Social Science Inquiry II

Week 8: Inference for multivariate regression, part I

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Loading packages for this class

```
> library(ggplot2)
> library(estimatr)
> library(gridExtra)
> set.seed(60637)
```

- Housekeeping.

Recall our multivariate regression model:

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- The model describes the true relationships among the variables.
- But the true population parameters are generally unknown.

- We estimate the parameter values for a given sample, as the values that minimize the sum of squared residuals.

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- We will think about our random sample being not just for one variable, but from the joint distribution of $(Y, X_1, X_2, \ldots, X_K)$.
- Then each $\hat{\beta}_k$ is also random, with its own sampling distribution.

- We can get a point estimate for each of the parameters, $\hat{\beta}_k$: the coefficients in our linear model.

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- We also want to get an estimate of the standard errors of the estimates, $\sqrt{\hat{\mathrm{Var}}[\hat{\beta}_k]}$, to describe how much we think these coefficients vary across samples.

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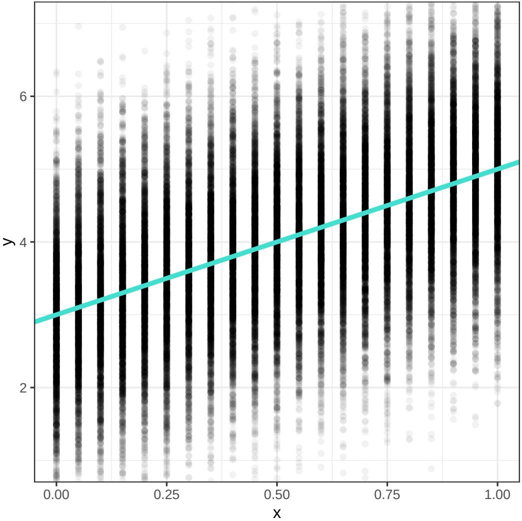
If we were to see the full data:



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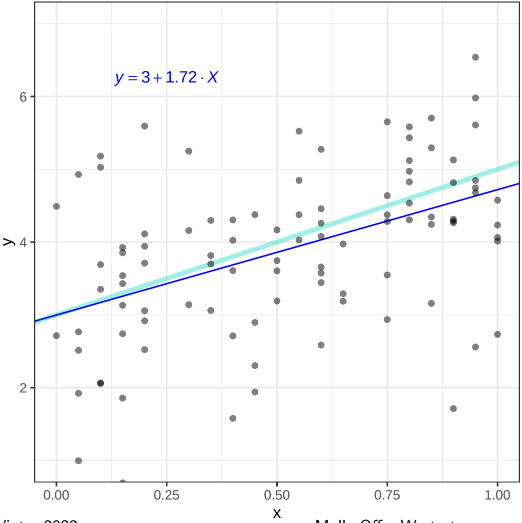
If we only saw 100 observations from the data:



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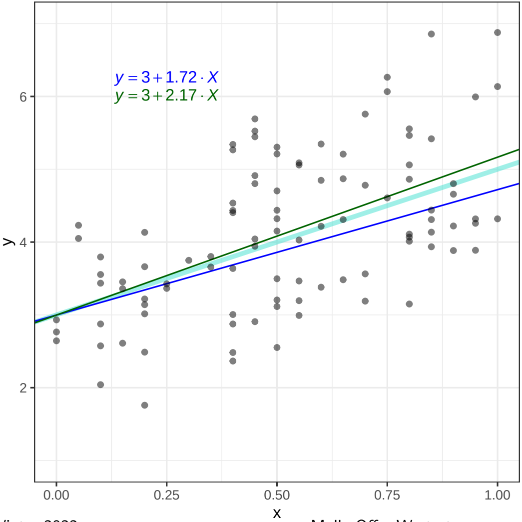

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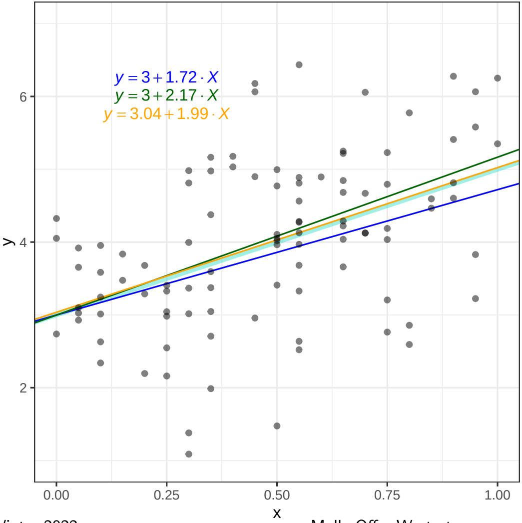

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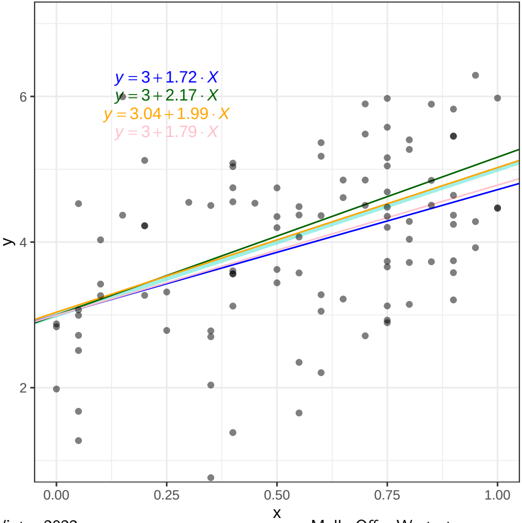

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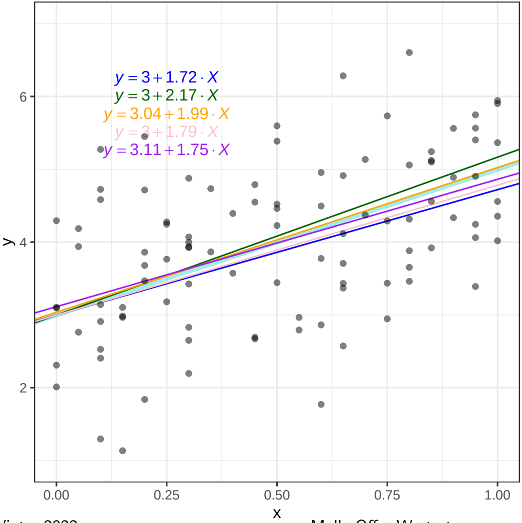

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- Our goal is to describe the *variability* in our parameter estimates.
- Here, we have a regression line with just an intercept and a slope. But we could consider the same resampling and fitting procedure for any joint distribution of $(Y, X_1, X_2, \ldots, X_K)$,

- We will use **robust** standard errors.

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- These standard errors don't require much beyond that our data is i.i.d.: random samples from the same joint distribution.

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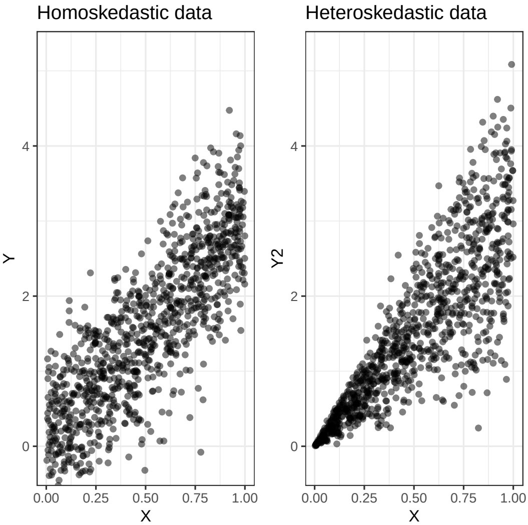
- These standard errors don't require much beyond that our data is i.i.d.: random samples from the same joint distribution.
- "Classical" regression modeling puts much stronger assumptions on the data, including that errors are "homoskedastic;" they don't vary with X


Homoskedastic data
Heteroskedastic data
Y
Y2
X
X
4
2
0
4
2
0
0.00
0.25
0.50
0.75
1.00
0.00
0.25
0.50
0.75
1.00

Applied example

Recall:

Pager, D. (2003). The mark of a criminal record. *American Journal of Sociology*, 108(5), 937-975.

```
> dfp <- data.frame(
+   black = rep(c(0, 1), times = c(300, 400)),
+   record = c(rep(c(0, 1), each = 150),
+              rep(c(0, 1), each = 200)),
+   call_back = c(
+     # whites without criminal records
+     rep(c(0, 1), times = c(99, 51)), # 150
+     # whites with criminal records
+     rep(c(0, 1), times = c(125, 25)), # 150;
+     # - callbacks could be 25 or 26
+     # blacks without criminal records
+     rep(c(0, 1), times = c(172, 28)), # 200
+     # blacks with criminal records
+     rep(c(0, 1), times = c(190, 10)) # 200
+   )
+ )
>
```

- Let's try this with the dfp data, where the outcome Y is `call_back`, regressed on `black` and `record`, interacted.

$$\hat{Y}_i = \hat{\beta}_0 + \hat{\beta}_1 \text{Black}_i + \hat{\beta}_2 \text{Record}_i + \hat{\beta}_3 \text{Black}_i \times \text{Record}_i$$

```
> model2 <- lm_robust(call_back ~ black*record, data = dfp)
```

- How do we go about interpreting these coefficients? confidence intervals? p-values?

```
> summary(model2)

Call:
lm_robust(formula = call_back ~ black * record, data = dfp)

Standard error type:  HC2

Coefficients:
             Estimate Std. Error t value Pr(>|t|) CI Lower CI Upper  DF
(Intercept)    0.3400     0.0388    8.76 1.46e-17   0.2638   0.4162 696
black         -0.2000     0.0459   -4.35 1.55e-05  -0.2902  -0.1098 696
record        -0.1733     0.0494   -3.51 4.76e-04  -0.2703  -0.0764 696
black:record   0.0833     0.0573    1.45 1.46e-01  -0.0291   0.1958 696

Multiple R-squared:  0.0771 ,       Adjusted R-squared:  0.0732
F-statistic: 18.4 on 3 and 696 DF,  p-value: 1.76e-11
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- A valid confidence interval CI_n for a target parameter θ with coverage $1 - \alpha$
$$\mathrm{P}[\theta \in CI_n] \geq 1 - \alpha$$

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- CI_n is a random interval. It is a function of the data we observe.
- θ is a fixed parameter. It does not move.
(In the frequentist view of statistics.)
- If you use valid confidence repeatedly in your work, 95% of the time, your confidence intervals will include the true value of the relevant θ.

- The formula for the 95% confidence interval is:

$$CI_n = \left(\hat{\theta}_n - 1.96 \times \hat{\text{se}},\ \theta_n + 1.96 \times \hat{\text{se}}\right)$$

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- The 1.96 value tells us how many standard errors away from the mean we need to include in our interval to get valid coverage.
- This formula is based on a *normal approximation*, i.e., we assume the data is going to look like a normal distribution.

- How do we go about interpreting these coefficients? confidence intervals? p-values?

```
> confint(model2)

              2.5 % 97.5 %
(Intercept)   0.264  0.416
black        -0.290 -0.110
record       -0.270 -0.076
black:record -0.029  0.196
```

P-values

Suppose $\hat{\theta}$ is the general form for an estimate produced by our estimator, and $\hat{\theta}^*$ is the value we have actually observed.

P-values

- A two-tailed p-value under the null hypothesis is

$$p = \mathrm{P}_0[|\hat{\theta}| \geq |\hat{\theta}^*|]$$

i.e., the probability *under the null distribution* that we would see an estimate of $\hat{\theta}$ as or more extreme as what we saw from the data.

- Confidence intervals and p-values help us get back to testing hypotheses.

Two-sided hypotheses

$$H_0 : \theta = 0$$

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Note that we are *not* imposing the sharp null of no individual effect here, we're looking at averages.

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- If the calculated two-tailed p-value is less than 0.05, reject the hypothesis.
- If the calculated two-tailed p-value is greater than 0.05, fail to reject the hypothesis.
- The θ_0 for which we would fail to reject the hypothesis lie within the 95% confidence interval.

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- If 0 is outside the 95% confidence interval, we would reject the hypothesis that $\theta = 0$ at $p = 0.05$.
- If 0 is outside the 99% confidence interval, we would reject the hypothesis that $\theta = 0$ at $p = 0.01$.
- If 0 is outside the 99.9% confidence interval, we would reject the hypothesis that $\theta = 0$ at $p = 0.001$.

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> summary(model2)

Call:
lm_robust(formula = call_back ~ black * record, data = dfp)

Standard error type:  HC2

Coefficients:
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Multiple R-squared:  0.0771 ,       Adjusted R-squared:  0.0732
F-statistic: 18.4 on 3 and 696 DF,  p-value: 1.76e-11

> round(model2$p.value,5)

 (Intercept)        black       record black:record
     0.00000      0.00002      0.00048      0.14622
```

Bootstrap estimation

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- Another approach to estimating the standard error of an estimate is to use bootstrapping.
- If we fully knew the joint distribution of our population, we would know exactly how to determine the sampling variation of our estimate.
- While we do not, we can *suppose* that the empirical joint distribution produced by the data that we observe is identical to the population joint distribution.
- We can then just re-sample with replacement from our observed data, and see how much our estimates vary across re-samples.

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- Repeat many times:
  1. Take a sample of size *n with replacement* from the observed data

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- Calculate the standard deviation of a parameter estimate across these many bootstrap estimates.

We can try this with the Pager (2003) data.

```
> outmat <- replicate(1000, # do this 1000 times
+                     {
+                       # Take a sample of size n with replacemetn from the data
+                       idx <- sample(1:nrow(dfp), replace = TRUE)
+                       # fit the model on the sampled data
+                       lmx <- lm_robust(call_back ~ black*record,
+                                        data = dfp[idx,])
+                       coef(lmx)
+                     })
> outmat <- t(outmat)
> dim(outmat)
```

```
[1] 1000    4
```

```
> head(outmat, 4)
```

```
     (Intercept) black record black:record
[1,]        0.30 -0.17  -0.12        0.057
[2,]        0.45 -0.32  -0.22        0.136
[3,]        0.33 -0.18  -0.19        0.078
[4,]        0.34 -0.18  -0.16        0.051
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Compare this to the robust standard errors from our model.

```
> model2$std.error
```

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1. Sort bootstrap estimates from smallest to largest
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```
> t(apply(outmat, 2, quantile, probs = c(0.025, 0.075)))

              2.5%    7.5%
(Intercept)   0.27  0.2867
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record       -0.27 -0.2455
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- There are options for different types of robust standard errors which have different small sample properties, but they're asymptotically equivalent.

References I

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