

# Test 03 - Regression diagnostics and tidy regression results

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# Load required packages

```
1 library(tidyverse)
2 # if you're using macOS, you can run: library(dplyr)
3 library(skimr)
4 library(broom)
5 library(modelr)
```

# Prepare Data

```
1 Hsb = read_csv("data/raw/hsb.csv")
2 Hsb = Hsb %>%
3   mutate(
4     race = as.factor(race),
5     schtyp = as.factor(schtyp),
6     prog = as.factor(prog)
7   )
```

# A regression

Recall that we run a regression between **write** score on **read** score and **female** (equal 1 for female students):

```
1 ols_reg_fit = lm(formula = write ~ read + female, data = Hsb)
2 summary(ols_reg_fit)
```

Call:

```
lm(formula = write ~ read + female, data = Hsb)
```

Residuals:

Min	1Q	Median	3Q	Max
-17.523	-5.658	0.168	5.043	15.175

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	20.22837	2.71376	7.454	2.80e-12	***
read	0.56589	0.04938	11.459	< 2e-16	***
female	5.48689	1.01426	5.410	1.82e-07	***

---

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

# Tidy the coefficients

- The about regressions results are in text format, which is time-consuming to copy to a report
- How about we transform it into a dataframe to easy to manipulate later: use function `tidy` from `broom` package
- For example, if we want to get the coefficient of `read`, we can easy `filter` and `select` to get the coefficient, rather than copy-and-paste:

```
1 tidy(ols_reg_fit)
```

```
# A tibble: 3 × 5
  term          estimate std.error statistic  p.value
<chr>         <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)    20.2        2.71        7.45 2.80e-12
```

# Get predictions and residuals

- Recall that in a regression

$$Y = a + bX + e$$

- So the prediction is:

$$\hat{Y} = \hat{a} + \hat{b}X$$

- and residuals:

$$\hat{e} = Y - \hat{Y}$$

- We have several ways to get the predictions and residuals

# 1st way: manual calculation

The fitted Y is the product of estimated coefficients and the corresponding X.

```
1 write_hat = 20.2283684 + 0.5658869*Hsb$read + 5.4868940*Hsb$female
2 head(write_hat)
```

```
[1] 52.48392 64.19557 45.12739 55.87924 46.82505 45.12739
```

The residuals is the difference between Y and fitted Y:

```
1 head(Hsb$write - write_hat)
```

```
[1] -0.4839217 -5.1955716 -12.1273920 -11.8792431 5.1749473 6.8726080
```



## 2nd way: use `tidy::augment`

This function added several new columns, including the fitted and residuals to the original data. Compare the results to the manual calculation above.

```
1 Hsb = augment(ols_reg_fit, Hsb)
2 Hsb %>%
3   select(.fitted:.std.resid) %>%
4   head()
```

# A tibble: 6 × 6

	.fitted <dbl>	.resid <dbl>	.hat <dbl>	.sigma <dbl>	.cooksd <dbl>	.std.resid <dbl>
1	52.5	-0.484	0.0118	7.15	0.0000186	-0.0683
2	64.2	-5.20	0.0219	7.14	0.00404	-0.737
3	45.1	-12.1	0.0147	7.10	0.0146	-1.71
4	55.9	-11.9	0.0160	7.10	0.0152	-1.68
5	46.8	5.17	0.0126	7.14	0.00227	0.730
6	45.1	6.87	0.0147	7.13	0.00469	0.971

# Training vs Test sample

- We often split our data into training vs test sample:
  - Training sample: to train historical data
  - Test sample: new data to make prediction
- e.g., Netflix uses our historical watched movies to recommend our next movies to watch

# Re-train our case

```
1 # train: use the first 150 obs
2 ols_reg_fit = lm(formula = write ~ read + female, data = Hsb[1:150,])
3 # test: use the last 50 obs
4 augment(ols_reg_fit, newdata = Hsb[151:200,])
```

# A tibble: 50 × 17

	id	female	race	ses	schtyp	prog	read	write	math	science	socst
.fitted	<dbl>	<dbl>	<fct>	<dbl>	<fct>	<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
<dbl>											
1	43	1	3	1	1	2	47	37	43	42	46
51.1											
2	96	1	4	3	1	2	65	54	61	58	56
61.7											
3	138	1	4	2	1	3	43	57	40	50	51
48.8											
4	10	1	1	2	1	1	47	54	49	53	61
51.1											
5	71	1	4	2	1	1	57	62	56	58	66
57.0											
6	120	1	4	2	1	2	60	50	61	55	71

# Regression diagnostics

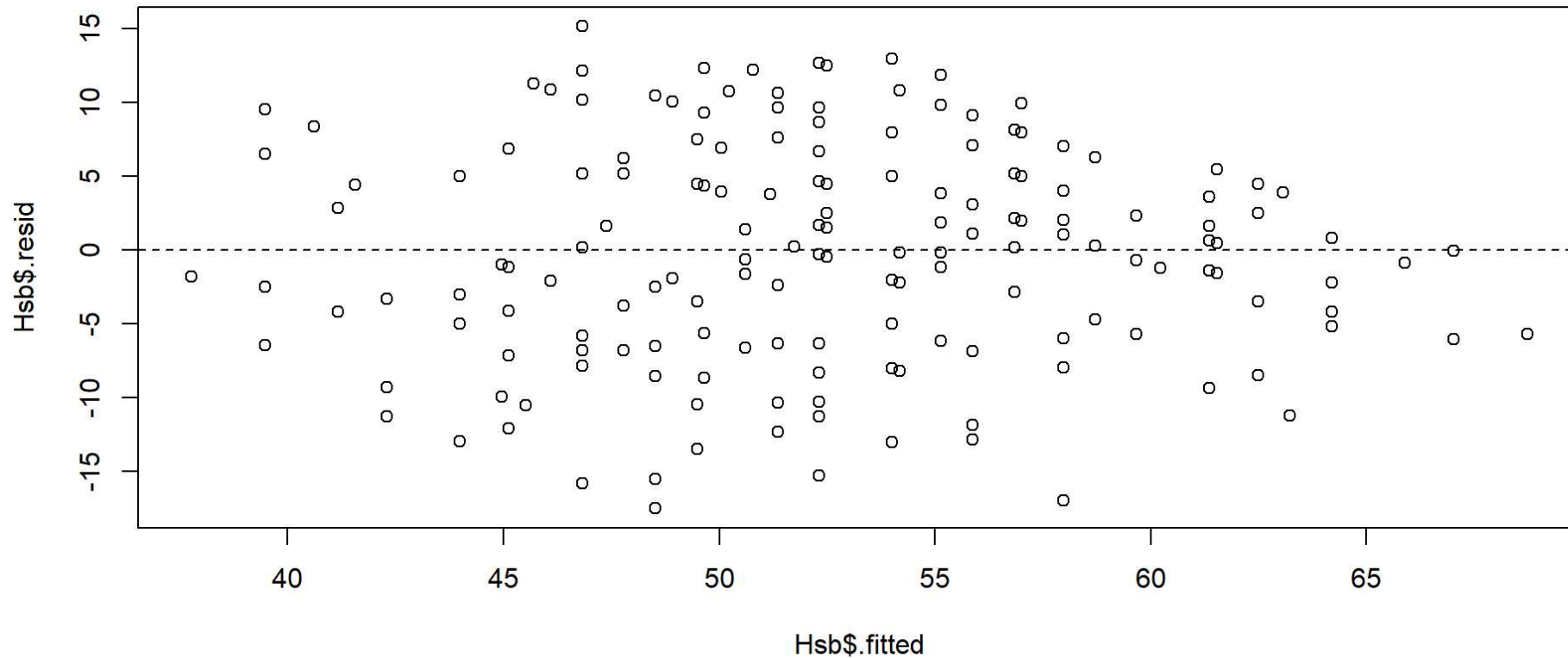
- The OLS regressions have several important assumptions, which we assume the data must be, to make sure the estimation is correct.
- Thus, after running regression, we often need to check these assumptions again to make sure
- This process is called as “regression diagnostics”
- I borrow a lot from [this slide note from UCLA](#)

# Assumption 1: Homogeneity of variance (homoscedasticity)

- It assumes that the variance of residuals is constant
- If the model is well-fitted, there should be no pattern to the residuals plotted against the fitted values.
- Let's plot to see:

# Plot of residuals

```
1 plot(Hsb$.resid ~ Hsb$.fitted)
2 abline(h = 0, lty = 2)
```



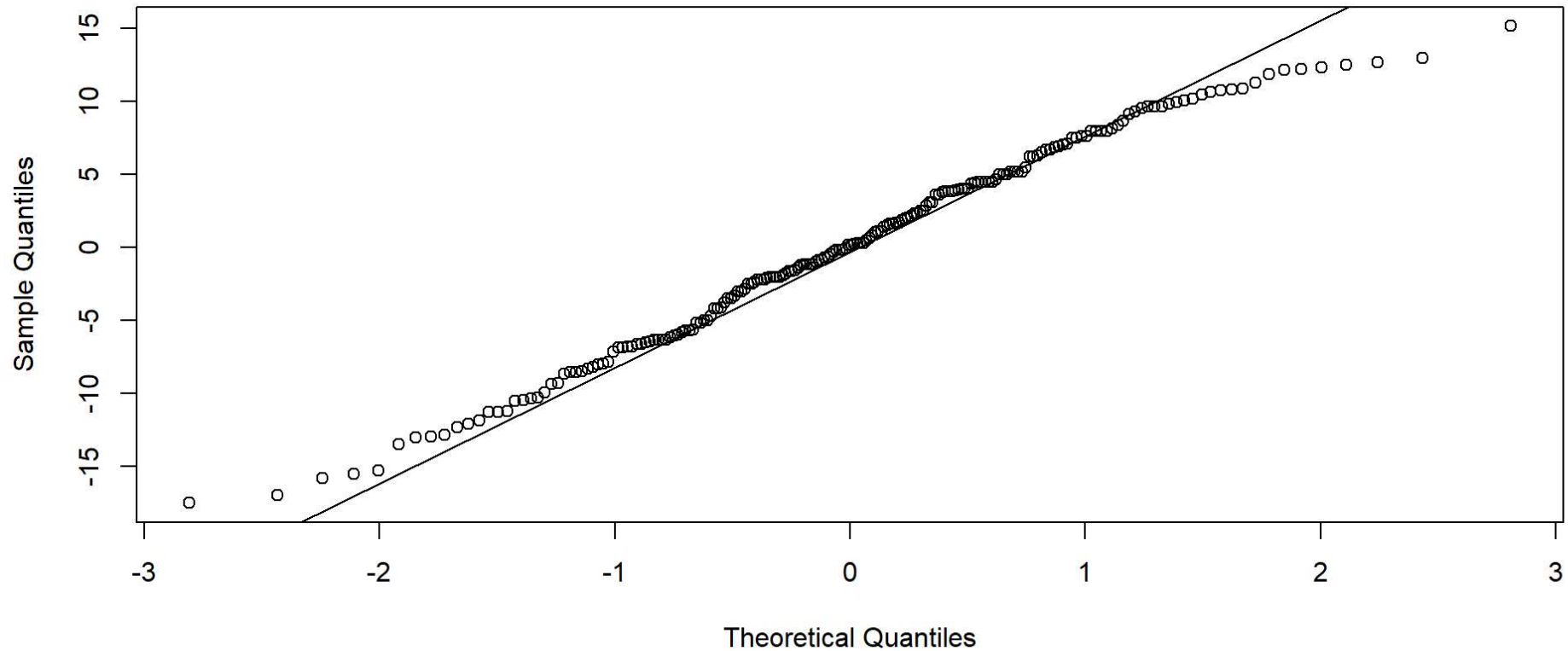
# Assumption 2: Normality of residuals

- It assumes that the residuals follow a normal distribution
- Thus, we need to test normality for the residuals

# Q-Q plot

```
1 qqnorm(Hsb$.resid)
2 qqline(Hsb$.resid)
```

Normal Q-Q Plot





# Normality test for residuals

Do you remember we have a test for normality?

# Assumption 3: Check for multicollinearity

- The term collinearity implies that two variables are near perfect linear combinations of one another.
- VIF, variance inflation factor, is used to measure the degree of multicollinearity.
- Rule-of-thumb:  $VIF \geq 10$  means that the variable could be considered as a linear combination of other independent variables.

# Multicollinearity check in R

- Install `car` package if not yet

```
1 # install.packages("car")  
2 car::vif(ols_reg_fit)
```

```
      read      female  
1.001121 1.001121
```

- All coefficients have low VIF
  - Less concern on multicollinearity problem

# Quiz time

Hmm...