Test 04B - Regression diagnostics and tidy regression results

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Load required packages

```
library(tidyverse)
```

```
## -- Attaching packages ---------------------------------
```

```
## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.1.1     v dplyr   1.0.5
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1
```

```
# if you're using macOS, you can run: library(dplyr)
library(skimr)
library(broom)
library(modelr)
```

Prepare Data

```
Hsb <- within(
  read.csv("https://stats.idre.ucla.edu/stat/data/hsb2.csv"
    race <- as.factor(race)
    schtyp <- as.factor(schtyp)
    prog <- as.factor(prog)
})
```

A regression

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

```
ols_reg_fit = lm(formula = write ~ read + female, data = Hs
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 ***
```

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
- 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:

```
tidy(ols_reg_fit)
```

```
## # A tibble: 3 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)   20.2      2.71       7.45 2.80e-12
## 2 read           0.566    0.0494    11.5  1.26e-23
## 3 female         5.49     1.01       5.41 1.82e- 7
```

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.

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

```
## [1] 52.48392 64.19557 45.12739 55.87924 46.82505 45.1273
```

The residuals is the difference between Y and fitted Y:

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

```
## [1]  -0.4839217  -5.1955716 -12.1273920 -11.8792431   5.
```

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.

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

```
## # A tibble: 6 x 6
##   .fitted  .resid   .hat .sigma   .cooksd .std.resid
##     <dbl>   <dbl>  <dbl>  <dbl>     <dbl>      <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
```

Regression diagnostics

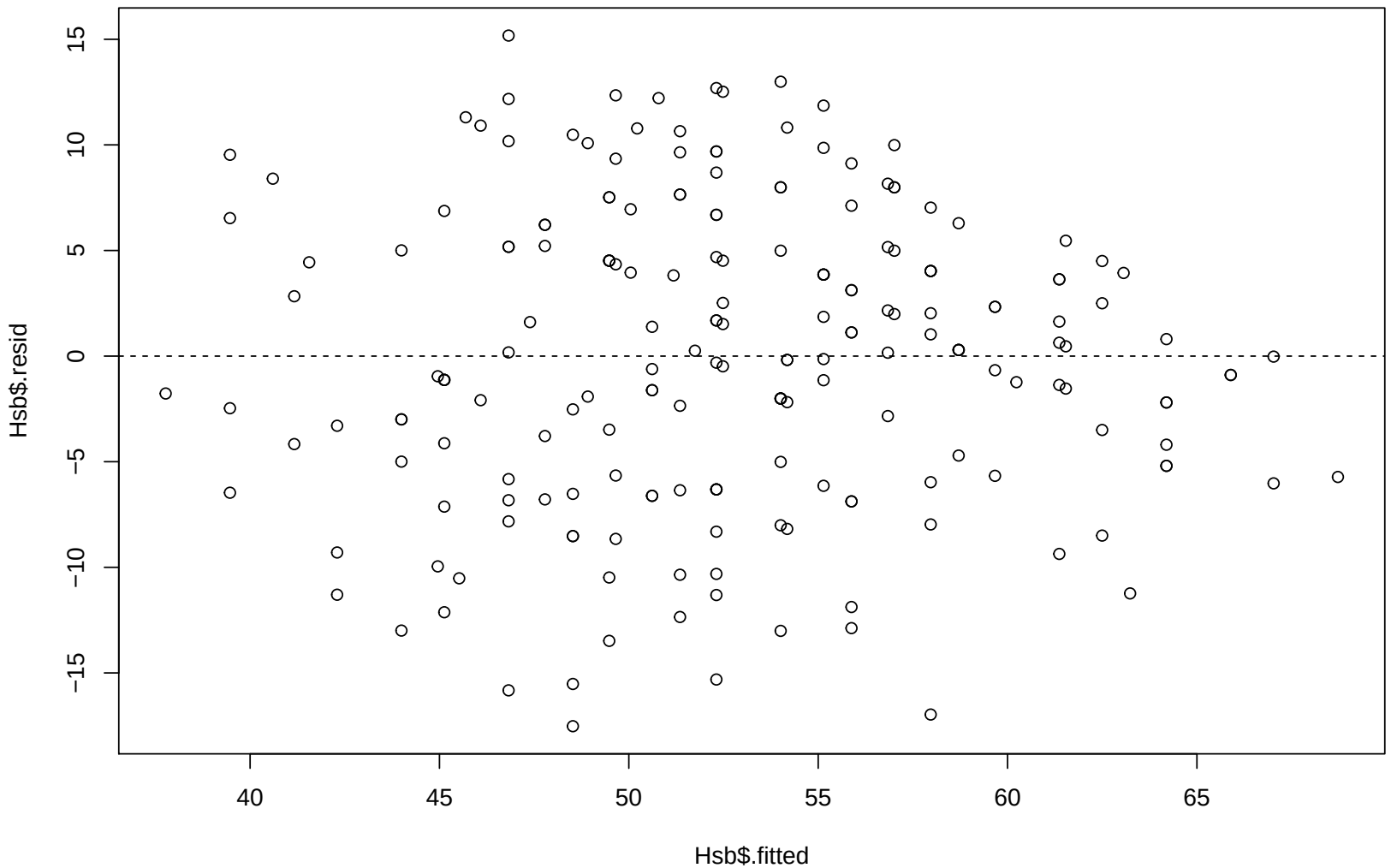
- The OLS regressions have several important assumptions, which we assume the data must be, to make sure the estimation is correct.
- Thus, after running regression, we often need to check these assumptions again to make sure
- This process is called as “regression diagnostics”
- I borrow a lot from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

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

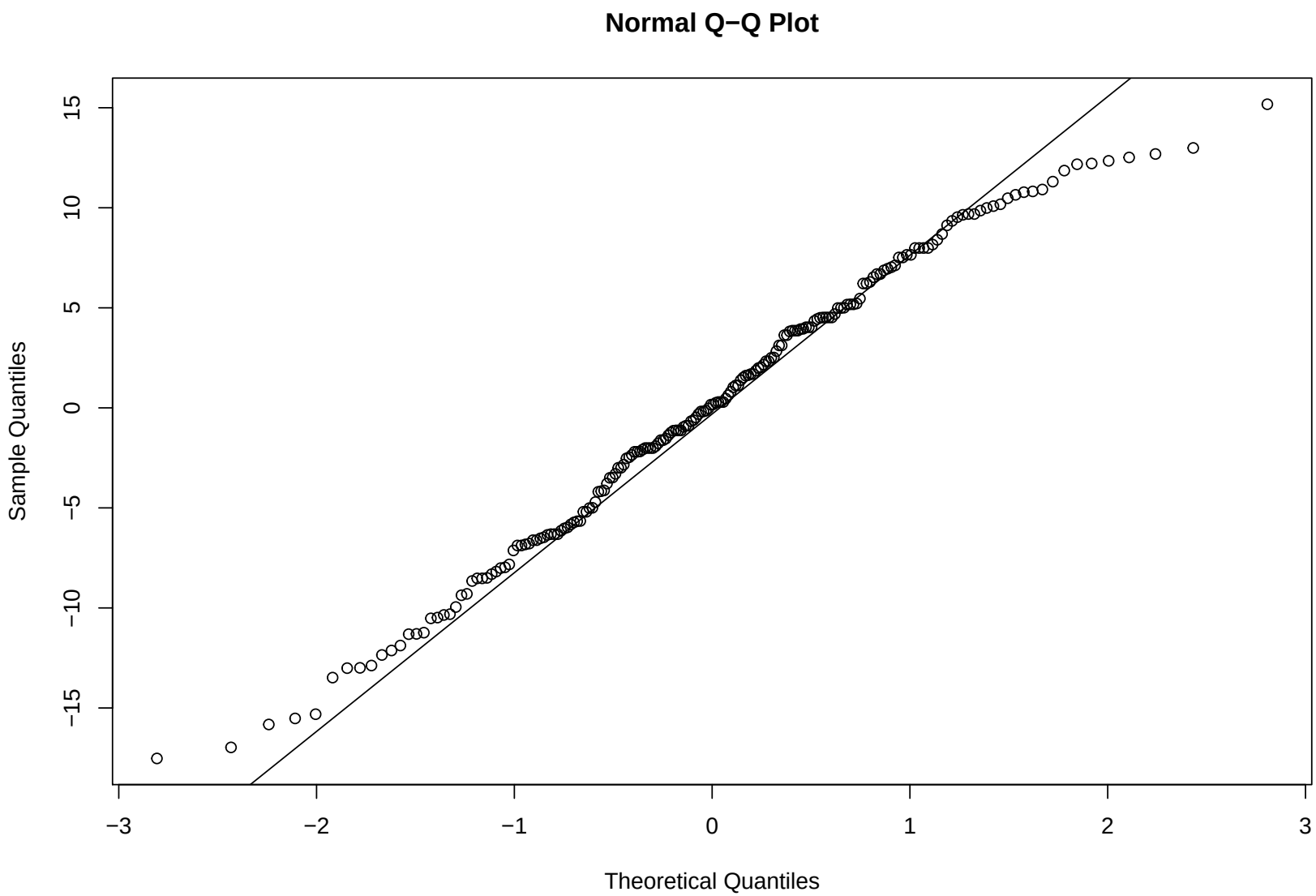


Assumption 2: Normality of residuals

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

Q-Q plot

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



Normality test for residuals

Do you remember we have a test for normality?

Assumption 3: Check for multicolinearity

- 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-thump: VIF $>=$ 10 means that the variable could be considered as a linear combination of other independent variables.

Multicolinearity check in R

- Install `car` package if not yet

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

```
##      read    female
## 1.002826 1.002826
```

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

Quiz time

Hmm...