Simple linear regression

WiSe23/24

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```r
library(broman)
# function to format p-values
format_pval <- function(pval){
    dplyr::case_when(
        pval < .001 ~ "< .001",
        pval < .01 ~ "< .01",
        pval < .05 ~ "< .05",
        TRUE ~ broman::myround(pval, 3)
    )
}

# round to nearest non-zero decimal
my_round = function(x, n=2) {
  max(abs(round(x, n)), abs(signif(x, 1))) * sign(x)
  }
```

Learning Objectives

Today we will learn…

- how to fit a simple linear model with the `lm()` function
- how to interpret our model output
- how to report our model

Workflow

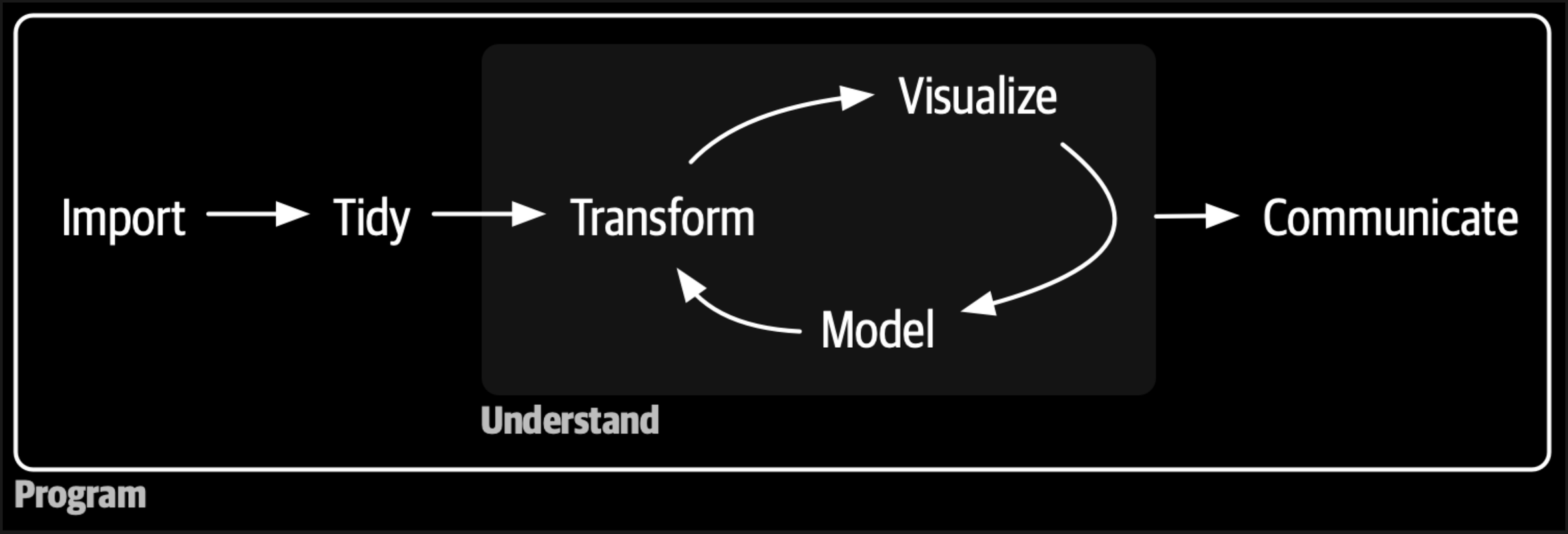


Figure 1: Image source: Wickham et al. (2023) (all rights reserved)

Set-up environment

- always start with a clean R Environment (`Session > Restart R`)
  - go to the `Session` > select `Restart R`
  - or use the keyboard shortcut :`Cmd/Ctrl+Shift+0`

- I usually run `options(scipen=999)` to supress scientific notation

```r
# suppress scientific notation
options(scipen=999)
```

- load in our required packages

```r
# load libraries
pacman::p_load(
               tidyverse,
               here,
               broom,
               lme4,
               janitor,
               languageR)
```

- and set my preferred `ggplot2` theme

```r
# set ggplot theme
theme_set(theme_bw())
```

Simple linear model: RT ~ frequency

- $y \sim x$ can be read as “y as a function of x”, or “y predicted by x”
- following Winter (2019), we will first model some word frequency data.
- our first model will be:

$$RT \sim frequency$$

Load data

- load our data using the `read_csv()` function from `readr`
- the `clean_names()` function from the `janitor` package tidies up variable names (e.g., no spaces, all lower case).

```
# load ELP_frequency.csv
df_freq <- read_csv(here("data", "ELP_frequency.csv")) |>
  clean_names()
```

Mini-EDA

- Exploratory Data Analysis is usually first step once collecting data
  - involves plotting and summarising variables of interest
- let’s explore the data a little bit, which is what we would normally do before fitting any models

head()

- let's use `head()` from base R to see the first 6 rows of our data

```
1 # print head of df_freq
2 head(df_freq)
```

```
# A tibble: 6 × 3
  word      freq    rt
  <chr>    <dbl> <dbl>
1 thing    55522  622.
2 life     40629  520.
3 door     14895  507.
4 angel     3992  637.
5 beer      3850  587.
6 disgrace   409  705
```

- 3 columns: `word`, `freq`, and `rt`
- we can assume that they correspond to the word, its frequency, and the reaction time, respectively
- We can also see in our global environment that there are 12 observations, meaning 12 rows

summary()

- `summary()` provides summaries of each variable in a dataframe
- numeric variables: descriptive statistics for the centre and spread of the data (mean, median, quartiles)
- categorical data: count per category
- character variables: number of observations

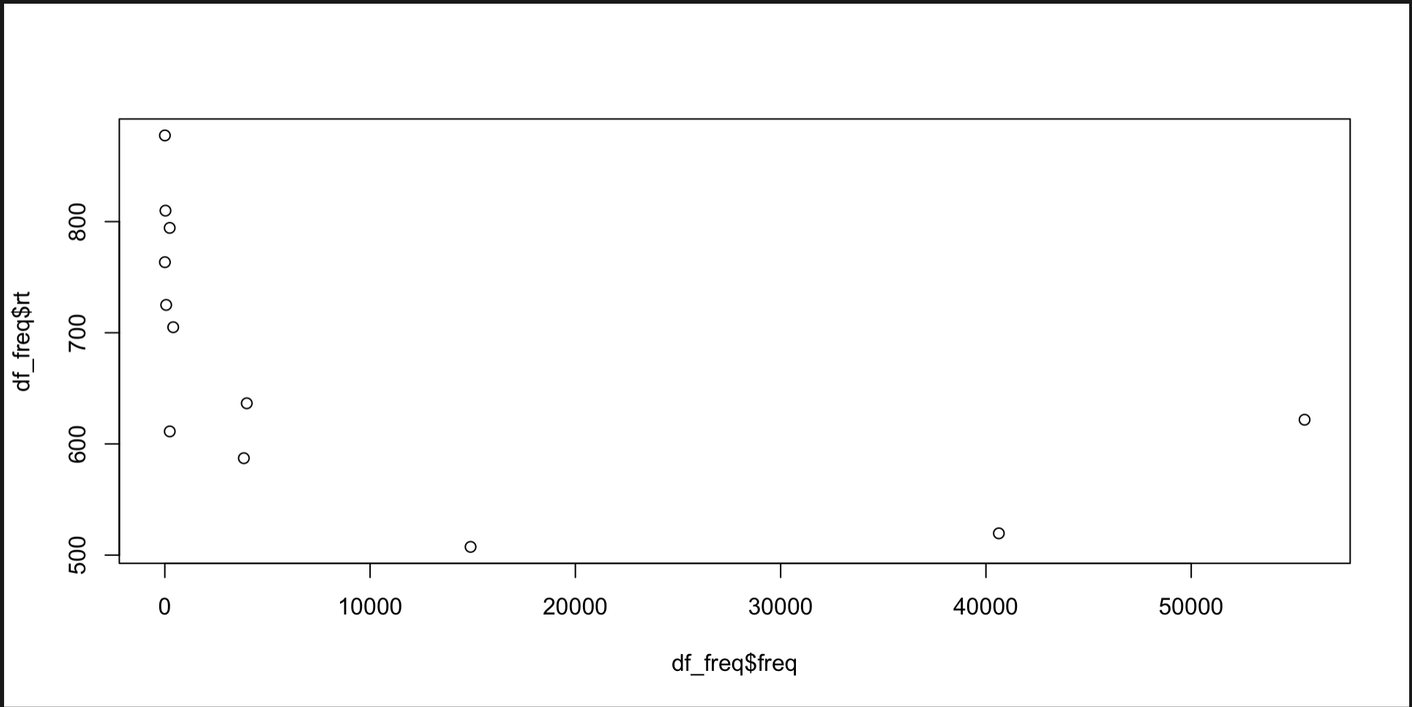
```
1  summary(df_freq)
```

```
     word                freq                rt
Length:12          Min.   :    4.0   Min.   :507.4
Class :character   1st Qu.:   57.5   1st Qu.:605.2
Mode  :character   Median :  325.0   Median :670.8
                   Mean   : 9990.2   Mean   :679.9
                   3rd Qu.: 6717.8   3rd Qu.:771.2
                   Max.   :55522.0   Max.   :877.5
```

Plotting

- what does the relationship between `freq` and `rt` look like?

```
1  plot(df_freq$freq, df_freq$rt)
```



- a lot of frequency values below roughly 400
  - these seem to have higher reaction times than those with a higher frequency value
- let’s fit these data to our first linear model to explore this effect of frequency on reaction times

`lm()`

- `lm()` function fits simple linear models
- as arguments it takes a formula (y x) and a dataset, at minimum
- for now, we will use 1 for our predictor, which is a placeholder for the intercept

$$\text{lm}(\text{outcome} \sim 1 + \text{predictor},\ \text{data} = \text{df\_name})$$

- the intercept is included by default
  - so if you omit the `1` the intercept is still included in the formula
- if you wanted to remove the intercept (which you often don't), you could replace `1` with `0`

Running a model

- to run such a model with our `df_freq` data:

```
1  lm(rt ~ 1, data = df_freq)
```

- or, to save the model as an object so that we can call on it later, assign it a name (`name <- value`)

```
1  fit_rt_1 <- lm(rt ~ 1, data = df_freq)
```

Object naming

- the letters `df` in `df_freq` stand for 'data frame'
  - this serves as a reminder of what exactly that object in our environment is
- we are saving our model as `fit_rt_1`, using 'fit' to signal that this object is a model fit. You could also save it as `mod_freq_1`, `lm_freq_1`, or whatever you see fit (there are no rules)
- if we plot the frequency data, we could call save the plot as `fig_freq` or `plot_freq`
- this simply helps keep our environment structured, which will become useful when you begin having more objects in your environment at a time

Model ouput

- print our model

```
1 # print model
2 fit_rt_1
```

```
Call:
lm(formula = rt ~ 1, data = df_freq)

Coefficients:
(Intercept)
      679.9
```

- `intercept` and `slope` are called `coefficients`
  - Why do we only see `Intercept`?
  - because we didn't include any predictors in our model.

- We typically use the `summary()` function to print full model outputs.

```
1 summary(fit_rt_1)
```

```
Call:
lm(formula = rt ~ 1, data = df_freq)

Residuals:
     Min       1Q   Median       3Q      Max
-172.537  -74.677   -9.137   91.296  197.613

Coefficients:
            Estimate Std. Error t value       Pr(>|t|)
(Intercept)   679.92      34.02   19.99 0.000000000538 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 117.8 on 11 degrees of freedom
```

broom package

The broom package has some useful functions for printing model outputs

- tidy() produces a tibble (type of dataframe) of the coefficients
- glance() produces goodness of fit measures (which we won't discuss)

The outputs from tidy() and glance() can be fed into kable and/or kable_styling() to create formatted tables

```
1  tidy(fit_rt_1)
```

```
# A tibble: 1 × 5
  term        estimate std.error statistic  p.value
  <chr>          <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)     680.      34.0      20.0 5.38e-10
```

```
1  glance(fit_rt_1)
```

```
# A tibble: 1 × 12
  r.squared adj.r.squared sigma statistic p.value    df logLik   AIC   BIC
      <dbl>         <dbl> <dbl>     <dbl>   <dbl> <dbl>  <dbl> <dbl> <dbl>
1         0             0  118.        NA      NA    NA  -73.7  151.  152.
# ℹ 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

augment() adds model values as columns to your dataframe (e.g., useful for plotting observed vs. fitted values).

```
1  augment(fit_rt_1, data = df_freq) %>% summary()
```

Interpreting model output

- let's take a closer look at our model summary

```
summary(fit_rt_1)
```

```
Call:
lm(formula = rt ~ 1, data = df_freq)

Residuals:
     Min       1Q   Median       3Q      Max
-172.537  -74.677   -9.137   91.296  197.613

Coefficients:
            Estimate Std. Error t value       Pr(>|t|)
(Intercept)   679.92      34.02   19.99 0.000000000538 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 117.8 on 11 degrees of freedom
```

① formula repetition

② residuals: differences between observed values and those predicted by the model

③ names for columns `Estimates`, `standard error`, `t-value`, `p-value` (`Pr(>|t|)`)

④ Intercept (b_0)

⑤ Significance codes

⑥ Standard deviation of residuals/error in our model (lower = better)

Intercept

- intercept is roughly 679.9 milliseconds; what does this number represent?

```
# print model intercept
coef(fit_rt_1)['(Intercept)']
```

```
(Intercept)
   679.9167
```

```
# print data mean
mean(df_freq$rt)
```

```
[1] 679.9167
```

- intercept corresponds to the mean reaction time value
  - why is this?

Plotting `rt ~ 1`

- Figure 2 shows the intercept (red dot) amongst the observed data (black dots)
  - along the x-axis we have abstract numerical units (the values don't mean anything)
  - what would the values of the intercept be?

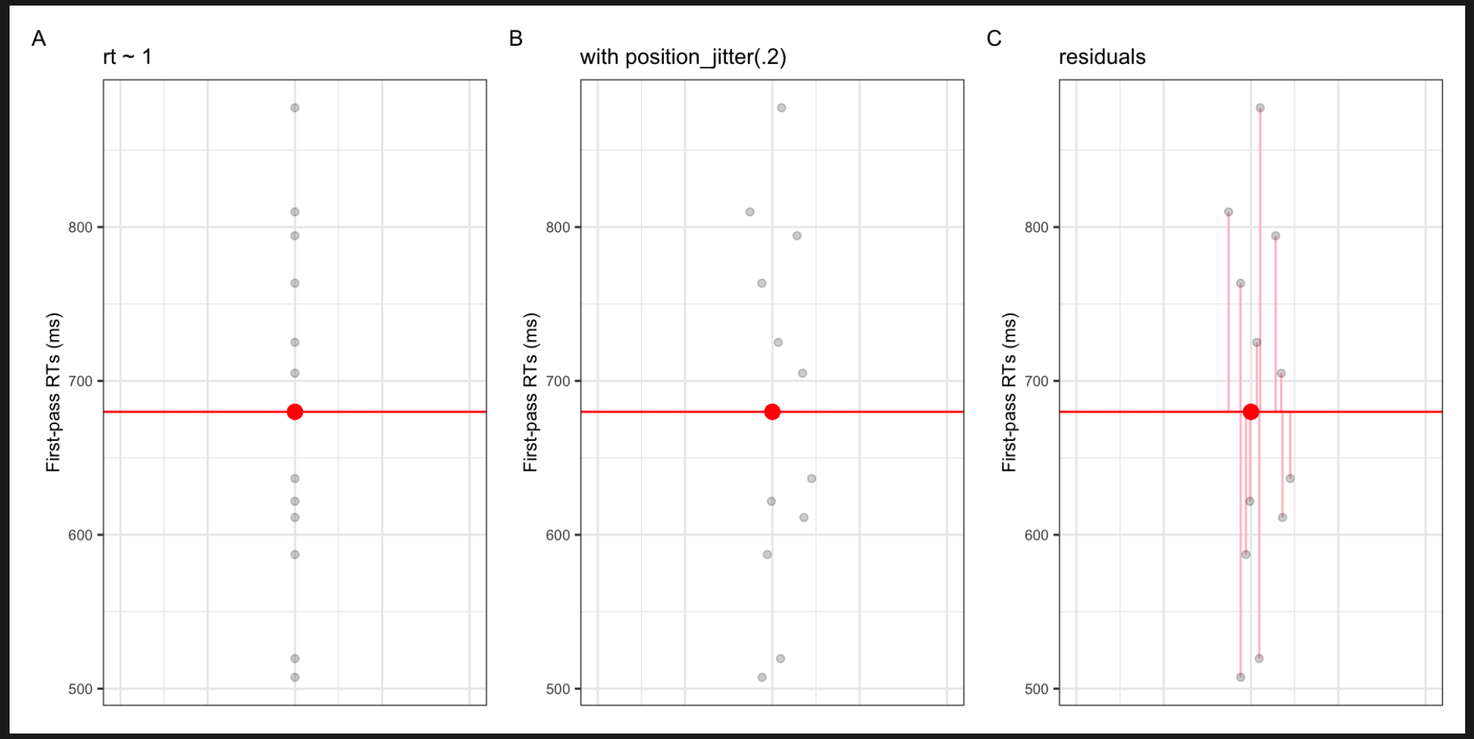


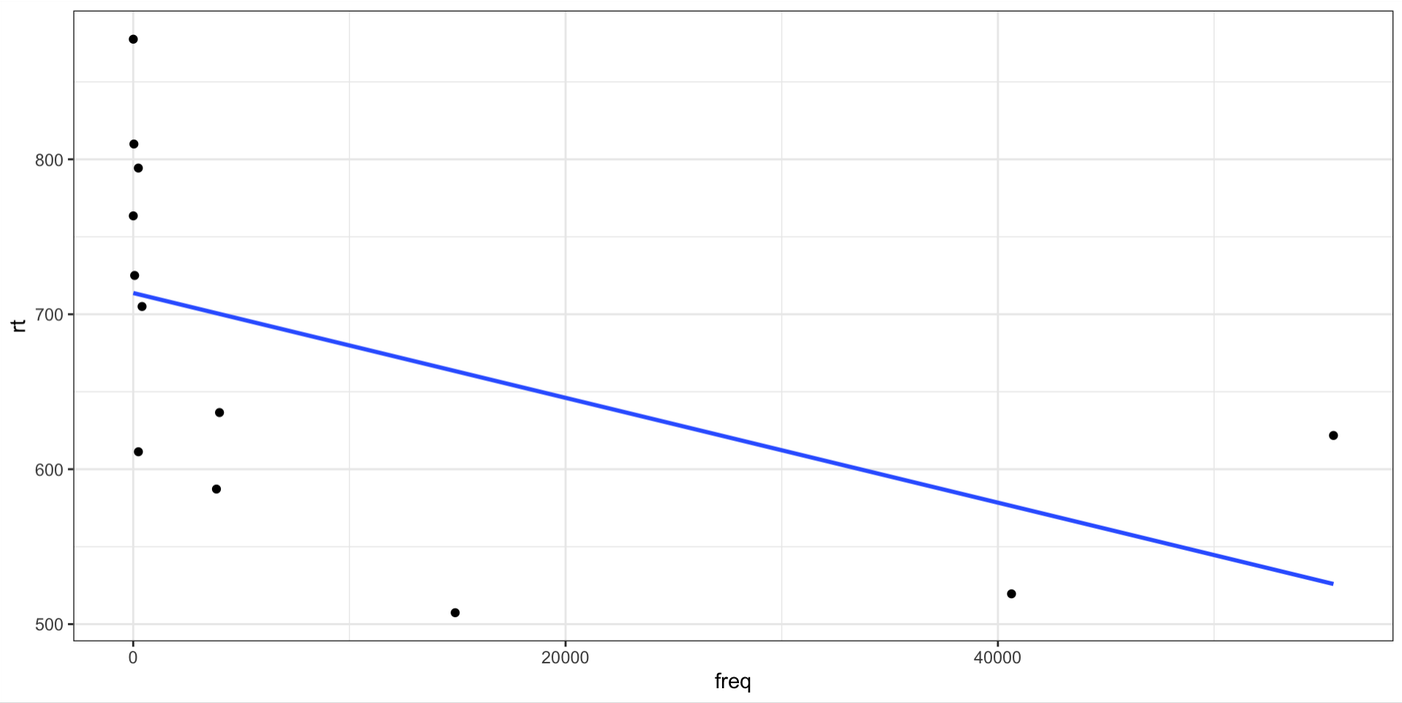
Figure 2: Visualisation of 'rt ~ 1': observed values (black) and mean (intercept; red). Residuals would be the distance from each black dot to the y-value of the read dot

Adding a fixed effect (slope)

- let's include a predictor, which will give us a *slope*
- the slope represents the change in y (DV: `rt`) when we move 1-unit along y (IV: `freq`)
  - it tells us the *effect* our IV has on the DV (although be weary of making causal inferences)

- let’s first plot the data again, but with a line:

```
df_freq |>
  ggplot() +
  aes(x = freq, y = rt) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



- what does this tell us?

Fit model (treatment contrasts)

```r
# fit simple linear model
fit_rt_freq <- lm(rt ~ freq, data = df_freq)
```

Model summary

```
1 summary(fit_rt_freq)
```

```
Call:
lm(formula = rt ~ freq, data = df_freq)

Residuals:
     Min       1Q   Median       3Q      Max
-155.947  -73.141    2.117   85.050  163.837

Coefficients:
             Estimate Std. Error t value     Pr(>|t|)
(Intercept) 713.706298  34.639105   20.60 0.0000000016 ***
freq         -0.003382   0.001699   -1.99       0.0746 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 104.6 on 10 degrees of freedom
```

Intercept

- our intercept is no longer the grand mean of first-pass reading times…what is it?

```
# print model intercept
coef(fit_rt_freq)['(Intercept)']
```

```
(Intercept)
   713.7063
```

```
# print data mean
mean(df_freq$rt)
```

```
[1] 679.9167
```

Slope

- the slope is -0.0033823
  - what does this correspond to?

```
1 # print slope
2 coef(fit_rt_freq)['freq']
```

```
        freq
-0.003382289
```

- change in y (our DV `rt`) for a 1-unit change in x (our IV: `freq`)
  - how we interpret this value depends on the measurement unit your variables are

Exploring the model

- we can extract information from our model and compare it to our observed data

```
# how many observed values did we enter into the model?
df_freq |>
  nrow()
```

```
[1] 12
```

```
# how many fitted values does our model have?
length(fitted(fit_rt_freq))
```

```
[1] 12
```

Exploring the model: residuals

```r
# what do our FITTED values look like?
head(fitted(fit_rt_freq))
```

```
       1        2        3        4        5        6
525.9148 576.2873 663.3271 700.2042 700.6845 712.3229
```

```r
# what do our OBSERVED values look like?
head(df_freq$rt)
```

```
[1] 621.77 519.56 507.38 636.56 587.18 705.00
```

```r
# what is the difference between the FITTED and OBSERVED values?
head(df_freq$rt) - head(fitted(fit_rt_freq))
```

```
         1          2          3          4          5          6
 95.855154  -56.727276 -155.947103  -63.644200 -113.504485   -7.322942
```

```r
# what are our RESIDUALS?
head(residuals(fit_rt_freq))
```

```
         1          2          3          4          5          6
 95.855154  -56.727276 -155.947103  -63.644200 -113.504485   -7.322942
```

Exploring the model: predicted values

- what were our coefficients?

```
coef(fit_rt_freq)
```

```
  (Intercept)          freq
713.706297951  -0.003382289
```

- what would be our predicted reaction time for a word with frequency of 0?

```
coef(fit_rt_freq)['(Intercept)'] + coef(fit_rt_freq)['freq'] * 0
```

```
(Intercept)
   713.7063
```

- ignore the `(Intercept)` label here, `R` just takes the first label when performing an operation on 2 vectors
- what is the predicted reaction time for a word with frequency score of `5000`?

```
coef(fit_rt_freq)['(Intercept)'] + coef(fit_rt_freq)['freq'] * 5000
```

```
(Intercept)
   696.7949
```

Model assumptions

- is our model a good fit for our data?
- linear regression makes assumptions about our data
  - these assumptions relate to the *residuals* of our model, not the raw data points themselves
- we'll focus on two assumptions for now:
  - assumptions of *normality* of the residuals
  - the constant *variance* of the residuals
- both assumptions are often diagnosed visually, so it takes some practice to learn what looks right

Normality

- a model's *residuals* (i.e., the difference between the *fitted* and *observed* values) should be approximately normally distributed
- Normality is typically visualised using a histogram (Figure 3 A) and/or a quantile-quantile (Q-Q) plot (Figure 3 B).

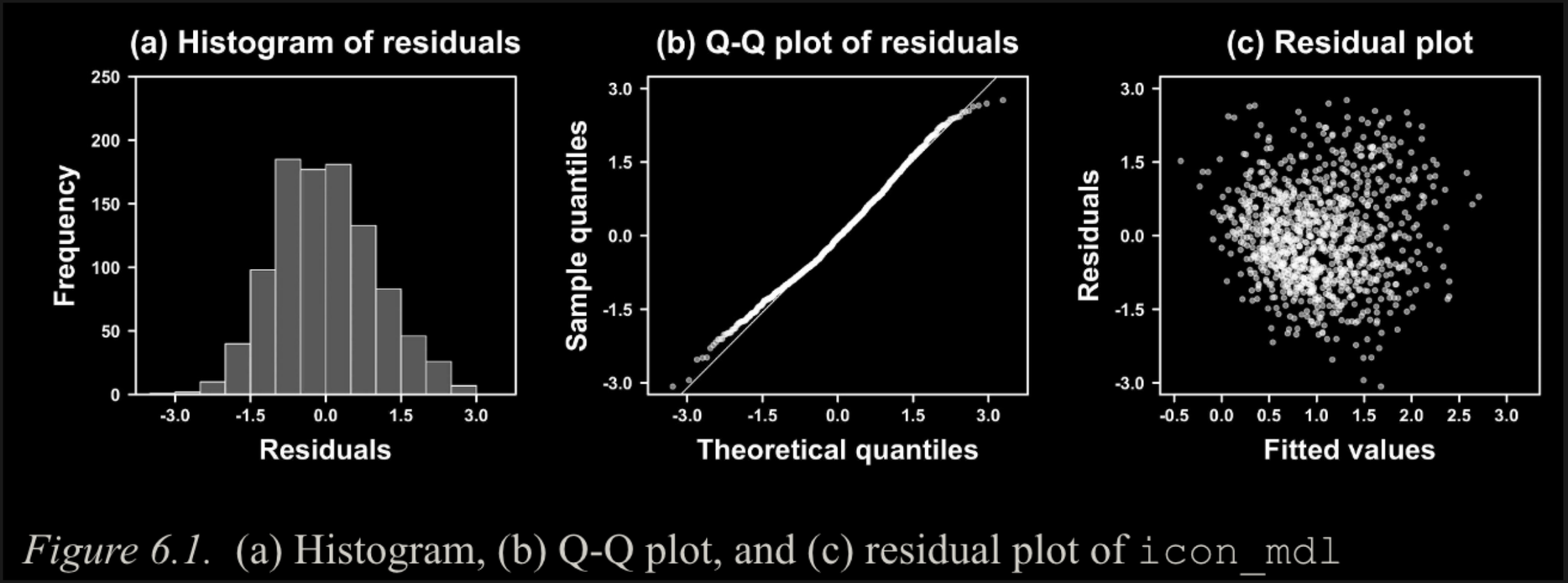


Figure 3: Image source: Winter (2019) (all rights reserved)

Constant variance

- if a model satisfies the constant variance assumption (also called *homoscedasticity*, or the absence of *heteroscedasticity*), the spread of residuals will be equal across the regression line
- typically visualised using a residual plot, which should look like a blob (Figure 3 C).

Visualising model assumptions

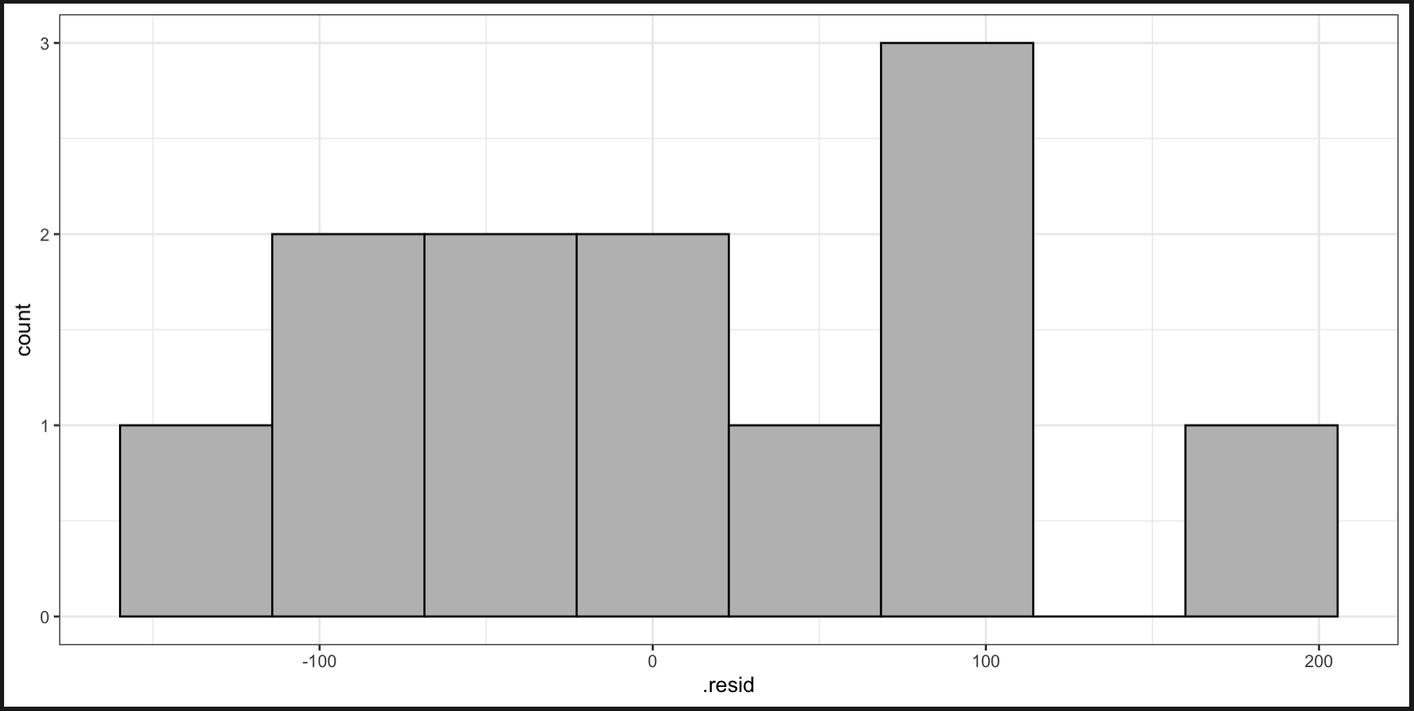
- let’s plot our residuals to assess whether our model satisfies the assumptions of normality and constant variance

Histogram

- let's use use the `augment()` function from `broom` to append model values to our original data frame, and then feed this into `ggplot()` from `ggplot2` (or even feed it into `hist()`).

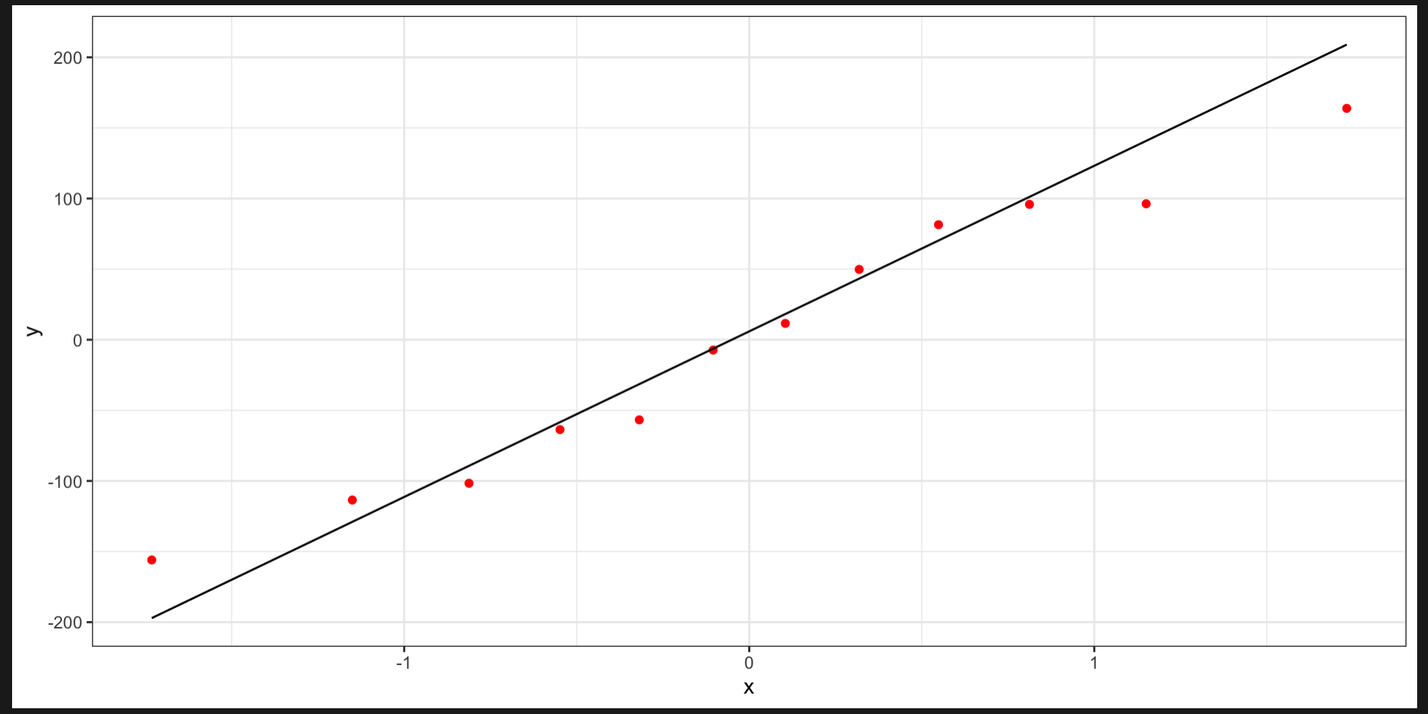
```
df_freq <- broom::augment(fit_rt_freq, df_freq)
```

```
# and create ggplot
df_freq |>
  ggplot() +
  aes(x = .resid) +
  geom_histogram(bins = 8, fill = "grey", colour = "black") +
  theme_bw()
```



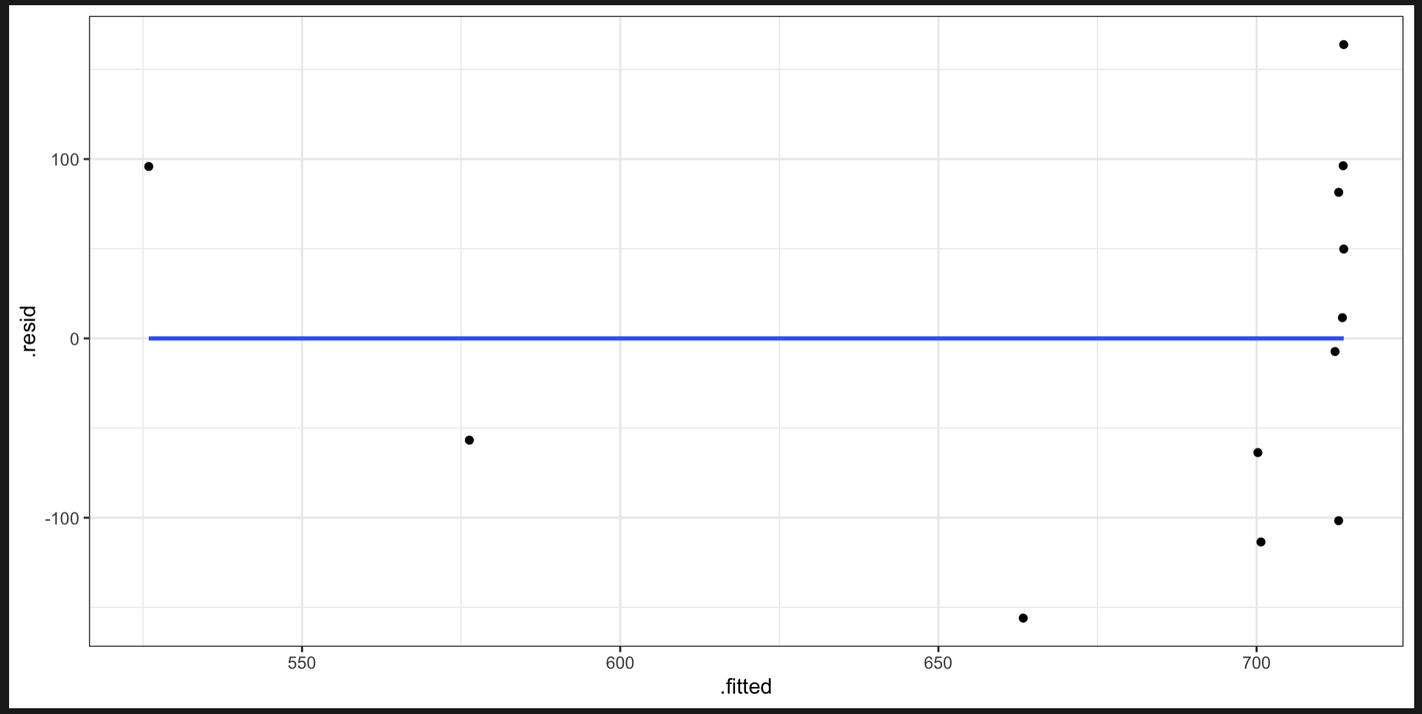
Q-Q plot

```
1 df_freq |>
2   ggplot() +
3   aes(sample = .resid) +
4   geom_qq(colour = "red") +
5   geom_qq_line()
```



Residual plot

```
1 df_freq |>
2   ggplot() +
3   aes(x = .fitted, y = .resid) +
4   geom_point() +
5   geom_smooth(method = "lm", se = F)
```



Reporting our model

- following Sonderegger (2023) (Section 4.6.1), we should report
  - our individual coefficients (coefficient estimate, standard error, test statistic (e.g., *t*-value) and corresponding *p*-value)
  - measures of model fit

Coefficients

- this can be written

> Higher-frequency words had longer reaction times, but this effect was not significant ($\hat{\beta}$ = -0.003; t = -1.99).

- and/or presented in a table

▶ Code

Coefficient	$\hat{\beta}$	SE	*t*	*p*
(Intercept)	713.706	34.639	20.6	< .001
freq	−0.003	0.002	−1.99	0.075

Model fit

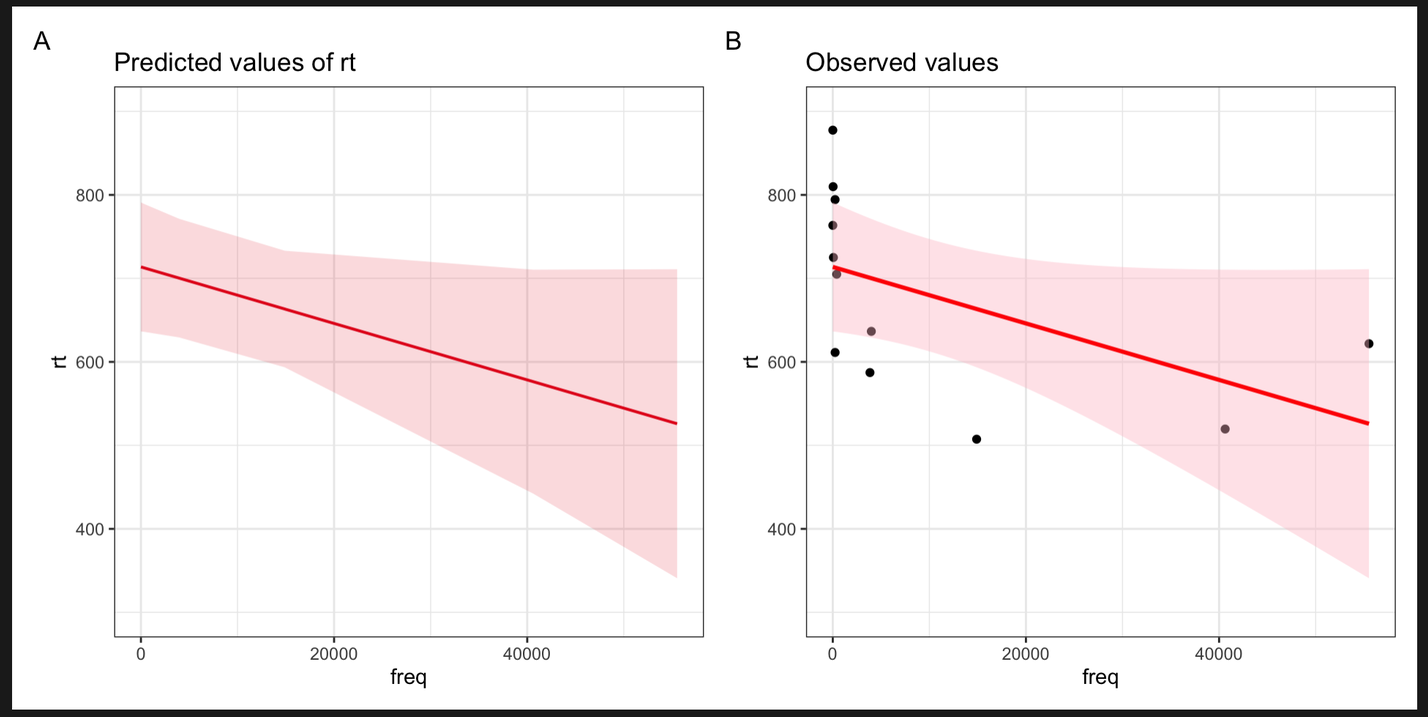
- R^2 is a measure of goodness of fit, representing the proportion of variance in the data that is described by our model
- AIC and BIC are also measures of goodness of fit (Akaike/Bayesian information criteria)
  - used to compare models
  - *lower* AIC/BIC values are better (when comparing models); think about temperatures: the colder the better
  - penalise for number of parameters in the model

▶ Code

R^2	sigma	df	AIC	BIC
0.284	104.595	1	149.469	150.924

- in addition, we should/could provide
  - visualisations (of model predictions or of the raw data)
  - confidence intervals for the coefficients
  - descriptive statistics where relevant (e.g., factorial designs)

▶ Code



Learning Objectives

Today we learned…

Task

Recycling the code above:

- run the model with `freq` as predictor
- extract the intercept
- extract the slope
- calculate the predicted reaction time for a word frequency of 462
- run assumption diagnostics
- assess model fit

Literaturverzeichnis

Sonderegger, M. (2023). *Regression Modeling for Linguistic Data*.

Wickham, H., Çetinkaya-Rundel, M., & Grolemund, G. (2023). *R for Data Science* (2nd ed.).

Winter, B. (2019). Statistics for Linguists: An Introduction Using R. In *Statistics for Linguists: An Introduction Using R*. Routledge. https://doi.org/10.4324/9781315165547