

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 $(Y, X_1, X_2, \dots, X_K)$.
- ▶ 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, $\sqrt{\hat{\text{Var}}[\hat{\beta}_k]}$, to describe how much we think these coefficients vary across samples.

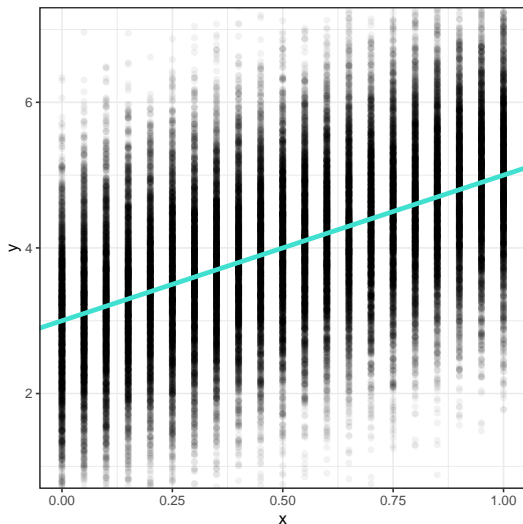
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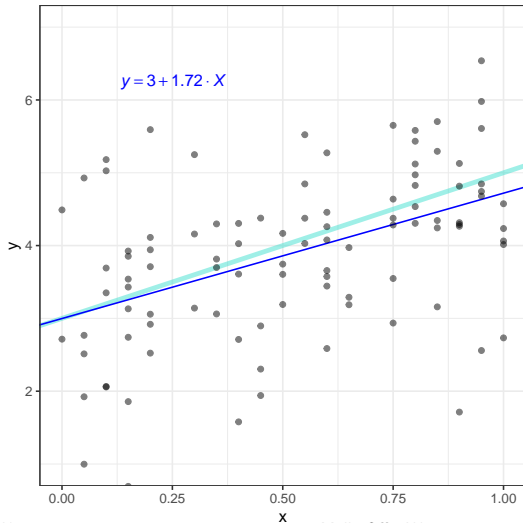
If we were to see the full data:



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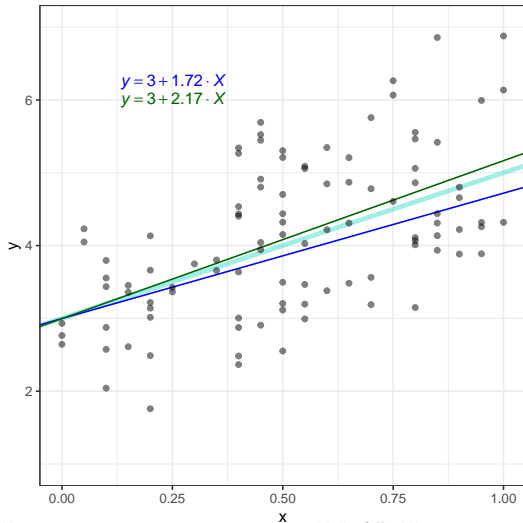
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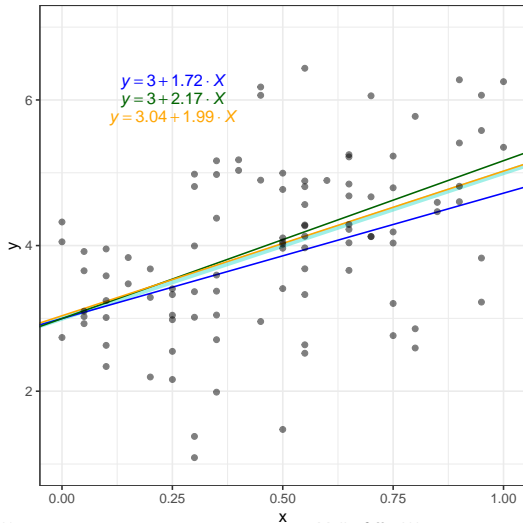
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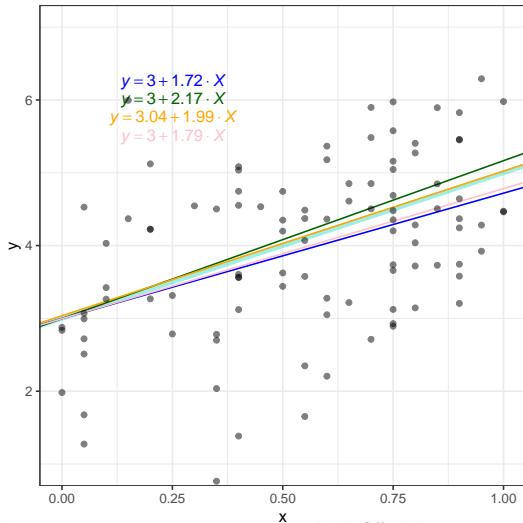
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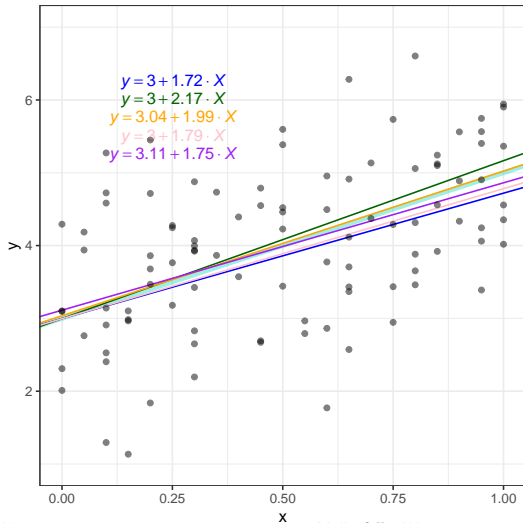
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- ▶ Our goal is to describe the *variability* in our parameter estimates.

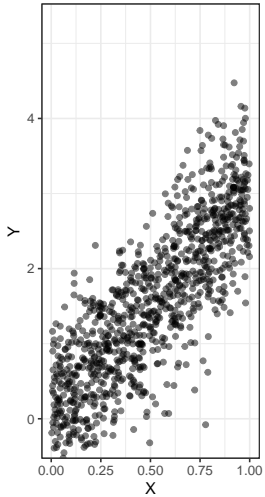
- ▶ Each time we sample from the population, we get a slightly different fit for our regression line.
- ▶ Our goal is to describe the *variability* in our parameter estimates.
- ▶ Here, we have a regression line with just an intercept and a slope. But we could consider the same resampling and fitting procedure for any joint distribution of $(Y, X_1, X_2, \dots, X_K)$,

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

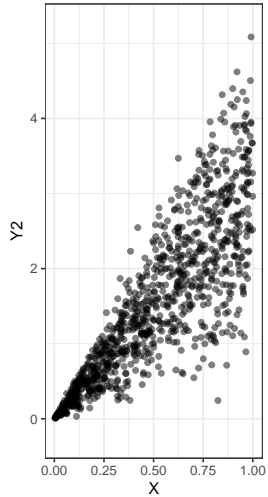
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- ▶ These standard errors don't require much beyond that our data is i.i.d.: random samples from the same joint distribution.
- ▶ "Classical" regression modeling puts much stronger assumptions on the data, including that errors are "homoskedastic;"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

Homoskedastic data



Heteroskedastic data



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

Confidence intervals

- ▶ A valid confidence interval CI_n for a target parameter θ with coverage $1 - \alpha$

$$P[\theta \in CI_n] \geq 1 - \alpha$$

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- ▶ 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:

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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

$$p = P_0[|\hat{\theta}| \geq |\hat{\theta}^*|]$$

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

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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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- ▶ 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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Multiple R-squared: 0.0771 , Adjusted R-squared: 0.0732

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```
> round(model2$p.value,5)
```

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

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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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- ▶ 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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> model2$std.error
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> t(apply(outmat, 2, quantile, probs = c(0.025, 0.075)))
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	2.5%	7.5%
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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

Pager, D. (2003). The mark of a criminal record. American journal of sociology, 108(5):937–975.