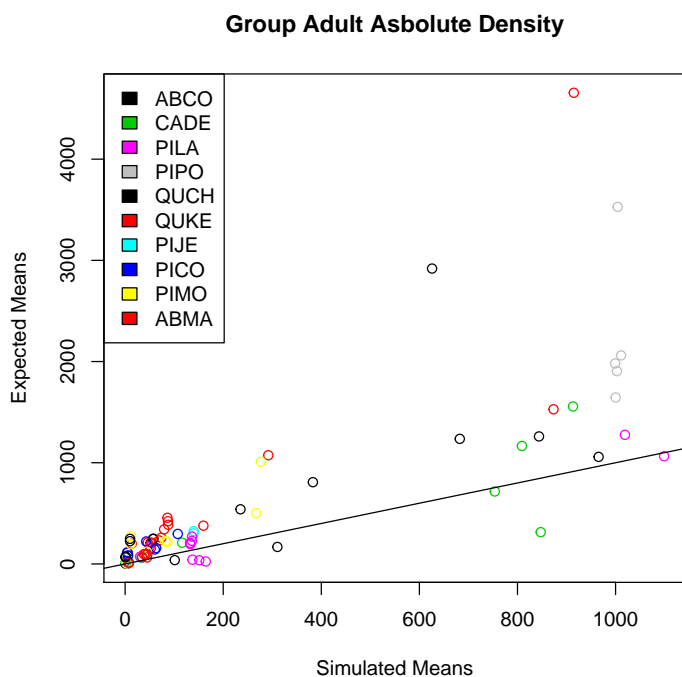
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	52.40326	22.34659	2.345	0.021 *
ExpAbsDen	0.34899	0.02576	13.549	<2e-16 ***

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

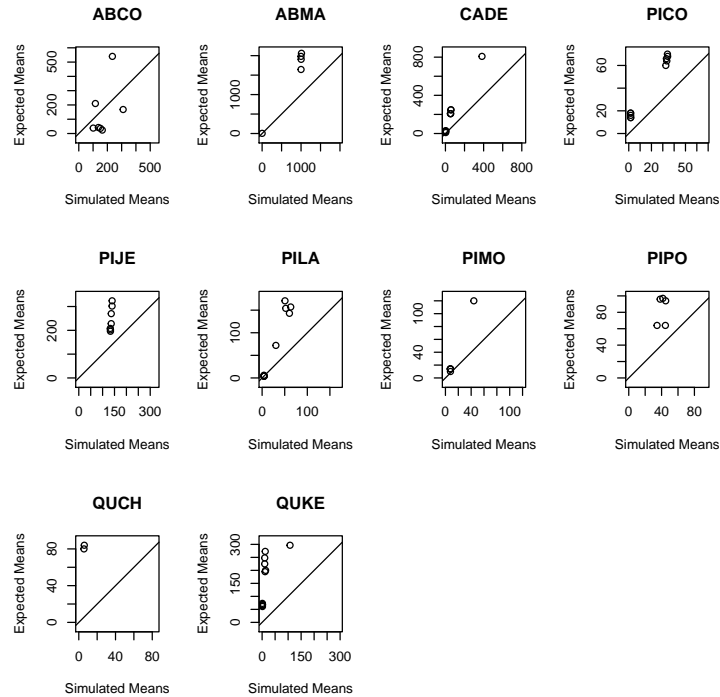
Residual standard error: 194.8 on 100 degrees of freedom

Multiple R-squared: 0.6474, Adjusted R-squared: 0.6438

F-statistic: 183.6 on 1 and 100 DF, p-value: < 2.2e-16



Now, how are the individual species doing?



> sppSlopes

	species	ba90	ba100	ba110	den90
1	ABCO	3.2109158	2.8679859	3.1087661	1.3363986
2	ABMA	0.9094796	0.8968508	0.9307194	2.2171767
3	CADE	0.9970746	0.9240230	0.9920768	2.3013607
4	PICO	0.9559808	0.9295847	0.9704309	1.5582780
5	PIJE	2.3726643	2.4811348	2.2106834	15.4895756
6	PILA	2.7357797	2.5907967	2.7875110	3.6350821
7	PIMO	2.8469262	0.9567542	0.9114492	4.0129953
8	PIPO	0.5107506	0.6919119	0.5507543	0.9001013
9	QUCH	21.0878545	7.0914178	5.3437429	-19.6701429
10	QUKE	1.0346412	1.0172449	1.0437060	2.5772572

6 At the original parameter designation

Call:

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

Residuals:

Min	1Q	Median	3Q	Max
-776.11	-73.57	-48.99	-4.74	687.39

Coefficients:

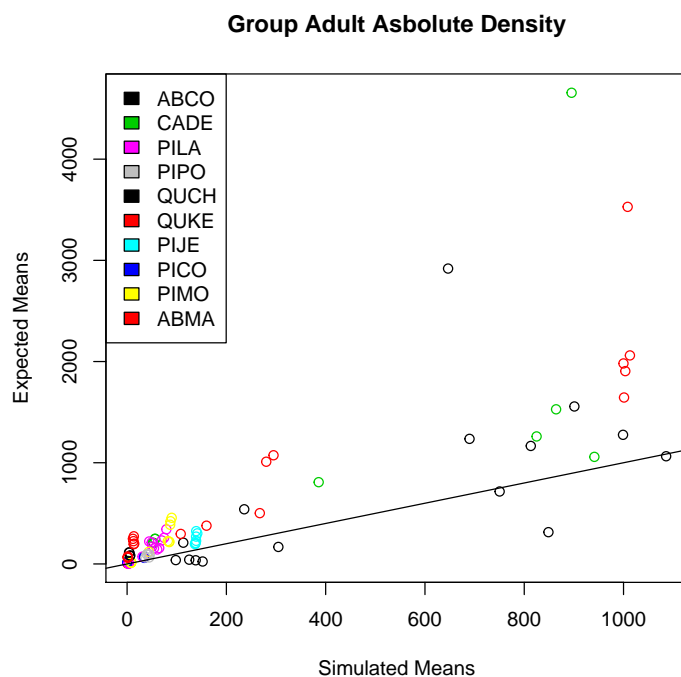
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	52.13734	22.09152	2.36	0.0202 *
ExpAbsDen	0.34780	0.02546	13.66	<2e-16 ***

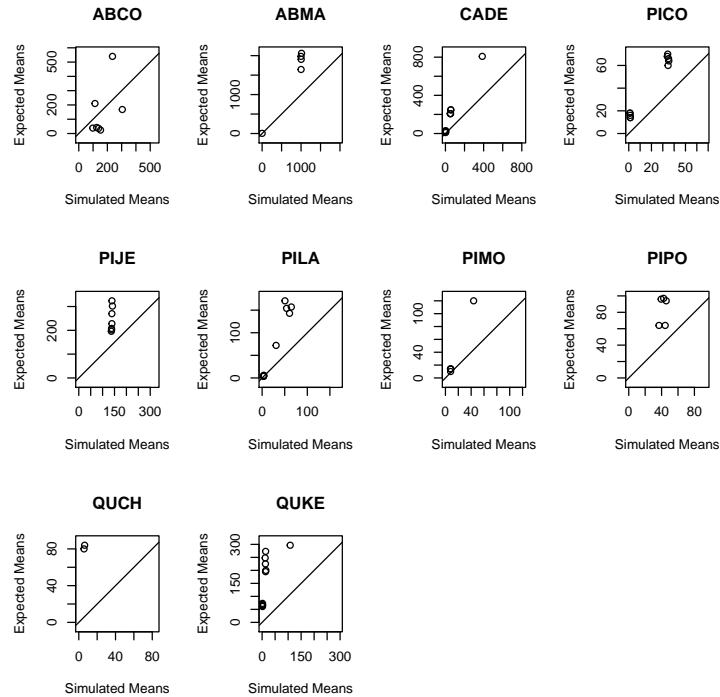
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 192.5 on 100 degrees of freedom

Multiple R-squared: 0.651, Adjusted R-squared: 0.6475

F-statistic: 186.6 on 1 and 100 DF, p-value: < 2.2e-16





> sppSlopes

	species	ba90	ba100	ba110	den90	den100
1	ABCO	3.2109158	2.8679859	3.1087661	1.3363986	1.366993
2	ABMA	0.9094796	0.8968508	0.9307194	2.2171767	2.218563
3	CADE	0.9970746	0.9240230	0.9920768	2.3013607	2.345902
4	PICO	0.9559808	0.9295847	0.9704309	1.5582780	1.479854
5	PIJE	2.3726643	2.4811348	2.2106834	15.4895756	27.477350
6	PILA	2.7357797	2.5907967	2.7875110	3.6350821	3.557684
7	PIMO	2.8469262	0.9567542	0.9114492	4.0129953	4.056143
8	PIPO	0.5107506	0.6919119	0.5507543	0.9001013	1.296860
9	QUCH	21.0878545	7.0914178	5.3437429	-19.6701429	-15.618990
10	QUKE	1.0346412	1.0172449	1.0437060	2.5772572	2.577005

7 At the one hundred and tenth percentile

Call:

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

Residuals:

Min	1Q	Median	3Q	Max
-753.63	-73.21	-49.58	-7.48	693.39

Coefficients:

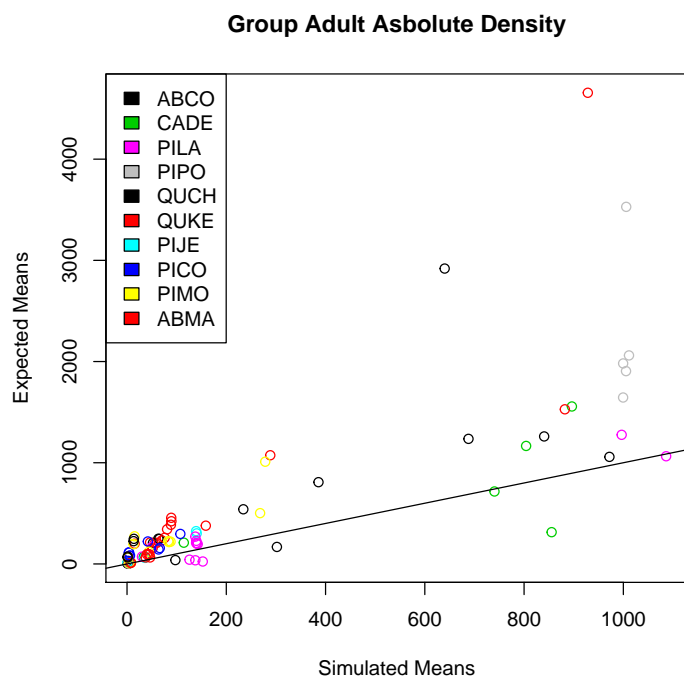
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	52.20678	22.07180	2.365	0.0199 *
ExpAbsDen	0.35006	0.02544	13.759	<2e-16 ***

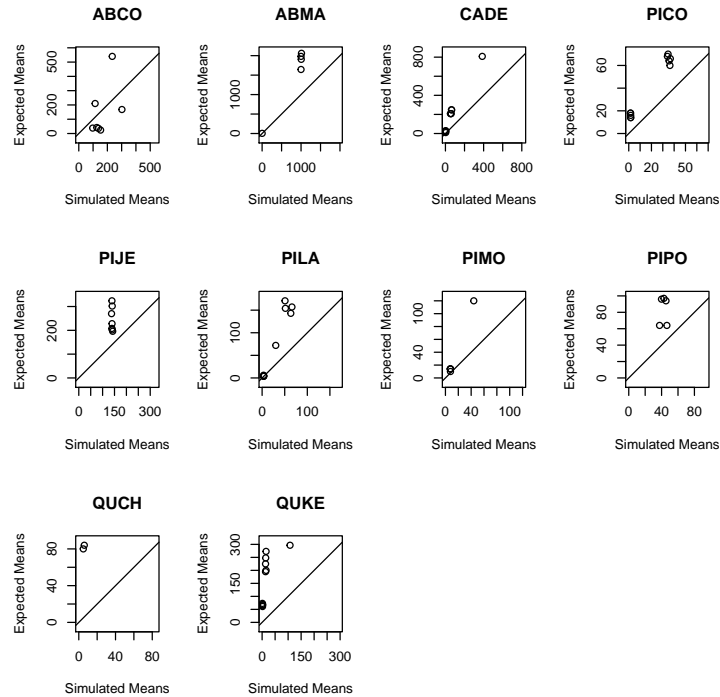
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 192.4 on 100 degrees of freedom

Multiple R-squared: 0.6544, Adjusted R-squared: 0.6509

F-statistic: 189.3 on 1 and 100 DF, p-value: < 2.2e-16





```
> sppSlopes
```

	species	ba90	ba100	ba110	den90	den100	den110
1	ABCO	3.2109158	2.8679859	3.1087661	1.3363986	1.366993	1.3618762
2	ABMA	0.9094796	0.8968508	0.9307194	2.2171767	2.218563	2.2173498
3	CADE	0.9970746	0.9240230	0.9920768	2.3013607	2.345902	2.3009673
4	PICO	0.9559808	0.9295847	0.9704309	1.5582780	1.479854	1.4610254
5	PIJE	2.3726643	2.4811348	2.2106834	15.4895756	27.477350	-15.3898886
6	PILA	2.7357797	2.5907967	2.7875110	3.6350821	3.557684	3.4773984
7	PIMO	2.8469262	0.9567542	0.9114492	4.0129953	4.056143	3.9741788
8	PIPO	0.5107506	0.6919119	0.5507543	0.9001013	1.296860	0.3865049
9	QUCH	21.0878545	7.0914178	5.3437429	-19.6701429	-15.618990	-14.8066538
10	QUKE	1.0346412	1.0172449	1.0437060	2.5772572	2.577005	2.5995907

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