Multiple Linear Regression

The Bootstrap, MVN

Math 392

Resampling methods: two methods

There are two general approaches to getting bootstrap intervals for your regression estimates (for β , $\hat{E}(Y|X)$, [Y|X]):

- 1. Bootstrap the cases.
- 2. Bootstrap the **residuals**.

Aside:

Bootstrap is not a good idea when your you have few observations, let's simulate a data set of moderate size.

```
set.seed(8134)
n <- 35
x0 <- 1
x1 <- rnorm(n)
x2 <- rnorm(n)
X <- as.matrix(data.frame(x0, x1, x2))
B <- c(-3, .5, 2)
sig_sq <- 2.25
epsilon <- rnorm(n, mean = 0, sd = sqrt(sig_sq))
Y <- X %*% B + epsilon
df <- data.frame(X, Y)</pre>
```

Bootstrap the cases

```
b1 <- sample_frac(df, replace = TRUE)
head(b1)
##
    x0
                x 1
                           x2
## 1 1 0.83535656 0.1209323 -2.536903
## 2 1 0.07239619 -1.8961143 -7.910420
## 3 1 -0.25058242 -1.3210614 -3.608330
## 4 1 -0.74282899 -1.1589374 -3.755188
## 5 1 -0.96462888 -0.1406838 -3.856865
## 6 1 0.57466246 -1.1905117 -4.296790
b2 <- sample_frac(df, replace = TRUE)
head(b2)
##
                           x2
                                       Υ
    x0
               x1
## 1 1 0.5631423 -0.82051067 -3.4623495
## 2 1 2.0582999 -1.24876981 -4.4920737
## 3 1 -0.2023860 0.06540560 -0.8649449
## 4 1 2.0582999 -1.24876981 -4.4920737
## 5 1 0.8353566 0.12093227 -2.5369027
```

6 1 0.6973097 0.04931632 -2.6266855

Compute estimates for each b

Full bootstrap

```
it <- 5000
beta_hp <- rep(NA, it)
for (i in 1:it) {
   b <- sample_frac(df, replace = TRUE)
   beta_hp[i] <- lm(Y ~ x1 + x2, data = b)$coef[2]
}
sd(beta_hp)</pre>
```

[1] 0.1955991

```
m1 <- lm(Y ~ x1 + x2, data = df)
summary(m1)$coef
```

```
## (Intercept) -3.0149299 0.2057590 -14.652724 9.591452e-16
## x1 0.4959268 0.2034211 2.437932 2.050589e-02
## x2 1.5608675 0.1950372 8.002922 3.894623e-09
```

Thoughts on that...

It seemed to work fine but it is a bit odd because the bootstrap procedure suggests that *both* the *X* and the *Y* are random variables.

Can we devise a procedure that is in closer accordance with our idea of regression as conditioning on the values of X?

After conditioning on the values of X, Y is only random through the random vector ϵ . Why don't we bootstrap that?

$$\mathbf{Y} = X\beta + \epsilon$$

Bootstrap Residuals visualized

Bootstrap residuals

```
it <- 5000
beta_hp <- rep(NA, it)
m1 <- lm(Y ~ x1 + x2, data = df)
b <- df
for (i in 1:it) {
   b$Y <- m1$fit + sample(m1$res, replace = TRUE)
   beta_hp[i] <- lm(Y ~ x1 + x2, data = b)$coef[2]
}
sd(beta_hp)</pre>
```

```
## [1] 0.1930897
```

```
summary(m1)$coef
```

```
## (Intercept) -3.0149299 0.2057590 -14.652724 9.591452e-16
## x1 0.4959268 0.2034211 2.437932 2.050589e-02
## x2 1.5608675 0.1950372 8.002922 3.894623e-09
```

Guidance on using the bootstrap

- If you are confident that you have the correct *mean function*, bootstrapping the residuals is more appropriate.
- If you have no idea about the form of the mean function, bootstrapping the cases is the safer / more conservative approach.

The Multivariate Normal Distribution

We can write any linear estimator as

$$\hat{eta} = CY$$

Therefore $\hat{\beta}$ is a linear combination of the Y. If we assume

$$Y \sim N(Xeta,\epsilon)$$

Then we know (through MGFs) that $\hat{\beta}$ is also normally distributed. More specifically, when $C = (X'X)^{-1}X'$,

$$\hat{eta} \sim N(eta, \sigma^2(X'X)^{-1})$$

The Multivariate Normal Distribution, cont.

The general form of the multivariate Normal distribution is

$$oldsymbol{X} \sim N(oldsymbol{\mu}, oldsymbol{\Sigma})$$

Where \boldsymbol{X} is a $n \times p$ matrix, $\boldsymbol{\mu}$ is a $p \times 1$ mean vector, and $\boldsymbol{\Sigma}$ is a $p \times p$ variance/covariance matrix.

You can access densities and random number generated for this distribution via the dmvnorm() and cmvnorm() functions

```
library(mvtnorm)
rmvnorm(n, mean = mu, sigma = Sigma)
```

Simulating from MVN

First, specify parameters,

```
## [,1] [,2] [,3]
## [1,] 0.5 0.0 0.7
## [2,] 0.0 0.5 0.0
## [3,] 0.7 0.0 2.0
```

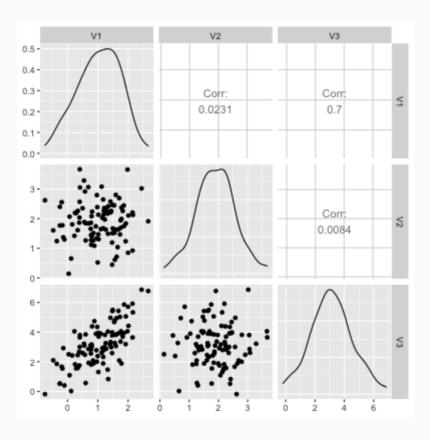
Simulating from MVN, cont.

then, generate random variables.

```
rmvnorm(1, mean = mu_vec, sigma = sigma_mat)
## [,1] [,2] [,3]
## [1,] 0.2138873 0.4631653 2.079299
rmvnorm(1, mean = mu_vec, sigma = sigma_mat)
## [,1] [,2] [,3]
## [1,] 1.223988 2.113755 3.117293
rmvnorm(10, mean = mu_vec, sigma = sigma_mat)
##
             [,1] [,2] [,3]
## [1,] 0.48087366 2.8899896 2.889368
##
   [2,] 1.29128984 2.5380857 4.171362
   [3,] 1.34164338 1.5339317 4.110056
##
  [4,] 1.31996910 0.5135465 3.566813
##
##
   [5,] 0.01468775 1.2799916 1.300745
```

Visualizing the MVN

```
X <- rmvnorm(100, mean = mu_vec, sigma = sigma_mat)
library(GGally)
ggpairs(as.data.frame(X))</pre>
```



Two ways to view a dataset $oldsymbol{Y}$

• n iid draws from $N(\mu, \sigma^2)$

• One draw from $N(\mu_n, \sum_{n \times n})$

Small example (n=3)

```
set.seed(8134)
n < -3
x0 <- 1
x1 < - rnorm(n)
x2 <- rnorm(n)
x3 <- rnorm(n)
x4 <- rnorm(n)
X \leftarrow as.matrix(data.frame(x0, x1, x2, x3, x4))
B \leftarrow c(-3, .5, 2, 1, -.8)
sig_sq <- 2.25
epsilon \leftarrow rnorm(n, mean = 0, sd = sqrt(sig_sq))
Y <- X %*% B + epsilon
df <- data.frame(Y, X)</pre>
df
```

```
## Y x0 x1 x2 x3 x4

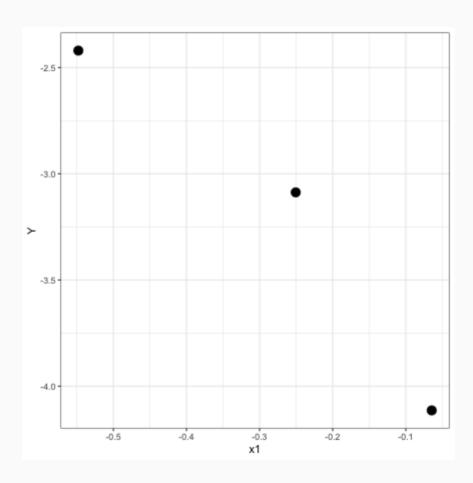
## 1 -2.420069 1 -0.54789199 0.6245961 -0.07552716 0.02026105

## 2 -4.114054 1 -0.06456819 -1.4713007 0.49497462 -0.39986583

## 3 -3.087447 1 -0.25058242 -0.9935656 0.34607212 -1.02113706
```

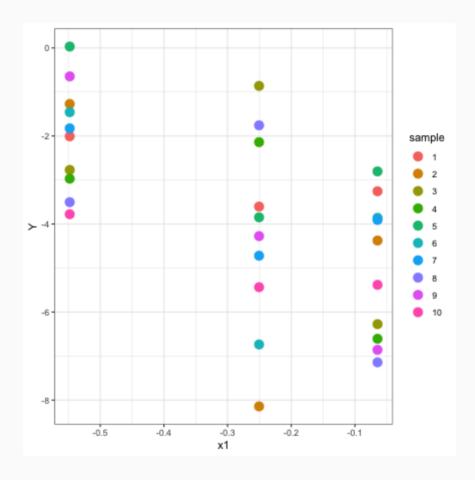
Three iid scalar draws

A partial view:



One vector draw

What does hypothetical resampling look like?



10 vector draws