Regression Modelling with a Categorical Exposure

Corinne Riddell (Instructor: Tomer Altman)

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Learning objectives for today

- Learn how to generalize the simple regression model to the case when the x variable is categorical (and y is still continuous)
- Learn how to run these models in R

Example

- Calcium is an essential mineral that regulates the heart
- It is important for blood clotting and for building healthy bones
- The National Osteoporosis Foundation recommends a daily calcium intake of 1,000-1,200 mg/day for adult men and women
- Most adults do not get enough calcium in their diets and take supplements
- Unfortunately some of the supplements have side effects such as gastric distress
    - Difficult for some

- A study is designed to test whether there is a difference in mean daily calcium intake in adults:
    - ... with normal bone density
    - ... with osteopenia (a low bone density which may lead to osteoporosis)
    - ... with osteoporosis
- SRS of Adults 60 years of age with normal bone density, osteopenia and osteoporosis from hospital records
    - Invited to participate in the study
- Each participant's daily calcium intake is measured

The data

```
##    calcium_intake          type type_num
## 1            1200        normal        1
## 2            1000        normal        1
## 3             980        normal        1
## 4             900        normal        1
## 5             750        normal        1
## 6             800        normal        1
## 7            1000    osteopenia        2
## 8            1100    osteopenia        2
## 9             700    osteopenia        2
## 10            800    osteopenia        2
## 11            500    osteopenia        2
## 12            700    osteopenia        2
## 13            890  osteoporosis        3
## 14            650  osteoporosis        3
## 15           1100  osteoporosis        3
## 16            900  osteoporosis        3
## 17            400  osteoporosis        3
```

Refresher on `lm()`

- So far, we ran linear regression when both the outcome and explanatory variables were continuous
- We can also use linear regression when the outcome is continuous, but the explanatory variable is categorical
- In today's lecture we learn how to run and interpret these kinds of models

Check your understanding!

Running linear regression using a categorical explanatory variable

The first thing you want to do is check how the categorical (or factor) variable is encoded, and change the order of the categorical variable if you need to:

```
str(calcium_data)
```

```
## 'data.frame':    18 obs. of  3 variables:
##  $ calcium_intake: num  1200 1000 980 900 750 800 1000 1
##  $ type          : chr  "normal" "normal" "normal" "norm
##  $ type_num      : num  1 1 1 1 1 1 2 2 2 2 ...
```

- This shows us that type is encoded as "chr", which stands for character
- This means it isn't yet stored as a factor variable
- We want to have the variable as factors for including in the analysis

Making type a factor variable

This code updated the variable `type` to be stored as a factor variable. We overwrote the original variable, but you might want to rename it `type2` within `mutate` so you can compare the new and old variables if you're doing this for your first time!

```
calcium_data <- calcium_data %>% mutate(type = factor(type)
str(calcium_data)
```

```
## 'data.frame':    18 obs. of  3 variables:
##  $ calcium_intake: num  1200 1000 980 900 750 800 1000 1
##  $ type          : Factor w/ 3 levels "normal","osteope
##  $ type_num      : num  1 1 1 1 1 1 2 2 2 2 ...
```

Now we can see that type is a factor variable with three levels. It is sorted alphabetically, which for our purposes is okay because we would like "normal", the first category, to be the **referent** group.

Referent group: The group that the others will be compared to. Here, we will compare the osteopenia and osteoporosis groups to the normal group. Oftentimes, we set the referent group to be the

Defining a new referent group

If you wanted to change the referent group, you can use `fct_relevel()`, which we used in Part I of the course:

```
#makes osteoporosis the referent level:
calcium_data <- calcium_data %>%
  mutate(type_reordered = fct_relevel(type, "osteoporosis"))

levels(calcium_data$type_reordered)
```

```
## [1] "osteoporosis" "normal"       "osteopenia"
```

- We will run two regressions to see how their outputs differ:
  - One with `type` as the explanatory variable
  - One with `type_reordered` as the explanatory variable

Linear regression when x is categorical

Recall the form of the regression model when x and y are both continuous:

$$y = mean(Y|X = x) = a + bx$$

We can write this more precisely. The predicted value for individual i is represented by:

$$\hat{y}_i = \hat{a} + \hat{b}x_i$$

Suppose you have a categorical variable with three levels. Then the new form of the regression model is:

$$\hat{y}_i = \hat{a} + \hat{b}_1 \times I_{type=osteopenia} + \hat{b}_2 \times I_{type=osteoporosis}$$

- The $I_{type=osteopenia}$ is called an indicator function or dummy variable

Linear regression when x is categorical

General form of regression model for categorical x variable with three levels:

$$\hat{y}_i = \hat{a} + \hat{b}_1 \times I_{type=osteopenia} + \hat{b}_2 \times I_{type=osteoporosis}$$

- Normal bone density category
  - `category == osteopenia` is `FALSE`
  - `category == osteoporosis` is `FALSE`
  - Both indicator variables are zero
  - The regression model simplifies to:

$$\hat{y}_i = \hat{a}$$

- Osteopenia bone density category
  - `category == osteopenia` is `TRUE`
  - `category == osteoporosis` is `FALSE`
  - The regression model simplifies to:

$$\hat{y}_i = \hat{a} + \hat{b}_1$$

- The osteoporosis bone density category
  - `category == osteopenia` is `FALSE`
  - `category == osteoporosis` is `TRUE`
  - The regression model simplifies to:

$$\hat{y}_i = \hat{a} + \hat{b}_2$$

Running `lm()` on categorical x data

```
library(broom)
calcium_lm <- lm(calcium_intake ~ type, data = calcium_data

tidy(calcium_lm)
```

```
## # A tibble: 3 x 5
##   term               estimate std.error statistic      p.v
##   <chr>                 <dbl>     <dbl>     <dbl>        <
## 1 (Intercept)            938.      95.4      9.83 0.00000
## 2 typeosteopenia        -138.     135.      -1.02 0.322
## 3 typeosteoporosis      -223.     135.      -1.65 0.119
```

Interpretation of the output:

- The intercept is equal to 938.33. This is the average calcium intake for a person with normal density.
- The coefficient for "osteopenia" is equal to -138.33. This means that individuals with osteopenia had calcium intakes that are on average 138.33 lower than individuals with normal bone density.

Running `lm()` on categorical x data

The coefficient estimates based on the model agree with what we calculate by hand:

```
calcium_data %>%
  group_by(type) %>%
  summarise(mean = mean(calcium_intake))
```

```
## # A tibble: 3 x 2
##   type          mean
##   <fct>        <dbl>
## 1 normal        938.
## 2 osteopenia    800
## 3 osteoporosis  715
```

- Note that 800 is 138.33 lower than 938.33
- Note that 715 is 223.33 lower that 938.33

Tests and p-values based on the linear model

```r
library(broom)
calcium_lm <- lm(calcium_intake ~ type, data = calcium_data

tidy(calcium_lm)
```

```
## # A tibble: 3 x 5
##   term               estimate std.error statistic      p.v
##   <chr>                 <dbl>     <dbl>     <dbl>        <
## 1 (Intercept)            938.      95.4      9.83 0.00000
## 2 typeosteopenia        -138.     135.      -1.02 0.322
## 3 typeosteoporosis      -223.     135.      -1.65 0.119
```

- We can also interpret these *p*-values. What is the null hypothesis?
- For the second row, the null hypothesis is that the regression coefficient for osteopenia is equal to 0. That is, the mean calcium intake for patients with osteopenia is equal to the mean for those with normal bone density
- $p = 0.32$, so we do not reject the null hypothesis

Get 95% confidence intervals using the predict function

We can use R code to calculate the 95% confidence intervals for the means:

```
#make a tiny data frame storing the three categorical leve
newdata = data.frame(type=c("normal", "osteopenia", "osteop

#predict calcium intake for each row in newdata, i.e., for
predictions <- data.frame(predict(calcium_lm, newdata, inte

#append another row to the data frame with the category la
predictions$type <- c("normal", "osteopenia", "osteoporosis

predictions
```

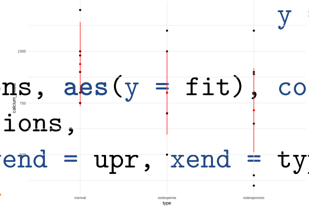
```
##        fit      lwr       upr         type
## 1 938.3333 734.9026 1141.7641       normal
## 2 800.0000 596.5693 1003.4307   osteopenia
## 3 715.0000 511.5693  918.4307 osteoporosis
```

Plot the observed data, the predicted means and their 95% CIs

```r
lm.cat.plot <- ggplot(data =                                    y = calcium_i

  geom_point() +
  geom_point(data = predictions, aes(y = fit), col = "red")
  geom_segment(data = predictions,
               aes(y = lwr, yend = upr, xend = type),
               col = "red") +
  theme_minimal()
```

```r
lm.cat.plot
```



- What does this remind you of?
- It looks like the plots we made when we did ANOVA!

Run the model again using the `type_reordered` as the exposure variable

- Recall that `type_reordered` contains the same factor variable but with osteoporosis as the reference group

```
levels(calcium_data$type_reordered)
```

```
## [1] "osteoporosis" "normal"       "osteopenia"
```

- Write the regression equation for the model with `type_reordered` as the `x` variable
- Before running the linear model, how do you expect the regression output to change?

Regression equation

$$\hat{y}_i = \hat{a} + \hat{b}_1 \times I_{type=normal} + \hat{b}_2 \times I_{type=osteopenia}$$

- a (the intercept) will be the average for patients with osteoporosis
- $a + b_1$ will be the average for patients with normal bone density
  - implying that b_1 will be the additional calcium intake for patients with normal bone density
- $a + b_2$ will be the average for patients with osteopenia
  - implying that b_2 will be the additional calcium intake for patients with osteopenia

The model

```
calcium_lm2 <- lm(calcium_intake ~ type_reordered, data = c

tidy(calcium_lm2)
```

```
## # A tibble: 3 x 5
##   term                        estimate std.error statistic
##   <chr>                          <dbl>     <dbl>     <dbl>
## 1 (Intercept)                     715.      95.4      7.49
## 2 type_reorderednormal            223.     135.       1.65
## 3 type_reorderedosteopenia         85      135.       0.630
```

- Can you interpret the intercept and other coefficients in this model?
- What is the average calcium intake for someone with osteopenia?
  - Is it lower or higher than someone with normal bone density?
  - By how much?

Another model: Mistaking categorical data for continuous data

- Recall that `type_num` is a numeric way of storing the categorical data stored in `type`

```
str(calcium_data$type_num)
```

```
##  num [1:18] 1 1 1 1 1 1 2 2 2 2 ...
```

- What happens if we run the regression on `type_num`?

Another model: Mistaking categorical data for continuous data

Run the regression on type_num:

```
calcium_lm3 <- lm(calcium_intake ~ type_num, data = calcium_

tidy(calcium_lm3)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic   p.value
##   <chr>          <dbl>     <dbl>     <dbl>     <dbl>
## 1 (Intercept)    1041.     141.       7.36 0.00000160
## 2 type_num       -112.      65.5     -1.71 0.107
```

- Notice that there is only one coefficient for type_num, but we were expecting two coefficients – one for the two non-referent levels of type.
  - What happened?
- Answer: R interpreted type_num as a continuous, not a categorical, variable. It estimated a regression slope term using $y = a + bx$, which is not what we want.
- This linear model makes the assumption that the increase in calcium intake

Changing a variable type from continuous to categorical

- If your factor variable was encoded numerically (like `type_num` in this example), R will interpret it as a continuous number and run simple linear regression on the underlying numbers. This is wrong, but can happen by mistake if you don't check.
- In this case you need to change the storage type using `your_data %>% mutate(var_categorical = as.factor(var_numeric, levels = c(<<YOUR LEVELS>>), labels = c(<<YOUR LABELS>>)))`
- In the code below, we update the storage type for `type_num` and store as a new categorical variable called `type_cat_ii`:

```
calcium_data <- calcium_data %>%
  mutate(type_cat_ii = factor(type_num, levels = c(1, 2, 3
                              labels = c("normal", "osteope

str(calcium_data)
```

```
## 'data.frame':    18 obs. of  5 variables:
##  $ calcium_intake: num  1200 1000 980 900 750 800 1000 1
```

Re-run the model

Re-run the model on `type_cat_ii`:

```
calcium_lm4 <- lm(calcium_intake ~ type_cat_ii, data = calc

tidy(calcium_lm4)
```

```
## # A tibble: 3 x 5
##   term                      estimate std.error statistic
##   <chr>                        <dbl>     <dbl>     <dbl>
## 1 (Intercept)                   938.      95.4      9.83 0
## 2 type_cat_iiosteopenia        -138.     135.      -1.02 0
## 3 type_cat_iiosteoporosis      -223.     135.      -1.65 0
```

- This looks better (we have two coefficients)

Recap

- We now know how to write linear models when y is continuous and x is either continuous or categorical
- When x is categorical we expect $k - 1$ regression coefficients, where k is the number of levels
- The regression coefficients correspond to the average value of y for each category, minus the intercept a
- When we have categorical data, it is important to make sure `R` knows it is categorical (by using `str()`) and setting the appropriate referent group
- Hypothesis tests as how much each group differs from the referent group

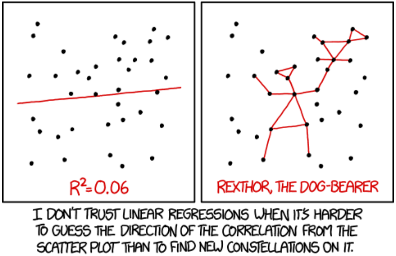
Check your understanding!

Future Statistics Classes

- We've only dealt with one x variable at a time. In future stat courses, you will learn how to model multiple x variables using multiple linear regression.
- This is important for prediction models (to get the best prediction you include every x variable that helps predict y)
- This is also important for causal models
- For these models, you are interested in the causal effect of a specific explanatory variable (e.g., x_1), but include other explanatory variables (e.g., x_2) to control for bias, such as confounding variables, and model interactions

The End!

- This lecture marks the end of the course material for PH 142
- Next lecture we will review
- Congratulations on making it this far!



https://xkcd.com/1725