Statistical Models in R

Applied Statistics and Data Science Group
with contributions from Yue Liu and Kim Dill-McFarland
U. of British Columbia

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```
set.seed(567)
```

Overview

In this workshop, we introduce various types of regression models and how they are implemented in R. We cover linear regression, ANOVA, ANCOVA, and mixed effects models for continuous response data, logistic regression binary response data, as well as Poisson and Negative Binomial regression for count response data.

You will learn:

- the different functions used to build a statistical model in R,
- the assumptions behind the different models,
- how the formula object in R is used to specify all the model terms,
- how to interpret the main effects and interaction terms in a model,
- various experimental design concepts that help maximize power.

This is an intermediate workshop series that assumes prior R experience including RStudio projects and the R tidyverse.

All code presented in this workshop is contained in the "stats_models_main.R" R script file. R script files are the primary way in which R facilitates reproducible research. You can follow along with the workshop by selecting the relevant line(s) of code and pressing ctrl+enter on Windows, cmd+enter on MacOS, or using the "Run" button in the upper right of your script window to execute it. There are also dedicated spaces in the R script for you to work on the given exercises which are indicated in the markdown with the RStudio logo  .

Prior to the workshop

Setup Instructions

Please come to the workshop with your laptop setup with the required software and data files as described in our setup instructions.

Data description

Unlike our other workshops, 'Statistical Models' utilizes several data sets in order to accurately demonstrate the use of statistical tests. You will find more information on each of these data sets in its relevant section(s) within the notes below.

Getting started

Making an RStudio Project

Projects allow you to divide your work into self-contained contexts.

Let's create a project to work in.

In the top-right corner of your RStudio window, click the "Project: (None)" button to show the projects drop-down menu. Select "New Project…" > "New Directory" > "New Project." Under directory name, input "statistical_models" and choose a parent directory to contain this project on your computer.

Installing and loading packages

At the beginning of every R script, you should have a dedicated space for loading R packages. R packages allow any R user to code reproducible functions and share them with the R community. Packages exist for anything ranging from microbial ecology to complex graphics to multivariate modeling and beyond.

In this workshop, we will use many different packages. Here, we load the necessary packages which *must already be installed* (see setup instructions for details).

```
# Suite of packages for data manipulation and visualization
library(tidyverse)
# puts output of statistical models in a nice data frame
library(broom)
# Split, process, and recombine data
library(plyr)
# Fit linear and generalized linear mixed-effects models
library(lme4)
# various functions, including Anova
library(car)
# least-square means
library(lsmeans)
## generalized linear model fitter
## Also has quine data  set
library(MASS)

# Data set libraries
## Fruitfly longevity, size, and sexual activity
library(faraway)
## Life expectancy, GDP and population by country
library(gapminder)
## A variety of data sets; we will use the plasma data
library(HSAUR3)
```

Experiment design

Key Aspects of experimental design include:

- Balanced designs
- Blocking factors and random effects
- Randomization

Balanced designs

- A balanced design has equal (or roughly equal) number of observations for each group
- Balance eliminates confounding factors and increases power

Blocking factors and random effects

- Blocking factors and random effects should be used/recorded to control sources of variation that exist but are otherwise not of interest

Randomization

- Subjects should be randomized to groups to help balance the unobserved factors in the experiment.
- Randomization should be done in a way to keep the controlled and observational factors (blocking factors and random effects) balanced.

Exercise: Experimental design


Exercise.

1. Discuss with following in pairs
   - What are some advantages and disadvantages of using a balanced experimental design?
   - Give an example of when a balanced design might not be possible.
   - There are 3 undergraduates assisting you with your experiment that assess the addiction potential of Saturday morning cartoons in rats. You need to run the experiments every Saturday, but one of your undergraduate assistants can only help out 2 Saturdays a month, while the other two undergraduate assistants can be there every Saturday. Rat behaviour is sensitive to handler. What should you do? (source)
2. *True or false.* A completely randomized design offers no control for lurking variables (a variable that is not included as an explanatory or response variable in the analysis).

Analysis of Variance (ANOVA)

ANOVA is used when you have data with:

- a quantitative response/dependent variable (Y) such as:
  - height
  - salary
  - number of offspring
- one or more categorical explanatory/independent variable(s) (X's) such as:
  - eye color
  - sex
  - genotype at a given locus

For example, you would use ANOVA to address questions like:

1. Does diet has an effect on weight gain?
   - response variable = weight gain (*e.g.* kg)
   - explanatory variable = type of diet (*e.g.* low vs. medium vs. high sugar)
2. Does the type sexual relationship practiced influence the fitness of male Red-winged Blackbirds?
   - response variable = fitness of male bird (*e.g.* # eggs laid)
   - explanatory variable = sexual relationship (*e.g.* monagamy vs. polygamy)

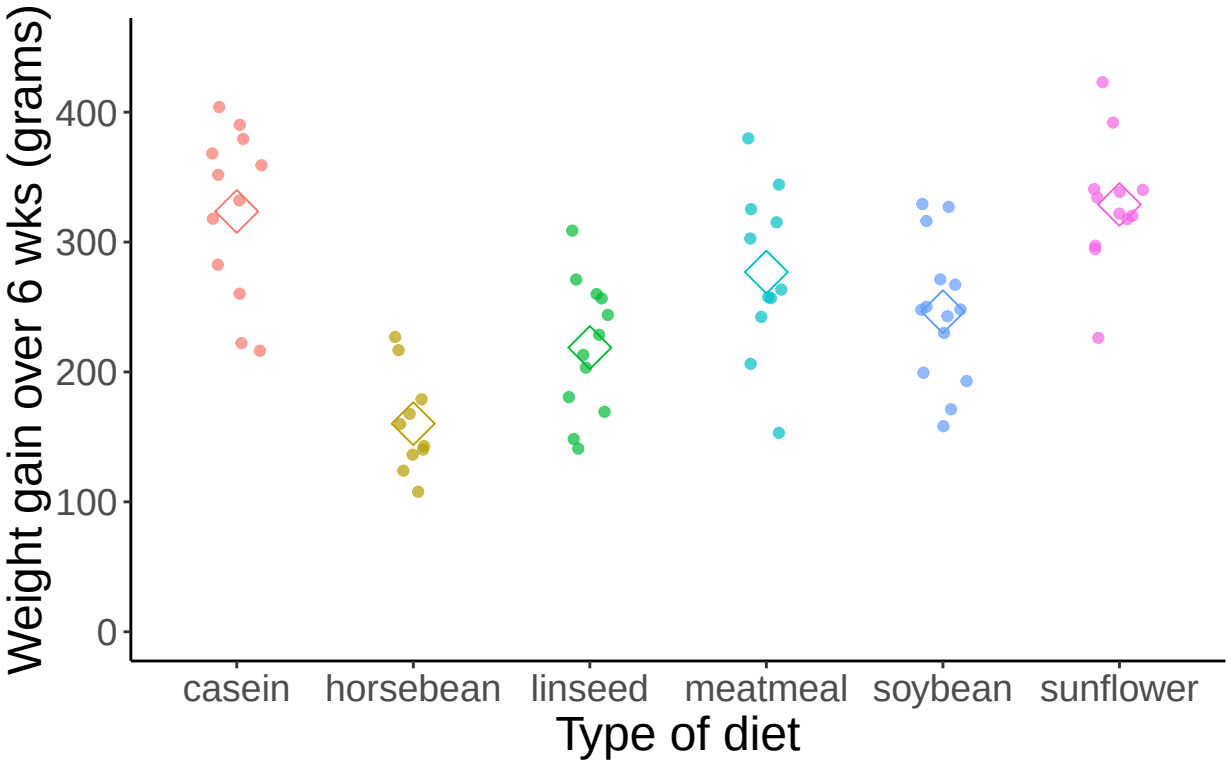
Key assumptions

- ANOVA is robust to the non-normality of sample data

- Balanced ANOVA (equal sample size between groups) is robust to unequal variance
- ANOVA is sensitive to sample independence

Example case

Let's explore an example case when we would use ANOVA. Here, we want to investigate if diet has an effect on chick weight. The data we have (from `chickwts` in R), look like so.



Thus, our variables are:

- response variable == chick weight (grams)
- explanatory variable == type of diet (6 levels)

And our hypotheses for an ANOVA are:

Null Hypothesis, H_0: $\mu_{caesin} = \mu_{horsebean} = \mu_{linseed} = \mu_{meatmeal} = \mu_{soybean} = \mu_{sunflower}$
Alternative Hypothesis, H_A: at least one group's population mean differs from that of the other groups

The gist of the math

When we run an ANOVA on these data, we calculate a test statistic (F-statistic) that compares the **between** group variation with the **within** group variation.

$$F = MSB/MSW$$

where MSB = Mean Square Between and MSW = Mean Square Within

Essentially, if there is greater variation between the groups than within the groups we will get a large test statistic value (and correspondingly, a small p-value) and reject that null hypothesis (H_0: population means of all groups are equal).

If you want to delve into ANOVA in more depth, checkout this video tutorial.

1-way ANOVA with 2 groups

Now let's run some ANOVAs on real data!

There are two perfectly acceptable statistical tests in R that we could apply to compare data in 2 groups. The first, which you may be very familiar with, is the *t*-test. The second is the topic of our lesson today, Analysis of Variance (or ANOVA). Interestingly, the *t*-test is really a special case of ANOVA that can be used when only comparing 2 groups. ANOVA is a more generalizable test that we will later see can be used with > 2 groups as well as more than one factor/category column.

Load and explore the data

The first experiment we are going to analyze was done to address the question of whether sexual activity effects the longevity of male fruit flies. To assess this, we are going to use a modified version of the `fruitfly` data from the `faraway` R package.

Our hypothesis for this experiment are as follows:

Null Hypothesis, H_0: Sexual activity has no effect on the population mean longevity of male fruit flies.
Alternative Hypothesis, H_A: Sexual activity has an effect on population mean longevity of male fruit flies.

Let's now load the fruit fly data from the `faraway` package, and create our categorical groups from the numerical variables. *If you are unfamiliar with the functions below, checkout our R tidyverse workshop.*

```
# Read in data from faraway package
data("fruitfly")

# Create categorical groups and subset data
fruitfly_2groups <- fruitfly %>%
  # Convert factors to character variables
  mutate_if(is.factor, as.character) %>%
  # Create 2-level activity variable
  mutate(activity = ifelse(activity %in% c("isolated", "one", "many"), "no", "yes")) %>%
  # Create 2-level size variable (for later ANOVA)
  mutate(thorax = ifelse(thorax <= 0.8, "short", "long")) %>%
  # Subset to equal group sizes for activity and size
  group_by(activity, thorax) %>%
  sample_n(20)
```

When we explore these data (ignoring thorax data for now)...

```
# get number of rows and columns
dim(fruitfly_2groups)
```

```
## [1] 80  3
```

```
# view first 6 records of data
head(fruitfly_2groups)
```

```
## # A tibble: 6 x 3
## # Groups:   activity, thorax [1]
##   thorax longevity activity
##   <chr>      <int> <chr>
## 1 long          70 no
```

```
## 2 long          75 no
## 3 long          96 no
## 4 long          77 no
## 5 long          81 no
## 6 long          77 no
```

```
# see summary of data
summary(fruitfly_2groups)
```

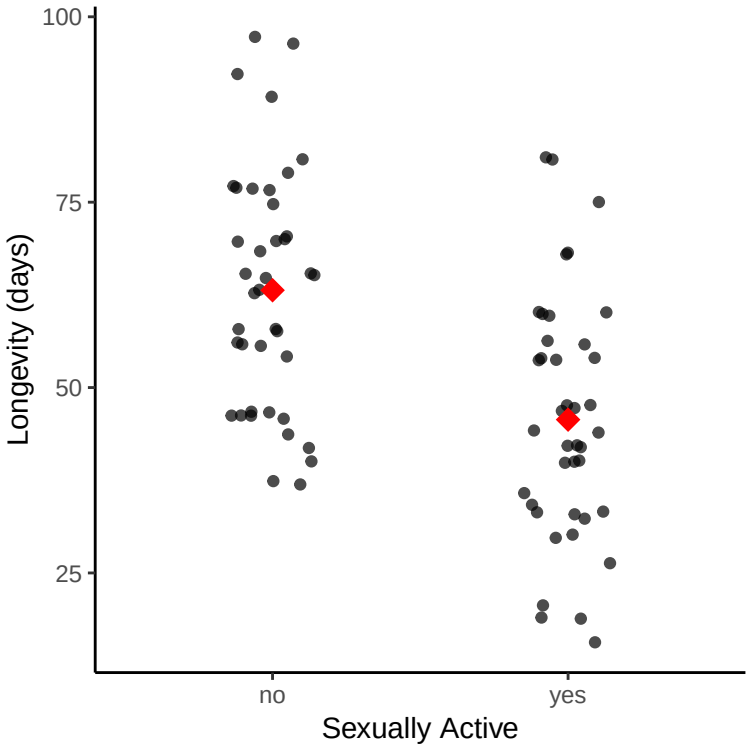
```
##     thorax            longevity      activity
##  Length:80          Min.   :16.0   Length:80
##  Class :character   1st Qu.:42.0   Class :character
##  Mode  :character   Median :54.0   Mode  :character
##                     Mean   :54.4
##                     3rd Qu.:68.0
##                     Max.   :97.0
```

We see that there are 2 columns of interest, `longevity` and `activity`. `longevity` is a quantitative variable, and is our response/dependent variable for this experiment. `activity`, on the other hand, is a categorical variable, and is our single explanatory/independent variable for this experiment. There are 2 levels to the `activity` variable, `yes` and `no`.

Let's visualize these data to get some intuition as to whether or not there is a difference in longevity between the male flies that are sexually active and those that are not.

Given that our sample sizes are not too large, the most informative plot we can make are strip plots. We will also add the mean to these:

```
# plot raw data points for each group as a transparent grey/black point
# overlay mean as a red diamond
ggplot(fruitfly_2groups, aes(x = activity, y = longevity)) +
  geom_jitter(position = position_jitter(0.15),
              alpha = 0.7) +
  stat_summary(fun.y = mean,
               geom = "point",
               shape = 18,
               size = 4,
               color="red") +
  xlab("Sexually Active") +
  ylab("Longevity (days)")
```



We can see that there is a difference between the mean of these two **samples**, but what can we say/infer about the **population** means of these two groups? To say anything meaningful from a statistical standpoint, we need to perform a statistical test that will guide us in rejecting, or failing to reject, our null hypothesis (*i.e* Sexual activity has no effect on the population mean longevity of male fruit flies).

Formula notation in R

To perform an ANOVA in R, we need to understand R's formula notation, as this is the first argument we give to the ANOVA function (`aov`). The formula notation starts with providing the response variable, then a special character, `~`, which can be read as "modeled as", and then the explanatory/independent variable(s). Thus, the formula notation for this experiment is:

```
longevity ~ activity
```

The formula notation can get more complex such as including additional explanatory/independent variables or interaction terms. We will introduce these are we attempt more complex analyses later on.

ANOVA in R

To do an ANOVA in R, we will use the `aov` function. As stated above, the first argument to this is the formula for the experiment/model, and the second argument we must provide is the name of the variable holding our data, here `fruitfly_2groups`.

The `aov` function returns us a "model" object, and we need to use another function to see the results of the analysis. I suggest using the `tidy` function from the `broom` R package as it returns the results in a nice data frame, that is easy to do further work with. Another, more traditional function to access these data is the `summary` function, but again, I don't recommend this as accessing the individual numbers from the output of `aov` from this model is a bit trickier.

```r
# create an ANOVA "model" object
fruitfly_2groups_model <- aov(longevity ~ activity,
                              data = fruitfly_2groups)

# view output of aov() as a nice dataframe using tidy() from the broom package
tidy(fruitfly_2groups_model)
```

```
## # A tibble: 2 x 6
##   term         df  sumsq meansq statistic     p.value
##   <chr>     <dbl>  <dbl>  <dbl>     <dbl>       <dbl>
## 1 activity      1  6090.  6090.      23.0  0.00000768
## 2 Residuals    78 20671.   265.       NA   NA
```

So, what does this output mean? The most important result in regards to rejecting (or failing to reject) our null hypothesis is the p-value. In this simple one-way ANOVA, we have a single p-value which has a very small value of 7.6845793×10^{-6}. Given that this is much much smaller than the commonly used threshold for rejecting the null hypothesis, $p < 0.05$, we can reject our null hypothesis that sexual activity has no effect on the population mean longevity of male fruit flies, and accept the alternative hypothesis that sexual activity **does** has an effect on population mean longevity of male fruit flies.

Exercise: 1-way ANOVA


Exercise.

1. Using ANOVA, test if fruit fly longevity is effected by size (as measured by thorax length). What are your null and alternate hypotheses? What can you conclude from these results?

1-way ANOVA with $>$ 2 groups

As mentioned at the start of this section, an ANOVA can be used when there are more than 2 levels in your categorical explanatory/independent variable (unlike a *t*-test). For example, we will consider the following case:

We are still interested in whether sexual activity effects the longevity of male fruit flies but want to understand this at a finer level (**e.g.** does the amount of sexual activity matter?). Thus, in this experiment, there are 3 categories for sexual `activity`. Specifically, males were kept:

1. `none` - alone
2. `low` - with a new virgin fruit fly every day
3. `high` - with a new set of eight virgin fruit flies every day

So, for this case, our hypotheses are as follows:

Null Hypothesis, H_0: $\mu_{isolated} = \mu_{low} = \mu_{high}$
Alternative Hypothesis, H_A: at least one group's population mean differs from that of the other groups

Reload and explore the data

Using the same original fruit fly data, now we create our 3-level activity group.

```r
# Create categorical groups and subset data
fruitfly_3groups <- fruitfly %>%
  # Convert factors to character variables
  mutate_if(is.factor, as.character) %>%
```

```
  # Create 3-level activity variable
  mutate(activity = ifelse(activity %in% c("isolated", "one", "many"), "none", activity)) %>%
  # Subset to equal group sizes for activity
  group_by(activity) %>%
  sample_n(25)
```

Let's explore these data (again, ignore the thorax variable).

```
# get number of rows and columns
dim(fruitfly_3groups)
```

```
## [1] 75  3
```

```
# view first 6 records of data
head(fruitfly_3groups)
```

```
## # A tibble: 6 x 3
## # Groups:   activity [1]
##   thorax longevity activity
##    <dbl>     <int> <chr>
## 1   0.84        47 high
## 2   0.76        42 high
## 3   0.78        33 high
## 4   0.88        60 high
## 5   0.8         26 high
## 6   0.88        54 high
```

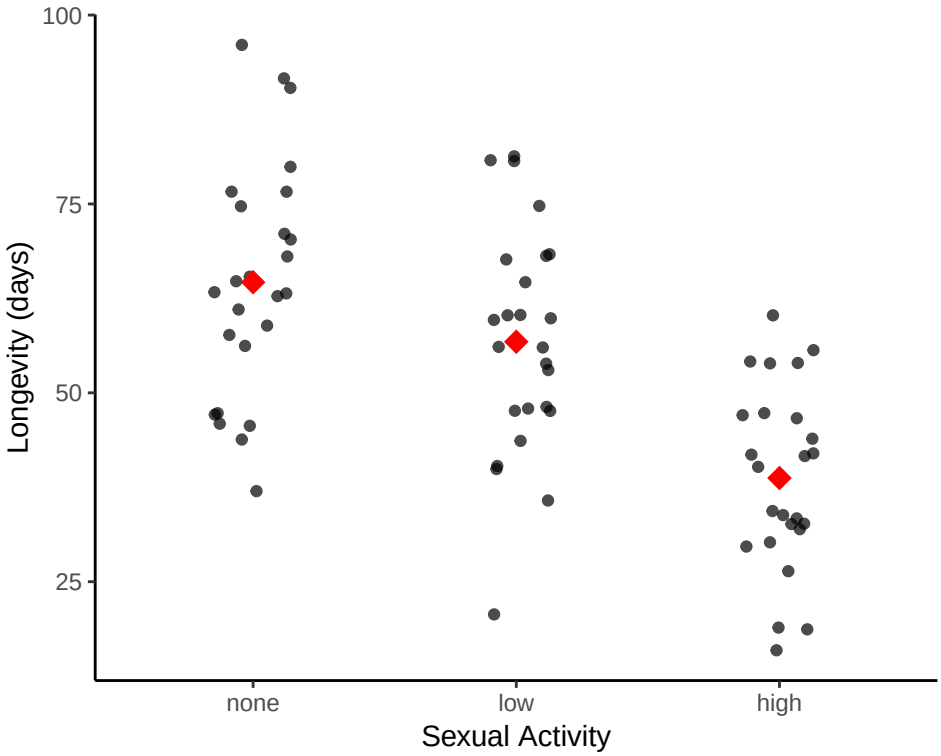
```
# see summary of data
summary(fruitfly_3groups)
```

```
##      thorax         longevity       activity
##  Min.   :0.6400   Min.   :16.00   Length:75
##  1st Qu.:0.7700   1st Qu.:42.00   Class :character
##  Median :0.8400   Median :54.00   Mode  :character
##  Mean   :0.8205   Mean   :53.37
##  3rd Qu.:0.8800   3rd Qu.:65.00
##  Max.   :0.9200   Max.   :96.00
```

And, again as a good practice, let's visualize the data before we perform our statistical analysis.

```
# re-order factors to make them show up how we would like them on the plot
# instead of alphabetically (default R behaviour)
fruitfly_3groups$activity <- factor(fruitfly_3groups$activity,
                                    levels = c("none","low","high"))

# plot raw data points for each group as a transparent grey/black point
# overlay mean as a red diamond
ggplot(fruitfly_3groups, aes(x = activity, y = longevity)) +
  geom_jitter(position = position_jitter(0.15),
              alpha = 0.7) +
  stat_summary(fun.y = mean,
               geom = "point",
               shape = 18,
               size = 4,
               color = "red") +
  xlab("Sexual Activity") +
  ylab("Longevity (days)")
```



So, it looks the sample means of longevity for both low and high activity are lower than the sample means of the isolated male fruit fly. Are these differences in the sample means indicating that there are differences in the true population means between any of these groups? Again we turn to ANOVA to answer this:

```
# create an ANOVA "model" object
fruitfly_3groups_model <- aov(longevity ~ activity,
                              data = fruitfly_3groups)

# view output of aov() as a nice dataframe using tidy() from the broom package
tidy(fruitfly_3groups_model)
```

```
## # A tibble: 2 x 6
##   term         df  sumsq meansq statistic       p.value
##   <chr>     <dbl>  <dbl>  <dbl>     <dbl>         <dbl>
## 1 activity      2  8828.  4414.      21.7  0.0000000422
## 2 Residuals    72 14647.   203.       NA   NA
```

So, what does this output mean? Similar to a 1-way, 2 group ANOVA, we look at the p-value to determine if we reject (or fail to reject) our null hypothesis. In this case, we have a single p-value which has a very small value of 4.2186266×10^{-8}. Given that this is much much smaller than the commonly used threshold for rejecting the null hypothesis, $p < 0.05$, we can reject our null hypothesis that all the population mean for longevity of male fruit flies is equal between all groups, and accept the alternative hypothesis that **at least** one group's population mean differs from that of the other groups.

But which one(s) differ?

Assess which groups differ

This is something ANOVA alone cannot tell us. To answer this, we need to either perform pair-wise *t*-tests (followed by an adjustment or correction for multiple comparisons, such as a Bonferroni correction, or False

Discovery Rate) OR follow the ANOVA with a contrast-test, such as Tukey's honestly significant difference (HSD) test. We'll do both here, and show that we get similar results:

```
# pairwise t-tests to observe group differences
tidy(pairwise.t.test(fruitfly_3groups$longevity,
                fruitfly_3groups$activity,
                p.adjust.method = "bonferroni",
                pool.sd = TRUE,
                paired = FALSE))
```

```
## # A tibble: 3 x 3
##   group1 group2      p.value
##   <chr>  <chr>         <dbl>
## 1 low    none   0.164
## 2 high   none   0.0000000374
## 3 high   low    0.0000850
```

```
# Tukey's HSD test to observe group differences
tidy(TukeyHSD(fruitfly_3groups_model, "activity"))
```

```
## # A tibble: 3 x 6
##   term     comparison estimate conf.low conf.high  adj.p.value
##   <chr>    <chr>         <dbl>    <dbl>     <dbl>        <dbl>
## 1 activity low-none      -7.88    -17.5      1.77 0.131
## 2 activity high-none    -25.9     -35.6    -16.3  0.0000000372
## 3 activity high-low     -18.0     -27.7     -8.39 0.0000834
```

From both of these multiple comparison tests, we see that there is no significant difference between the population mean longevity of male fruit flies who had no or little sexual activity. However, high sexual activity does appear to matter, as the population mean longevity of male fruit flies who had high sexual activity is significantly different from that of male flies who had either no or low sexual activity.

2-way ANOVA with 2 groups

Let's continue to add complexity to our ANOVA model. In this experiment, we not only interested in how sexual activity might effect longevity; we are also interested in body size (assessed via thorax length). We do this because the literature indicates body size affects fruit fly longevity. Thus, now we have two categories/explanatory variables to look at sexual activity (back to our first version with levels `no` and `yes`) and thorax length (with levels `short` and `long`).

For this experiment, we have two sets of null and alternative hypotheses:

Hypotheses for sexual activity

Null Hypothesis, H_0: $\mu_{No} = \mu_{Yes}$
Alternative Hypothesis, H_A: $\mu_{No} \neq \mu_{Yes}$

Hypotheses for thorax length

Null Hypothesis, H_0: $\mu_{short} = \mu_{long}$
Alternative Hypothesis, H_A: $\mu_{short} \neq \mu_{long}$

Now that we have our case setup, let's re-look at our 2 level data but now notice the thorax information.

```
# get number of rows and columns
dim(fruitfly_2groups)
```

```
## [1] 80  3
```

```r
# view first 6 records of data
head(fruitfly_2groups)
```

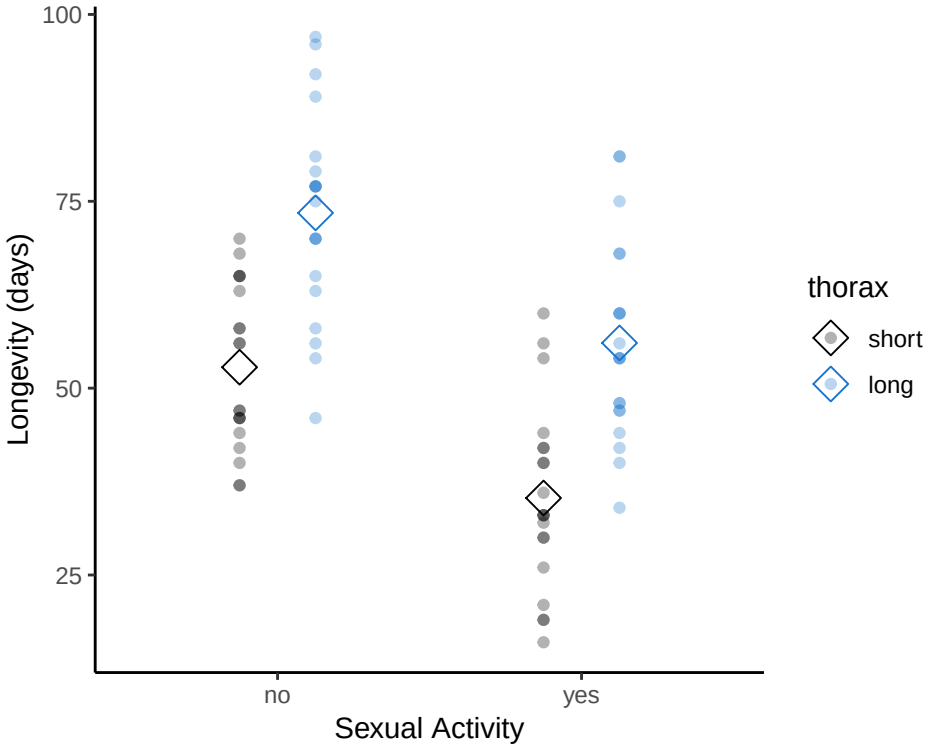
```
## # A tibble: 6 x 3
## # Groups:   activity, thorax [1]
##   thorax longevity activity
##   <chr>      <int> <chr>
## 1 long          70 no
## 2 long          75 no
## 3 long          96 no
## 4 long          77 no
## 5 long          81 no
## 6 long          77 no
```

```r
# see summary of data
summary(fruitfly_2groups)
```

```
##     thorax            longevity      activity
##  Length:80          Min.   :16.0   Length:80
##  Class :character   1st Qu.:42.0   Class :character
##  Mode  :character   Median :54.0   Mode  :character
##                     Mean   :54.4
##                     3rd Qu.:68.0
##                     Max.   :97.0
```

Next, let's plot these data.

```r
# re-order factors to make them show up how we would like them on the plot
# instead of alphabetically (default R behaviour)
fruitfly_2groups$thorax <- factor(fruitfly_2groups$thorax,
                                  levels = c("short","long"))
# plot strip charts of longevity, grouped by sexual activity
# and colored by thorax length
ggplot(fruitfly_2groups,
       aes(x = activity, y = longevity, color = thorax)) +
  stat_summary(fun.y = mean,
               geom = "point",
               shape = 5,
               size = 4,
               position = position_dodge(0.5)) +
  geom_jitter(position = position_dodge(0.5), alpha = 0.3) +
  scale_color_manual(values=c("black", "dodgerblue3")) +
  xlab("Sexual Activity") +
  ylab("Longevity (days)")
```



This data visualization suggests that both sexual activity and body size/thorax length may effect longevity. Let's confirm (or disprove) this intuition by performing a 2-way (or 2-factor) ANOVA.

To perform a 2-way ANOVA, we modify the formula notation that we pass into to `aov` function by adding an additional factor/category/explanatory variable through the use of the `+` sign and the name of the new variable. Thus, our formula for this case is:

```
longevity ~ activity + thorax
```

Everything else remains the same:

```
# create an ANOVA "model" object
fruitfly_2var_model <- aov(longevity ~ activity + thorax,
                           data = fruitfly_2groups)

# view output of aov() as a nice dataframe using tidy() from the broom package
tidy(fruitfly_2var_model)
```

```
## # A tibble: 3 x 6
##   term         df  sumsq meansq statistic   p.value
##   <chr>     <dbl>  <dbl>  <dbl>     <dbl>     <dbl>
## 1 activity      1  6090.  6090.      38.8  2.34e- 8
## 2 thorax        1  8570.  8570.      54.5  1.54e-10
## 3 Residuals    77 12101.   157.      NA   NA
```

Now, we see that we get back an additional line in our results summary that corresponds to the hypotheses regarding the effect of body size/thorax length on longevity. The p-values for both sexual activity (2.3379708×10^{-8}) and size ($1.5438099 \times 10^{-10}$) are very, very small. Thus, we can reject both of our null hypotheses and infer that both sexual activity and size have statistically significant effect on longevity.

2-way ANOVA with 2 groups including an interaction term

Oftentimes when we are dealing with experiments/cases where we have 2 or more factor/category/explanatory variables, we first want to ask if there is an interaction effect between them and their influences/effects on the response variable.

What do we mean by interaction effect? Essentially, an interaction effect is observed when the effect of two explanatory variables on the response variable is not additive (for example, their effect could instead be synergistic).

Our hypotheses for whether or not there is an interaction are:

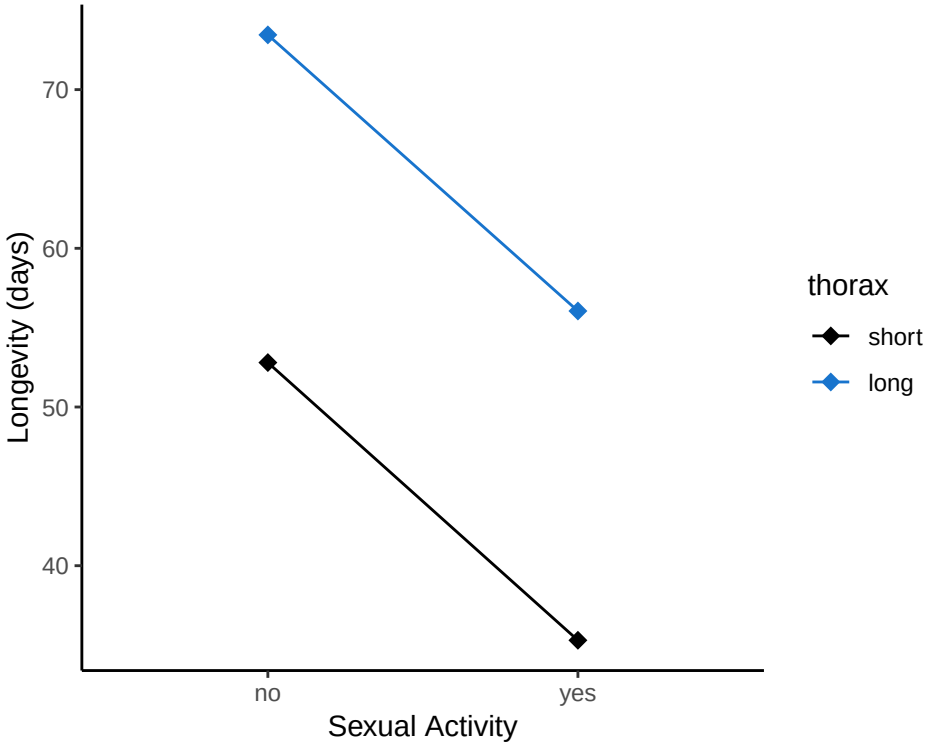
Null Hypothesis, H_0: There is **no** interaction effect between sexual activity and thorax length on the mean longevity of the population.
Alternative Hypothesis, H_A: There is an interaction effect between sexual activity and thorax length on the mean longevity of the population.

In a simple case, as presented in this experiment, we first assess the hypotheses in regards to the presence or absence of interaction. If we reject the interaction effect null hypothesis, then we interpret the data only in regards to this null hypothesis. If we fail to reject the interaction effect null hypothesis, then we can proceed and investigate/test the hypotheses for each individual factor/category/explanatory variable (often referred to as "main effects").

Can we get an intuitive sense for this via visualization? Yes we can by making an interaction plot (see example below). Here, we are looking at the slope of the lines that connects the means. If the slopes of the interaction lines are parallel, then the ANOVA results will very likely tell us that we will fail to reject the interaction effect null hypothesis. On the other hand, if they are not parallel, the ANOVA results will very likely tell us to reject the interaction effect null hypothesis, and we can infer that there is an interaction effect on the response variable between the two factor/category/explanatory variables.

Let's look at the interaction plot for our case:

```
# plot to investigate possible interaction effect of sexual
# activity and thorax length on longevity
ggplot(fruitfly_2groups,
       aes(x = activity, y = longevity, color = thorax)) +
  stat_summary(fun.y = mean,
               geom = "point",
               shape = 18,
               size = 3) +
  stat_summary(fun.y = mean,
               geom = "line",
               aes(group = thorax)) +
  scale_color_manual(values=c("black", "dodgerblue3")) +
  xlab("Sexual Activity") +
  ylab("Longevity (days)")
```



Although not perfectly parallel, the lines on the interaction plot are pretty close to parallel. So, the ANOVA results will very likely tell us that we will fail to reject the interaction effect null hypothesis. Let's proceed with the analysis to be sure.

One way to include an interaction term in your ANOVA model is to use the `*` symbol between two factor/category/explanatory variables. This causes R to test the null hypotheses for the effect of each individual factor/category/explanatory variables as well as the combined effect of these two explanatory variables. Thus, for us, our formula notation is now:

```
longevity ~ activity * thorax
```

Importantly, using `*` causes R to test all possible interactions. So if we had a formula `A * B * C`, it would test all combinations of the 3 variables. If instead, you want to specify specific interaction term(s), you can use `:`. In the case of our formula, this is the same as `*` but serves as an example of the other notation type.

```
longevity ~ activity + thorax + activity:thorax
```

Everything else about our input `aov` remains the same as our previous model.

```
# create an ANOVA "model" object
fruitfly_2var_model2 <- aov(longevity ~ activity * thorax,
                            data = fruitfly_2groups)

# view output of aov() as a nice dataframe using tidy() from the broom package
tidy(fruitfly_2var_model2)
```

```
## # A tibble: 4 x 6
##   term              df    sumsq  meansq statistic   p.value
##   <chr>          <dbl>    <dbl>   <dbl>     <dbl>     <dbl>
## 1 activity           1  6090.   6090.   38.2       2.88e- 8
## 2 thorax             1  8570.   8570.   53.8       2.03e-10
## 3 activity:thorax    1     0.05    0.05  0.000314  9.86e- 1
```

```
## 4 Residuals          76 12101.    159.   NA        NA
```

As stated above, as a rule of thumb for cases such as these, the first hypotheses we should attend to are those regarding the interaction effect (or lack thereof). We can see our output from ANOVA now has an additional line that refers to the testing of the interaction effect hypothesis.

$activity : thorax, 1, 0.05, 0.05, 3.1401585 \times 10^{-4}, 0.9859083$

We observe that the p-value from this line is not very small, 0.9859083, and not less than the standard p-value threshold for rejecting null hypotheses (0.05). Thus, as our interaction plot suggested, we fail to reject the null hypotheses and conclude that there is **no** interaction effect between sexual activity and thorax length on the mean longevity of the population).

We would then proceed to investigate the hypotheses of each main effect independently. This could be done by either interpreting the relevant p-values from our current ANOVA results table, or re-running the analysis without the interaction term (as done in the previous case).

Exercise: ANOVA

Exercise. Determine whether the following statements are *true or false*?

1. ANOVA tests the null hypothesis that the sample means are all equal?
2. We use ANOVA to compare the variances of the population?
3. A one-way ANOVA is equivalent to a t-test when there are 2 groups to be compared.
4. In rejecting the null hypothesis, one can conclude that all the population means are different from one another?

Questions courtesy of Dr. Gabriela Cohen Freue's DSCI 562 course (UBC)

If you are attending a 3 x 2-hour workshop, this is the end of day 1

Linear regression

oad and explore the data

Now, we will work with a data frame that Jennifer Bryan (U. of British Columbia, RStudio) put together in the `gapminder` package.

Unlike the fruit fly data, no pre-manipulation is needed so let's view these data as is.

```
gapminder
```

```
## # A tibble: 1,704 x 6
##    country     continent  year lifeExp      pop gdpPercap
##    <fct>       <fct>     <int>   <dbl>    <int>     <dbl>
##  1 Afghanistan Asia       1952    28.8  8425333      779.
##  2 Afghanistan Asia       1957    30.3  9240934      821.
##  3 Afghanistan Asia       1962    32.0 10267083      853.
##  4 Afghanistan Asia       1967    34.0 11537966      836.
##  5 Afghanistan Asia       1972    36.1 13079460      740.
##  6 Afghanistan Asia       1977    38.4 14880372      786.
```

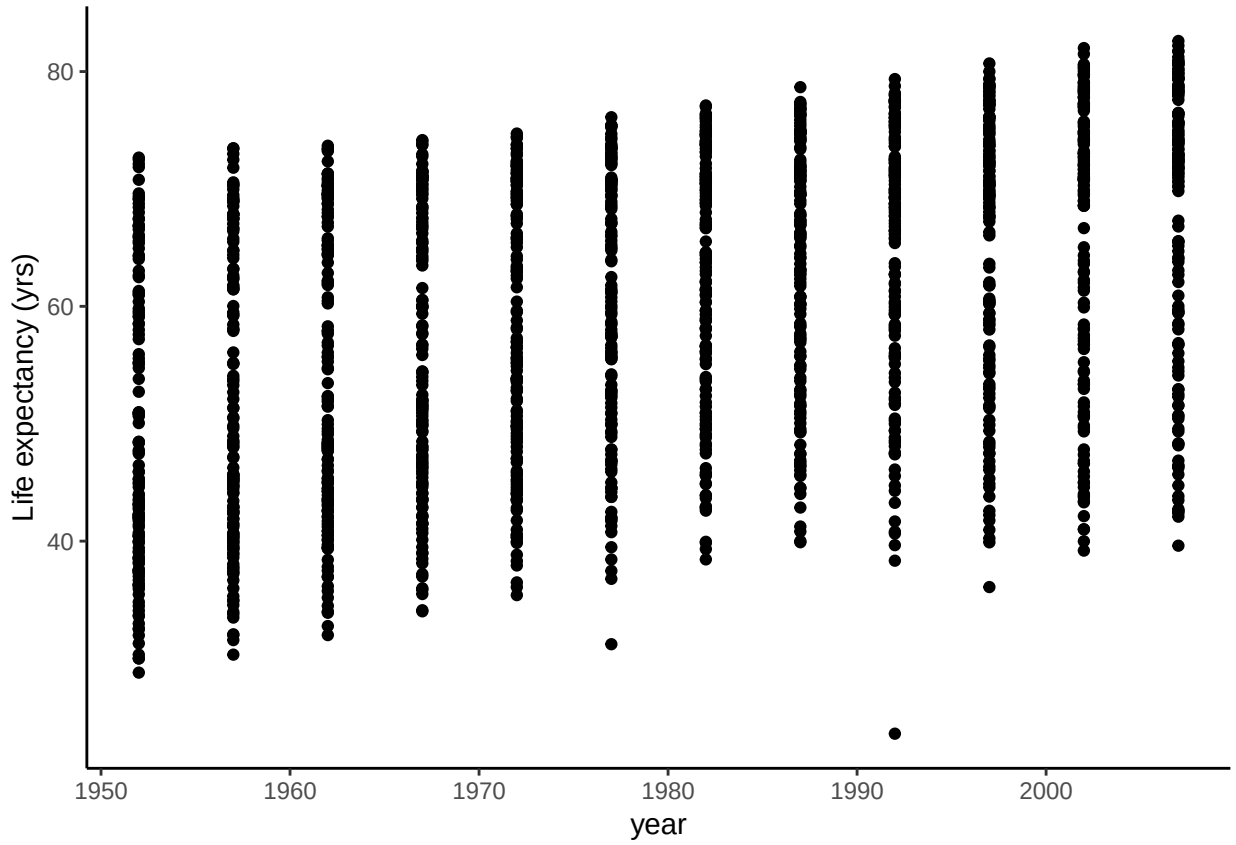
```
##  7 Afghanistan Asia       1982    39.9 12881816      978.
##  8 Afghanistan Asia       1987    40.8 13867957      852.
##  9 Afghanistan Asia       1992    41.7 16317921      649.
## 10 Afghanistan Asia       1997    41.8 22227415      635.
## # ... with 1,694 more rows
```

We see that the data contain information on life expectancy (lifeExp), population (pop), and gross domestic product per capita (gdpPercap, a rough measure of economical richness) for many countries across many years.

A very naive working hypothesis that you may come to is that our life expectancy grew with time. This would be represent in r with `lifeExp ~ year`.

We can explore this hypothesis graphically.

```
gapminder %>%
  ggplot(aes(x = year, y = lifeExp)) +
  geom_point() +
  labs(y="Life expectancy (yrs)")
```

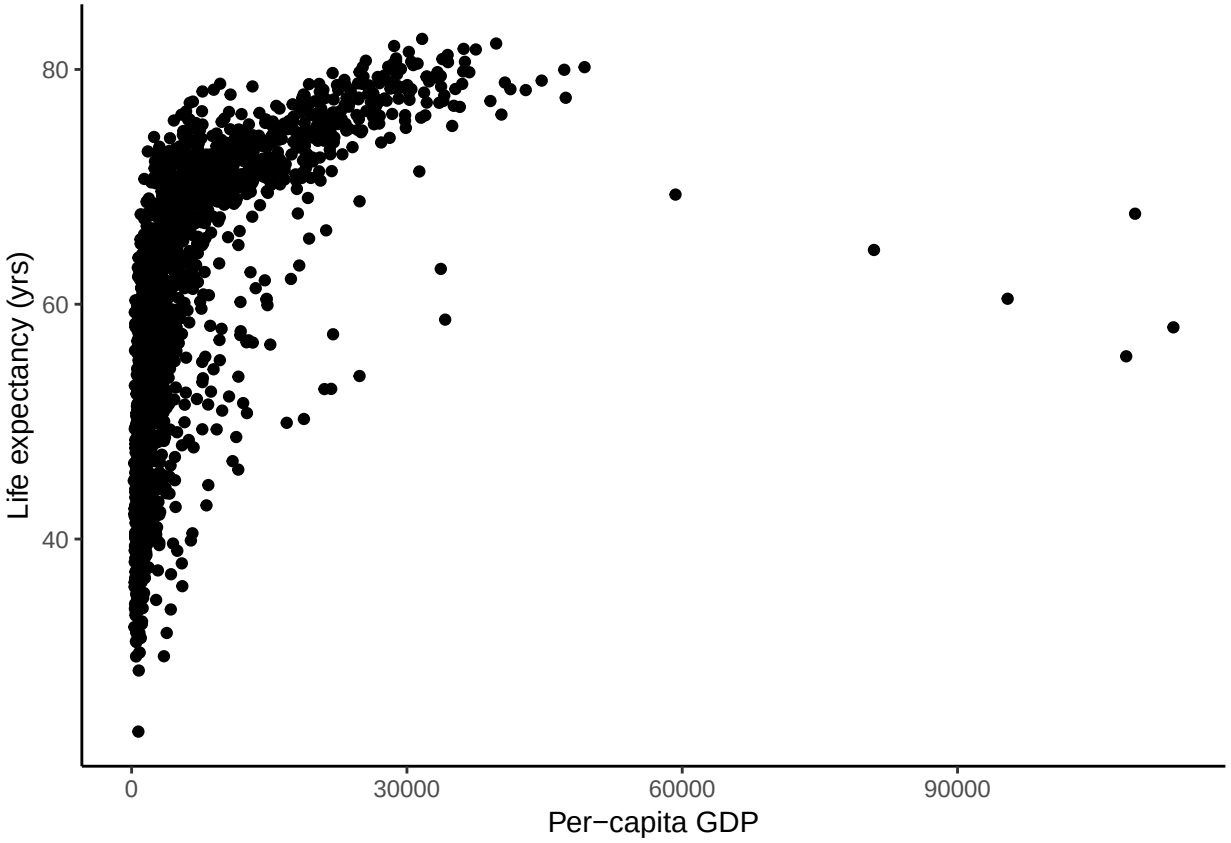


Although there is very high variance, we do see a certain trend with mean life expectancy increasing over time.

Similarly, we can naively hypothesize that life expectancy is higher where the per-capita gdp is higher. In R, this is `lifeExp ~ gdpPercap`.

```
gapminder %>%
  ggplot(aes(x = gdpPercap, y = lifeExp)) +
  geom_point() +
```

```
labs(y="Life expectancy (yrs)", x="Per-capita GDP")
```



Linear models

A **linear regression** model describes the change of a *dependent* variable, say `lifeExp`, as a *linear* function of one or more *explanatory* variables, say `year`. This means that increasing by x the variable `year` will have an effect $\beta \cdot x$ on the *dependent* variable `lifeExp`, whatever the value x is. In mathematical terms:

$$\text{lifeExp} = \alpha + \beta \cdot \text{year}$$

We call α the intercept of the model, or the value of `lifeExp` when `year` is equal to zero. When we go forward in time, increasing `year`, `lifeExp` increases (if β is positive, otherwise it decreases):

$$\alpha + \beta \cdot (\text{year} + x) = \alpha + \beta \cdot \text{year} + \beta \cdot x = \text{lifeExp} + \beta \cdot x$$

A### Key assumptions number of assumptions must be satisfied for a linear model to be reliable. These are:

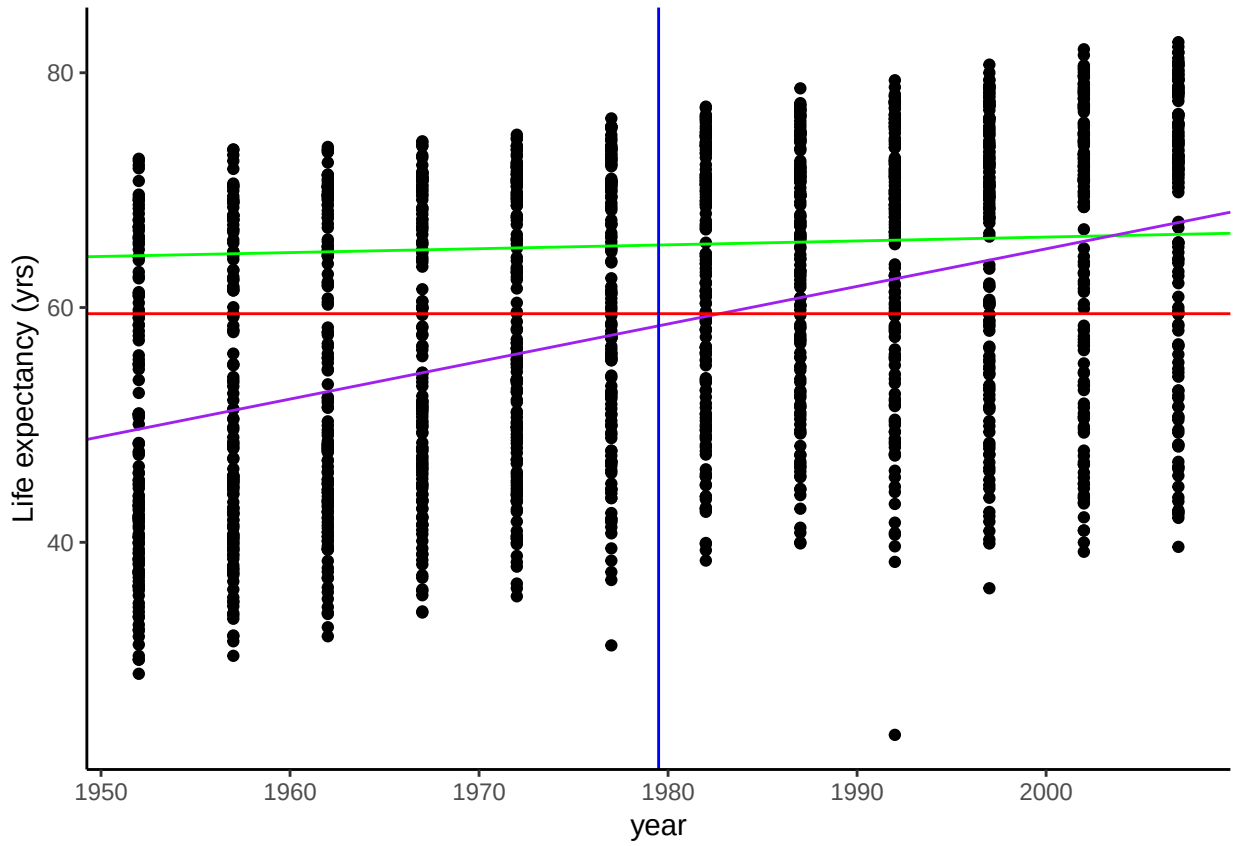
- the predictor variables should be measured with not too much error (**weak exogeneity**)
- the variance of the response variable should be roughly the same across the range of its predictors (**homoscedasticity**, a fancy pants word for "constant variance")
- the discrepancies between observed and predicted values should be **independent**
- the predictors themselves should be **non-colinear** (a rather technical issues, given by the way we solve the model, that may happen when two predictors are perfectly correlated or we try to estimate the effect of too many predictors with too little data).

Here, we only mention these assumptions, but for more details, take a look at wiki.

When we have only one predictive variable (what is called a *simple* linear regression model), the formula we just introduced describes a straight line. The task of a linear regression method is identifying the *best fitting* slope and intercept of that straight line. But what does *best fitting* means in this context? We will first adopt a heuristic definition of it but will rigorously define it later on.

Let's consider a bunch of straight lines in our first plot:

```
gapminder %>%
  ggplot(aes(x = year, y = lifeExp)) +
  geom_point() +
  geom_abline(intercept = 0, slope = 0.033, colour = "green") +
  geom_abline(intercept = -575, slope = 0.32, colour = "purple") +
  geom_hline(aes(yintercept = mean(lifeExp)), colour = "red") +
  geom_vline(aes(xintercept = mean(year)), colour = "blue") +
  labs(y="Life expectancy (yrs)")
```



Exercise: Best fit lines

Exercise. At your table, discuss the following questions.

1. Which line best describes the data?
2. The red one is a horizontal line at the overall mean life expectancy. It seems a reasonable model, but what is missing?

Simple linear regression

To obtain the slope and intercept of the green line, we can use the built-in R function `lm()`. This function works very similarly to the `aov` function we used earlier in that we must give it a model and data. The output of `lm()` is also messy but we want to use `summary` instead of `tidy` in order to see all the relevant results.

```
# create a lm "model" object
lifeExp_model1 <- lm(lifeExp ~ year,
                     data = gapminder)

# view output of lm() as using summary()
summary(lifeExp_model1)
```

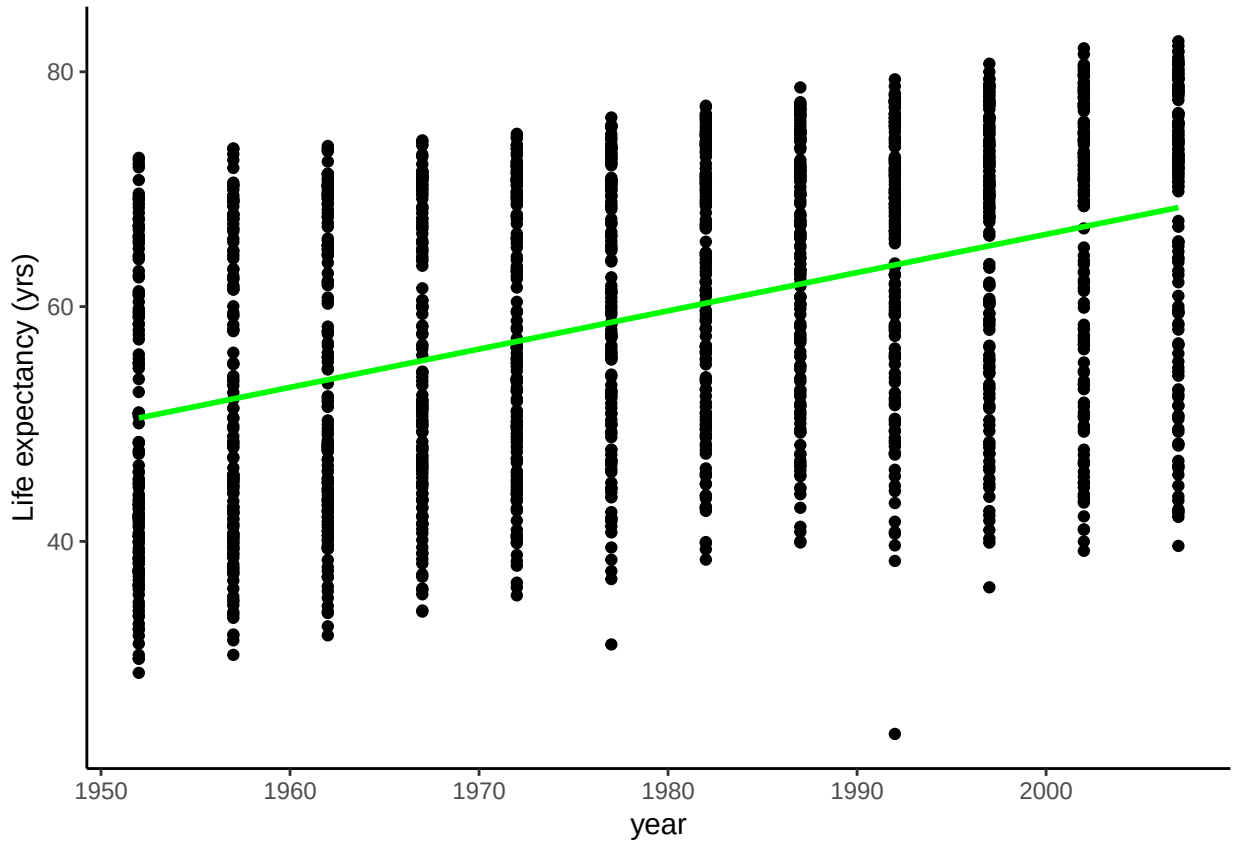
```
##
## Call:
## lm(formula = lifeExp ~ year, data = gapminder)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -39.949  -9.651   1.697  10.335  22.158
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -585.65219   32.31396  -18.12   <2e-16 ***
## year           0.32590    0.01632   19.96   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.63 on 1702 degrees of freedom
## Multiple R-squared:  0.1898, Adjusted R-squared:  0.1893
## F-statistic: 398.6 on 1 and 1702 DF,  p-value: < 2.2e-16
```

Now, however, we are interested in more than just the p-value.

The `Estimate` values are the best fit for the intercept, α, and the slope, β. The slope, the parameter the links `year` to `lifeExp`, is a positive value: every 1 year, the life expectancy increases of 0.3259038 years. This is in line with our hypothesis. Moreover, its p-value, the probability of finding a correlation at least as strong between predictive and response variable, is rather low at $7.5467946 \times 10^{-80}$ (but see this for a cautionary tale about p-values!).

Using this slope and intercept, we can plot this best fit line on our data.

```
gapminder %>%
  ggplot(aes(x = year, y = lifeExp)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, colour = "green") +
  labs(y="Life expectancy (yrs)")
```

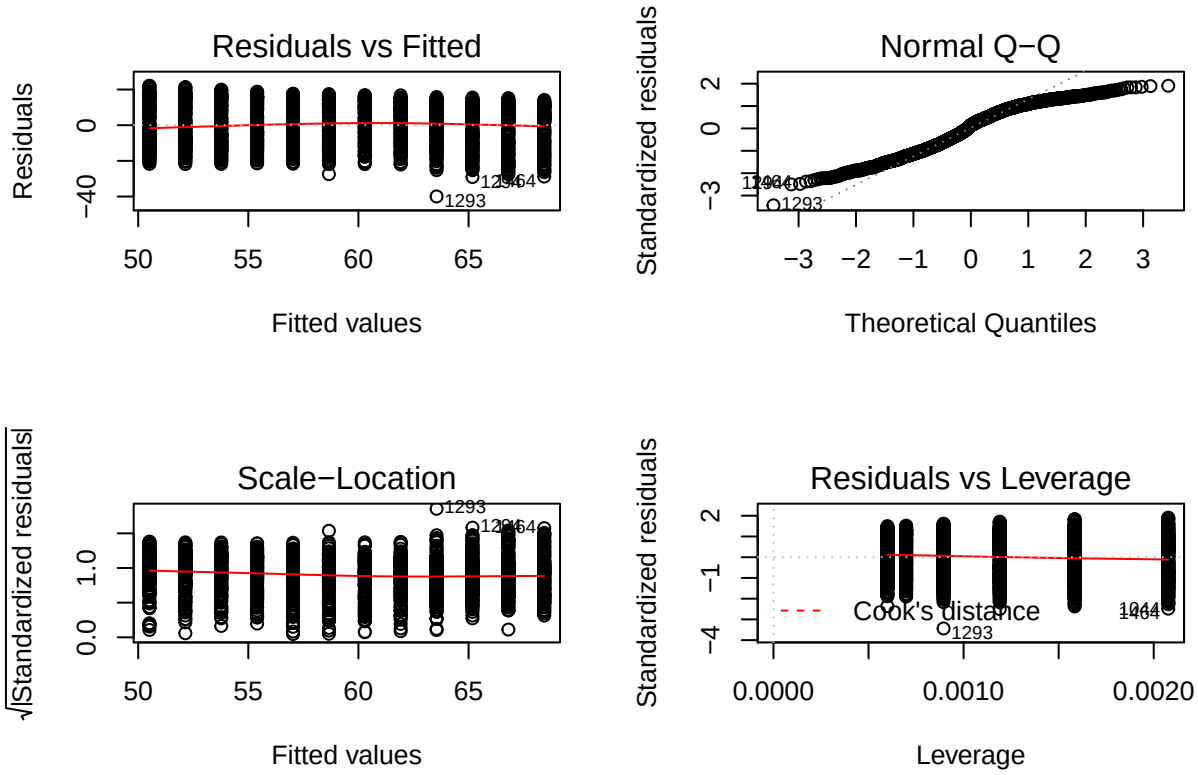


Another important bit of information in our results is the R-squared values, both are the *Multiple* and *Adjusted R-squared*. These tell us how much of *variance* in the life expectancy data is explained by the year. In this case, not much (0.1897571, 0.1892811, respectively)

Residuals

We can further explore our linear model by plotting some diagnostic plots. Base R provides a quick and easy way to view all of these plots at once with `plot`.

```
# Set plot frame to 2 by 2
par(mfrow=c(2,2))
# Create diagnostic plots
plot(lifeExp_model1)
```



Whoa right?! Let's break it down. Overall, these diagnostic plots are useful for understanding the model *residuals*. The residuals are the discrepancies between the life expectancy we would have guessed by the model and the observed values in the available data. In other words, the distances between the straight line and actual data points. In a linear regression model, these residuals are the values we try to minimize when we fit the straight line.

There is a lot of information contained in these 4 plots, and you can find in-depth explanations here. For our purposes today, let's focus on just the Residuals vs Fitted and Normal Q-Q plots.

The Residuals vs Fitted plot shows the differences between the best fit line and all the available data points. When the model is a good fit for the data, this plot should have no discernible pattern. That is, the red line should not form a shape like an 'S' or a parabola. Another way to look it is that the points should look like 'stars in the sky', *e.g.* random. This second description is not great for these data since year is an integer (whole number) but we do see that the red line is relatively straight and without pattern.

The Normal Q-Q plot directly compares the best fit and actual data values. A good model closely adheres to dotted line and points that fall off the line should not portray any pattern. In our case, this plot indicates that this simple linear model may not be the best fit for these data. Notice how either end deviates more and more from the line and the plot forms somewhat of an 'S' pattern.

These ends are particularly important in a linear model. Because we've chosen to use a simple linear model, *outliers*, or observed values that are very far away from our best fit line, are very important (in jargon, they have a high *leverage*, see the fourth diagnostic plot). This is especially true if the outliers are at the edge of the predicting variable ranges such as we see in our Q-Q plot.

Exercise: Linear models

Exercise. At your table, discuss the following questions.

1. Looking at the summary plots above, do you feel that our model can be extrapolated to a much wider `year` range? Why or why not?
2. Fit a linear model of life expectancy as a function of per-capita gdp. Using the summary table and diagnostic plots, discuss whether or not you think this is a good fit for these data.

Cautions when using linear models

R (and most other statistical software) will fit, plot, summarize, etc. a linear model regardless of whether that model is a good fit for the data.

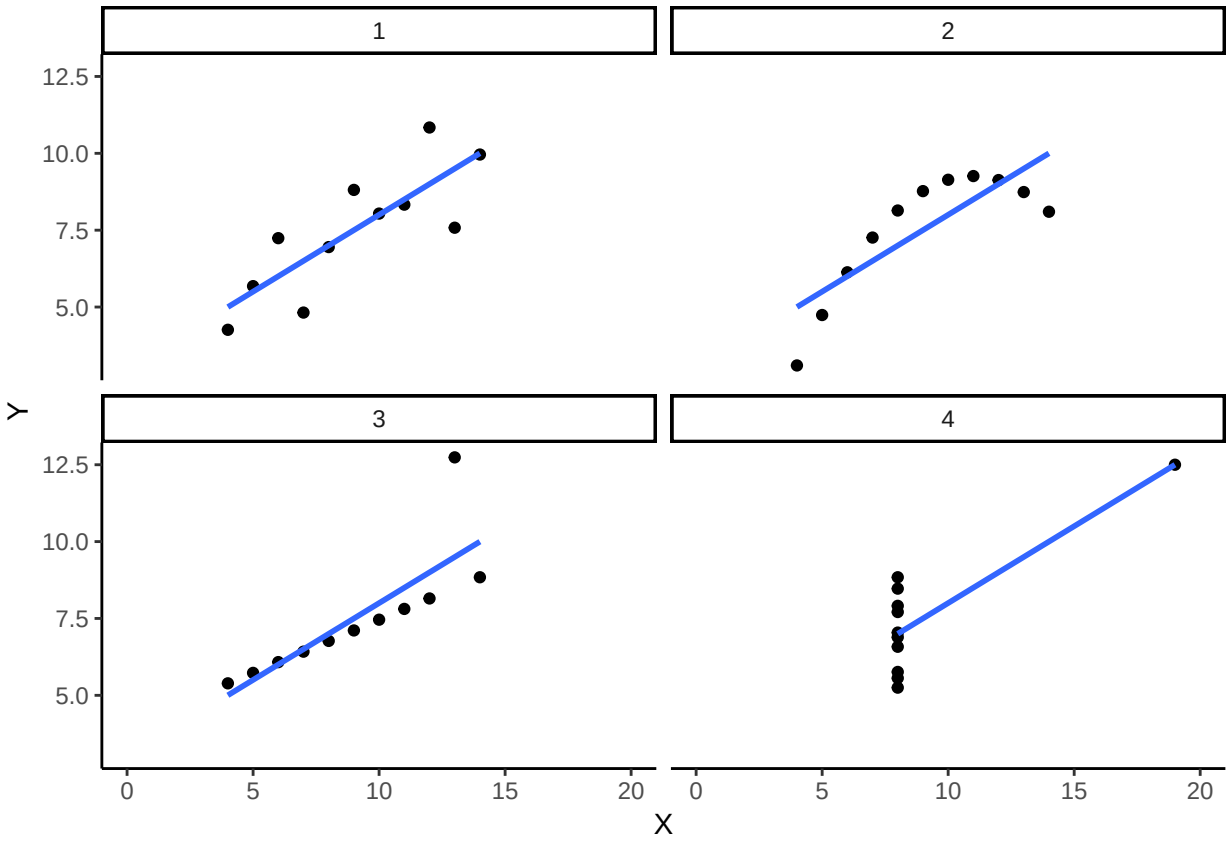
For example, the Anscombe data sets are very different data that give the *same slope, intercept, and mean* in a linear model.

We can access these data in R and format them with

```
absc <- with(datasets::anscombe,
             tibble(X=c(x1,x2,x3,x4),
                        Y=c(y1,y2,y3,y4),
        anscombe_quartet=gl(4,nrow(datasets::anscombe))
                    )
             )
```

Plotting these data reveals the problem.

```
absc %>%
  ggplot(aes(x=X,y=Y,group=anscombe_quartet)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  scale_x_continuous(limits = c(0,20)) +
  facet_wrap(~anscombe_quartet)
```



This is why you should always, always, always plot your data before attempting regression!

If you are attending a 2 x 3-hour workshop, this is the end of day 1

Multiple linear regression

So far, we have dealt with simple regression models, where we had only one predictor variable. However, `lm()` handles much more complex models. Consider for example a model of life expectancy as a function of both the year and the per-capita gdp.

```
lifeExp ~ year + gdpPercap
```

```
## lifeExp ~ year + gdpPercap
```

This formula does not describe a straight line anymore, but a plane in a 3D space. Still a very flat thingy.

Let's fit this model.

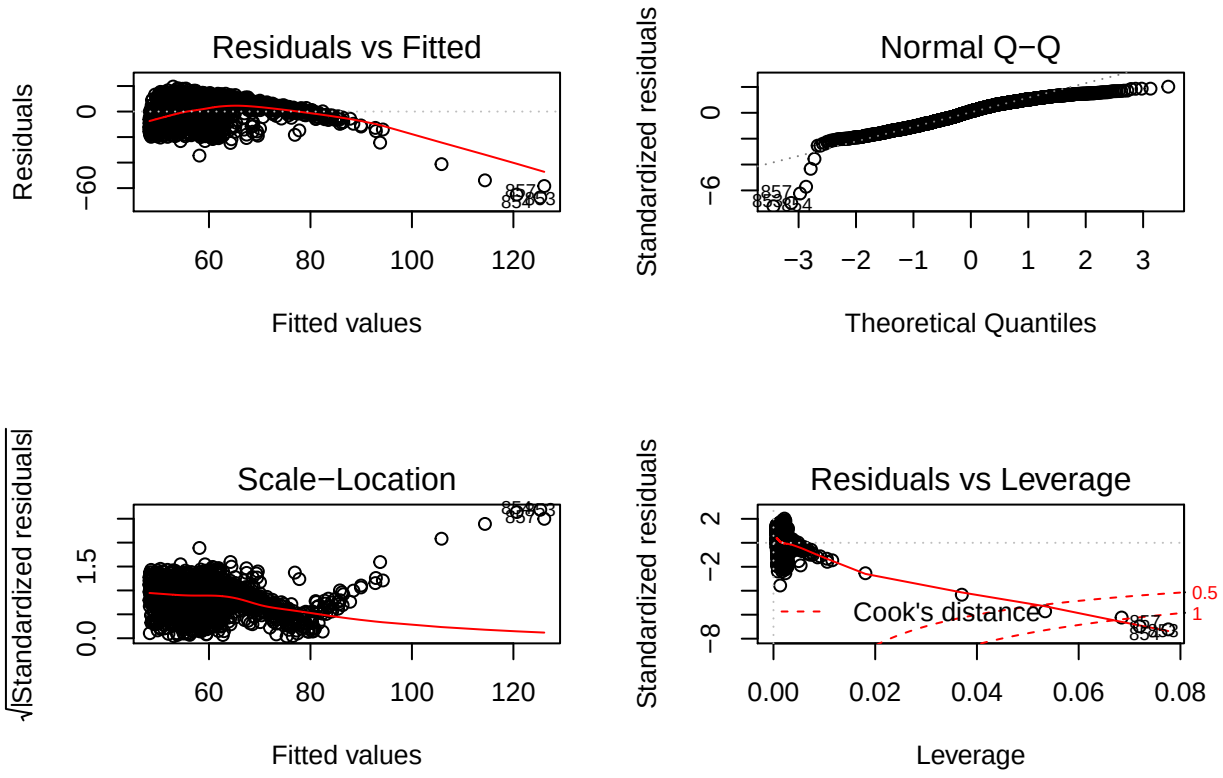
```
# create a lm "model" object
lifeExp_model2 <- lm(lifeExp ~ year + gdpPercap,
                     data = gapminder)

# view output of lm() as using summary()
summary(lifeExp_model2)
```

```
##
## Call:
## lm(formula = lifeExp ~ year + gdpPercap, data = gapminder)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -67.262  -6.954   1.219   7.759  19.553
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -4.184e+02  2.762e+01  -15.15   <2e-16 ***
## year         2.390e-01  1.397e-02   17.11   <2e-16 ***
## gdpPercap    6.697e-04  2.447e-05   27.37   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.694 on 1701 degrees of freedom
## Multiple R-squared:  0.4375, Adjusted R-squared:  0.4368
## F-statistic: 661.4 on 2 and 1701 DF,  p-value: < 2.2e-16
```

We can assess this model with plots similar to our simple linear regression.

```
par(mfrow=c(2,2))
plot(lifeExp_model2)
```



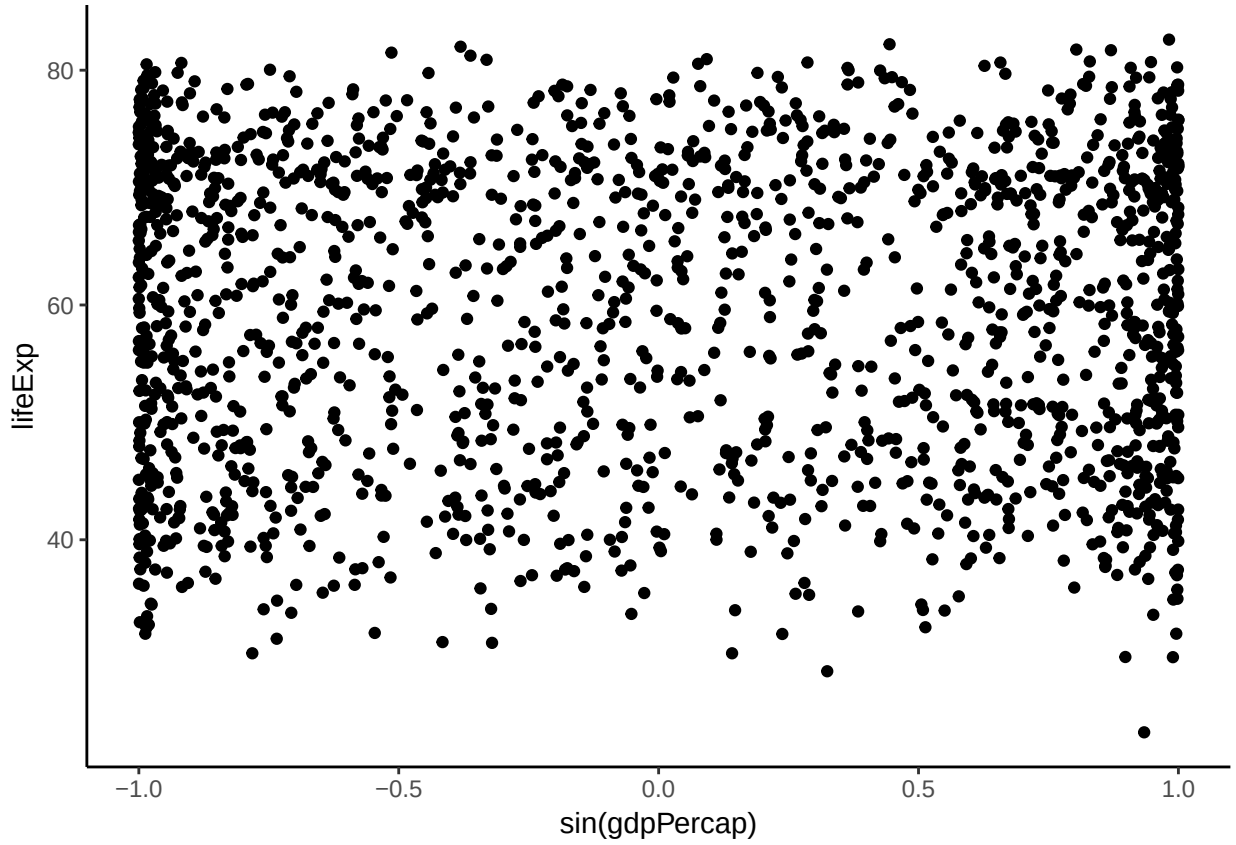
Linear is the formula, not the predictor

The linearity of a model is in how the predictive variables are put together, not necessarily in the predictors themselves. In the last exercise, you saw that `gdpPercap` is not the best predictor of `lifeExp` because it does not seem to fit linearly. This carries forward into our multiple linear regression as is apparent in the last plot.

One way to improve our model is to use a transformed `gdpPercap` predictor. But transformed how?

Let's pick a (silly) function to start. Here, we take the sine of the `gdpPercap`.

```
gapminder %>%
  ggplot(aes(x = sin(gdpPercap), y = lifeExp)) +
  geom_point()
```



Doesn't look much better.

Exercise: Tranforming predictors


Exercise.

1. Find a function that makes the plot more "linear" and fit a model of life expectancy as a function of the transformed per-capita gdp. Is it a better model?
   - Go back to your original `gdpPercap` vs. `lifeExp` plot and think about what function creates a similar trend.

Tranforming predictors: log

Let's use a transformed predictor for creating a new (and hopefully better) model. There are two ways. We can include the function directly into the formula (similar to the last plot) and fit the model.

```
lifeExp_model3a <- lm(lifeExp ~ year + log(gdpPercap),
                      data = gapminder)
```

Or we can create a new variable in the data frame and use that variable in the model

```
gapminder <- gapminder %>%
  mutate(log_gdp = log(gdpPercap))

lifeExp_model3b <- lm(lifeExp ~ year + log_gdp,
             data = gapminder)
```

Both yield the same result.

```
summary(lifeExp_model3a)
```

```
##
## Call:
## lm(formula = lifeExp ~ year + log(gdpPercap), data = gapminder)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -27.2291  -3.8454   0.6065   4.7737  17.8644
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -3.911e+02  1.942e+01  -20.14   <2e-16 ***
## year            1.956e-01  9.927e-03   19.70   <2e-16 ***
## log(gdpPercap)  7.770e+00  1.381e-01   56.27   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.877 on 1701 degrees of freedom
## Multiple R-squared:  0.7169, Adjusted R-squared:  0.7165
## F-statistic:  2153 on 2 and 1701 DF,  p-value: < 2.2e-16
```

```
summary(lifeExp_model3b)
```

```
##
## Call:
## lm(formula = lifeExp ~ year + log_gdp, data = gapminder)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -27.2291  -3.8454   0.6065   4.7737  17.8644
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -3.911e+02  1.942e+01  -20.14   <2e-16 ***
## year         1.956e-01  9.927e-03   19.70   <2e-16 ***
## log_gdp      7.770e+00  1.381e-01   56.27   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 6.877 on 1701 degrees of freedom
## Multiple R-squared:  0.7169, Adjusted R-squared:  0.7165
## F-statistic:  2153 on 2 and 1701 DF,  p-value: < 2.2e-16
```

Tranforming predictors: polynomial

Another option is using a *polynomial* transformation of our model.

```
lifeExp_model4 <- lm(lifeExp ~ year + poly(gdpPercap),
                     data = gapminder)
summary(lifeExp_model4)
```

```
##
## Call:
## lm(formula = lifeExp ~ year + poly(gdpPercap), data = gapminder)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -67.262  -6.954   1.219   7.759  19.553
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -413.59192   27.65674  -14.95   <2e-16 ***
## year               0.23898    0.01397   17.11   <2e-16 ***
## poly(gdpPercap)  272.44154    9.95433   27.37   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.694 on 1701 degrees of freedom
## Multiple R-squared:  0.4375, Adjusted R-squared:  0.4368
## F-statistic: 661.4 on 2 and 1701 DF,  p-value: < 2.2e-16
```

Or explicit write a polynomial equation for one of our predictor.

```
lifeExp_model5 <- lm(lifeExp ~ year + gdpPercap + I(gdpPercap^2),
                     data = gapminder)
summary(lifeExp_model5)
```

```
##
## Call:
## lm(formula = lifeExp ~ year + gdpPercap + I(gdpPercap^2), data = gapminder)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -31.1048  -6.3211   0.3511   6.8441  25.7228
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -3.088e+02  2.426e+01  -12.73   <2e-16 ***
## year            1.819e-01  1.228e-02   14.81   <2e-16 ***
## gdpPercap       1.396e-03  3.671e-05   38.02   <2e-16 ***
## I(gdpPercap^2) -1.344e-08  5.558e-10  -24.18   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 8.364 on 1700 degrees of freedom
## Multiple R-squared:  0.5814, Adjusted R-squared:  0.5807
## F-statistic: 787.1 on 3 and 1700 DF,  p-value: < 2.2e-16
```

Note that we must use `I(gdpPercap^2)` instead of `gdpPercap^2` because the symbols `^`, `*`, and `:` have a particular meaning in a linear model. As we saw in ANOVA, these symbols are used to specify *interactions* between predicting variables.

Exercise: Multiple linear regression

 Exercise.

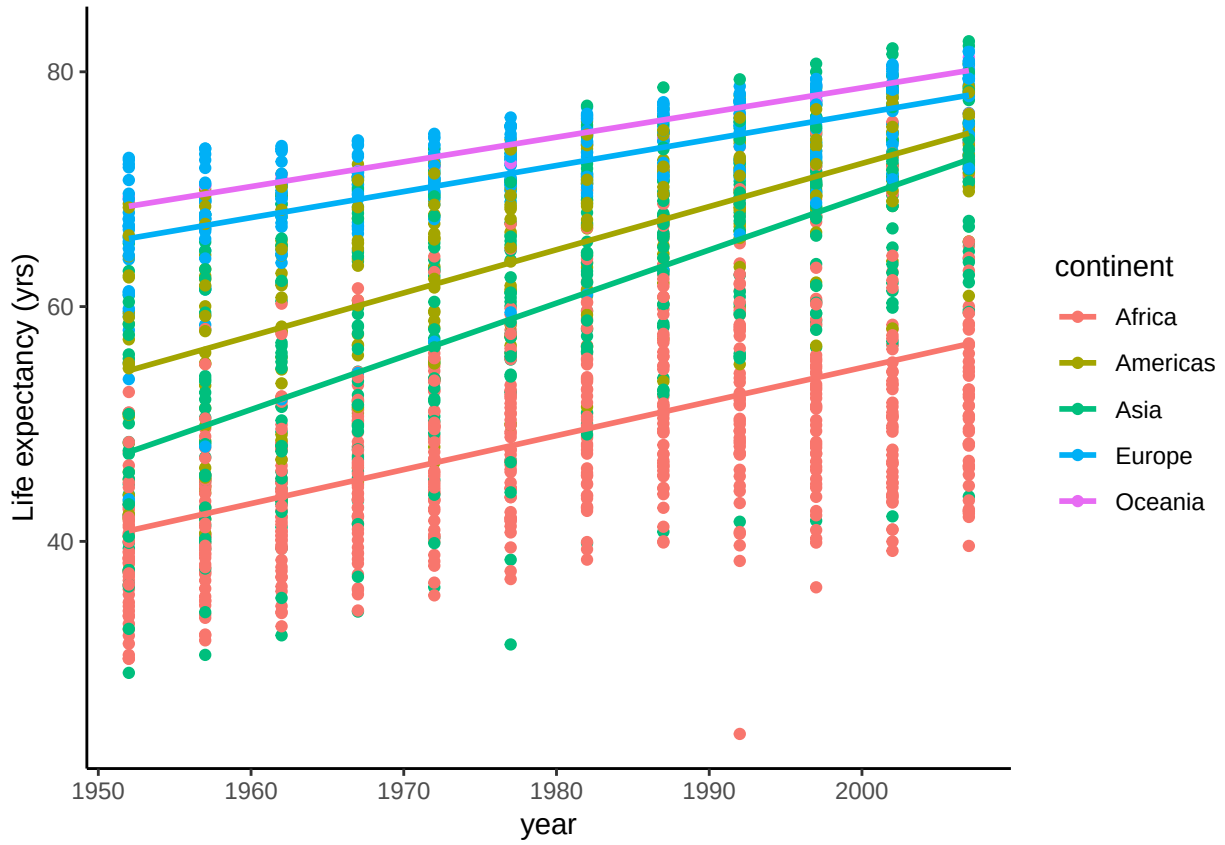
1. So far, we have worked with `lifeExp` as our independent variable. Now, in small groups, try to produce a model of population (`pop`) using one or more of the variables available in `gapminder`.

Interactions and ANalysis of COVAriance (ANCOVA)

So far, our models for life expectancy have built upon continuous (or discrete but incremental) variables. However, we may wonder if being in one continent rather than another has a differential effect on the correlation between `year` and `lifeExp`.

Let's take a look at our data set now with continent in mind.

```
gapminder %>%
  ggplot(aes(x = year, y = lifeExp, colour = continent)) +
  geom_point() +
  geom_smooth(method = "lm", se= FALSE) +
  labs(y="Life expectancy (yrs)")
```



The slopes for each continent seem different, but how can we tell if the difference is significant? Here's where we can combine our linear model with the ANOVA function we learned earlier!

First, using the special character `*`, we model the effects of year, continent, and their interaction on life expectancy.

```
lifeExp_model6 <- lm(lifeExp ~ year*continent,
                     data = gapminder)
```

Then, we call the ANOVA function `aov()` on the model:

```
summary(aov(lifeExp_model6))
```

```
##                  Df Sum Sq Mean Sq F value   Pr(>F)
## year              1  53919   53919  1046.0  < 2e-16 ***
## continent         4 139343   34836   675.8  < 2e-16 ***
## year:continent    4   3566     892    17.3 6.46e-14 ***
## Residuals      1694  87320      52
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Based on these results, it really seems that the continent should have a role in the model. However, it is not always like this. Let's take a closer look at Europe and Oceania.

```
gapminder %>%
  filter(continent %in% c("Oceania","Europe")) %>%
  lm(lifeExp ~ year*continent, data = .) %>%
  aov() %>%
  summary()
```

```
##                  Df Sum Sq Mean Sq F value  Pr(>F)
## year              1   5598    5598 399.070 < 2e-16 ***
## continent         1    132     132   9.414 0.00231 **
## year:continent    1      1       1   0.065 0.79895
## Residuals       380   5330      14
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Note that this is an example of how the tidyverse can be used to link together a bunch of functions, instead of creating many new R objects as we've been doing thus far.

When just looking at Oceania and Europe, continent has a significant effect on the *intercept* of the model, but not on its *slope*. This makes sense since in our plot, these lines (blue and purple) appear parallel but with different y-intercepts.

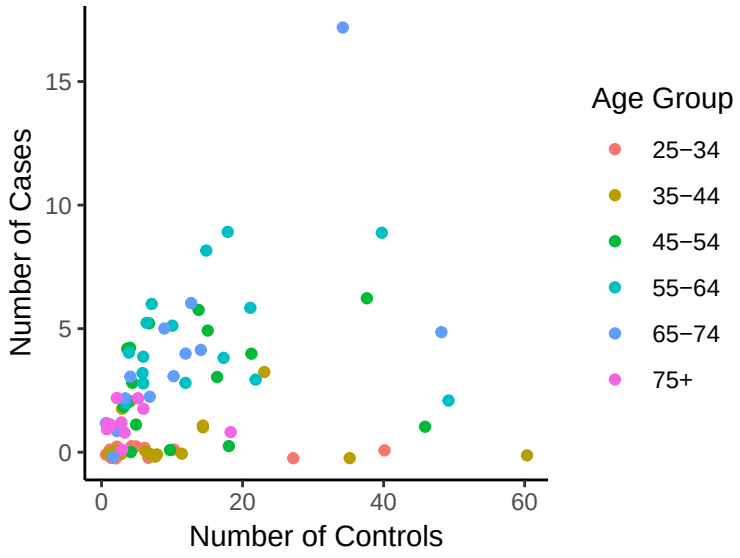
Linear Mixed Effects models

Motivation for LME

Let's take a look at the `esoph` data set, which comes pre-downloaded in R. These data contain information on smoking, alcoholism, and (o)esophageal cancer. Specifically, we are interested in if the number of controls `ncontrols` affects the number of cases `ncases` of cancer for each age group `agegp`.

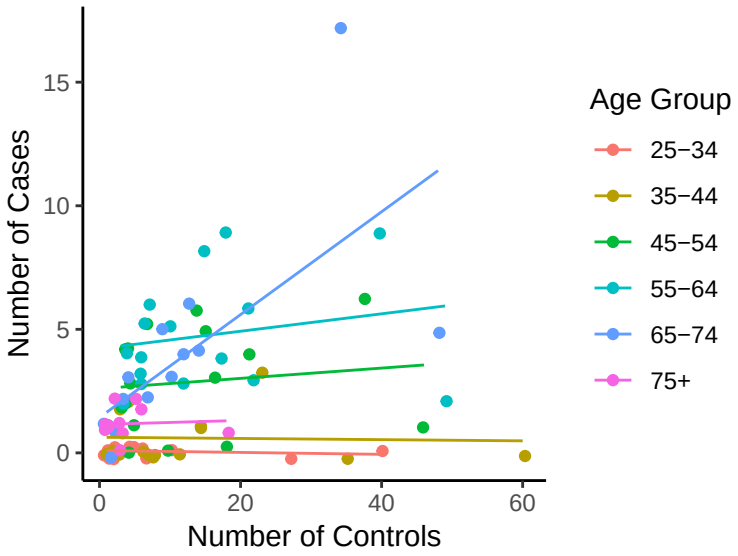
Here's what the data look like (with a tad bit of vertical jitter):

```
p <- ggplot(esoph, aes(ncontrols, ncases, group=agegp, colour=agegp)) +
    geom_jitter(height=0.25) +
    scale_colour_discrete("Age Group") +
    ylab("Number of Cases") + xlab("Number of Controls")
p
```



It seems each age group has a different relationship. Should we then fit regression lines for each group separately? Here's what we get, if we do.

```
p + geom_smooth(method="lm", se=FALSE, size=0.5)
```



But each group has so few observations which makes the regression less powerful.

```
esoph %>%
    group_by(agegp) %>%
    dplyr::summarise(n=length(ncases)) %>%
    as.data.frame
```

```
##   agegp  n
## 1 25-34 15
## 2 35-44 15
## 3 45-54 16
## 4 55-64 16
## 5 65-74 15
## 6   75+ 11
```

Question: can we borrow information across groups to strengthen regression, while still allowing each group to have its own regression line?

Yes – we can use *Linear Mixed Effects* (LME) models. An LME model is just a linear regression model for each group, with different slopes and intercepts, but the collection of slopes and intercepts *is assumed to come from some normal distribution.*

Definition

With one predictor (X), we can write an LME as follows:

$$Y = (\beta_0 + b_0) + (\beta_1 + b_1)\, X + \varepsilon,$$

where the error term ε has mean zero, and the b_0 and b_1 terms are normally distributed having a mean of zero, and some unknown variances and correlation. The b_0 and b_1 terms indicate group-to-group differences from average.

The β terms are called the *fixed effects*, and the b terms are called the *random effects*. Since the model has both types of effects, it's said to be a *mixed* model – hence the name of "LME".

Note that we don't have to make *both* the slope and intercept random. For example, we can remove the b_0 term, which would mean that each group is forced to have the same (fixed) intercept β_0. Also, we can add more predictors (X variables).

Fitting LME

Two R packages exist for working with mixed effects models: `lme4` and `nlme`. We'll be using the `lme4` package (check out this discussion on Cross Validated for a comparison of the two packages).

Let's fit the model. Just like our other models we need to give a formula and data.

```
esoph_model <- lmer(ncases ~ ncontrols + (ncontrols | agegp),
                    data=esoph)
```

Let's take a closer look at the *formula*, which in this case is `ncases ~ ncontrols + (ncontrols | agegp)`.

On the left of the `~` is the response variable, as usual (just like for `lm`). On the right, we need to specify both the fixed and random effects. The **fixed effects** part is the same as usual: `ncontrols` indicates the explanatory variables that get a fixed effect. Then, we need to indicate which explanatory variables get a **random effect**. The random effects can be indicated in parentheses, separated by `+`, followed by a `|`, after which the variable(s) that you wish to group by are indicated. So `|` can be interpreted as "grouped by".

Now let's look at the model output:

```
summary(esoph_model)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: ncases ~ ncontrols + (ncontrols | agegp)
##    Data: esoph
##
## REML criterion at convergence: 388.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.6508 -0.3710 -0.1302  0.3683  4.8056
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  agegp    (Intercept) 1.693347 1.30129
##           ncontrols   0.005728 0.07569  0.26
##  Residual             3.733047 1.93211
## Number of obs: 88, groups:  agegp, 6
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  1.63377    0.59979   2.724
## ncontrols    0.04972    0.03676   1.352
##
## Correlation of Fixed Effects:
##           (Intr)
## ncontrols 0.038
```

The random and fixed effects are indicated here.

- Under the "Random effects:" section, we have the variance of each random effect, and the lower part of the correlation matrix of these random effects.
- Under the "Fixed effects:" section, we have the estimates of the fixed effects, as well as the uncertainty in the estimate (indicated by the Std. Error).

We can extract the collection of slopes and intercepts for each group with our handy `tidy` function.

```
tidy(esoph_model, "ran_modes")
```

```
##    level group        term     estimate  std.error
## 1  25-34 agegp (Intercept)  0.267552852 0.51616109
## 2  25-34 agegp   ncontrols -0.002921620 0.03733551
## 3  35-44 agegp (Intercept)  0.722809516 0.55421797
## 4  35-44 agegp   ncontrols -0.001129813 0.02796924
## 5  45-54 agegp (Intercept)  2.283244800 0.57000244
## 6  45-54 agegp   ncontrols  0.036595805 0.03162986
## 7  55-64 agegp (Intercept)  3.510436639 0.59270544
## 8  55-64 agegp   ncontrols  0.064260084 0.03052225
## 9  65-74 agegp (Intercept)  1.870096879 0.54057859
## 10 65-74 agegp   ncontrols  0.171908841 0.03206950
## 11   75+ agegp (Intercept)  1.148485219 0.54951890
## 12   75+ agegp   ncontrols  0.029578210 0.06006128
```

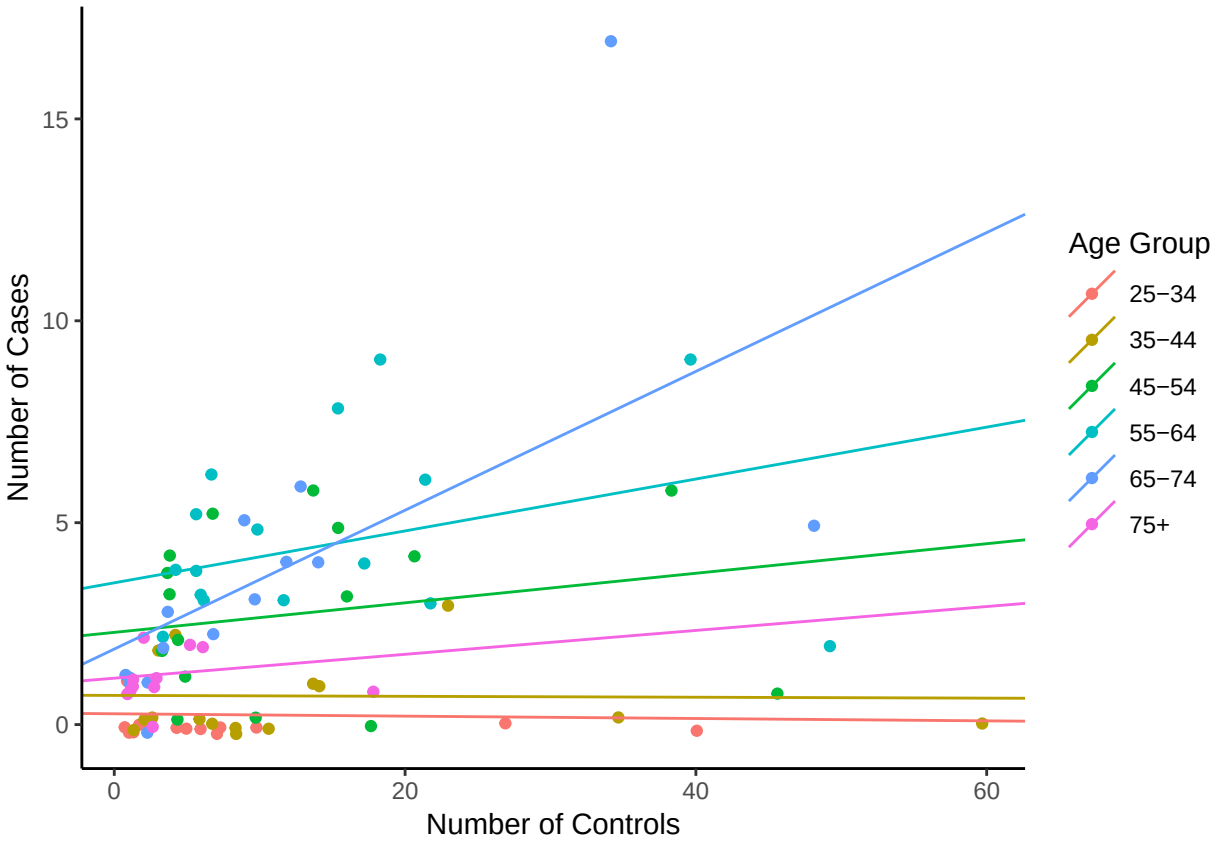
Alternatively, we can use the `coef` function:

```
coef(esoph_model)
```

```
## $agegp
##       (Intercept)    ncontrols
## 25-34   0.2675529 -0.002921620
## 35-44   0.7228095 -0.001129813
## 45-54   2.2832448  0.036595805
## 55-64   3.5104366  0.064260084
## 65-74   1.8700969  0.171908841
## 75+     1.1484852  0.029578210
##
## attr(,"class")
## [1] "coef.mer"
```

Let's put these regression lines on the plot.

```
## Plot
ggplot(esoph, aes(ncontrols, ncases, group=agegp, colour=agegp)) +
    geom_jitter(height=0.25) +
    geom_abline(aes(intercept=intercept, slope=slope, colour=agegp)) +
    scale_colour_discrete("Age Group") +
    ylab("Number of Cases") + xlab("Number of Controls")
```



So, each group still gets its own regression line, but tying the parameters together with a normal distribution gives us a more powerful regression.

Exercise: LME


Exercise.

1. Using the `sleepstudy` dataset, fit an LME on Reaction against Days, grouped by Subject.
2. What is the intercept and slope of subject #310 in the model from question 1?
3. CHALLENGE. Using the Teams dataset from the `Lahman` package, fit a model on runs (`R`) from the variables 'walks' (`BB`) and 'Hits' (`H`), grouped by team (`teamID`).
    - *Hint*: wrap the scale function around each predictor variable.

If you are attending a 3 x 2-hour workshop, this is the end of day 2

Generalized Linear Models

In the linear models discussed so far, we always assumed that the response can take any numeric value or at least any numeric value in a large range.

However, we often have response data that does not quite fit this assumption. This includes, for instance, count data that can only take non-negative integer values (*i.e.* 0, 1, 2, 3, …). Another example is binary data, where the response can take only one of two values (*e.g.* yes/no, low/high, 0/1, etc.).

Definition

Generalized Linear Models (GLMs) are exactly what their name suggests, a generalization of linear models introduced to different kinds of data. With GLMs, we want to model the *mean* μ (or rather a function called *link*) of the assumed distribution as a linear function of some covariates.

The model can be written as

$$g(\mu) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p$$

and we want to estimate the parameters β_0 to β_p for the p covariates from the available data.

The choice of the distribution is guided by the type of the response data (and the limited set of distributions for GLMs). The link function $g()$ is needed to convert the mean of the assumed distribution into a linear function of the model parameters, but it also makes it more difficult to interpret the parameters. The distributions usually have a "natural" link function, but other choices would be available too.

Before we discuss this in more detail, let's see how we can actually fit a GLM in R.

Fitting GLMs

To fit a generalized linear model in R, we use the function `glm` which works very similarly to the already known `lm` function. However, it allows us to specify the distribution we want to use via the argument `family`. Each family comes with a default link function. The help page for `?family` lists all supported types of GLMs. We explore some of them below.

Logistic regression (`family = binomial`)

We will first discuss the case of binary response data (*e.g.* no/yes, 0/1, failure/success, …). Oftentimes, we are interested in the probability of a *success* under certain circumstances, *i.e.* we want to model the success probability given a set of covariates.

The natural choice for this kind of data is to use the Binomial distribution. This distribution corresponds to the number of successes in m trials, if each trial is independent and has the same success probability. Binary data can be thought of as a single trial (*i.e.* $m = 1$). The mean of the Binomial distribution is the success probability p and the usual link function is the log of the odds.

This gives us the logistic regression model:

$$\log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p$$

Importantly, each trial needs to be independent and must have the same success probability!

As a first example, we will try logistic regression on the UC Berkeley Admission data (`UCBAdmissions`, pre-installed in R). We want to model log odds of being admitted, using the biological sex (incorrectly attributed as gender in the data set) of the applicant and the department as covariates.

Note: The data set does not contain one row per applicant, but rather has the *number of applications* that fall in each of the possible combinations. This can be easily used in R via the `weights` argument to `glm`.

```r
# Load and format data
ucb <- as.data.frame(UCBAdmissions) %>%
  dplyr::rename(sex=Gender)

# Fit GLM binomial
ucb_model <- glm(Admit ~ sex * Dept,
                 data = ucb,
                 family = binomial,
                 weights = Freq)

summary(ucb_model)
```

```
##
## Call:
## glm(formula = Admit ~ sex * Dept, family = binomial, data = ucb,
##     weights = Freq)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -22.1022  -15.6975    0.3243   13.0256   24.6314
##
## Coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -0.49212    0.07175  -6.859 6.94e-12 ***
## sexFemale       -1.05208    0.26271  -4.005 6.21e-05 ***
## DeptB           -0.04163    0.11319  -0.368  0.71304
## DeptC            1.02764    0.13550   7.584 3.34e-14 ***
## DeptD            1.19608    0.12641   9.462  < 2e-16 ***
## DeptE            1.44908    0.17681   8.196 2.49e-16 ***
## DeptF            3.26187    0.23120  14.109  < 2e-16 ***
## sexFemale:DeptB  0.83205    0.51039   1.630  0.10306
## sexFemale:DeptC  1.17700    0.29956   3.929 8.53e-05 ***
## sexFemale:DeptD  0.97009    0.30262   3.206  0.00135 **
## sexFemale:DeptE  1.25226    0.33032   3.791  0.00015 ***
## sexFemale:DeptF  0.86318    0.40267   2.144  0.03206 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 6044.3  on 23  degrees of freedom
## Residual deviance: 5167.3  on 12  degrees of freedom
## AIC: 5191.3
##
## Number of Fisher Scoring iterations: 6
```

The summary of the `glm` output shows us the value of each of the parameters as well as whether they are significantly different from 0. However, since our covariates are *categorical*, each of the two are reflected by multiple parameters (one for each "level" and combination of levels).

With the `Anova` function from the package `car`, we can check the significance of each of the two covariates as a whole.

```r
Anova(ucb_model)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Admit
##          LR Chisq Df Pr(>Chisq)
## sex          1.53  1   0.215928
## Dept       763.40  5  < 2.2e-16 ***
## sex:Dept    20.20  5   0.001144 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

This tells us that `sex` by itself has no significant effect on the log-odds of being admitted, but the interaction effect with the department seems to be important. Hence, we can not remove any of the covariates without significantly degrading the fit.

```
drop1(ucb_model, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## Admit ~ sex * Dept
##          Df Deviance    AIC    LRT Pr(>Chi)
## <none>        5167.3 5191.3
## sex:Dept  5   5187.5 5201.5 20.204 0.001144 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In GLMs with a link function (as in logistic regression), the interpretation of the parameters can be tricky. The sign of the parameter (*i.e.* is it positive or negative) can be interpreted as whether the covariate increases ("+") or decreases ("-") the odds, and hence, the probability of success. Also, the relative magnitudes tell you which covariate increases/decreases the probability more. However, the magnitude itself is not directly interpretable, *i.e.* you can not say "the probability of being admitted is 1.05 less for females than for males".

We can make statements about the probabilities themselves. The `lsmeans` function provides a nice overview of the fitted "success" (in our case "being admitted") probabilities for the different combinations of the predictors, including a confidence interval.

```
ucb_model_sum <- lsmeans(ucb_model, ~ sex + Dept, type = "response")
ucb_model_sum
```

```
##  sex    Dept  prob     SE  df asymp.LCL asymp.UCL
##  Male   A    0.379 0.0169 Inf     0.347     0.413
##  Female A    0.176 0.0366 Inf     0.115     0.259
##  Male   B    0.370 0.0204 Inf     0.331     0.410
##  Female B    0.320 0.0933 Inf     0.169     0.522
##  Male   C    0.631 0.0268 Inf     0.577     0.682
##  Female C    0.659 0.0195 Inf     0.620     0.696
##  Male   D    0.669 0.0230 Inf     0.622     0.713
##  Female D    0.651 0.0246 Inf     0.601     0.697
##  Male   E    0.723 0.0324 Inf     0.655     0.781
##  Female E    0.761 0.0215 Inf     0.716     0.800
##  Male   F    0.941 0.0122 Inf     0.912     0.961
##  Female F    0.930 0.0139 Inf     0.897     0.952
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
```

This summary can also be grouped by one of the predictors, *e.g.* by the department.

```
summary(ucb_model_sum, by = "Dept")
```

```
## Dept = A:
##  sex     prob     SE  df asymp.LCL asymp.UCL
##  Male   0.379 0.0169 Inf     0.347     0.413
##  Female 0.176 0.0366 Inf     0.115     0.259
##
## Dept = B:
##  sex     prob     SE  df asymp.LCL asymp.UCL
##  Male   0.370 0.0204 Inf     0.331     0.410
##  Female 0.320 0.0933 Inf     0.169     0.522
##
## Dept = C:
##  sex     prob     SE  df asymp.LCL asymp.UCL
##  Male   0.631 0.0268 Inf     0.577     0.682
##  Female 0.659 0.0195 Inf     0.620     0.696
##
## Dept = D:
##  sex     prob     SE  df asymp.LCL asymp.UCL
##  Male   0.669 0.0230 Inf     0.622     0.713
##  Female 0.651 0.0246 Inf     0.601     0.697
##
## Dept = E:
##  sex     prob     SE  df asymp.LCL asymp.UCL
##  Male   0.723 0.0324 Inf     0.655     0.781
##  Female 0.761 0.0215 Inf     0.716     0.800
##
## Dept = F:
##  sex     prob     SE  df asymp.LCL asymp.UCL
##  Male   0.941 0.0122 Inf     0.912     0.961
##  Female 0.930 0.0139 Inf     0.897     0.952
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
```

Similarly, we can get the *odds ratio* between males and females in each department. This basically tells us how different the odds are between male and female applicants in each department.

```
contrast(ucb_model_sum, "pairwise", by = "Dept")
```

```
## Dept = A:
##  contrast      odds.ratio    SE  df z.ratio p.value
##  Male / Female      2.864 0.752 Inf  4.005  0.0001
##
## Dept = B:
##  contrast      odds.ratio    SE  df z.ratio p.value
##  Male / Female      1.246 0.545 Inf  0.503  0.6151
##
## Dept = C:
##  contrast      odds.ratio    SE  df z.ratio p.value
##  Male / Female      0.883 0.127 Inf -0.868  0.3855
##
## Dept = D:
##  contrast      odds.ratio    SE  df z.ratio p.value
##  Male / Female      1.085 0.163 Inf  0.546  0.5852
```

```
##
## Dept = E:
##  contrast      odds.ratio    SE  df z.ratio p.value
##  Male / Female      0.819 0.164 Inf -1.000  0.3174
##
## Dept = F:
##  contrast      odds.ratio    SE  df z.ratio p.value
##  Male / Female      1.208 0.369 Inf  0.619  0.5359
##
## Tests are performed on the log odds ratio scale
```

This tells us that sex seems to make a significant difference in Department A but not so in the other departments. This, in turn, causes the significant interaction effect we saw before.

Exercise: Logistic GLM


Exercise.

1. In the plasma data (from the `HSAUR3` package), use logistic regression to estimate the probabilities of ESR > 20, given the level of fibrinogen in the blood.
2. Using the `womensrole` data set from the `HSAUR3` package, try to fit a logistic regression to the agreement with the statement, given the years of education and the respondent's sex (also attributed as `gender` in these data).

Count Data (`family = poisson`)

When we are dealing with count data, the Poisson distribution is often used as a model. The Poisson distribution models the number of events during a fixed period of time (or space, etc.). It is completely characterized by the *rate* parameter μ. Both the mean and the variance of the Poisson distribution are equal to the *rate* parameter. In other words, a larger *rate* also implies a larger spread of the data. This is a rather strong assumption and we will learn how to check if this assumption is reasonable for a given data set. The usual link function for Poisson GLMs is the log, so our GLM for the rate μ is:

$$\log(\mu) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p.$$

Let's use this model on the `polyps` data set (pre-installed). We want to explain the number of colonic polyps at 12 months by means of the age of the patient and whether they are in the treatment group.

```
polyps_model1 <- glm(number ~ treat + age,
                     data = polyps,
                     family = poisson)
summary(polyps_model1)
```

```
##
## Call:
## glm(formula = number ~ treat + age, family = poisson, data = polyps)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.2212  -3.0536  -0.1802   1.4459   5.8301
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)  4.529024   0.146872   30.84  < 2e-16 ***
## treatdrug   -1.359083   0.117643  -11.55  < 2e-16 ***
## age         -0.038830   0.005955   -6.52 7.02e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 378.66  on 19  degrees of freedom
## Residual deviance: 179.54  on 17  degrees of freedom
## AIC: 273.88
##
## Number of Fisher Scoring iterations: 5
```

We assumed that the mean and the variance are equal. But how close is this assumption to the truth? R supports the "quasi-" family which allows for the variance to be different.

```
polyps_model2 <- glm(number ~ treat + age,
                     data = polyps,
                     family = quasipoisson)
summary(polyps_model2)
```

```
##
## Call:
## glm(formula = number ~ treat + age, family = quasipoisson, data = polyps)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.2212  -3.0536  -0.1802   1.4459   5.8301
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.52902    0.48106   9.415 3.72e-08 ***
## treatdrug   -1.35908    0.38533  -3.527  0.00259 **
## age         -0.03883    0.01951  -1.991  0.06284 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 10.72805)
##
##     Null deviance: 378.66  on 19  degrees of freedom
## Residual deviance: 179.54  on 17  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

The fitted quasi-Poisson model results in dispersion parameter different from 1, which makes the assumption of equal mean and variance highly questionable. If the assumption of equal mean and variance is wrong, the standard errors of the parameters are grossly underestimated. The uncoupling of the mean and the variance does not change the parameter estimates, but the significance of the parameters in the model will be different.

Similarly to logistic regression, we can investigate the difference in the rate between two levels of a categorical covariate:

```
polyps_model2_sum <- lsmeans(polyps_model2, ~ treat,
                             type = "response")
```

```r
contrast(polyps_model2_sum, "pairwise")
```

```
##  contrast       ratio  SE  df z.ratio p.value
##  placebo / drug  3.89 1.5 Inf 3.527   0.0004
##
## Tests are performed on the log scale
```

The significant (p= 4.2012649×10^{-4}) `rate.ratio` of 3.8926236 tells us that the rate of the number of colonic polyps at 12 months for subjects in the placebo group is 3.8926236 times higher than for subjects in the treatment group.

Exercise: Poisson GLM


Exercise.

1. Check which *covariates* have a significant effect on the response in the model fitted with the Poisson family and with the quasi-Poisson family and compare the results. What do you observe?

Negative binomial model for count data

An over-dispersed Poisson regression model (*i.e.* fitted with quasi-Poisson) is similar to a Negative Binomial (NB) regression model. This can be fitted with the `glm.nb` function from the `MASS` package. For instance, we can model the days absent from school based on the sex of students, their age, ethnic background, and learner status. These data are within `quine` from this same package.

```r
quine_model <- glm.nb(Days ~ Sex * (Age + Eth * Lrn),
                      data = quine)
## equivalent to
## quine_model <- glm.nb(Days ~ Sex * Age + Sex * Eth * Lrn, data = quine)
summary(quine_model)
```

```
##
## Call:
## glm.nb(formula = Days ~ Sex * (Age + Eth * Lrn), data = quine,
##     init.theta = 1.597990733, link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.8950  -0.8827  -0.2299   0.5669   2.1071
##
## Coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)      3.01919    0.29706  10.163  < 2e-16 ***
## SexM            -0.47541    0.39550  -1.202 0.229355
## AgeF1           -0.70887    0.32321  -2.193 0.028290 *
## AgeF2           -0.61486    0.37141  -1.655 0.097826 .
## AgeF3           -0.34235    0.32717  -1.046 0.295388
## EthN            -0.07312    0.26539  -0.276 0.782908
## LrnSL            0.94358    0.32246   2.926 0.003432 **
## EthN:LrnSL      -1.35849    0.37719  -3.602 0.000316 ***
## SexM:AgeF1      -0.01486    0.46225  -0.032 0.974353
## SexM:AgeF2       1.24328    0.46134   2.695 0.007040 **
## SexM:AgeF3       1.49319    0.45337   3.294 0.000989 ***
```

```
## SexM:EthN       -0.60586    0.36896  -1.642 0.100572
## SexM:LrnSL      -0.70467    0.46536  -1.514 0.129966
## SexM:EthN:LrnSL  2.11991    0.58056   3.651 0.000261 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.598) family taken to be 1)
##
##     Null deviance: 234.56  on 145  degrees of freedom
## Residual deviance: 167.56  on 132  degrees of freedom
## AIC: 1093
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  1.598
##           Std. Err.:  0.213
##
##  2 x log-likelihood:  -1063.025
```

```
Anova(quine_model)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Days
##             LR Chisq Df Pr(>Chisq)
## Sex           0.9284  1  0.3352783
## Age          14.9609  3  0.0018503 **
## Eth          16.9573  1  3.823e-05 ***
## Lrn           5.6903  1  0.0170588 *
## Eth:Lrn       2.5726  1  0.1087268
## Sex:Age      19.8297  3  0.0001841 ***
## Sex:Eth       0.6547  1  0.4184372
## Sex:Lrn       1.4965  1  0.2212106
## Sex:Eth:Lrn  12.9647  1  0.0003174 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From the ANOVA table we see that several terms are not significant, but the highest order term involving any of the four factors is significant. Therefore we cannot remove any terms from the model.

```
drop1(quine_model, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## Days ~ Sex * (Age + Eth * Lrn)
##             Df Deviance    AIC    LRT  Pr(>Chi)
## <none>           167.56 1091.0
## Sex:Age      3   187.39 1104.8 19.830 0.0001841 ***
## Sex:Eth:Lrn  1   180.52 1102.0 12.965 0.0003174 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can use `lsmeans` to compare groups but the relationships are hard to interpret because there are high order interaction terms in the model.

```
quine_model_sum1 <- lsmeans(quine_model, ~ Sex + Eth + Lrn, type = "response")
summary(quine_model_sum1, by = c("Sex", "Eth"))
```

```
## Sex = F, Eth = A:
##  Lrn response   SE  df asymp.LCL asymp.UCL
##  AL     13.50 2.78 Inf      9.01      20.2
##  SL     34.68 7.63 Inf     22.53      53.4
##
## Sex = M, Eth = A:
##  Lrn response   SE  df asymp.LCL asymp.UCL
##  AL     16.57 3.12 Inf     11.46      24.0
##  SL     21.04 5.73 Inf     12.35      35.9
##
## Sex = F, Eth = N:
##  Lrn response   SE  df asymp.LCL asymp.UCL
##  AL     12.55 2.49 Inf      8.50      18.5
##  SL      8.29 1.87 Inf      5.33      12.9
##
## Sex = M, Eth = N:
##  Lrn response   SE  df asymp.LCL asymp.UCL
##  AL      8.40 1.60 Inf      5.78      12.2
##  SL     22.85 5.76 Inf     13.94      37.5
##
## Results are averaged over the levels of: Age
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

```
summary(quine_model_sum1, by = c("Eth", "Lrn"))
```

```
## Eth = A, Lrn = AL:
##  Sex response   SE  df asymp.LCL asymp.UCL
##  F      13.50 2.78 Inf      9.01      20.2
##  M      16.57 3.12 Inf     11.46      24.0
##
## Eth = N, Lrn = AL:
##  Sex response   SE  df asymp.LCL asymp.UCL
##  F      12.55 2.49 Inf      8.50      18.5
##  M       8.40 1.60 Inf      5.78      12.2
##
## Eth = A, Lrn = SL:
##  Sex response   SE  df asymp.LCL asymp.UCL
##  F      34.68 7.63 Inf     22.53      53.4
##  M      21.04 5.73 Inf     12.35      35.9
##
## Eth = N, Lrn = SL:
##  Sex response   SE  df asymp.LCL asymp.UCL
##  F       8.29 1.87 Inf      5.33      12.9
##  M      22.85 5.76 Inf     13.94      37.5
##
## Results are averaged over the levels of: Age
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

```
quine_model_sum2 <- lsmeans(quine_model, ~ Sex + Age, type = "response")
summary(quine_model_sum2, by = "Sex")
```

```
## Sex = F:
##  Age response   SE  df asymp.LCL asymp.UCL
##  F0     22.53 6.11 Inf     13.23     38.35
##  F1     11.09 1.73 Inf      8.16     15.06
##  F2     12.18 2.68 Inf      7.92     18.74
##  F3     16.00 3.70 Inf     10.16     25.19
##
## Sex = M:
##  Age response   SE  df asymp.LCL asymp.UCL
##  F0     12.36 2.58 Inf      8.21     18.60
##  F1      5.99 1.49 Inf      3.68      9.76
##  F2     23.16 4.26 Inf     16.15     33.22
##  F3     39.05 9.80 Inf     23.88     63.87
##
## Results are averaged over the levels of: Eth, Lrn
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

```
summary(quine_model_sum2, by = "Age")
```

```
## Age = F0:
##  Sex response   SE  df asymp.LCL asymp.UCL
##  F      22.53 6.11 Inf     13.23     38.35
##  M      12.36 2.58 Inf      8.21     18.60
##
## Age = F1:
##  Sex response   SE  df asymp.LCL asymp.UCL
##  F      11.09 1.73 Inf      8.16     15.06
##  M       5.99 1.49 Inf      3.68      9.76
##
## Age = F2:
##  Sex response   SE  df asymp.LCL asymp.UCL
##  F      12.18 2.68 Inf      7.92     18.74
##  M      23.16 4.26 Inf     16.15     33.22
##
## Age = F3:
##  Sex response   SE  df asymp.LCL asymp.UCL
##  F      16.00 3.70 Inf     10.16     25.19
##  M      39.05 9.80 Inf     23.88     63.87
##
## Results are averaged over the levels of: Eth, Lrn
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

Exercise: Quasi-poisson vs. negative binomial GLM


Exercise.

1. Fit the above model with a Quasi-Poisson family and check the over-dispersion in that fit. Is there a difference in the significance of any terms compared to the NB model? Would a Poisson model be appropriate as well?

Survey

Please provide us with feedback through this short survey.