Univariate and multivariable regression

::: callout-tip ## Extended Materials

You can find the original, extended version of this chapter here. ::

This page demonstrates the use of **base** R regression functions such as `glm()` and the **gtsummary** package to look at associations between variables (e.g. odds ratios, risk ratios and hazard ratios). It also uses functions like `tidy()` from the **broom** package to clean-up regression outputs.

Data Preparation

Load packages

```
pacman::p_load(
  rio,          # File import
  here,         # File locator
  tidyverse,    # data management + ggplot2 graphics,
  stringr,      # manipulate text strings
  purrr,        # loop over objects in a tidy way
  gtsummary,    # summary statistics and tests
  broom,        # tidy up results from regressions
  lmtest,       # likelihood-ratio tests
  parameters,   # alternative to tidy up results from regressions
  see          # alternative to visualise forest plots
  )
```

Import data

We import the dataset of cases from a simulated Ebola epidemic. If you want to follow along, click to download the "clean" linelist (as .rds file).

```
# import the linelist
linelist <- import("linelist_cleaned.rds")
```

Clean data

* Store explanatory variables

We store the names of the explanatory columns as a character vector. This will be referenced later.

```
## define variables of interest
explanatory_vars <- c("gender", "fever", "chills", "cough", "aches", "vomit")
```

* Convert to 1's and 0's

Below we convert the explanatory columns from "yes"/"no", "m"/"f", and "dead"/"alive" to **1 / 0**, to cooperate with the expectations of logistic regression models. To do this efficiently, used `across()` from **dplyr** to transform multiple columns at one time. The function we apply to each column is `case_when()` (also **dplyr**) which applies logic to convert specified values to 1's and 0's.

Note: the "." below represents the column that is being processed by `across()` at that moment.

```
## convert dichotomous variables to 0/1
linelist <- linelist %>%
  mutate(across(
    .cols = all_of(c(explanatory_vars, "outcome")),  ## for each column listed and "outc
    .fns = ~case_when(
      . %in% c("m", "yes", "Death")   ~ 1,           ## recode male, yes and death to 1
      . %in% c("f", "no",  "Recover") ~ 0,           ## female, no and recover to 0
      TRUE                            ~ NA_real_)    ## otherwise set to missing
    )
  )
```

* Drop rows with missing values

To drop rows with missing values, can use the **tidyr** function `drop_na()`. However, we only want to do this for rows that are missing values in the columns of interest.

The first thing we must to is make sure our `explanatory_vars` vector includes the column `age` (`age` would have produced an error in the previous `case_when()` operation, which was only for dichotomous variables). Then we pipe the `linelist` to `drop_na()` to remove any rows with missing values in the `outcome` column or any of the `explanatory_vars` columns.

Before running the code, the number of rows in the `linelist` is `nrow(linelist)`.

```
## add in age_category to the explanatory vars
explanatory_vars <- c(explanatory_vars, "age_cat")

## drop rows with missing information for variables of interest
linelist <- linelist %>%
  drop_na(any_of(c("outcome", explanatory_vars)))
```

> The number of rows remaining in `linelist` is `nrow(linelist)`.

Univariate

Your use case will determine which R package you use. We present two options for doing univariate analysis:

- Use functions available in **base** R to quickly print results to the console. Use the **broom** package to tidy up the outputs.
- Use the **gtsummary** package to model and get publication-ready outputs

base R

* Linear regression

The **base** R function `lm()` perform linear regression, assessing the relationship between numeric response and explanatory variables that are assumed to have a linear relationship.

Provide the equation as a formula, with the response and explanatory column names separated by a tilde `~`. Also, specify the dataset to `data =`. Define the model results as an R object, to use later.

```
lm_results <- lm(ht_cm ~ age, data = linelist)
```

You can then run `summary()` on the model results to see the coefficients (Estimates), P-value, residuals, and other measures.

```
summary(lm_results)
```

```
Call:
lm(formula = ht_cm ~ age, data = linelist)

Residuals:
     Min       1Q   Median       3Q      Max
-128.579  -15.854    1.177   15.887  175.483

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  69.9051     0.5979   116.9   <2e-16 ***
```

```
age           3.4354     0.0293   117.2   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 23.75 on 4165 degrees of freedom
Multiple R-squared:  0.7675,    Adjusted R-squared:  0.7674
F-statistic: 1.375e+04 on 1 and 4165 DF,  p-value: < 2.2e-16
```

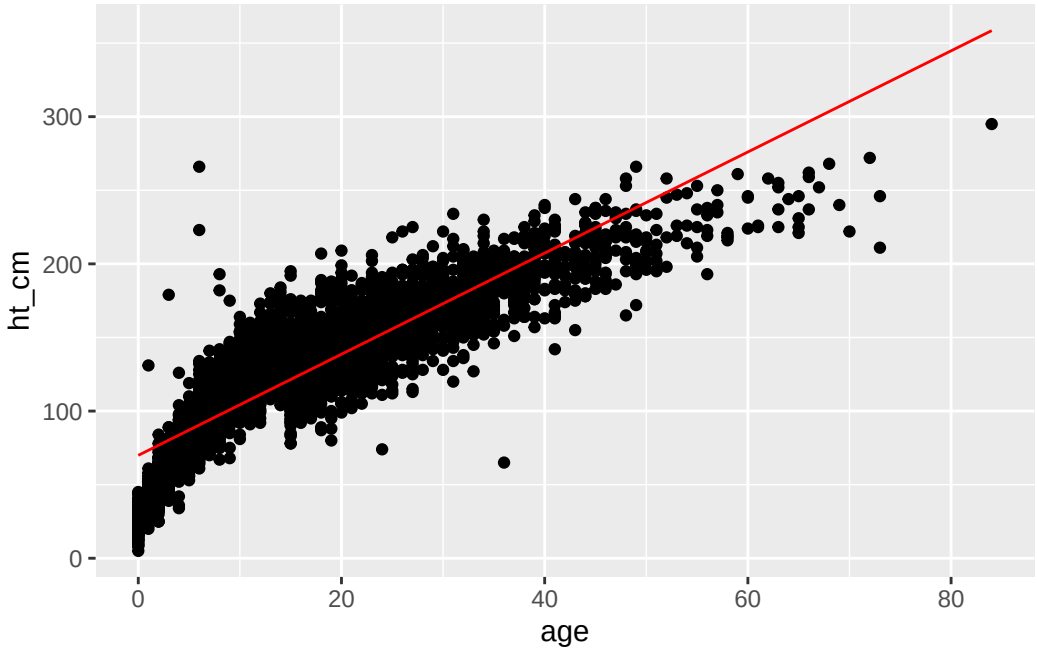
Alternatively you can use the `tidy()` function from the **broom** package to pull the results in to a table. What the results tell us is that for each year increase in age the height increases by 3.5 cm and this is statistically significant.

```
tidy(lm_results)
```

```
# A tibble: 2 x 5
  term        estimate std.error statistic p.value
  <chr>          <dbl>     <dbl>     <dbl>   <dbl>
1 (Intercept)    69.9     0.598       117.        0
2 age             3.44    0.0293      117.        0
```

You can then also use this regression to add it to a **ggplot**, to do this we first pull the points for the observed data and the fitted line in to one data frame using the `augment()` function from **broom**.

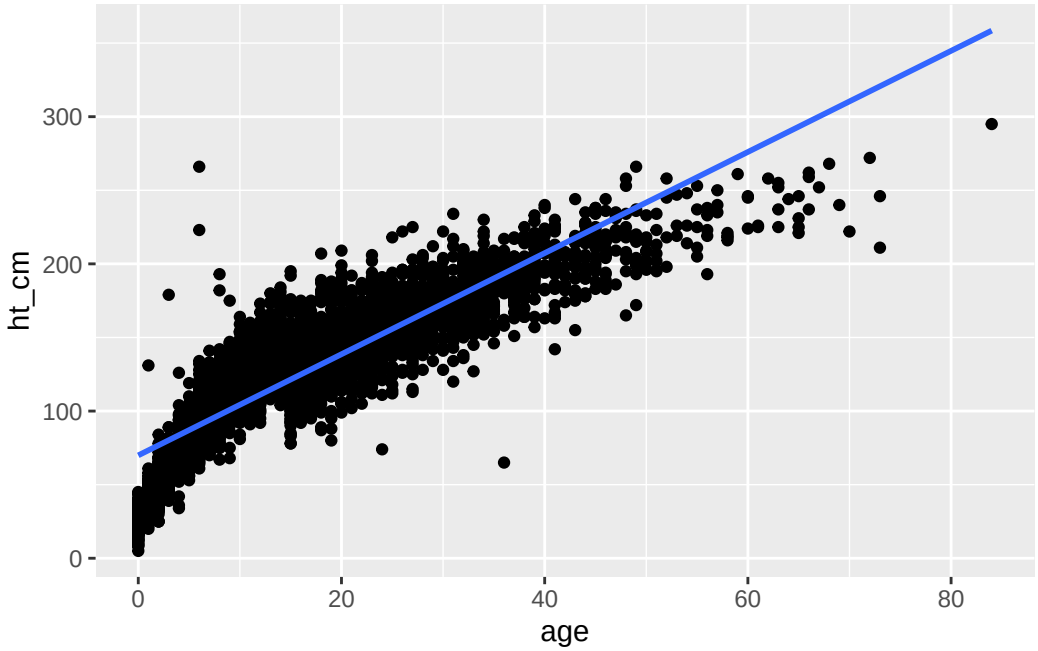
```
## pull the regression points and observed data in to one dataset
points <- augment(lm_results)

## plot the data using age as the x-axis
ggplot(points, aes(x = age)) +
  ## add points for height
  geom_point(aes(y = ht_cm)) +
  ## add your regression line
  geom_line(aes(y = .fitted), colour = "red")
```



It is also possible to add a simple linear regression straight straight in **ggplot** using the `geom_smooth()` function.

```
## add your data to a plot
 ggplot(linelist, aes(x = age, y = ht_cm)) +
  ## show points
  geom_point() +
  ## add a linear regression
  geom_smooth(method = "lm", se = FALSE)
```

```
`geom_smooth()` using formula = 'y ~ x'
```



See the Resource section at the end of this chapter for more detailed tutorials.

* Logistic regression

The function `glm()` from the **stats** package (part of **base** R) is used to fit Generalized Linear Models (GLM).

`glm()` can be used for univariate and multivariable logistic regression (e.g. to get Odds Ratios). Here are the core parts:

```
# arguments for glm()
glm(formula, family, data, weights, subset, ...)
```

- `formula =` The model is provided to `glm()` as an equation, with the outcome on the left and explanatory variables on the right of a tilde `~`.
- `family =` This determines the type of model to run. For logistic regression, use `family = "binomial"`, for poisson use `family = "poisson"`. Other examples are in the table below.
- `data =` Specify your data frame

If necessary, you can also specify the link function via the syntax `family = familytype(link = "linkfunction"))`. You can read more in the documentation about other families and optional arguments such as `weights =` and `subset =` (`?glm`).

Family	Default link function
"binomial"	(link = "logit")
"gaussian"	(link = "identity")
"Gamma"	(link = "inverse")
"inverse.gaussian"	(link = "1/mu^2")
"poisson"	(link = "log")
"quasi"	(link = "identity", variance = "constant")
"quasibinomial"	(link = "logit")
"quasipoisson"	(link = "log")

When running `glm()` it is most common to save the results as a named R object. Then you can print the results to your console using `summary()` as shown below, or perform other operations on the results (e.g. exponentiate).

* Univariate `glm()`

In this example we are assessing the association between different age categories and the outcome of death (coded as 1 in the Preparation section). Below is a univariate model of `outcome` by `age_cat`. We save the model output as `model` and then print it with `summary()` to the console. Note the estimates provided are the *log odds* and that the baseline level is the first factor level of `age_cat` ("0-4").

```
model <- glm(outcome ~ age_cat, family = "binomial", data = linelist)
summary(model)
```

```
Call:
glm(formula = outcome ~ age_cat, family = "binomial", data = linelist)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.233738   0.072805   3.210  0.00133 **
age_cat5-9   -0.062898   0.101733  -0.618  0.53640
age_cat10-14  0.138204   0.107186   1.289  0.19726
age_cat15-19 -0.005565   0.113343  -0.049  0.96084
age_cat20-29  0.027511   0.102133   0.269  0.78765
```

```
age_cat30-49  0.063764   0.113771   0.560  0.57517
age_cat50-69 -0.387889   0.259240  -1.496  0.13459
age_cat70+   -0.639203   0.915770  -0.698  0.48518
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 5712.4  on 4166  degrees of freedom
Residual deviance: 5705.1  on 4159  degrees of freedom
AIC: 5721.1

Number of Fisher Scoring iterations: 4
```

To alter the baseline level of a given variable, ensure the column is class Factor and move the desired level to the first position with `fct_relevel()`. For example, below we take column `age_cat` and set "20-29" as the baseline before piping the modified data frame into `glm()`.

```r
linelist %>%
  mutate(age_cat = fct_relevel(age_cat, "20-29", after = 0)) %>%
  glm(formula = outcome ~ age_cat, family = "binomial") %>%
  summary()
```

```
Call:
glm(formula = outcome ~ age_cat, family = "binomial", data = .)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.26125    0.07163   3.647 0.000265 ***
age_cat0-4   -0.02751    0.10213  -0.269 0.787652
age_cat5-9   -0.09041    0.10090  -0.896 0.370220
age_cat10-14  0.11069    0.10639   1.040 0.298133
age_cat15-19 -0.03308    0.11259  -0.294 0.768934
age_cat30-49  0.03625    0.11302   0.321 0.748390
age_cat50-69 -0.41540    0.25891  -1.604 0.108625
age_cat70+   -0.66671    0.91568  -0.728 0.466546
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)
```

```
    Null deviance: 5712.4  on 4166  degrees of freedom
Residual deviance: 5705.1  on 4159  degrees of freedom
AIC: 5721.1

Number of Fisher Scoring iterations: 4
```

* Printing results

For most uses, several modifications must be made to the above outputs. The function `tidy()` from the package **broom** is convenient for making the model results presentable.

Here we demonstrate how to combine model outputs with a table of counts.

1) Get the *exponentiated* log odds ratio estimates and confidence intervals by passing the model to `tidy()` and setting `exponentiate = TRUE` and `conf.int = TRUE`.

```
model <- glm(outcome ~ age_cat, family = "binomial", data = linelist) %>%
  tidy(exponentiate = TRUE, conf.int = TRUE) %>%        # exponentiate and produce CIs
  mutate(across(where(is.numeric), round, digits = 2))  # round all numeric columns
```

```
Warning: There was 1 warning in `mutate()`.
i In argument: `across(where(is.numeric), round, digits = 2)`.
Caused by warning:
! The `...` argument of `across()` is deprecated as of dplyr 1.1.0.
Supply arguments directly to `.fns` through an anonymous function instead.

  # Previously
  across(a:b, mean, na.rm = TRUE)

  # Now
  across(a:b, \(x) mean(x, na.rm = TRUE))
```

Below is the outputted tibble `model`:

Show 8 entries Search:

term			estimate		std.
(Intercept)	1.26	0.07	3.21	0	1.1	1.4
age_cat5-9	0.94	0.1	-0.62	0.54	0.77	1.1
age_cat10-14	1.15	0.11	1.29	0.2	0.93	1.4
age_cat15-19	0.99	0.11	-0.05	0.96	0.8	1.2
age_cat20-29	1.03	0.1	0.27	0.79	0.84	1.2
age_cat30-49	1.07	0.11	0.56	0.58	0.85	1.3
age_cat50-69	0.68	0.26	-1.5	0.13	0.41	1.1
age_cat70+	0.53	0.92	-0.7	0.49	0.07	3

Showing 1 to 8 of 8 entries Previous 1 Next

2) Combine these model results with a table of counts. Below, we create the a counts cross-table with the `tabyl()` function from **janitor**.

```
counts_table <- linelist %>%
  janitor::tabyl(age_cat, outcome)
```

Here is what this `counts_table` data frame looks like:

Show 8 entries Search:

age_cat		
0-4	338	427
5-9	365	433
10-14	273	396
15-19	238	299
20-29	345	448
30-49	228	307
50-69	35	30
70+	3	2

Showing 1 to 8 of 8 entries Previous 1 Next

Now we can bind the `counts_table` and the `model` results together horizontally with `bind_cols()` (**dplyr**). Remember that with `bind_cols()` the rows in the two data frames must be aligned perfectly. In this code, because we are binding within a pipe chain, we use `.` to represent the piped object `counts_table` as we bind it to `model`. To finish the process, we use `select()` to pick the desired columns and their order, and finally apply the **base** R `round()` function across all numeric columns to specify 2 decimal places.

```
combined <- counts_table %>%           # begin with table of counts
  bind_cols(., model) %>%              # combine with the outputs of the regression
  select(term, 2:3, estimate,          # select and re-order cols
         conf.low, conf.high, p.value) %>%
  mutate(across(where(is.numeric), round, digits = 2)) ## round to 2 decimal places
```

Here is what the combined data frame looks like, printed nicely as an image with a function from **flextable**. The [Tables for presentation] explains how to customize such tables with **flextable**, or or you can use numerous other packages such as **knitr** or **GT**.

```
combined <- combined %>%
  flextable::qflextable()
```

* Looping multiple univariate models

Below we present a method using `glm()` and `tidy()` for a more simple approach, see the section on **gtsummary**.

To run the models on several exposure variables to produce univariate odds ratios (i.e. not controlling for each other), you can use the approach below. It uses `str_c()` from **stringr** to create univariate formulas (see [Characters and strings]), runs the `glm()` regression on each formula, passes each `glm()` output to `tidy()` and finally collapses all the model outputs together with `bind_rows()` from **tidyr**. This approach uses `map()` from the package **purrr** to iterate.

1) Create a vector of column names of the explanatory variables. We already have this as `explanatory_vars` from the Preparation section of this page.
2) Use `str_c()` to create multiple string formulas, with `outcome` on the left, and a column name from `explanatory_vars` on the right. The period `.` substitutes for the column name in `explanatory_vars`.

```
explanatory_vars %>% str_c("outcome ~ ", .)
```

```
[1] "outcome ~ gender"  "outcome ~ fever"   "outcome ~ chills"
```

```
[4] "outcome ~ cough"   "outcome ~ aches"   "outcome ~ vomit"
[7] "outcome ~ age_cat"
```

3) Pass these string formulas to `map()` and set `~glm()` as the function to apply to each input. Within `glm()`, set the regression formula as `as.formula(.x)` where `.x` will be replaced by the string formula defined in the step above. `map()` will loop over each of the string formulas, running regressions for each one.

4) The outputs of this first `map()` are passed to a second `map()` command, which applies `tidy()` to the regression outputs.

5) Finally the output of the second `map()` (a list of tidied data frames) is condensed with `bind_rows()`, resulting in one data frame with all the univariate results.

```
models <- explanatory_vars %>%       # begin with variables of interest
  str_c("outcome ~ ", .) %>%         # combine each variable into formula ("outcome ~ vari

  # iterate through each univariate formula
  map(
    .f = ~glm(                       # pass the formulas one-by-one to glm()
      formula = as.formula(.x),      # within glm(), the string formula is .x
      family = "binomial",           # specify type of glm (logistic)
      data = linelist)) %>%          # dataset

  # tidy up each of the glm regression outputs from above
  map(
    .f = ~tidy(
      .x,
      exponentiate = TRUE,           # exponentiate
      conf.int = TRUE)) %>%          # return confidence intervals

  # collapse the list of regression outputs in to one data frame
  bind_rows() %>%

  # round all numeric columns
  mutate(across(where(is.numeric), round, digits = 2))
```

This time, the end object `models` is longer because it now represents the combined results of several univariate regressions. Click through to see all the rows of `model`.

Show 5 entries Search:

term			estimate			std.erro
(Intercept)	1.28	0.04	5.67	0	1.18	1.4
gender	1	0.06	-0.04	0.97	0.88	1.13
(Intercept)	1.28	0.07	3.44	0	1.11	1.48
fever	1	0.08	0.01	0.99	0.85	1.17
(Intercept)	1.28	0.03	6.98	0	1.19	1.37

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As before, we can create a counts table from the `linelist` for each explanatory variable, bind it to `models`, and make a nice table. We begin with the variables, and iterate through them with `map()`. We iterate through a user-defined function which involves creating a counts table with **dplyr** functions. Then the results are combined and bound with the `models` model results.

```
## for each explanatory variable
univ_tab_base <- explanatory_vars %>%
  map(.f =
    ~{linelist %>%                ## begin with linelist
        group_by(outcome) %>%     ## group data set by outcome
        count(.data[[.x]]) %>%    ## produce counts for variable of interest
        pivot_wider(              ## spread to wide format (as in cross-tabulation)
          names_from = outcome,
          values_from = n) %>%
        drop_na(.data[[.x]]) %>%         ## drop rows with missings
        rename("variable" = .x) %>%      ## change variable of interest column to "variabl
        mutate(variable = as.character(variable))} ## convert to character, else non-dicho
     ) %>%

  ## collapse the list of count outputs in to one data frame
  bind_rows() %>%

  ## merge with the outputs of the regression
  bind_cols(., models) %>%

  ## only keep columns interested in
  select(term, 2:3, estimate, conf.low, conf.high, p.value) %>%

  ## round decimal places
  mutate(across(where(is.numeric), round, digits = 2))
```

Below is what the data frame looks like.

Show 5 entries Search:

term			0		1	
(Intercept)	909	1168	1.28	1.18	1.4	0
gender	916	1174	1	0.88	1.13	0.97
(Intercept)	340	436	1.28	1.11	1.48	0
fever	1485	1906	1	0.85	1.17	0.99
(Intercept)	1472	1877	1.28	1.19	1.37	0

Showing 1 to 5 of 20 entries Previous 1 2 3 4 Next

gtsummary package

Below we present the use of `tbl_uvregression()` from the **gtsummary** package. **gtsummary** functions do a good job of running statistics *and* producing professional-looking outputs. This function produces a table of univariate regression results.

We select only the necessary columns from the `linelist` (explanatory variables and the outcome variable) and pipe them into `tbl_uvregression()`. We are going to run univariate regression on each of the columns we defined as `explanatory_vars` in the data Preparation section (gender, fever, chills, cough, aches, vomit, and age_cat).

Within the function itself, we provide the `method =` as `glm` (no quotes), the `y =` outcome column (`outcome`), specify to `method.args =` that we want to run logistic regression via `family = binomial`, and we tell it to exponentiate the results.

The output is HTML and contains the counts

```
univ_tab <- linelist %>%
  dplyr::select(explanatory_vars, outcome) %>% ## select variables of interest

  tbl_uvregression(                           ## produce univariate table
    method = glm,                             ## define regression want to run (generalised
    y = outcome,                              ## define outcome variable
    method.args = list(family = binomial),    ## define what type of glm want to run (logist
    exponentiate = TRUE                       ## exponentiate to produce odds ratios (rather
  )

## view univariate results table
univ_tab
```

Characteristic	N	OR	95% CI	p-value
gender	4,167	1.00	0.88, 1.13	>0.9
fever	4,167	1.00	0.85, 1.17	>0.9
chills	4,167	1.03	0.89, 1.21	0.7
cough	4,167	1.15	0.97, 1.37	0.11
aches	4,167	0.93	0.76, 1.14	0.5
vomit	4,167	1.09	0.96, 1.23	0.2
age_cat	4,167			
0-4		—	—	
5-9		0.94	0.77, 1.15	0.5
10-14		1.15	0.93, 1.42	0.2
15-19		0.99	0.80, 1.24	>0.9
20-29		1.03	0.84, 1.26	0.8

Characteristic	N	OR	95% CI	p-value
30-49		1.07	0.85, 1.33	0.6
50-69		0.68	0.41, 1.13	0.13
70+		0.53	0.07, 3.20	0.5

There are many modifications you can make to this table output, such as adjusting the text labels, bolding rows by their p-value, etc. See tutorials here and elsewhere online.

Multivariable

For multivariable analysis, we again present two approaches:

- `glm()` and `tidy()`
- **gtsummary** package

The workflow is similar for each and only the last step of pulling together a final table is different.

Conduct multivariable

Here we use `glm()` but add more variables to the right side of the equation, separated by plus symbols (+).

To run the model with all of our explanatory variables we would run:

```
mv_reg <- glm(outcome ~ gender + fever + chills + cough + aches + vomit + age_cat, family

summary(mv_reg)
```

```
Call:
glm(formula = outcome ~ gender + fever + chills + cough + aches +
    vomit + age_cat, family = "binomial", data = linelist)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.069054   0.131726   0.524    0.600
gender       0.002448   0.065133   0.038    0.970
fever        0.004309   0.080522   0.054    0.957
```

```
chills         0.034112   0.078924   0.432    0.666
cough          0.138584   0.089909   1.541    0.123
aches         -0.070705   0.104078  -0.679    0.497
vomit          0.086098   0.062618   1.375    0.169
age_cat5-9    -0.063562   0.101851  -0.624    0.533
age_cat10-14   0.136372   0.107275   1.271    0.204
age_cat15-19  -0.011074   0.113640  -0.097    0.922
age_cat20-29   0.026552   0.102780   0.258    0.796
age_cat30-49   0.059569   0.116402   0.512    0.609
age_cat50-69  -0.388964   0.262384  -1.482    0.138
age_cat70+    -0.647443   0.917375  -0.706    0.480

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 5712.4  on 4166  degrees of freedom
Residual deviance: 5700.2  on 4153  degrees of freedom
AIC: 5728.2

Number of Fisher Scoring iterations: 4
```

If you want to include two variables and an interaction between them you can separate them with an asterisk `*` instead of a `+`. Separate them with a colon `:` if you are only specifying the interaction. For example:

```
glm(outcome ~ gender + age_cat * fever, family = "binomial", data = linelist)
```

Optionally, you can use this code to leverage the pre-defined vector of column names and re-create the above command using `str_c()`. This might be useful if your explanatory variable names are changing, or you don't want to type them all out again.

```
## run a regression with all variables of interest
mv_reg <- explanatory_vars %>%  ## begin with vector of explanatory column names
  str_c(collapse = "+") %>%     ## combine all names of the variables of interest separate
  str_c("outcome ~ ", .) %>%    ## combine the names of variables of interest with outcome
  glm(family = "binomial",      ## define type of glm as logistic,
      data = linelist)          ## define your dataset
```

***** Building the model

You can build your model step-by-step, saving various models that include certain explanatory variables. You can compare these models with likelihood-ratio tests using `lrtest()` from the package **lmtest**, as below:

NOTE: Using **base** `anova(model1, model2, test = "Chisq)` produces the same results

```
model1 <- glm(outcome ~ age_cat, family = "binomial", data = linelist)
model2 <- glm(outcome ~ age_cat + gender, family = "binomial", data = linelist)

lmtest::lrtest(model1, model2)
```

```
Likelihood ratio test

Model 1: outcome ~ age_cat
Model 2: outcome ~ age_cat + gender
  #Df  LogLik Df Chisq Pr(>Chisq)
1   8 -2852.6
2   9 -2852.6  1 2e-04     0.9883
```

Another option is to take the model object and apply the `step()` function from the **stats** package. Specify which variable selection direction you want use when building the model.

```
## choose a model using forward selection based on AIC
## you can also do "backward" or "both" by adjusting the direction
final_mv_reg <- mv_reg %>%
  step(direction = "forward", trace = FALSE)
```

You can also turn off scientific notation in your R session, for clarity:

```
options(scipen=999)
```

As described in the section on univariate analysis, pass the model output to `tidy()` to exponentiate the log odds and CIs. Finally we round all numeric columns to two decimal places. Scroll through to see all the rows.

```
mv_tab_base <- final_mv_reg %>%
  broom::tidy(exponentiate = TRUE, conf.int = TRUE) %>%  ## get a tidy dataframe of estima
  mutate(across(where(is.numeric), round, digits = 2))          ## round
```

Here is what the resulting data frame looks like:

Show 10 entries Search:

term			estimate		std.
(Intercept)	1.07	0.13	0.52	0.6	0.83	1.3
gender	1	0.07	0.04	0.97	0.88	1.1
fever	1	0.08	0.05	0.96	0.86	1.1
chills	1.03	0.08	0.43	0.67	0.89	1.2
cough	1.15	0.09	1.54	0.12	0.96	1.3
aches	0.93	0.1	-0.68	0.5	0.76	1.1
vomit	1.09	0.06	1.37	0.17	0.96	1.2
age_cat5-9	0.94	0.1	-0.62	0.53	0.77	1.1
age_cat10-14	1.15	0.11	1.27	0.2	0.93	1.4
age_cat15-19	0.99	0.11	-0.1	0.92	0.79	1.2

Showing 1 to 10 of 14 entries Previous 1 2 Next

Combine univariate and multivariable

* Combine with **gtsummary**

The **gtsummary** package provides the `tbl_regression()` function, which will take the outputs from a regression (`glm()` in this case) and produce an nice summary table.

```
## show results table of final regression
mv_tab <- tbl_regression(final_mv_reg, exponentiate = TRUE)
```

Let's see the table:

```
mv_tab
```

```
Table printed with `knitr::kable()`, not {gt}. Learn why at
https://www.danieldsjoberg.com/gtsummary/articles/rmarkdown.html
To suppress this message, include `message = FALSE` in code chunk header.
```

Characteristic	OR	95% CI	p-value
gender	1.00	0.88, 1.14	>0.9
fever	1.00	0.86, 1.18	>0.9
chills	1.03	0.89, 1.21	0.7
cough	1.15	0.96, 1.37	0.12
aches	0.93	0.76, 1.14	0.5
vomit	1.09	0.96, 1.23	0.2
age_cat			
0-4	—	—	
5-9	0.94	0.77, 1.15	0.5
10-14	1.15	0.93, 1.41	0.2
15-19	0.99	0.79, 1.24	>0.9
20-29	1.03	0.84, 1.26	0.8
30-49	1.06	0.85, 1.33	0.6
50-69	0.68	0.40, 1.13	0.14
70+	0.52	0.07, 3.19	0.5

You can also combine several different output tables produced by **gtsummary** with the `tbl_merge()` function. We now combine the multivariable results with the **gtsummary** *univariate* results that we created above:

```r
## combine with univariate results
tbl_merge(
  tbls = list(univ_tab, mv_tab),                          # combine
  tab_spanner = c("**Univariate**", "**Multivariable**")) # set header names
```

```
Table printed with `knitr::kable()`, not {gt}. Learn why at
https://www.danieldsjoberg.com/gtsummary/articles/rmarkdown.html
To suppress this message, include `message = FALSE` in code chunk header.
```

Characteristic	N	OR	95% CI	p-value	OR	95% CI	p-value
gender	4,167	1.00	0.88, 1.13	>0.9	1.00	0.88, 1.14	>0.9
fever	4,167	1.00	0.85, 1.17	>0.9	1.00	0.86, 1.18	>0.9
chills	4,167	1.03	0.89, 1.21	0.7	1.03	0.89, 1.21	0.7
cough	4,167	1.15	0.97, 1.37	0.11	1.15	0.96, 1.37	0.12
aches	4,167	0.93	0.76, 1.14	0.5	0.93	0.76, 1.14	0.5
vomit	4,167	1.09	0.96, 1.23	0.2	1.09	0.96, 1.23	0.2
age_cat	4,167						
0-4		—	—		—	—	
5-9		0.94	0.77, 1.15	0.5	0.94	0.77, 1.15	0.5
10-14		1.15	0.93, 1.42	0.2	1.15	0.93, 1.41	0.2
15-19		0.99	0.80, 1.24	>0.9	0.99	0.79, 1.24	>0.9
20-29		1.03	0.84, 1.26	0.8	1.03	0.84, 1.26	0.8
30-49		1.07	0.85, 1.33	0.6	1.06	0.85, 1.33	0.6
50-69		0.68	0.41, 1.13	0.13	0.68	0.40, 1.13	0.14
70+		0.53	0.07, 3.20	0.5	0.52	0.07, 3.19	0.5

* Combine with **dplyr**

An alternative way of combining the `glm()`/`tidy()` univariate and multivariable outputs is with the **dplyr** join functions.

- Join the univariate results from earlier (`univ_tab_base`, which contains counts) with the tidied multivariable results `mv_tab_base`
- Use `select()` to keep only the columns we want, specify their order, and re-name them
- Use `round()` with two decimal places on all the column that are class Double

```r
  ## combine univariate and multivariable tables
  left_join(univ_tab_base, mv_tab_base, by = "term") %>%
    ## choose columns and rename them
    select( # new name =  old name
      "characteristic" = term,
      "recovered"      = "0",
      "dead"           = "1",
      "univ_or"        = estimate.x,
      "univ_ci_low"    = conf.low.x,
      "univ_ci_high"   = conf.high.x,
      "univ_pval"      = p.value.x,
      "mv_or"          = estimate.y,
      "mvv_ci_low"     = conf.low.y,
      "mv_ci_high"     = conf.high.y,
      "mv_pval"        = p.value.y
    ) %>%
    mutate(across(where(is.double), round, 2))
```

```
# A tibble: 20 x 11
   characteristic recovered  dead univ_or univ_ci_low univ_ci_high univ_pval
   <chr>              <dbl> <dbl>   <dbl>       <dbl>        <dbl>     <dbl>
 1 (Intercept)          909  1168    1.28        1.18         1.4       0
 2 gender               916  1174    1           0.88         1.13      0.97
 3 (Intercept)          340   436    1.28        1.11         1.48      0
 4 fever               1485  1906    1           0.85         1.17      0.99
 5 (Intercept)         1472  1877    1.28        1.19         1.37      0
 6 chills               353   465    1.03        0.89         1.21      0.68
 7 (Intercept)          272   309    1.14        0.97         1.34      0.13
 8 cough               1553  2033    1.15        0.97         1.37      0.11
 9 (Intercept)         1636  2114    1.29        1.21         1.38      0
10 aches                189   228    0.93        0.76         1.14      0.51
11 (Intercept)          931  1144    1.23        1.13         1.34      0
12 vomit                894  1198    1.09        0.96         1.23      0.17
13 (Intercept)          338   427    1.26        1.1          1.46      0
14 age_cat5-9           365   433    0.94        0.77         1.15      0.54
15 age_cat10-14         273   396    1.15        0.93         1.42      0.2
16 age_cat15-19         238   299    0.99        0.8          1.24      0.96
17 age_cat20-29         345   448    1.03        0.84         1.26      0.79
18 age_cat30-49         228   307    1.07        0.85         1.33      0.58
19 age_cat50-69          35    30    0.68        0.41         1.13      0.13
20 age_cat70+             3     2    0.53        0.07         3.2       0.49
# i 4 more variables: mv_or <dbl>, mvv_ci_low <dbl>, mv_ci_high <dbl>,
```

```
#   mv_pval <dbl>
```