CHAPTER 9 Multicollinearity

Introduction

- Multicollinearity is a problem that plagues many regression models
- Multicollinearity impacts the estimates of the individual regression coefficients
- Uses of regression:
 - Identifying the relative effects of the regressor variables
 - Prediction and/or estimation
 - Selection of an appropriate set of variables for the model

Introduction

- If all regressors are orthogonal, then multicollinearity does not exist
- This is a rare situation in regression analysis
- Often there are near-linear dependencies among the regressors such that

$$\sum_{j=1}^{p} t_{j} \mathbf{X}_{j} \approx \mathbf{0}$$

 If this sum holds exactly for a subset of regressors, then (X'X)⁻¹ does not exist.

- Four primary sources
 - The data collection method employed
 - Constraints on the model or in the population
 - Model specification
 - An overdefined model

Data collection method employed

- Occurs when only a subsample of the entire sample space has been selected.
- Example: Soft drink delivery: number of cases and distance tend to be correlated
- Have data where only a small number of cases are paired with short distances, large number of cases paired with longer distances
- May be able to reduce this multicollinearity through the sampling technique used

- Constraints on the model or in the population
 - Electricity consumption: two variables x_1 family income and x_2 house size
 - Physical constraints are present, multicollinearity will exist regardless of collection method

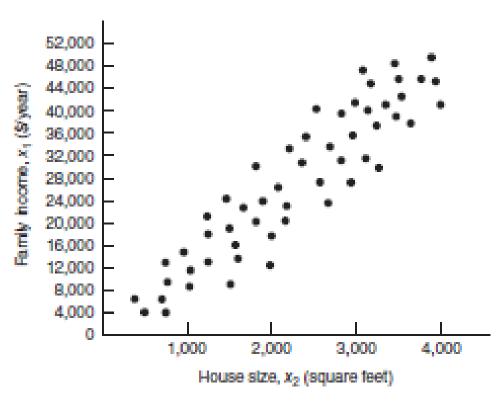


Figure 9.1 Levels of family income and house size for a study on residential electricity consumption.

Model Specification

- Polynomial terms can cause ill-conditioning in the X'X matrix
- This is especially true if range on a regressor variable,
 x, is small

Overdefined model

- More regressor variables than observations
- The best way to counter this is to remove regressor variables
- Recommendations:
 - Redefine the model using smaller set of regressors
 - Do preliminary studies using subsets of regressors
 - Use principal components type regressor methods to remove regressors

Effects of Multicollinearity

 Strong multicollinearity can result in large variances and covariances for the least squares estimates of the coefficients

• Recall **C** = (**X'X**)⁻¹ and
$$C_{jj} = \frac{1}{1 - R_j^2}$$

- Strong multicollinearity between x_j and any other regressor variable will cause R_j^2 to be large, and thus C_{ij} to be large.
- Thus the variance of the least squares estimate of the coefficient will be very large

Effects of Multicollinearity

 Strong multicollinearity can also produce leastsquares estimates of the coefficients that are too large in absolute value

Effects of Multicollinearity

Informal Diagnostics

- Large changes in the estimated regression coefficients when a predictor variable is added or deleted
- Nonsignificant results in individual tests of regression coefficients for important predictors
- Regression coefficients with a sign that is opposite of that expected
- Large coefficients of simple correlation between pairs of predictor variables
- Wide confidence intervals for the regression coefficients for important predictors

Multicollinearity Diagnostics

- Ideal characteristics of a multicollinearity diagnostic:
 - Want the procedure to correctly indicate if multicollinearity is present
 - 2. Want the procedure to provide some insight as to which regressors are causing the problem

Multicollinearity Diagnostics

Correlation Coefficients

- $_{\circ}$ The pairwise correlation between two variables $x_{_{i}}$ and $x_{_{j}}$ is denoted $r_{_{ij}}$
- |r_{ii}| close to unity is an indication of multicollinearity
- However, there may be instances when multicollinearity is present, but the pairwise correlations do not indicate a problem

Data Analysis Methods

TABLE 9.4 Unstandardized Regressor and Response Variables from Webster, Gunst, and Mason [1974]

Observation, i	y_i	$x_{\rm sl}$	x_{i2}	x_{i3}	x_{i4}	$x_{\rm f5}$	x_{i6}
1	10.006	8.000	1.000	1.000	1.000	0.541	-0.099
2	9.737	8.000	1.000	1.000	0.000	0.130	0.070
3	15.087	8.000	1.000	1.000	0.000	2.116	0.115
4	8.422	0.000	0.000	9.000	1.000	-2.397	0.252
5	8.625	0.000	0.000	9.000	1.000	-0.046	0.017
6	16.289	0.000	0.000	9.000	1.000	0.365	1.504
7	5.958	2.000	7.000	0.000	1.000	1.996	-0.865
8	9.313	2.000	7.000	0.000	1.000	0.228	-0.055
9	12.960	2.000	7.000	0.000	1.000	1.380	0.502
10	5.541	0.000	0.000	0.000	10.000	-0.798	-0.399
11	8.756	0.000	0.000	0.000	10.000	0.257	0.101
12	10.937	0.000	0.000	0.000	10.000	0.440	0.432

Multicollinearity Diagnostics

Mason, Gunst & Webster data

$$\mathbf{X'X} = \begin{bmatrix} 1.000 & 0.052 & -0.343 & -0.498 & 0.417 & -0.192 \\ 1.000 & -0.432 & -0.371 & 0.485 & -0.317 \\ 1.000 & -0.355 & -0.505 & 0.494 \\ 1.000 & -0.215 & -0.087 \\ 1.000 & -0.123 \\ 1.000 & Symmetric \end{bmatrix}$$

Variance Inflation Factors

 Variance inflation factors are very useful in determining if multicollinearity is present.

$$VIF_{j} = C_{jj} = (1 - R_{j}^{2})^{-1}$$

- VIFs > 5 to 10 are considered significant
- The regressors that have high VIFs may have poorly estimated regression coefficients

Data Analysis Methods

R code

- #Webster data
- W <- read.csv("Webster.csv",h=T)
- pairs(W,pch=20)
- cor(W)
- library(car)
- $model1=lm(y\sim x1+x2+x3+x4+x5+x6,data=W)$
- vif(model1)
- # Acetylene data
- A <- read.csv("Acetylene.csv",h=T)
- pairs(A,pch=20)
- A\$x12=A\$x1*A\$x2
- A\$x13=A\$x1*A\$x3
- A\$x23=A\$x2*A\$x3
- Ax1sq=A$x1^2$
- Ax2sq=A$x2^2$
- Ax3sq=A$x3^2$
- names(A)
- cor(A)
- library(car)
- library(MASS)
- $model1=lm(y\sim x1+x2+x3+x12+x13+x23+x1sq+x2sq+x3sq,data=A)$
- vif(model1)
- # standardized Acetylene
- A_standard=as.data.frame(apply(A,2,function(x) $\{(x-mean(x))/sd(x)\}$))
- A_standard\$x12=A_standard\$x1*A_standard\$x2
- A standard\$x13=A standard\$x1*A standard\$x3
- A standard\$x23=A standard\$x2*A standard\$x3
- A standard\$x1sq=A standard\$x1^2
- A_standard\$x2sq=A_standard\$x2^2
- A_standard\$x3sq=A_standard\$x3^2
- A standard\$y=A\$y
- $model1=Im(y\sim x1+x2+x3+x12+x13+x23+x1sq+x2sq+x3sq,data=A_standard)$
- $model1=lm(y\sim x1+x2+x3+x12+x13+x23+x1sq+x2sq+x3sq,data=A)$
- vif(model1)

Variance Inflation Factors

TABLE 9.5 VIFs for Acetylene Data and Webster, Gunst, and Mason Data

Data, (A) Acetylene Centered Term VIF	Data, (B) Acetylene Uncentered Term VIF	Data, (C) Webster, Gunst, and Mason Term VIF
$x_1 = 374$ $x_2 = 1.74$ $x_3 = 679.11$ $x_1x_2 = 31.03$ $x_1x_3 = 6565.91$ $x_2x_3 = 35.60$	$x_1 = 2,856,749$ $x_2 = 10,956.1$ $x_3 = 2,017,163$ $x_1x_2 = 2,501,945$ $x_1x_3 = 65.73$ $x_2x_3 = 12,667.1$	$x_1 = 181.83$ $x_2 = 161.40$ $x_3 = 265.49$ $x_4 = 297.14$ $x_5 = 1.74$ $x_6 = 1.44$
$x_1^2 = 1762.58$ $x_2^2 = 3.17$ $x_3^2 = 1158.13$ Maximum VIF = 6565.91	$x_1^2 = 9802.9$ $x_2^2 = 1,428,092$ $x_3^2 = 240.36$ Maximum VIF = 2,856,749	Maximum VIF = 297.14

Variance Inflation Factors

VIFs: A Second Look and Interpretation

- The square root of the jth VIF provides a measure of how much longer the confidence interval for the jth regression coefficient is because of multicollinearity
- For example, if $VIF_3 = 10$, then $\sqrt{VIF_3} \cong 3.3$ and the confidence interval is 3.3 times longer than if the regressors had been *orthogonal*

- Collect more data
- Respecify the model
- Use Ridge Regression

Least squares estimation gives an unbiased estimate,

$$E(\hat{\beta}) = \beta$$

with minimum variance but may be very large

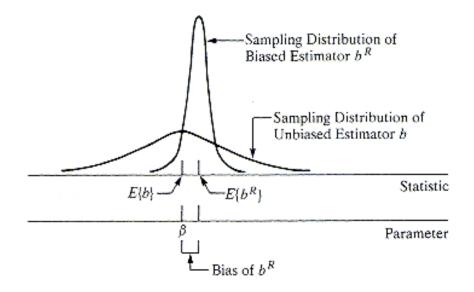
 Alternative: Find an estimate that is biased but with a smaller variance

- Ridge Estimator $\hat{\beta}_R$

$$\hat{\boldsymbol{\beta}}_{R} = (\mathbf{X}'\mathbf{X} + k\mathbf{I})^{-1}\mathbf{X}'\mathbf{y}$$
$$= (\mathbf{X}'\mathbf{X} + k\mathbf{I})^{-1}\mathbf{X}'\mathbf{X}\hat{\boldsymbol{\beta}}$$
$$= \mathbf{Z}_{k}\hat{\boldsymbol{\beta}}$$

- ∘ *k* is a "biasing parameter"
- ok usually between 0 and 1

- Ridge Regression
 - Modifies method of least squares to biased estimators of the regression coefficients



Ridge Trace

- Plots k against the coefficient estimates
- Will show impact of multicollinearity in the stability of the coefficients
- $_{\odot}$ Choose k such that $\hat{\beta}_{\it R}$ is stable and the MSE is acceptable
- Ridge regression is a good alternative if the model user wants to have all regressors in the model

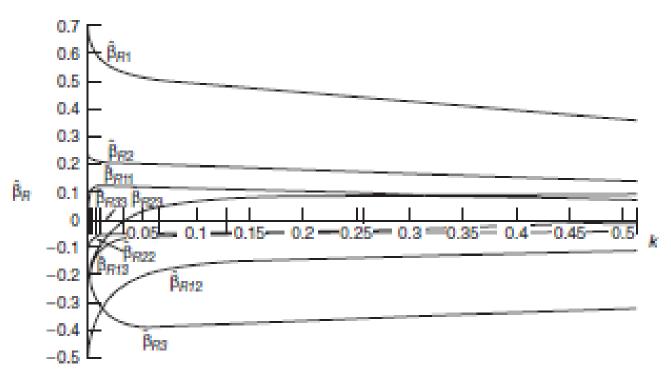
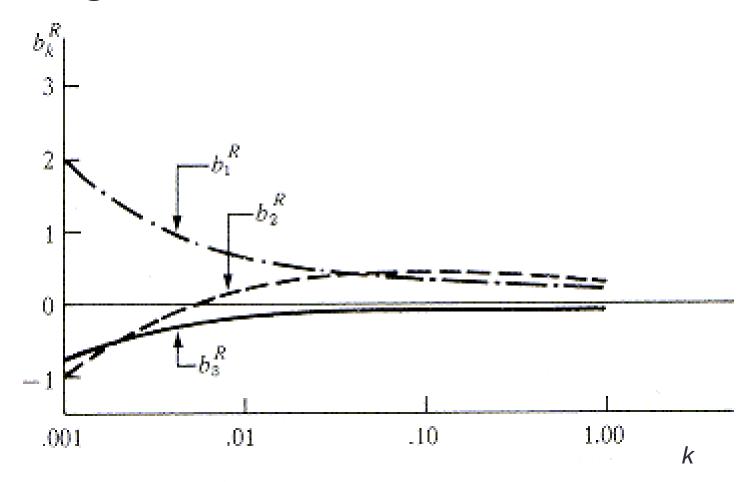


Figure 9.5 Ridge trace for acetylene data using nine regressors.

Ridge Trace



Ridge Regression

k	$(VIF)_1$	$(VIF)_2$	$(VIF)_3$	R^2
.000	708.84	564.34	104.61	.8014
.002	50.56	40.45	8.28	.7901
.004	16.98	13.73	3.36	.7864
.006	8.50	6.98	2.19	.7847
.008	5.15	4.30	1.62	.7838
.010	3.49	2.98	1.38	.7832
.020	1.10	1.08	1.01	.7818
.030	.63	.70	.92	.7812
.040	.45	.56	.88	.7808
.050	.37	.49	.85	.7804
.100	.25	.37	.76	.7784
.500	.15	.21	.40	.7427
1.000	.11	.14	.23	.6818
k	b_1^R	b_2^2	R 2	b_3^R
.000	4.264	-2.9	929	-1.561
.002	1.441	4	1113	4813
.004	1.006	0)248	3149
.006	.8300	.1	314	2472
.008	.7343	.2	2158	2103
.010	.6742	.2	2684	1870
.020	.5463	.3	3774	1369
.030	.5004	.4	1134	1181
.040	.4760	.4	1302	1076
.050	.4605	.4	1392	1005
.100	.4234	.4	1490	0812
.500	.3377	.3	3791	0295
1.000	.2798	.3	3101	0059

- Ridge Regression
 - Comments
 - R² can be defined analogously to OLS
 - Estimates are more stable than OLS estimates and little affected by small changes in the data
 - Estimates provide good estimates of mean responses for levels of the predictor variables outside the region of the observations
 - Inferential procedures are not applicable since exact distributions are not known
 - Selection of k is judgmental
 - Exploratory tool used to reduce the number of predictor variables

R code

```
install.packages("genridge")
install.packages("pls")
library (genridge)
library(pls)
library(MASS)
library(car)
# body fat example
rm(list=ls())
BF <- read.csv("BodyFat.csv",h=T)
pairs(BF,pch=20)
cor(BF)
model1=lm(y~x1+x2+x3,data=BF)
vif(model1)
rreg <- Im.ridge(y~x1+x2+x3, BF, lambda=seq(0,1,.05))
select(rreg)
temp <- lm(y~x1+x2+x3, data=BF)
y <- BF[,"y"]
X0 <- model.matrix(temp)[,-1]
lambda <- seq(0, 1, 0.05)
aridge <- ridge(y, X0, lambda=lambda)
traceplot(aridge)
coef(aridge)
vridge <- vif(aridge)
rreg <- Im.ridge(y~x1+x2+x3, BF, lambda=.31)
temp <- princomp(bodyfat)
summary(temp)
outpcr <- pcr(y~x1+x2+x3, data=BF,ncomp=2)
summary(outpcr)
outpcr <- pcr(y~x1+x2+x3, data=BF,ncomp=3)
summary(outpcr)
# table B21
B21 <- read.csv("data-table-B21.csv",h=T)
pairs(B21,pch=20)
cor(B21)
library(car)
model1=lm(y~x1+x2+x3+x4,data=B21)
rreg <- lm.ridge(y~x1+x2+x3+x4, B21, lambda=seq(0,1,.05))
select(rreg)
temp <- Im(y~x1+x2+x3+x4, data=B21)
y <- B21[,"y"]
X0 <- model.matrix(temp)[,-1]
lambda <- seq(0, 1, 0.05)
aridge <- ridge(y, X0, lambda=lambda)
traceplot(aridge)
coef(aridge)
vridge <- vif(aridge)
rreg <- Im.ridge(y~x1+x2+x3+x4, B21, lambda=.08)
```

R code

```
# webster
W <- read.csv("Webster.csv",h=T)
pairs(W,pch=20)
library(car)
model1=Im(y\sim x1+x2+x3+x4+x5+x6,data=W)
vif(model1)
rreg <- Im.ridge(y~x1+x2+x3+x4+x5+x6, W, lambda=seq(0,1,.05))
select(rreg)
temp <- Im(y\sim x1+x2+x3+x4+x5+x6, data=W)
X0 <- model.matrix(temp)[,-1]
lambda <- seq(0, 1, 0.05)
aridge <- ridge(y, X0, lambda=lambda)
traceplot(aridge)
coef(aridge)
vridge <- vif(aridge)
vridge
rreg <- Im.ridge(y~x1+x2+x3+x4+x5+x6, W, lambda=.25)
# acetylene
A <- read.csv("Acetylene.csv",h=T)
pairs(A,pch=20)
A$x12=A$x1*A$x2
A$x13=A$x1*A$x3
A$x23=A$x2*A$x3
A$x1sq=A$x1^2
A$x2sq=A$x2^2
A$x3sq=A$x3^2
names(A)
cor(A)
library(car)
library(MASS)
model1=lm(y~x1+x2+x3+x12+x13+x23+x1sq+x2sq+x3sq,data=A)
rreg <- lm.ridge(y~x1+x2+x3+x12+x13+x23+x1sq+x2sq+x3sq, A, lambda=seq(0,1,.05))
select(rreg)
y <- A[,"y"]
X0 <- model.matrix(model1)[,-1]
lambda <- seq(0, 1, 0.05)
library(genridge)
aridge <- ridge(y, X0, lambda=lambda)
traceplot(aridge)
coef(aridge)
vridge <- vif(aridge)
```

rreg <- Im.ridge(y~x1+x2+x3+x4+x5+x6, W, lambda=.25)

R code

- A_standard=as.data.frame(apply(A,2,function(x){(x-mean(x))/sd(x)}))
- A standard\$x12=A standard\$x1*A standard\$x2
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- A standard\$x2sq=A standard\$x2^2
- A_standard\$x3sq=A_standard\$x3^2
- A_standard\$y=A\$y
- model1=lm(y~x1+x2+x3+x12+x13+x23+x1sq+x2sq+x3sq,data =A_standard)
- vif(model1)
- model1=lm(y~x1+x2+x3+x12+x13+x23+x1sq+x2sq+x3sq,data =A)
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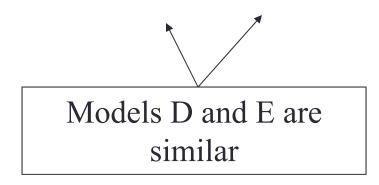
Principal-Component Regression

- Provides composites that are linear combinations of the original variables
- Creates composites are uncorrelated
- Utilizes a subset of the components as the regressors that explain much of the variance
- May be limited by inability to attach concrete meanings to the composites

Data Analysis Methods

TABLE 9.12 Principal Components Regression for the Acetylene Data

Principal Components in Model										
	A z ₁		B z _b z ₂		C z ₁ , z ₂ , z ₃		D Z1, Z3 Z3, Z4		E Z1, Z3 Z3, Z4 Z5	
Parameter										
	Standarized Estimate	Original Estimate	Standardized Estimate	Original Estimate	Standardized Estimate	Original Estimate	Standar dized Estimate	Original Estimate	Standardized Estimate	Original Estimate
β_v	.0000	42.1943	.0000	42.2219	.0000	36.6275	.0000	34.6688	.0000	34.7517
β_1	.1193	1.4194	.1188	1.4 141	.5087	6.0508	.5070	6.0324	.50.56	6.0139
β_2	.0466	.5530	.0450	.5346	.0409	.4885	. 2139	25438	.2195	26129
B	1457	-1.7327	1453	-1.7281	4272	-5.0830	4100	-4.8803	4099	4.8757
β_{12}	0772	-1.0369	0798	-1.0738	0260	3502	1123	-1.5115	1107	-1.4885
β_{12}	.1583	2.0968	.1578	2.0922	0143	1843	0597	7926	0588	7788
β_{23}	.0889	1.2627	.0914	1.2950	.0572	.8111	.1396	1.9816	.1377	1.9493
β_{11}	1429	-2.1429	1425	-21383	.1 219	1.8295	.1751	26268	.1738	26083
β_{22}	.0091	.0968	.0065	.0691	1280	-1.3779	0460	4977	0533	5760
β_{22}	1644	-1.9033	1639	-1.8986	0786	9125	0467	5392	0463	5346
R^2	.5217		.5218		.9320		. 991.4		.9915	
MS_{Ra}	.079713		.079705		.011333		.001427		.00142	



Data Analysis Methods

R code

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- install.packages("pls")
- library (genridge)
- library(pls)
- library(MASS)
- library(car)
- # body fat example
- rm(list=ls())
- BF <- read.csv("BodyFat.csv",h=T)
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- vif(model1)
- rreg <- Im.ridge(y~x1+x2+x3, BF, lambda=seq(0,1,.05))
- select(rreg)
- temp <- Im(y~x1+x2+x3, data=BF)
- y <- BF[,"y"]
- X0 <- model.matrix(temp)[,-1]
- lambda <- seq(0, 1, 0.05)
- aridge <- ridge(y, X0, lambda=lambda)
- traceplot(aridge)
- coef(aridge)
- vridge <- vif(aridge)
- vridge
- rreg <- Im.ridge(y~x1+x2+x3, BF, lambda=.31)
- temp <- princomp(bodyfat)
- summary(temp)
- outpcr <- pcr(y~x1+x2+x3, data=BF,ncomp=2)
- summary(outper)
- outpcr <- pcr(y~x1+x2+x3, data=BF,ncomp=3)
- summary(outpcr)