

# Homework 4

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## 1 Effects of collinearity on variances of betas and Yhats.

### 1.1

Make a MLR model with all explanatory variables and bd as the response variable. Report the code and the summary for the model. Determine is there is excessive collinearity. [10]

#### 1.1.1 Code and Relevant Output

```
library(car)
library(HH)
library(leaps)
library(MASS)
library(DAAG)

birds<-read.table("C:\\Users\\gitanshu\\Desktop\\birds.csv",header=T,sep=",")
model<-lm(bd~grzinv+dist+height+peri+mammal+area+leg,birds)
summary(model)
```

Call:

```
lm(formula = bd ~ grzinv + dist + height + peri + mammal + area + leg, data = birds)
```

Residuals:

Min	1Q	Median	3Q	Max
-3.5284	-0.7912	0.2158	0.9800	3.0052

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	25.0481	0.1461	171.419	<2e-16 ***
grzinv	-1.7224	5.7661	-0.299	0.766
dist	-218.5275	499.9072	-0.437	0.663
height	196.6375	446.3263	0.441	0.661
peri	162.1747	368.9310	0.440	0.661
mammal	-8.2513	18.5205	-0.446	0.657
area	-1.0341	5.0022	-0.207	0.837
leg	-223.5453	507.8320	-0.440	0.661

---

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

Residual standard error: 1.386 on 92 degrees of freedom

Multiple R-squared: 0.7428, Adjusted R-squared: 0.7232

F-statistic: 37.96 on 7 and 92 DF, p-value: < 2.2e-16

```
vif(model)
```

grzinv	dist	height	peri	mammal	area	leg
1617.970	12783783.739	12502844.195	6570401.610	15350.575	1105.641	14149460.854

Variance Inflation Factor (VIF) values over 5 are undesirable and over 10 indicate excessive collinearity. As demonstrated by the above results, **indeed there is excessive collinearity** in the current model as all VIF values are above 10.

## 1.2

Pretend that the first explanatory variable was not measured and create a second model without it. Report the same as in 3.1 [10]

### 1.2.1 Code and Relevant Output

```
modelminus<-lm(bd~dist+height+peri+mammal+area+leg,birds)
summary(modelminus)
```

Call:

```
lm(formula = bd ~ dist + height + peri + mammal + area + leg,
    data = birds)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-3.4687	-0.8002	0.1927	0.9408	2.9999

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	25.0549	0.1436	174.474	< 2e-16 ***
dist	-69.2525	13.0098	-5.323	7.04e-07 ***
height	63.3618	11.5795	5.472	3.75e-07 ***
peri	52.0097	9.5733	5.433	4.42e-07 ***
mammal	-2.7214	0.5311	-5.124	1.61e-06 ***
area	0.4590	0.1947	2.357	0.0205 *
leg	-71.9034	13.1469	-5.469	3.79e-07 ***

---

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

Residual standard error: 1.379 on 93 degrees of freedom

Multiple R-squared: 0.7426, Adjusted R-squared: 0.726

F-statistic: 44.71 on 6 and 93 DF, p-value: < 2.2e-16

```
vif(modelminus)
```

	dist	height	peri	mammal	area	leg
	8743.655474	8498.801023	4467.834812	12.746025	1.691853	9576.817202

As demonstrated by the above results, **indeed there is excessive collinearity** in the current model as all VIF values except one (area) are above 10. However, the reduction in VIF values in comparison to the full model must be noted

## 1.3

Compare the estimated parameters in 3.1 and 3.2 and explain how and why they differ. Then, use the results as an example to briefly explain the effects of not including all variables in the model. [10]

Although both models found excessive collinearity, the estimates were much improved by removing the first explanatory variable as demonstrated by the **decrease in the std. error** for each of the estimates. Getting rid of that collinear variable's contribution to noise helped improve our ability to estimate by **reducing redundancy**. These results make the case for not including redundant variables and also for a stepwise removal of such redundancy, if found in the model, in order to **improve the signal to noise ratio**. Furthermore, removing such redundancy is advised as excessive collinearity coupled with extreme outliers could spell disaster for an analysis.

## 1.4

Start with all variables again and develop a good model using `regsubsets()` from the `leaps` package. Select the model with the minimum BIC. Report the model selected and its summary and analysis of variance. [10]

### 1.4.1 Code and Relevant Output

```
birds.best<-summary(best<-regsubsets(bd~., birds, nbest=1, nvmax=7, method=c("exhaustive")))
which.min(birds.best$bic)
birds.best$which[which.min(birds.best$bic),]
```

	X	grzinv	dist	height	peri	mammal	area	leg
	FALSE	TRUE	TRUE	FALSE	FALSE	FALSE	TRUE	FALSE

Based on the above stated results, the best model with the minimum BIC includes 3 explanatory variables (grzinv, dist, area).

```
bestmodel<-lm(bd~grzinv+dist+area,birds)
summary(bestmodel)
```

Call:

```
lm(formula = bd ~ grzinv + dist + area, data = birds)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-3.4996	-0.9005	0.1404	0.9458	3.1988

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	25.0591	0.1435	174.676	< 2e-16 ***
grzinv	0.8147	0.1474	5.527	2.80e-07 ***
dist	1.5452	0.1454	10.630	< 2e-16 ***
area	1.1167	0.1518	7.356	6.39e-11 ***

---

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

Residual standard error: 1.381 on 96 degrees of freedom

Multiple R-squared: 0.7337, Adjusted R-squared: 0.7254

F-statistic: 88.18 on 3 and 96 DF, p-value: < 2.2e-16

```
anova(bestmodel)
```

Analysis of Variance Table

Response: bd

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
grzinv	1	129	128.8	67.6	9.7e-13 ***
dist	1	272	272.3	142.9	< 2e-16 ***
area	1	103	103.1	54.1	6.4e-11 ***
Residuals	96	183	1.9		

---

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

## 1.5

Make predictions for bird abundance using the model from part a and the model from part d and two sets of predictor values: all predictors at their average value and all predictors equal average + 2 standard deviations. Obtain standard errors for all predictions. Compare predictions and s.e.'s and discuss the effects of collinearity and removal of redundant variables. How does the variance of  $\hat{Y}$  change as function of predictor values and presence of collinearity? [10]

### 1.5.1 Code and Relevant Output

```
xvals<-as.data.frame(t(colMeans(birds[,c(3:9)])))
vars <- apply(birds[,c(3:9)],2,var)
xvals <- rbind(xvals,t(t(xvals)+2*sqrt(vars)))

predict(model, xvals, interval="confidence", level=0.90, se=T)
```

```
$fit
      fit      lwr      upr
1   25.2    24.9    25.4
2 -144.3  -808.7  520.1

$se.fit
      1      2
0.139 399.844

$df
[1] 92

$residual.scale
[1] 1.39
```

```
predict(bestmodel,xvals[,c(1,2,6)],interval="confidence",level=0.9,se=T)
```

```
$fit
      fit      lwr      upr
1  25.2    24.9    25.4
2  31.9    31.1    32.6

$se.fit
      1      2
0.138 0.455

$df
[1] 96

$residual.scale
[1] 1.38
```

Comparing the above results makes it clear that there is not much difference in the ability to make predictions for the mean as the results using all predictors at their average values were nearly identical.

The real difference lies in making predictions about points far away from the mean as the results using all predictors at their average values summed + 2 standard deviations were found to be very different. The standard error for the fit of the reduced model was found to be higher than the full model which is as expected since we removed 4 explanatory variables. The fact that these variables were redundant is indicated in the observation that the standard error for the model fit is not impressively higher in their absence.

The confidence interval around the predicted values for bird abundance using the reduced model were found to be much narrower in comparison the confidence interval around the prediction for the full model. This observation makes the case for removing reducing excessive collinearity by removing redundant variables in order to improve our ability to estimate.

## 2 Regression diagnostics and validation.

### 2.1

Do a multiple linear regression of SalePr on YrHgt, FtFrBody, PrctFFB, Frame, BkFat, SaleHt and SaleWt.

#### 2.1.1 Code and Relevant Output

```
bulls<-read.table("C:\\Users\\gitanshu\\Desktop\\Bulls.txt",header=T,sep=",")
bully<- lm(SalePr ~ YrHgt + FtFrBody + PrctFFB + Frame + BkFat + SaleHt + SaleWt, bulls)
summary(bully)
```

Call:

```
lm(formula = SalePr ~ YrHgt + FtFrBody + PrctFFB + Frame + BkFat +
    SaleHt + SaleWt, data = bulls)
```

Residuals:

Min	1Q	Median	3Q	Max
-927	-280	-44	220	1613

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-3156.894	4105.719	-0.77	0.4446
YrHgt	25.931	111.403	0.23	0.8166
FtFrBody	-2.201	1.071	-2.06	0.0437 *
PrctFFB	-30.098	26.717	-1.13	0.2639
Frame	360.317	172.903	2.08	0.0409 *
BkFat	2571.550	790.788	3.25	0.0018 **
SaleHt	84.397	64.091	1.32	0.1923
SaleWt	0.363	0.608	0.60	0.5523

---

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

Residual standard error: 461 on 68 degrees of freedom

Multiple R-squared: 0.504, Adjusted R-squared: 0.453

F-statistic: 9.86 on 7 and 68 DF, p-value: 2.01e-08

## 2.2

Test the assumption of normality. [5]

### 2.2.1 Code and Relevant Output

```
shapiro.test(residuals(bully))  
qqplot(bully)
```

```
Shapiro-Wilk normality test  
  
data:  residuals(bully)  
W = 0.925, p-value = 0.0002499
```

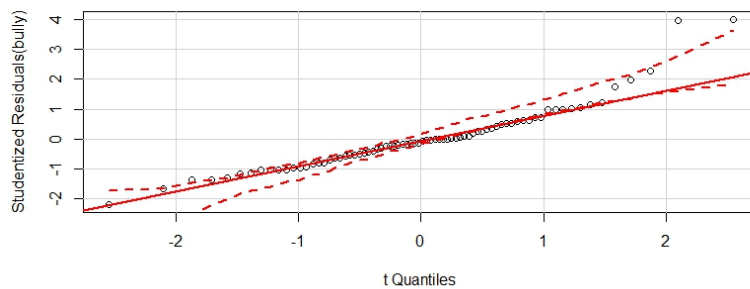


Figure 1: Quantile plot of residuals to test for normality

The significant p-value for the above produced Shapiro-Wilk test indicates that assumption of normality has been violated i.e. the **residuals are NOT normally distributed**. One possible cause for this violation could be extreme outliers (we see two such points lying outside the confidence interval). The other possibility could be lack of homogeneity of variances which might need a transformation to remedy.

## 2.3

Test the homogeneity of variance. In addition to other potential checks, use Breed as grouping variable. [10]

### 2.3.1 Code and Relevant Output

```
residualPlots(bully)
```

	Test stat	Pr(> t )
YrHgt	0.677	0.501
FtFrBody	-0.715	0.477
PrctFFB	-1.565	0.122
Frame	0.528	0.599
BkFat	-1.197	0.235
SaleHt	0.146	0.884
SaleWt	-0.256	0.799
Tukey test	4.441	0.000

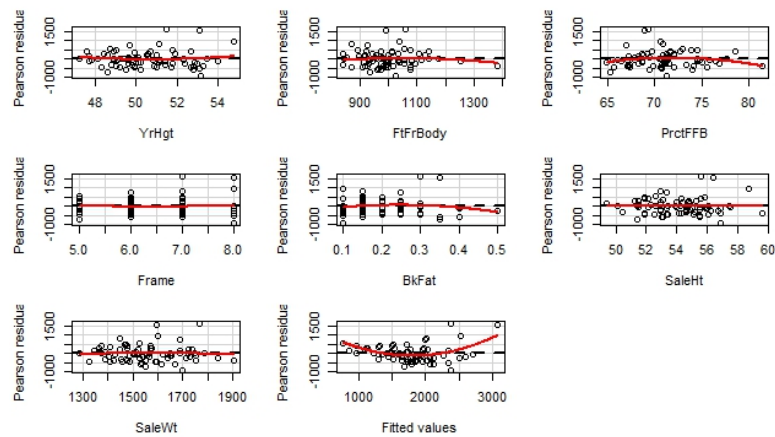


Figure 2: Residual plots

The above results from the residual plots indicate that indeed all variances are homogenous as the p-values for the supporting test, " $\Pr(>|t|)$ ", were found to be not significant at the 95 percent significance level. However, the plot for Residual Vs Fitted values was found to be non-linear indicating that the assumption regarding additivity might be violated (again, possibly remedied by removal of redundancy and/or transformation).

```
leveneTest(residuals(bully)~as.factor(Breed),bulls)
```

Levene's Test for Homogeneity of Variance (center = median)

	Df	F value	Pr(>F)
group	2	0.51	0.6
	73		

The levene's test for homogeneity of variances using Breed as a grouping variable was found to be not significant at the 95 percent significant level indicating that the variances were homogenous.

## 2.4

Inspect the added variable or "leverage" plots to test for lack of linearity. [5]

### 2.4.1 Code and Relevant Output

```
avPlots(bully)
```

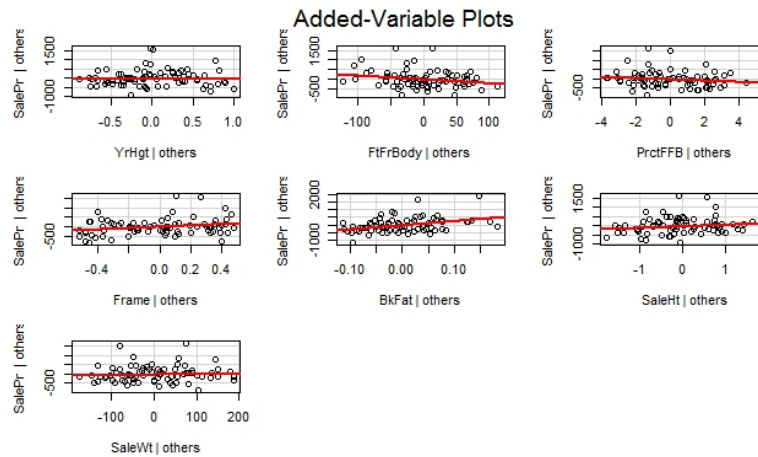


Figure 3: Added Variable plots

The added variable plots indicated **no departure from linearity**.

## 2.5

Determine if there is excessive collinearity. [10]

### 2.5.1 Code and Relevant Output

```
vif(bully)
```

YrHgt	FtFrBody	PrctFFB	Frame	BkFat	SaleHt	SaleWt
13.13	3.48	2.69	9.06	1.77	5.83	2.20

As mentioned earlier, VIF values above 5 are undesirable and above 10 are excessive. Using that definition, indeed **there is evidence for excessive collinearity**.



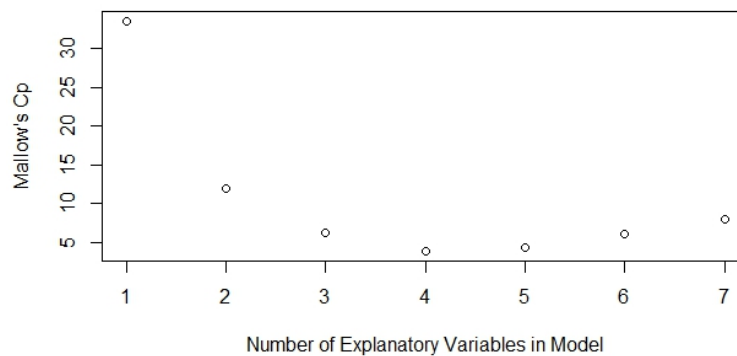
## 2.6

Use the leaps package to select a good reduced model as necessary. [10]

### 2.6.1 Code and Relevant Output

```
bestbulls<-summary(best<-regsubsets(SalePr ~ .-Breed, bulls, nbest=1,
nvmax=7, method=c("exhaustive")))

plot(bestbulls$cp~1+as.numeric(rownames(bestbulls$which)),
xlab="Number of Explanatory Variables in Model",ylab="Mallow's Cp")
```



```
bestbulls$which[which.min(bestbulls$cp),]
```

YrHgt	FtFrBody	PrctFFB	Frame	BkFat	SaleHt	SaleWt
FALSE	TRUE	FALSE	TRUE	TRUE	TRUE	FALSE

The best model was thus picked by minimizing Mallow's Cp. This model included four explanatory variables (FtFrBody, Frame, BkFat, and SaleHt).

```
betterbully<-update(bully, ~ .- YrHgt -PrctFFB - SaleWt)
summary(betterbully)
```

Call:

```
lm(formula = SalePr ~ FtFrBody + Frame + BkFat + SaleHt, data = bulls)
```

Residuals:

Min	1Q	Median	3Q	Max
-841.4	-329.9	-40.1	193.2	1687.2

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	-4511.119	2047.267	-2.20	0.0308	*
FtFrBody	-2.745	0.802	-3.42	0.0010	**
Frame	375.466	95.807	3.92	0.0002	***
BkFat	3157.195	616.125	5.12	2.5e-06	***
SaleHt	110.763	49.709	2.23	0.0290	*

---

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

Residual standard error: 457 on 71 degrees of freedom

Multiple R-squared: 0.49, Adjusted R-squared: 0.462

F-statistic: 17.1 on 4 and 71 DF, p-value: 7.49e-10

## 2.7

Perform a k-fold validation. Report your choice of k, the average MSE and compare with the original MSE. [10]

### 2.7.1

For the analysis here, a K value of 5 was chosen so as to allow sufficient observations for each K group while not compromising on number of groups.

### 2.7.2 Code and Relevant Output

```
cv.lm(df=bulls, betterbully, m=5, seed=floor(1000*runif(1)))
```

#### Analysis of Variance Table

Response: SalePr

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
FtFrBody	1	302808	302808	1.45	0.233
Frame	1	7981585	7981585	38.19	3.6e-08 ***
BkFat	1	4950958	4950958	23.69	6.6e-06 ***
SaleHt	1	1037571	1037571	4.97	0.029 *
Residuals	71	14837102	208973		

---

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

#### fold 1

Observations in test set: 15

	7	10	16	17	22	23	30	37	45	55	58	59	65	68	69
Predicted	2097	1763	2503	1933.1	1460.8	2442.3	1235	1428.7	1740	1738	2458	2042	1817	1383	1842
cvpred	2068	1833	2631	1983.9	1521.4	2414.9	1239	1424.8	1800	1687	2344	1959	1788	1357	1811
SalePr	2250	1525	2300	1900.0	1500.0	2400.0	1400	1500.0	1325	1800	3450	1650	2200	1250	1350
CV residual	182	-308	-331	-83.9	-21.4	-14.9	161	75.2	-475	113	1106	-309	412	-107	-461

Sum of squares = 2227846      Mean square = 148523      n = 15

#### fold 2

Observations in test set: 16

	2	3	8	14	25	33	40	44	47	49	51	62	64	66	67
76															
Predicted	1990	1321	2313	2204	1408.8	1648	1865	1595	1266	1072	1929	1508.9	1733	2309	1679
cvpred	1973	1350	2293	2199	1452.1	1656	1888	1610	1333	1151	1837	1501.8	1752	2353	1693
SalePr	2250	1625	4000	1550	1525.0	2000	1500	975	1025	975	1450	1550.0	1475	1850	1550
CV residual	277	275	1707	-649	72.9	344	-388	-635	-308	-176	-387	48.2	-277	-503	-143

Sum of squares = 5036765      Mean square = 314798      n = 16

#### fold 3

Observations in test set: 15

	1	4	6	18	19	24	26	32	34	41	42	54	56	61
74														
Predicted	1880	3119	1204.5	1072	1976	1074	1941	915	1334.9	1304.0	1710	2291	1632.4	1967.2
cvpred	1808	2983	1181.8	1053	1933	1094	1840	930	1329.9	1262.4	1646	2296	1612.9	1936.6
SalePr	2200	4600	1225.0	1400	1650	1425	1800	1400	1300.0	1325.0	1800	1450	1525.0	1850.0
CV residual	392	1617	43.2	347	-283	331	-40	470	-29.9	62.6	154	-846	-87.9	-86.6

Sum of squares = 4069311      Mean square = 271287      n = 15

#### fold 4

Observations in test set: 15

	12	20	21	28	31	36	38	46	48	52	53	57	60	70	75
Predicted	2062	2085	1787	1643	1174	767	1204.4	1733	805	1784	1940.5	1617	2096	1797.1	1421
cvpred	2009	2117	1787	1720	1164	717	1182.4	1711	677	1774	1928.2	1596	2125	1795.9	1419
SalePr	2850	1500	1375	1600	1300	1300	1225.0	1850	1000	1200	2000.0	1925	1900	1725.0	1250
CV residual	841	-617	-412	-120	136	583	42.6	139	323	-574	71.8	329	-225	-70.9	-169

Sum of squares = 2284133      Mean square = 152276      n = 15

fold 5

Observations in test set: 15

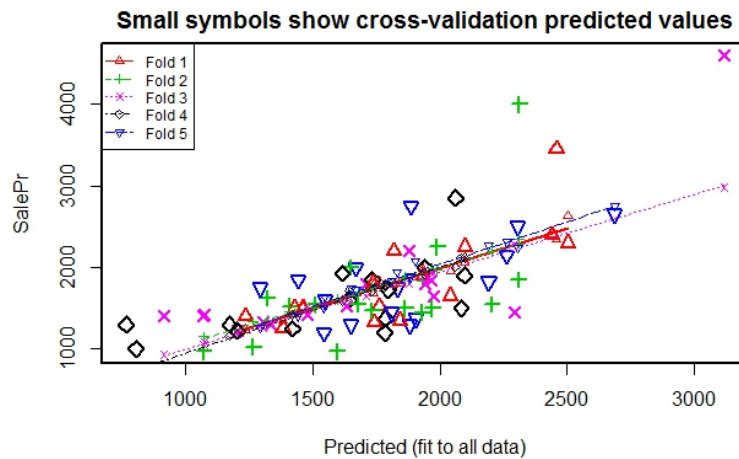
	5	9	11	13	15	27	29	35	39	43	50	63	71	72	73
Predicted	2264	1547.7	1441	2688	1670	2307	1883	1651	1884	1904	1832	2192	1294	1810	1542
cvpred	2310	1640.5	1402	2758	1725	2241	1874	1737	1890	2082	1945	2269	1268	1841	1502
SalePr	2150	1600.0	1850	2650	2000	2500	1300	1300	2750	1375	1750	1825	1750	1450	1200
CV residual	-160	-40.5	448	-108	275	259	-574	-437	860	-707	-195	-444	482	-391	-302

Sum of squares = 2854132      Mean square = 190275      n = 15

Overall (Sum over all 15 folds)

ms

216739



The average MSE calculated from the above validation (216739) was found to be 1.03 times the original MSE (208973) indicating that our reduced model is indeed good. Within reasonable limitations, our reduced model is able to make roughly accurate predictions.