Adjusting Individual Parameters

Samantha L. Davis October 15, 2015

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 Seedling Absolute Density

Call:

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

Residuals:

Min 1Q Median 3Q Max -531.26 -62.29 -58.81 -26.74 635.60

Coefficients:

Estimate Std. Error t value Pr(>|t|)
(Intercept) 58.71876 12.61262 4.656 5.96e-06 ***
ExpAbsDen 0.08706 0.01496 5.819 2.40e-08 ***

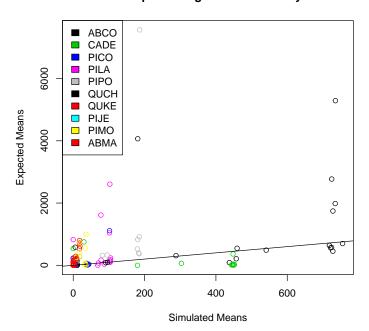
Signif. codes: 0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

Residual standard error: 166.9 on 195 degrees of freedom

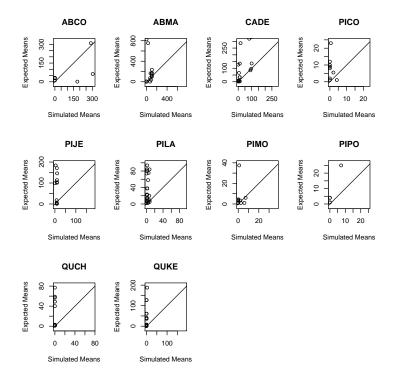
Multiple R-squared: 0.1479, Adjusted R-squared: 0.1436

F-statistic: 33.86 on 1 and 195 DF, p-value: 2.399e-08

Group Seedling Absolute Density



Now, how are the individual species doing?



> sppSlopes

	species	sdlDen
1	ABCO	2.157439
2	ABMA	3.380833
3	CADE	10.706891
4	PICO	3.295118
5	PIJE	-6.009182
6	PILA	7.852920
7	PIMO	5.585802
8	PIPO	3.642160
9	QUCH	-180.534271
10	QUKE	29.951049

3 Sapling Density

Call:

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

Residuals:

Min 1Q Median 3Q Max -629.40 -31.75 0.88 6.35 696.04

Coefficients:

Estimate Std. Error t value Pr(>|t|)
(Intercept) -6.46008 14.50988 -0.445 0.657
ExpAbsDen 1.08447 0.08344 12.997 <2e-16 ***

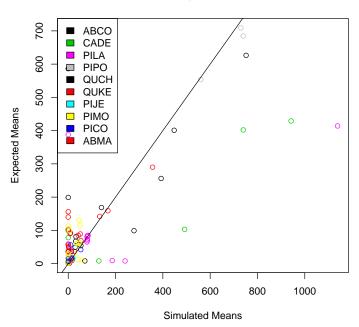
Signif. codes: 0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

Residual standard error: 131.5 on 110 degrees of freedom

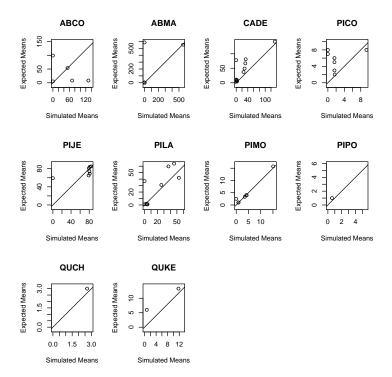
Multiple R-squared: 0.6056, Adjusted R-squared: 0.602

F-statistic: 168.9 on 1 and 110 DF, p-value: < 2.2e-16

Group Sapling Asbolute Density



Now, how are the individual species doing?



> sppSlopes

```
species
                 sdlDen
                              {\tt saplDen}
1
      ABCO
               2.157439
                           0.34272634
2
      ABMA
               3.380833
                           0.77941696
3
              10.706891
      CADE
                           0.61776581
4
      PICO
               3.295118
                           0.48216647
5
      PIJE
              -6.009182
                           0.22176447
6
      PILA
               7.852920
                           1.11587597
7
      PIMO
               5.585802
                           0.73830836
8
               3.642160
      PIP0
                           0.09804478
9
      QUCH -180.534271
                        -14.87905328
      QUKE
              29.951049
                           0.19570718
10
```

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