DSA 8020 R Session 2: Multiple Linear Regression I

Whitney

January 16, 2023

Contents

Species diversity on the Galapagos Islands

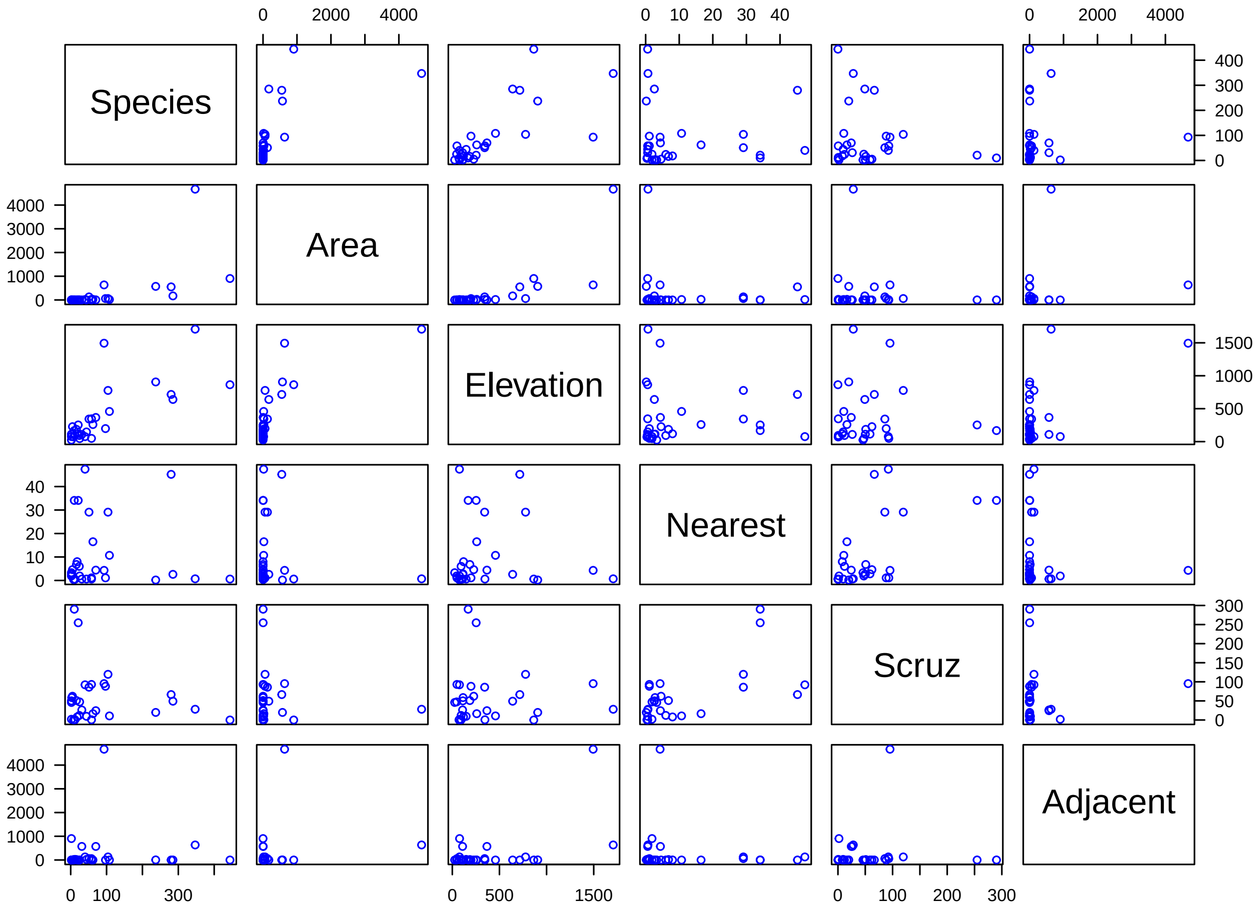
First Step: Load the data

```r
#installinstall.packages("faraway")
library(faraway)
data(gala)
head(gala)
```

```
##              Species Endemics  Area Elevation Nearest Scruz Adjacent
## Baltra            58       23 25.09       346     0.6   0.6     1.84
## Bartolome         31       21  1.24       109     0.6  26.3   572.33
## Caldwell           3        3  0.21       114     2.8  58.7     0.78
## Champion          25        9  0.10        46     1.9  47.4     0.18
## Coamano            2        1  0.05        77     1.9   1.9   903.82
## Daphne.Major      18       11  0.34       119     8.0   8.0     1.84
```

Plot the pairwise scatterplots

```r
pairs(gala[, -2], cex = 0.95, col = "blue", las = 1)
```



Correlation matrix

```r
cor(gala[, -2])
```

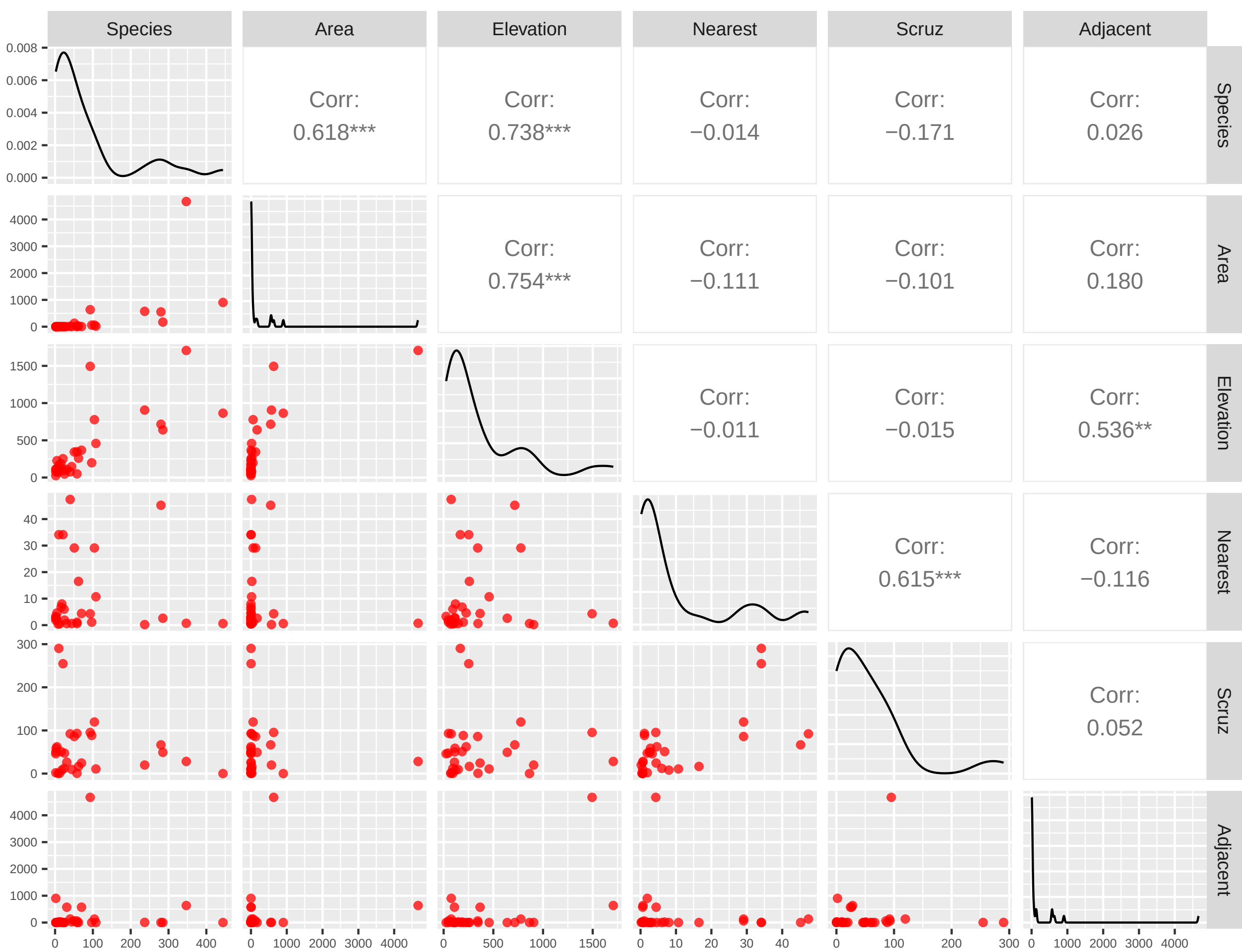
```
##              Species       Area   Elevation     Nearest       Scruz
## Species    1.00000000  0.6178431  0.73848666 -0.01409407 -0.17114244
## Area       0.61784307  1.0000000  0.75373492 -0.11110320 -0.10078493
## Elevation  0.73848666  0.7537349  1.00000000 -0.01107698 -0.01543829
## Nearest   -0.01409407 -0.1111032 -0.01107698  1.00000000  0.61541036
## Scruz     -0.17114244 -0.1007849 -0.01543829  0.61541036  1.00000000
## Adjacent   0.02616635  0.1800376  0.53645782 -0.11624788  0.05166066
##             Adjacent
## Species    0.02616635
## Area       0.18003759
## Elevation  0.53645782
## Nearest   -0.11624788
## Scruz      0.05166066
## Adjacent   1.00000000
```

Using *ggpairs* to combine scatterplot and correlation matrix

```
library(ggplot2)
library(GGally)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2

##
## Attaching package: 'GGally'

## The following object is masked from 'package:faraway':
##
##     happy
```

```
pm <- ggpairs(gala[, -2],
              lower = list(continuous = wrap("points", alpha = 0.75, colour = "red")))
pm + theme(axis.text = element_text(size = 6))
```



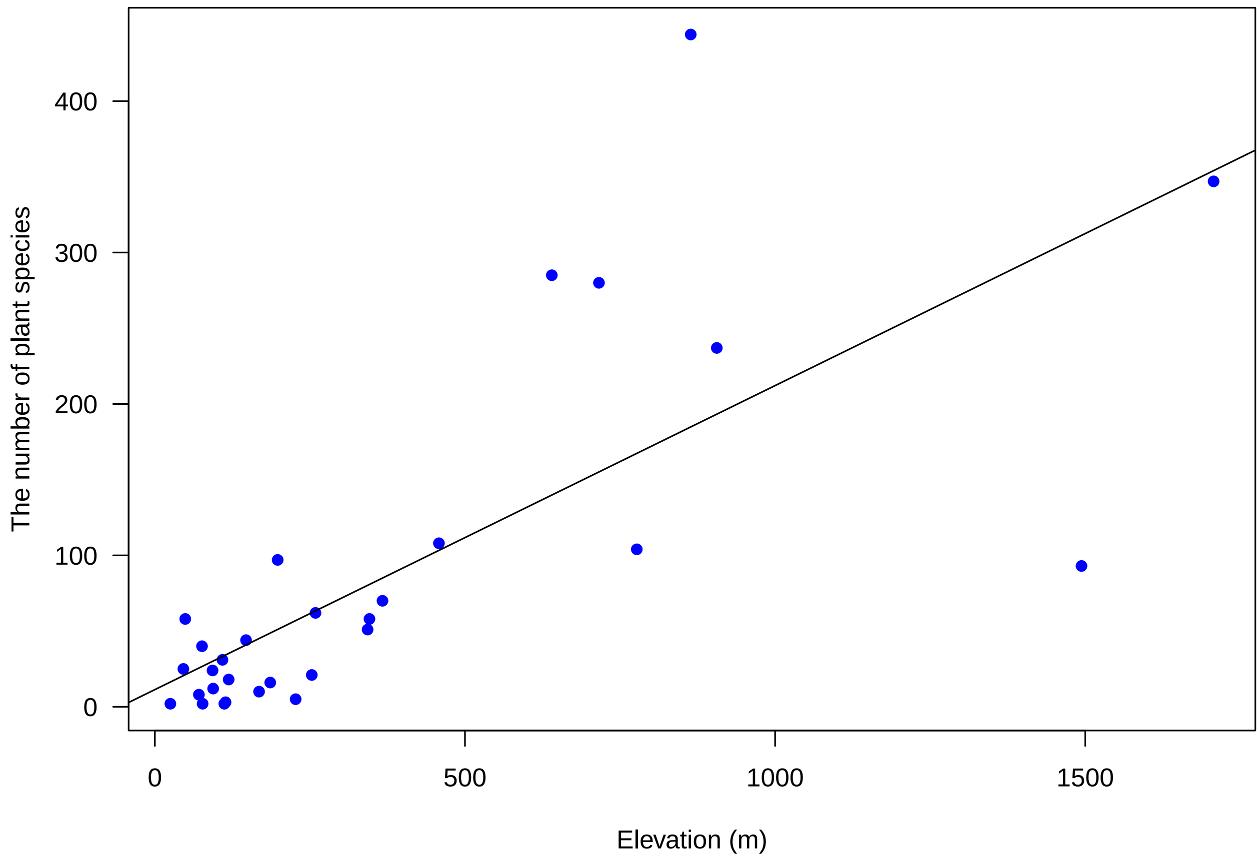
Model 1: Fitting a simple linear regression

Here we use *Elevation* as the predictor as it has the highest correlation with *Species*

```
M1 <- lm(Species ~ Elevation, data = gala)
summary(M1)
```

```
##
## Call:
## lm(formula = Species ~ Elevation, data = gala)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -218.319  -30.721  -14.690    4.634  259.180
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 11.33511   19.20529   0.590     0.56
## Elevation    0.20079    0.03465   5.795 3.18e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 78.66 on 28 degrees of freedom
## Multiple R-squared:  0.5454, Adjusted R-squared:  0.5291
## F-statistic: 33.59 on 1 and 28 DF,  p-value: 3.177e-06
```

```
plot(gala$Elevation, gala$Species, xlab = "Elevation (m)",
     ylab = "The number of plant species", las = 1, pch = 16, col = "blue")
abline(M1)
```



Regression equation:

$$y_{species} = 11.335 + 0.201x_{elevation}.$$

(Estimated) error standard deviation $\hat{\sigma} = 78.6615407$.

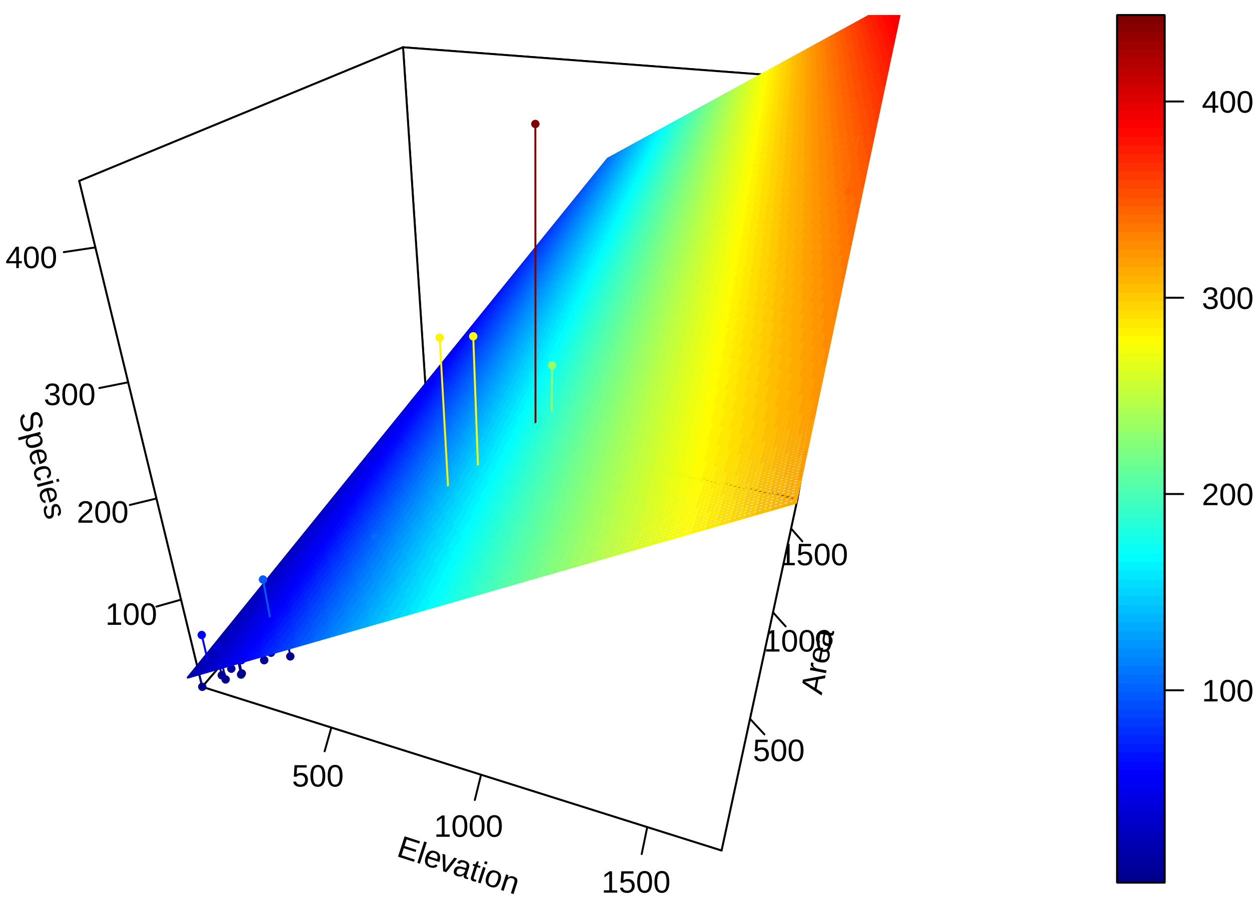
Model 2: Adding *Area*

```
M2 <- lm(Species ~ Elevation + Area, data = gala)
summary(M2)
```

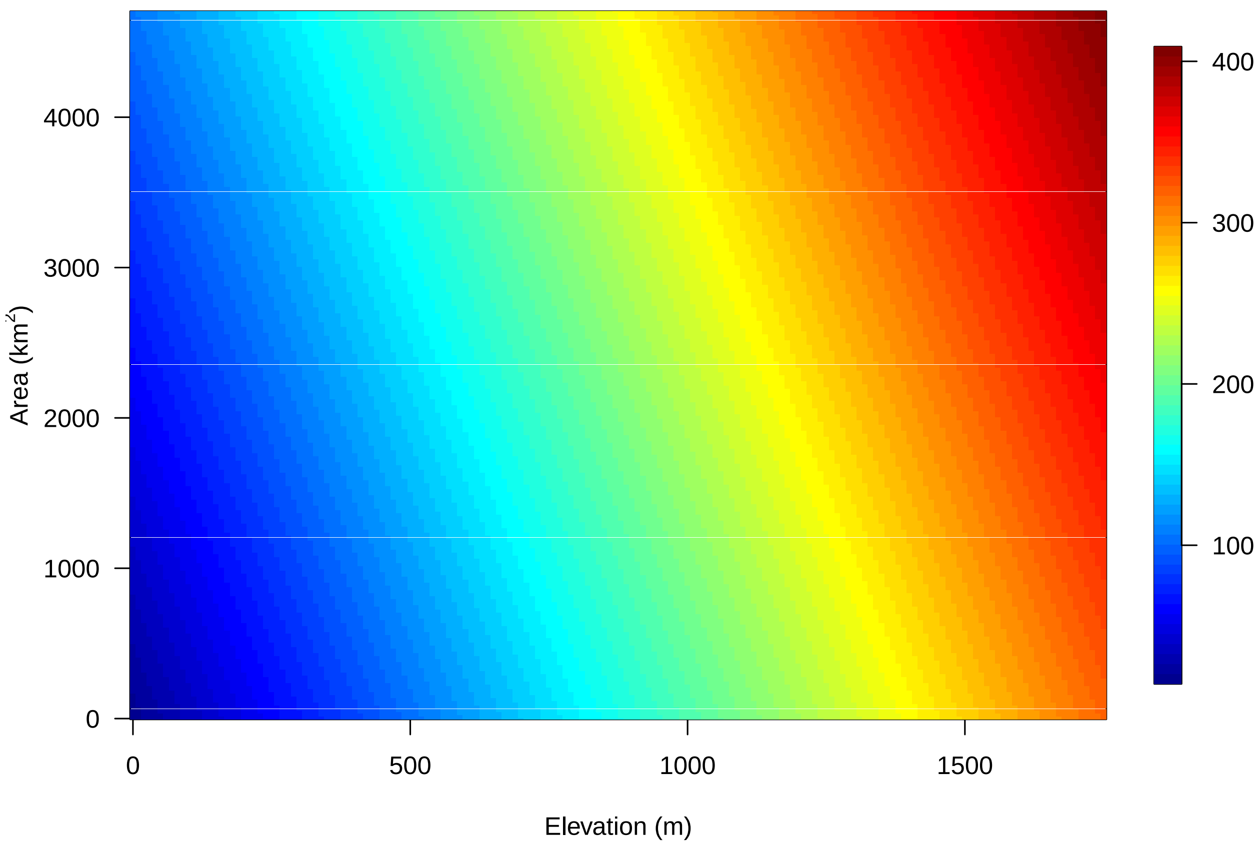
```
##
## Call:
## lm(formula = Species ~ Elevation + Area, data = gala)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -192.619  -33.534  -19.199    7.541  261.514
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 17.10519   20.94211   0.817  0.42120
## Elevation    0.17174    0.05317   3.230  0.00325 **
## Area         0.01880    0.02594   0.725  0.47478
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 79.34 on 27 degrees of freedom
## Multiple R-squared:  0.554,  Adjusted R-squared:  0.521
## F-statistic: 16.77 on 2 and 27 DF,  p-value: 1.843e-05
```

```r
Elevation_grid <- seq(0, 1750, 10)
Area_grid <- seq(0, 4700, 10)
temp <- expand.grid(Elevation_grid, Area_grid)
x_new <- data.frame(Elevation = temp$Var1, Area = temp$Var2)

y_pred <- matrix(predict(M2, x_new), nrow = length(Elevation_grid))

library(plot3D)
# fitted points for droplines to surface
fitpoints <- predict(M2)
# scatter plot with regression plane
scatter3D(gala$Elevation, gala$Elevation, gala$Species,
          pch = 16, cex = 0.6, theta = 20, phi = 30,
          ticktype = "detailed",
          xlab = "Elevation", ylab = "Area", zlab = "Species",
          surf = list(x = Elevation_grid, y = Area_grid,
                      z = y_pred, facets = NA, fit = fitpoints))
```



```r
library(fields)
image.plot(Elevation_grid, Area_grid,  y_pred, las = 1,
           xlab = "Elevation (m)", ylab = expression(paste("Area (", km^2, ")")))
```



Model 3: Adding *Adjacent*

```r
M3 <- lm(Species ~ Elevation + Area + Adjacent, data = gala)
summary(M3)
```

```
##
## Call:
## lm(formula = Species ~ Elevation + Area + Adjacent, data = gala)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -124.064  -34.283   -8.733   27.972  195.973
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -5.71893   16.90706  -0.338  0.73789
## Elevation    0.31498    0.05211   6.044  2.2e-06 ***
## Area        -0.02031    0.02181  -0.931  0.36034
## Adjacent    -0.07528    0.01698  -4.434  0.00015 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 61.01 on 26 degrees of freedom
## Multiple R-squared:  0.746,  Adjusted R-squared:  0.7167
## F-statistic: 25.46 on 3 and 26 DF,  p-value: 6.683e-08
```

Full Model

```
M4 <- lm(Species ~ Elevation + Area + Adjacent + Nearest + Scruz, data = gala)
summary(M4)
```

```
##
## Call:
## lm(formula = Species ~ Elevation + Area + Adjacent + Nearest +
##     Scruz, data = gala)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -111.679  -34.898   -7.862   33.460  182.584
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  7.068221  19.154198   0.369 0.715351
## Elevation    0.319465   0.053663   5.953 3.82e-06 ***
## Area        -0.023938   0.022422  -1.068 0.296318
## Adjacent    -0.074805   0.017700  -4.226 0.000297 ***
## Nearest      0.009144   1.054136   0.009 0.993151
## Scruz       -0.240524   0.215402  -1.117 0.275208
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 60.98 on 24 degrees of freedom
## Multiple R-squared:  0.7658, Adjusted R-squared:  0.7171
## F-statistic:  15.7 on 5 and 24 DF,  p-value: 6.838e-07
```

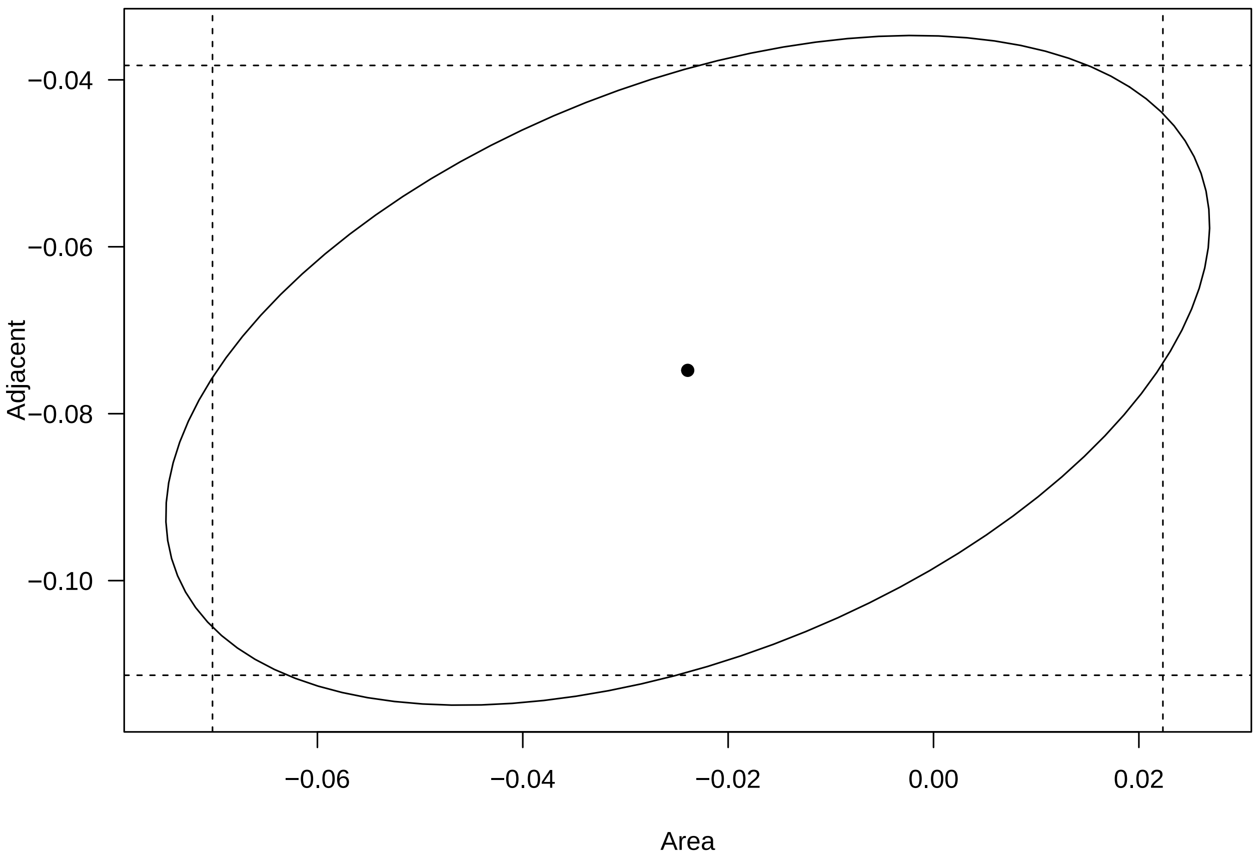
```
predict(M4)
```

```
##       Baltra    Bartolome     Caldwell     Champion      Coamano Daphne.Major
##  116.7259460   -7.2731544   29.3306594   10.3642660  -36.3839155   43.0877052
## Daphne.Minor       Darwin         Eden      Enderby     Espanola   Fernandina
##   33.9196678   -9.0189919   28.3142017   30.7859425   47.6564865   96.9895982
##     Gardner1     Gardner2     Genovesa      Isabela     Marchena       Onslow
##   -4.0332759   64.6337956   -0.4971756  386.4035578   88.6945404    4.0372328
##        Pinta       Pinzon   Las.Plazas       Rabida SanCristobal  SanSalvador
##  215.6794862  150.4753750   35.0758066   75.5531221  206.9518779  277.6763183
##    SantaCruz      SantaFe   SantaMaria      Seymour      Tortuga         Wolf
##  261.4164131   85.3764857  195.6166286   49.8050946   52.9357316   26.7005735
```

```
confint(M4)
```

```
##                    2.5 %      97.5 %
## (Intercept) -32.4641006 46.60054205
## Elevation     0.2087102  0.43021935
## Area         -0.0702158  0.02233912
## Adjacent     -0.1113362 -0.03827344
## Nearest      -2.1664857  2.18477363
## Scruz        -0.6850926  0.20404416
```

```
require(ellipse)
plot(ellipse(M4, c(3, 4), level = 0.95^2), type = "l", las = 1)
points(coef(M4)[3], coef(M4)[4], pch = 19)
abline(v = confint(M4)[3,], lty = 2)
abline(h = confint(M4)[4,], lty = 2)
```



Parameter Estimation

```
X <- model.matrix(M4)
y <- gala$Species
# regression parameters
(beta_hat <- solve(t(X) %*% X) %*% t(X) %*% y)
```

```
##                     [,1]
## (Intercept)  7.068220709
## Elevation    0.319464761
```

```
## Area        -0.023938338
## Adjacent    -0.074804832
## Nearest      0.009143961
## Scruz       -0.240524230
```

```
beta_hat_faster <- solve(crossprod(X), crossprod(X, y))
# fitted values
(y_hat <- X %*% solve(t(X) %*% X) %*% t(X) %*% y)
```

```
##                     [,1]
## Baltra       116.7259460
## Bartolome     -7.2731544
## Caldwell      29.3306594
## Champion      10.3642660
## Coamano      -36.3839155
## Daphne.Major  43.0877052
## Daphne.Minor  33.9196678
## Darwin        -9.0189919
## Eden          28.3142017
## Enderby       30.7859425
## Espanola      47.6564865
## Fernandina    96.9895982
## Gardner1      -4.0332759
## Gardner2      64.6337956
## Genovesa      -0.4971756
## Isabela      386.4035578
## Marchena      88.6945404
## Onslow         4.0372328
## Pinta        215.6794862
## Pinzon       150.4753750
## Las.Plazas    35.0758066
## Rabida        75.5531221
## SanCristobal 206.9518779
## SanSalvador  277.6763183
## SantaCruz    261.4164131
## SantaFe       85.3764857
## SantaMaria   195.6166286
## Seymour       49.8050946
## Tortuga       52.9357316
## Wolf          26.7005735
```

ANOVA

```
anova(M4)
```

```
## Analysis of Variance Table
##
## Response: Species
##             Df Sum Sq Mean Sq F value    Pr(>F)
## Elevation    1 207828  207828 55.8981 1.023e-07 ***
## Area         1   3307    3307  0.8895 0.3550197
```

```
## Adjacent   1  73171   73171 19.6804 0.0001742 ***
## Nearest    1   2909    2909  0.7823 0.3852165
## Scruz      1   4636    4636  1.2469 0.2752082
## Residuals 24  89231    3718
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Monte Carlo Simulation to Study R^2 vs. R^2_{adj}

Step I

Simulating a large number of independent replications from the true linear regression model $Y = 5 + 2x_1 + \varepsilon$, where each having the same predictor values but (slightly) different responses (due to random error $\varepsilon \sim N(0, \sigma^2)$).

```
set.seed(123)
N = 500; n = 30; sigma = 1
x1 <- replicate(N, rnorm(n))
x2 <- replicate(N, rnorm(n))
y <- apply(x1, 2, function(x) 5 + 2 * x + rnorm(n, 0, sigma))
```

Step II

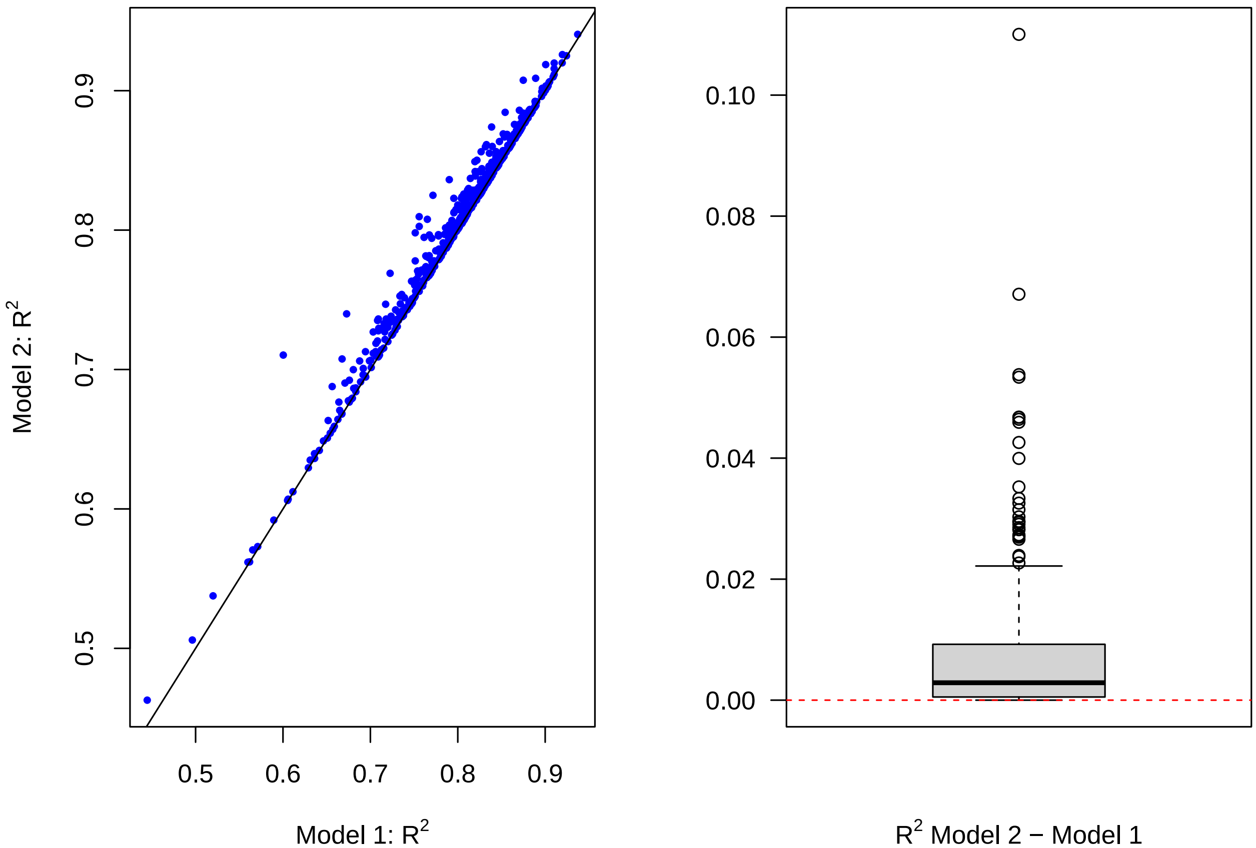
Fitting model 1: $Y = \beta_0 + \beta_1 x_1 + \varepsilon^1$ (true model) and model 2: $Y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \varepsilon^2$, respectively for each simulating data set and calculating their R^2 and R^2_{adj}.

```
R.sq <- array(dim = c(N, 4))
for (i in 1:N){
  m1 <- lm(y[, i] ~ x1[, i])
  R.sq[i, 1] = summary(m1)$r.squared
  R.sq[i, 2] = summary(m1)$adj.r.squared
  m2 <- lm(y[, i] ~ x1[, i] + x2[, i])
  R.sq[i, 3] = summary(m2)$r.squared
  R.sq[i, 4] = summary(m2)$adj.r.squared
}
```

Step III

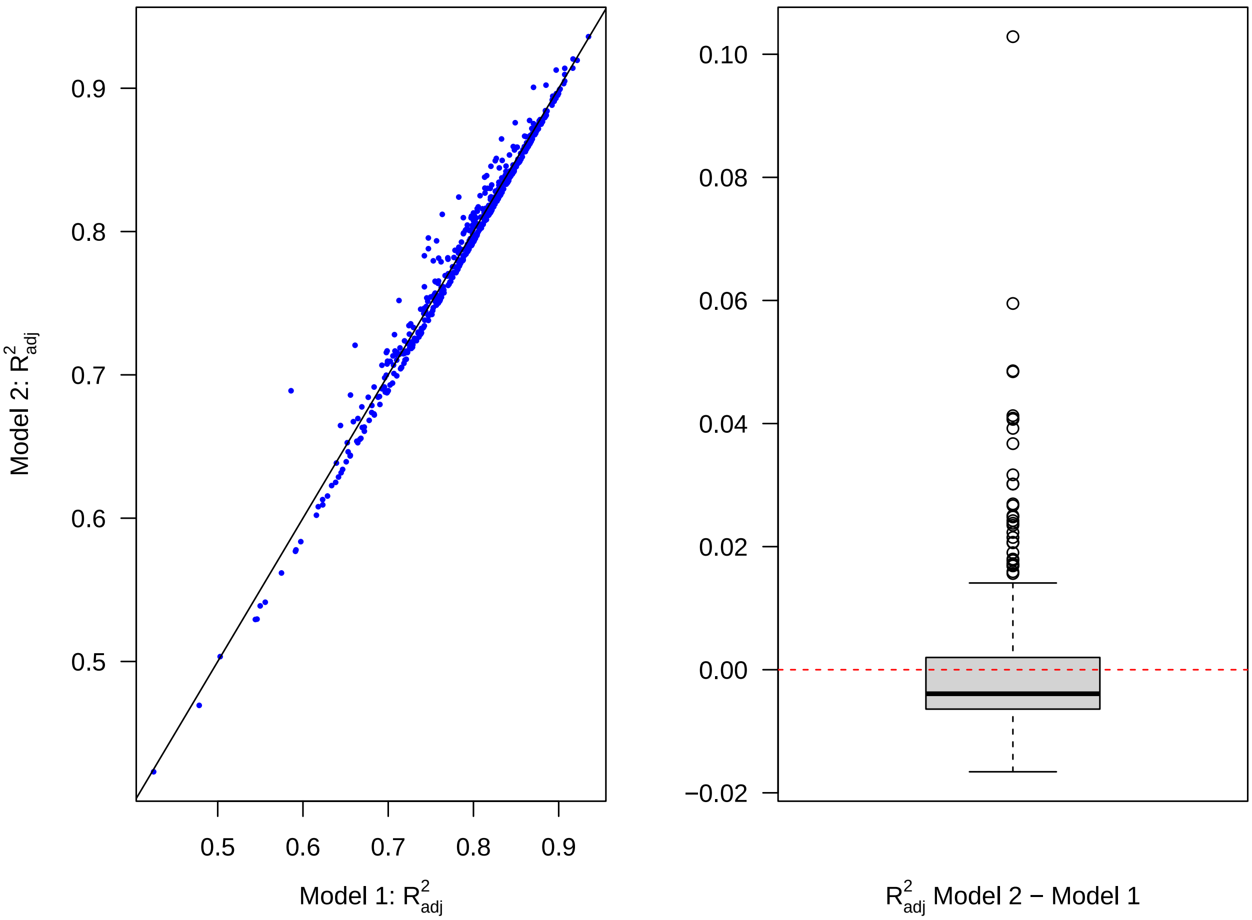
Summarizing the result. First, let's compare model 1 and model 2 via R^2.

```
par(mfrow = c(1, 2))
plot(R.sq[, 1], R.sq[, 3], pch = 16, cex = 0.65, col = "blue",
     xlab = expression(paste("Model 1: ", R^2)),
     ylab = expression(paste("Model 2: ", R^2)))
abline(0, 1)

boxplot(R.sq[, 3] - R.sq[, 1], las = 1, xlab = expression(paste(R^2, " Model 2 - Model 1")))
abline(h = 0, lty = 2, col = "red")
```



Next, let's compare model 1 and model 2 via R^2_{adj}.

```
par(las = 1, mfrow = c(1, 2), mar = c(5.1, 4.6, 1.1, 1.1))
plot(R.sq[, 2], R.sq[, 4], pch = 16, cex = 0.5, col = "blue",
     xlab = expression(paste("Model 1: ", R[adj]^2)),
     ylab = expression(paste("Model 2: ", R[adj]^2)))
abline(0, 1)

boxplot(R.sq[, 4] - R.sq[, 2], las = 1, xlab = expression(paste(R[adj]^2, " Model 2 - Model 1")))
abline(h = 0, lty = 2, col = "red")
```



Model 2: R^2_{adj}
0.9
0.8
0.7
0.6
0.5
0.5
0.6
0.7
0.8
0.9
Model 1: R^2_{adj}
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
R^2_{adj} Model 2 − Model 1