

STAT 8020 R Lab 5: Multiple Linear Regression I

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Species diversity on the Galapagos Islands

First Step: Load the data

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

gala

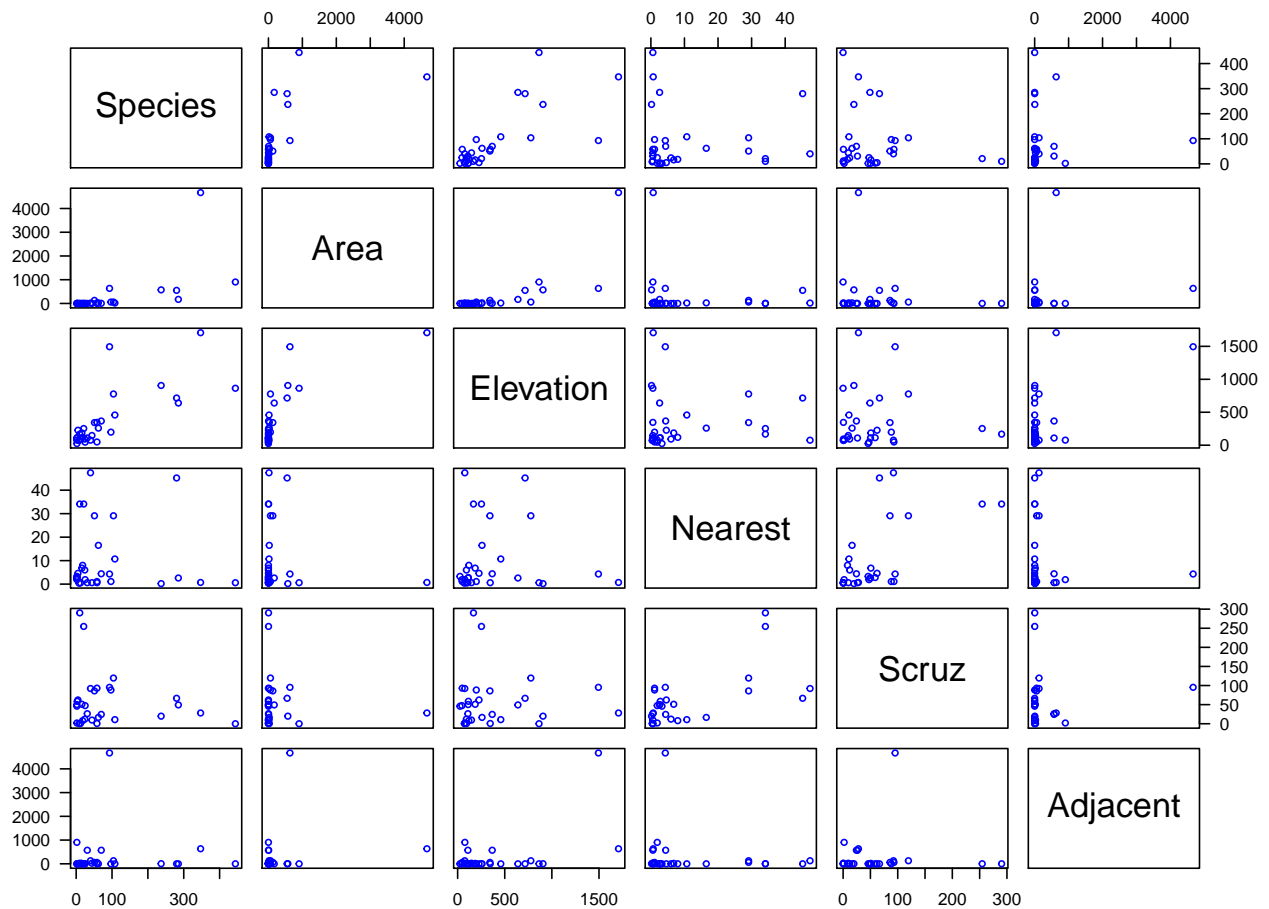
##	Species	Endemics	Area	Elevation	Nearest	Scruz	Adjacent	
##	Baltra	58	23	25.09	346	0.6	0.6	1.84
##	Bartolome	31	21	1.24	109	0.6	26.3	572.33
##	Caldwell	3	3	0.21	114	2.8	58.7	0.78
##	Champion	25	9	0.10	46	1.9	47.4	0.18
##	Coamano	2	1	0.05	77	1.9	1.9	903.82
##	Daphne.Major	18	11	0.34	119	8.0	8.0	1.84
##	Daphne.Minor	24	0	0.08	93	6.0	12.0	0.34
##	Darwin	10	7	2.33	168	34.1	290.2	2.85
##	Eden	8	4	0.03	71	0.4	0.4	17.95
##	Enderby	2	2	0.18	112	2.6	50.2	0.10
##	Espanola	97	26	58.27	198	1.1	88.3	0.57
##	Fernandina	93	35	634.49	1494	4.3	95.3	4669.32
##	Gardner1	58	17	0.57	49	1.1	93.1	58.27
##	Gardner2	5	4	0.78	227	4.6	62.2	0.21
##	Genovesa	40	19	17.35	76	47.4	92.2	129.49
##	Isabela	347	89	4669.32	1707	0.7	28.1	634.49
##	Marchena	51	23	129.49	343	29.1	85.9	59.56
##	Onslow	2	2	0.01	25	3.3	45.9	0.10
##	Pinta	104	37	59.56	777	29.1	119.6	129.49

```
## Pinzon          108      33  17.95      458    10.7  10.7    0.03
## Las.Plazas      12       9   0.23       94     0.5   0.6    25.09
## Rabida          70      30   4.89      367    4.4  24.4   572.33
## SanCristobal   280     65  551.62     716   45.2  66.6    0.57
## SanSalvador    237     81  572.33     906    0.2  19.8    4.89
## SantaCruz      444     95  903.82     864    0.6   0.0    0.52
## SantaFe        62      28  24.08     259   16.5  16.5    0.52
## SantaMaria     285     73  170.92     640    2.6  49.2    0.10
## Seymour        44      16   1.84     147    0.6   9.6    25.09
## Tortuga        16       8   1.24     186    6.8  50.9   17.95
## Wolf           21      12   2.85     253   34.1 254.7    2.33
```

```
#Out the data in csv
#write.csv(gala, file = "gala.csv")
```

Plot the pairwise scatterplots

```
plot(gala[, -2], cex = 0.75, col = "blue", las = 1)
```



Correlation matrix

```
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
```

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
```

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
```

Model 3: Adding *Adjacent*

```
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 + Scrutz, data = gala)
summary(M4)
```

```
##
## Call:
## lm(formula = Species ~ Elevation + Area + Adjacent + Nearest +
##      Scrutz, 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
```

Parameter Estimation

```
X <- model.matrix(M4)
y <- gala$Species
# regression parameters
beta_hat <- solve(t(X) %*% X) %*% t(X) %*% y
#beta_hat_faster <- solve(crossprod(X), crossprod(X, y))
# fitted values
y_hat <- X %*% solve(t(X) %*% X) %*% t(X) %*% y
```

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
```

General Linear Test

```
anova(M1, M2)
```

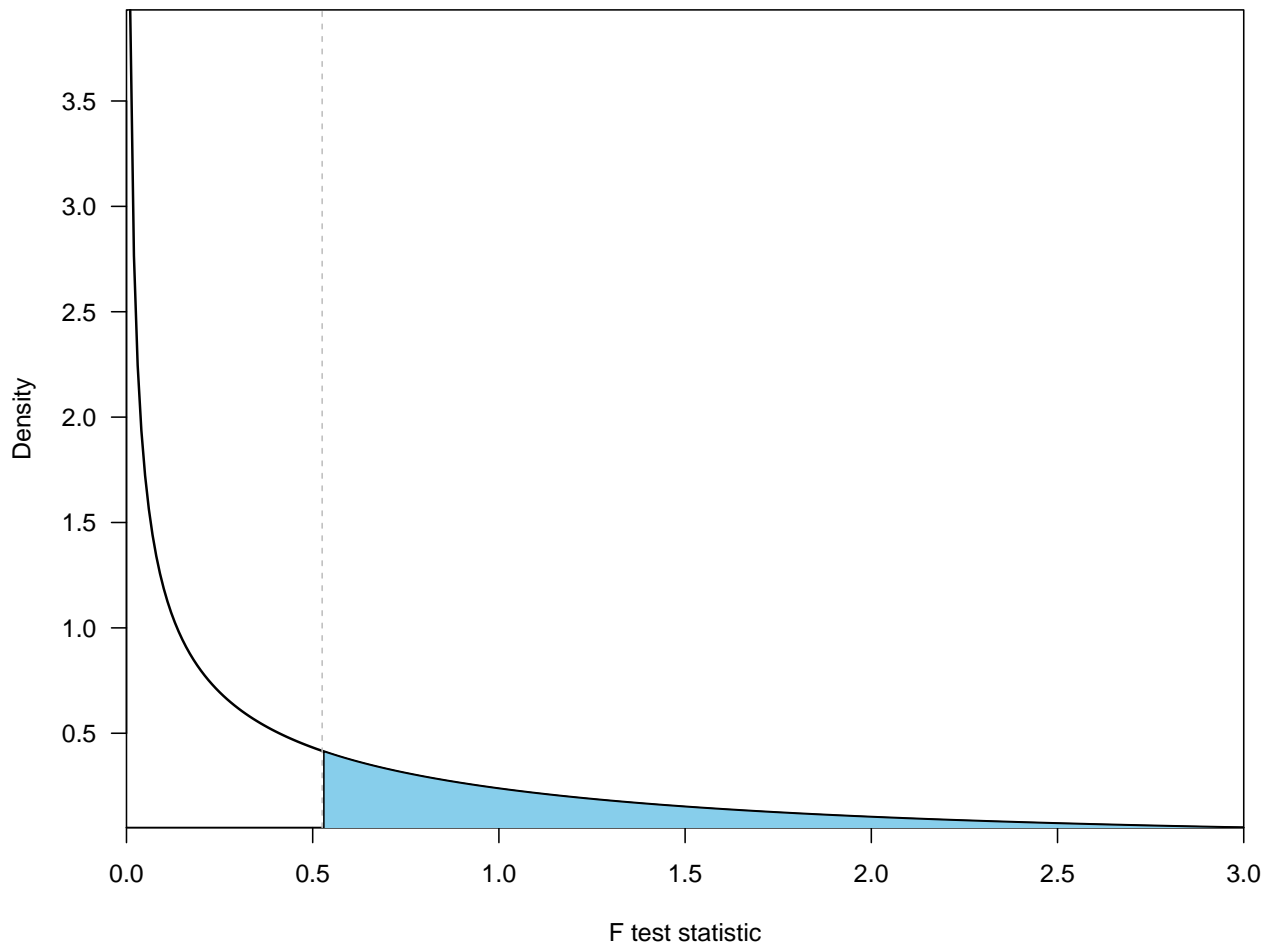
```
## Analysis of Variance Table
##
## Model 1: Species ~ Elevation
## Model 2: Species ~ Elevation + Area
##   Res.Df  RSS Df Sum of Sq    F Pr(>F)
## 1      28 173254
## 2      27 169947  1      3307 0.5254 0.4748
```

```
par(las = 1, mar = c(4.1, 4.1, 1.1, 1.1))
xg <- seq(0, 3, 0.01)
yg <- df(xg, 1, 27)
plot(xg, yg, type = "l", xaxs = "i", yaxs = "i", lwd = 1.6,
      xlab = "F test statistic", ylab = "Density")
```

```

abline(v = 0.5254, lty = 2, col = "gray")
polygon(c(xg[xg > 0.5254], rev(xg[xg > 0.5254])),
        c(yg[xg > 0.5254], rep(0, length(yg[xg > 0.5254]))),
        col = "skyblue")

```



Simulation

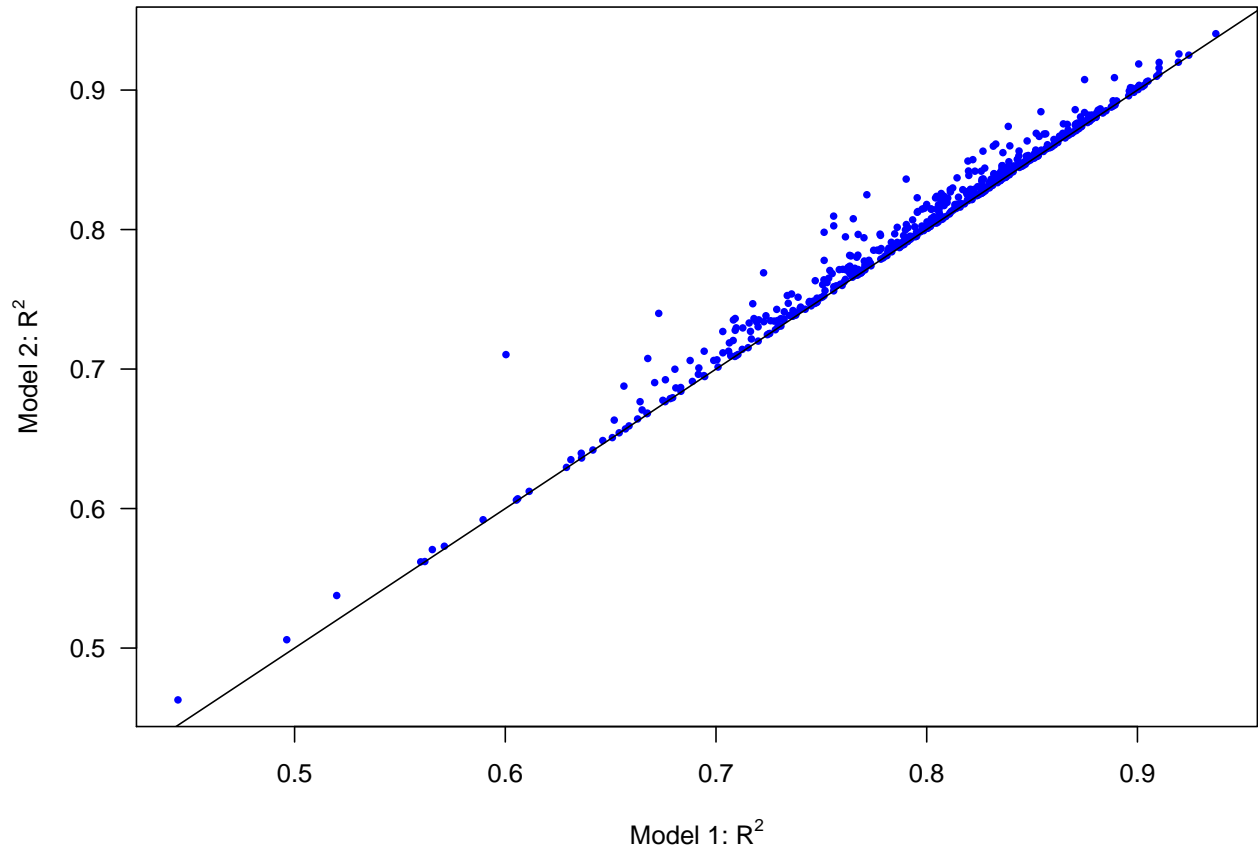
R^2 vs. R^2_{adj}

```

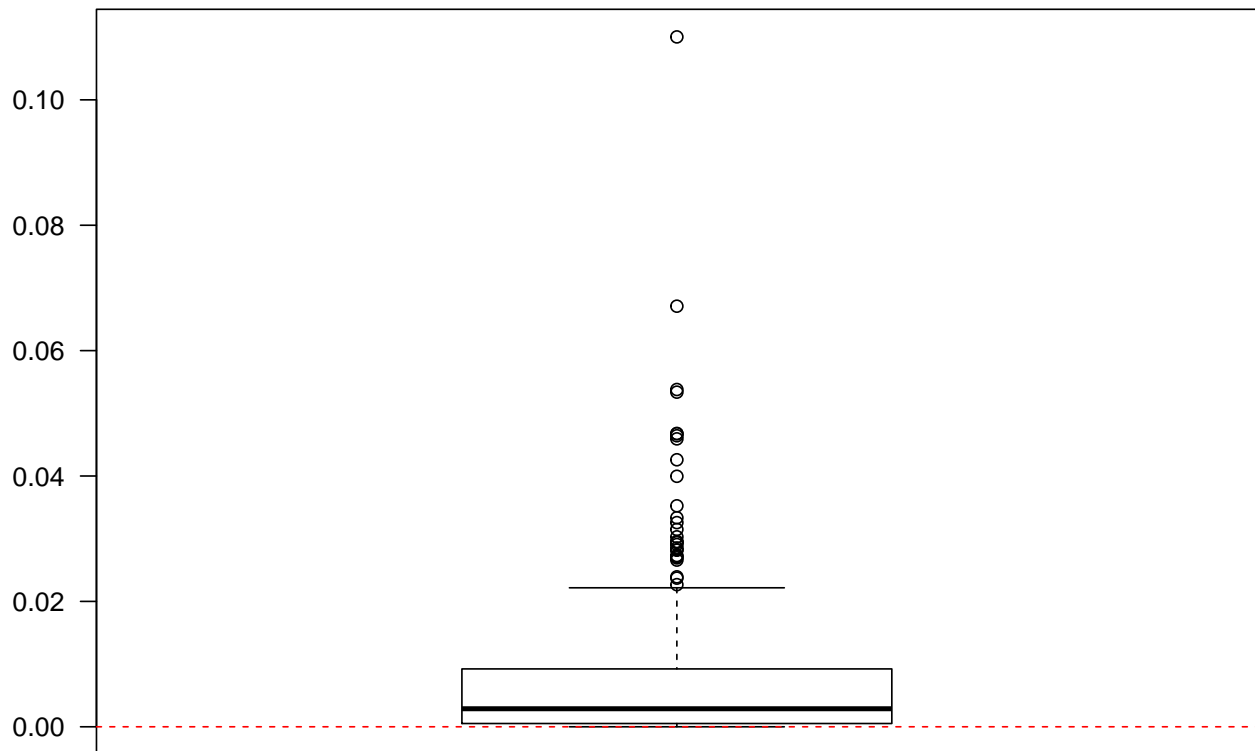
set.seed(123)
N = 500
x1 <- replicate(N, rnorm(30))
x2 <- replicate(N, rnorm(30))
y1 <- apply(x1, 2, function(x) 5 + 2 * x + rnorm(30, 0, 1))
R.sq <- array(dim = c(N, 4))
for (i in 1:N){
  R.sq[i, 1] = summary(lm(y1[, i] ~ x1[, i]))$r.squared
  R.sq[i, 2] = summary(lm(y1[, i] ~ x1[, i]))$adj.r.squared
  R.sq[i, 3] = summary(lm(y1[, i] ~ x1[, i] + x2[, i]))$r.squared
  R.sq[i, 4] = summary(lm(y1[, i] ~ x1[, i] + x2[, i]))$adj.r.squared
}

```

```
par(las = 1)
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)
```

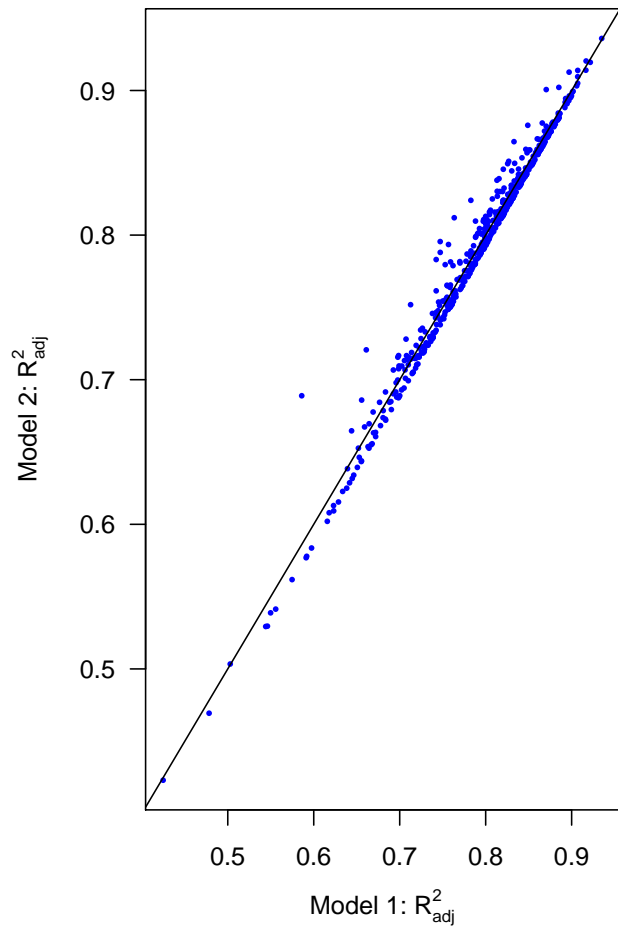
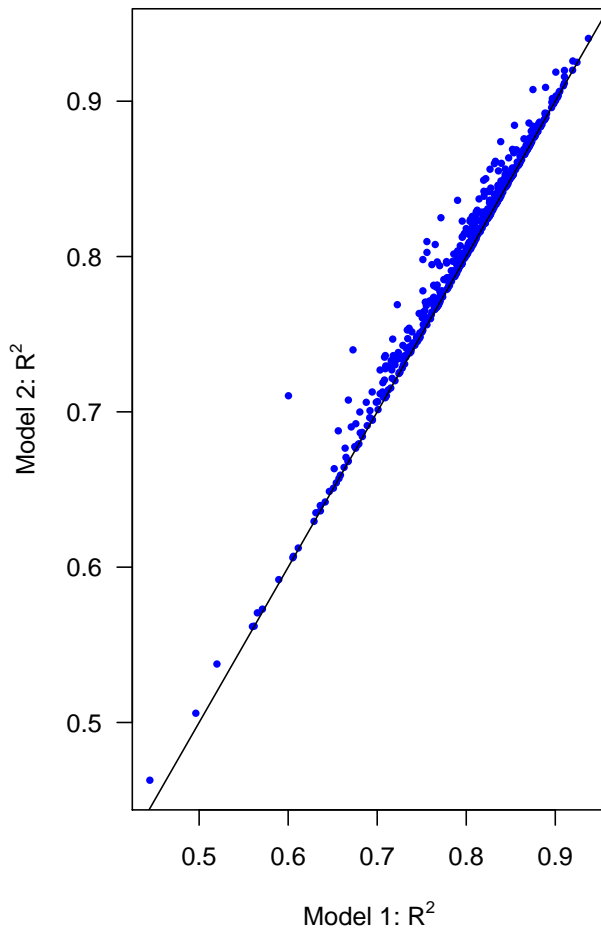


```
boxplot(R.sq[, 3] - R.sq[, 1], las = 1)
abline(h = 0, lty = 2, col = "red")
```



```
par(las = 1, mfrow = c(1, 2), mar = c(5.1, 4.6, 1.1, 1.1))
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)

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)
```

```

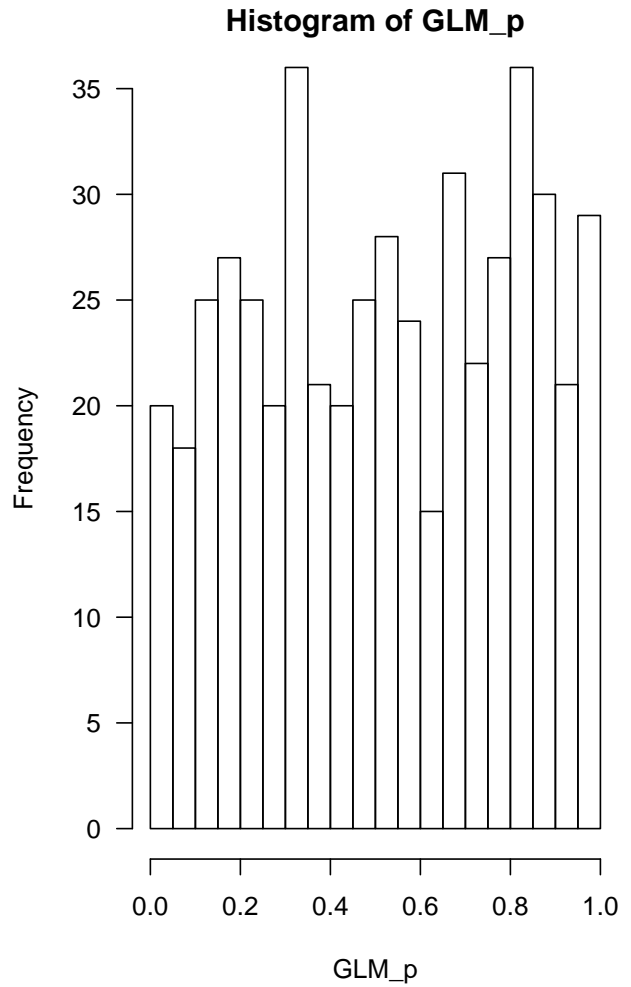
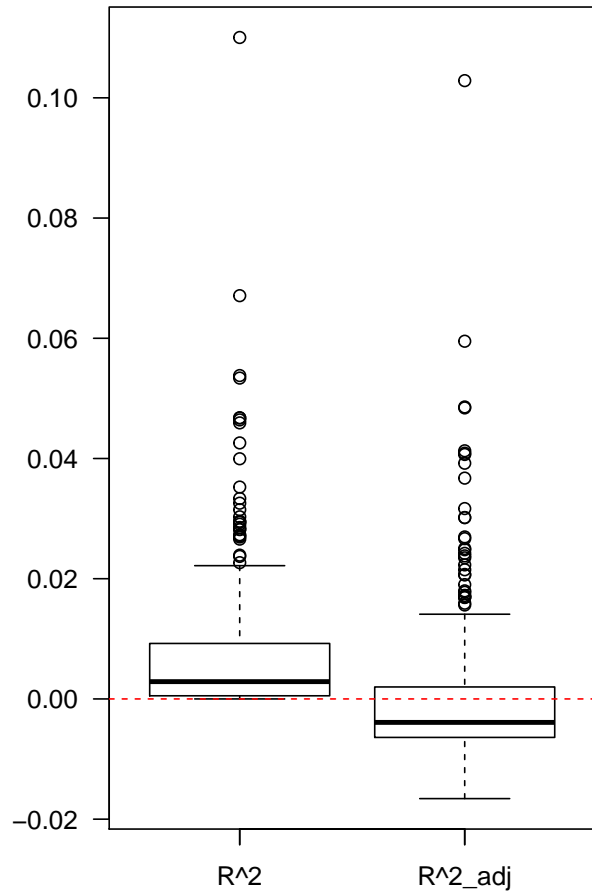
boxplot(R.sq[, 3] - R.sq[, 1], R.sq[, 4] - R.sq[, 2], las = 1)
abline(h = 0, lty = 2, col = "red")
axis(1, at = 1:2, labels = c("R^2", "R^2_adj"))

GLM_p <- numeric(500)

for (i in 1:500){
  reduce <- lm(y1[, i] ~ x1[, i])
  full <- lm(y1[, i] ~ x1[, i] + x2[, i])
  GLM_p[i] <- anova(reduce, full)$`Pr(>F)`[2]
}

hist(GLM_p, 30, las = 1)

```



Multicollinearity

```
library(MASS)

x <- replicate(N, mvrnorm(n = 30, c(0, 0), matrix(c(1, 0.9, 0.9, 1), 2)))
y <- array(dim = c(30, N))
for (i in 1:N){
  y[, i] = 4 + 0.8 * x[, 1, i] + 0.6 * x[, 2, i] + rnorm(30)
}
beta <- array(dim = c(3, N))
for (i in 1:N){
  beta[, i] <- lm(y[, i] ~ x[, 1, i] + x[, 2, i])$coefficients
}
```