Example Manuscript Template for a Data Analysis Project

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The structure below is one possible setup for a manuscript, or a general data analysis project (including the course project). Adjust as needed. You don’t need to have exactly these sections, but the content covering those sections should be addressed.

This uses MS Word as output format. [See here](https://quarto.org/docs/output-formats/ms-word.html) for more information. You can switch to other formats, like html or pdf. See [the Quarto documentation](https://quarto.org/) for other formats.

Warning: package 'here' was built under R version 4.4.2

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# 1. Summary/Abstract

*Write a summary of your project.* MADA PROJECT PART 1:

TITLE: Sex-based analysis/Differences in TB Immune Activation.

This project is aimed at looking at the differences in the Tuberculosis immune activation between males and females.( Sex-based analysis/Differences in TB Immune Activation Research Question)

we shall use data from a tuberculosis public repository. • Data source: Tidyverse https://dataverse.unc.edu/dataset.xhtml?persistentId=doi:10.15139/S3/AYOFEU with a Sample size of 60 individuals. The data includes 60 different individual that accepted to take part in the study.

The key variables that we shall look at are;

Key variables: - CD4 Immune activation count - Disease severity indicators(Extent of lung disease andNumber of lungs involved) -Fat in kgs - Sex/Gender - BMI - Age of the participant

#load packages  
library("readxl")  
library("readr")  
library("dplyr")

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':  
  
 filter, lag

The following objects are masked from 'package:base':  
  
 intersect, setdiff, setequal, union

library("ggplot2")  
library("tidyverse")

Warning: package 'tidyverse' was built under R version 4.4.2

Warning: package 'stringr' was built under R version 4.4.2

── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──  
✔ forcats 1.0.0 ✔ stringr 1.5.1  
✔ lubridate 1.9.3 ✔ tibble 3.2.1  
✔ purrr 1.0.2 ✔ tidyr 1.3.1

── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
✖ dplyr::filter() masks stats::filter()  
✖ dplyr::lag() masks stats::lag()  
ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

library("here")  
  
# follow through with the code folder to see the #variables in the data and how i selected the #variables make this data set.   
#location of the data  
data\_location <- here::here("data","processed-data","Tb\_immune\_data.rds")  
  
#loading the data  
data<- read\_rds(data\_location)  
  
#summary of the data  
summary(data)

ID Sex Participant age BMI   
 Min. :50004 Length:61 Min. :17.00 Min. :15.55   
 1st Qu.:50020 Class :character 1st Qu.:23.00 1st Qu.:18.09   
 Median :50035 Mode :character Median :28.00 Median :19.25   
 Mean :50035 Mean :30.02 Mean :19.83   
 3rd Qu.:50050 3rd Qu.:35.00 3rd Qu.:21.47   
 Max. :50067 Max. :70.00 Max. :28.15   
 NA's :1 NA's :1   
 Dose Fat in kg LBM in kg Fat %   
 Min. :29.61 Min. :-96.640 Min. :-41.98 Min. :-177.647   
 1st Qu.:29.99 1st Qu.: 3.554 1st Qu.: 39.13 1st Qu.: 6.629   
 Median :30.00 Median : 8.704 Median : 43.43 Median : 16.685   
 Mean :29.99 Mean : 9.615 Mean : 43.02 Mean : 17.950   
 3rd Qu.:30.00 3rd Qu.: 13.364 3rd Qu.: 49.82 3rd Qu.: 25.987   
 Max. :30.15 Max. : 80.979 Max. :151.04 Max. : 207.639   
 NA's :1 NA's :1 NA's :1 NA's :1   
 LBM in % CD4+ CD4 Immune activation count  
 Min. :-107.64 Min. : 8.636 Min. : 84.0   
 1st Qu.: 74.01 1st Qu.:185.006 1st Qu.: 914.8   
 Median : 83.32 Median :317.941 Median : 1384.5   
 Mean : 82.05 Mean :337.364 Mean : 1948.1   
 3rd Qu.: 93.37 3rd Qu.:484.889 3rd Qu.: 2057.5   
 Max. : 277.65 Max. :785.896 Max. :17872.0   
 NA's :1 NA's :1 NA's :1

Proposed Analysis Method

• Compare immune activation levels between males and females

• Correlate immune markers with disease severity measures/Correlation between activation levels and disease severity

• Use linear regression to analyze relationships between variables

• Control for potential confounding factors

These are some of our Expected Outcomes.

• Check and Identify any sex-based differences in immune response.

• Quantify the relationship between immune activation and disease severity.

• Propose any insights for sex-specific treatment approaches

# 2. Introduction

## 2.1 General Background Information

*Provide enough background on your topic that others can understand the why and how of your analysis* Tuberculosis (TB) remains a significant global public health challenge. According to the World Health Organization (WHO), reports show that 10 million new cases and 1.4 million deaths in 2023 (1) were as a result of Tuberculosis. The spread of M. tuberculosis, as the pathogen of TB, has long been hypothesized to occur more often in the household than in the community(2). While most of the M.Tuberculosis transmission in the community is attributed to the unknown contact networks that occurs between individuals, this accounts upto 90% of the transmission. The recent outbreak of Tuberculosis in the united states clearly explains the contact network phenomena. Overall, TB accounts for one quarter of the annual deaths that happen worldwide. An estimated 10.0 million people fell ill with TB in 2018. Geographically, Southeast Asia ranked highest (44%), followed by Africa (24%) and the Western Pacific (18%), with lesser percentages in the Eastern Mediterranean (8%), the Americas (3%), and Europe (3%). Among women of reproductive years, TB is the largest cause of death (3). Global Strategies made by WHO, aim at ending the TB epidemic, with targets to reduce the number of deaths caused by TB by 95% and to decrease new cases by 90% from 2015 to 2035(4).

Mycobacterium tuberculosis infection is acquired mostly through sharing air space with an individual who has active tuberculosis and inhaling droplet aerosols produced by that person. Since this bacterium is transmitted via the respiratory route to susceptible individuals in the community, the household of an infectious person is an environment for intense transmission of M. tuberculosis where most new cases of infection and diseases might be detected and treated. According some reports,they suggest that there are differences in the responses to tuberculosis between men and women. These reports highlight greater barrier to early detection and treatment of tuberculosis to be greater for women than men.

The World Health Organisations, among others, attributed to the differences in the tuberculosis trends between men and women to access to care and treatment, pregnancy effects and gender rules that diminish the social capital of women hence lowering incidence among them(5). Not forgetting that biological mechanisms might influence these differences, previous studies show that men have a higher incidence and prevalence of disease and this might lead to bad treatment outcomes as compared to women.

Since the balance of fat and lean tissue differ in men and women especially at the time of presentation, the objective of this study will be to find out whether the more immune activation there is, the more infected / sicker is the person.

## 2.2 Description of data and data source

The data we used for this project was got from the TRAC dataverse and is fully accessible to everyone. This is considered a safe place where the the Tuberculosis data from the TRAc project is kept and can be used by anyone who wants contribute to TB research. More details about the data can be found [here]!(https://dataverse.unc.edu/dataset.xhtml?persistentId=doi:10.15139/S3/AYOFEU). The data is publicaly available and can be accessed by anyone.

## 2.3 Questions/Hypotheses to be addressed

*State the research questions you plan to answer with this analysis.* Since the balance of fat and lean tissue differ in men and women especially at the time of tuberculosis presentation, the objective of this study will be to find out whether there are differences in the Tuberculosis immune activation between males and females. We shall hypothesize on the more immune activation there is, the more infected / sicker the person.

# 3. Methods

*Describe your methods. That should describe the data, the cleaning processes, and the analysis approaches. You might want to provide a shorter description here and all the details in the supplement.* Study Design This study utilized a cohort design analyzing data from 2021. We included all patients that were 15 years and older. The candidate must have had TB as their first episode, not on any hormonal therapy and does not take any hormonal birth control. The participant was not supposed to have diabetes melitus, cancer or HIV.Similarly,the exclusion criteria applied. All participants that were below the age of 15, reported TB as their second episode, took any form of hormanl therapy or biirth control , had diabetes melitus, cancer or HIV were excluded from the study. The variables of interest were extracted from the TRAC dataset and exported to an MS Excel sheet. The outcome variable was CD4+ immune activatin counts. The primary independent variable was sex (cis-gender) and this was categorized as male and female. The covariates were age at diagnosis,BMI, Fat in Kg, lean body mass in kg(LBM in kg), CD4+ and CD4 immune activation counts.

## 3.1 Schematic of workflow

Chromosomal sex and hormones play a role in the modulation of immune responses to Mtb and thereby contribute to the general outcome of disease. The first cells that encounter Mtb are known as Macrophages. These initiate a local inflammatory reaction which may differ between the sexes(6). This causes the long term containment of TB infection to differ between men and women since their adaptive immune responses are different. (**tbfig-1?**)

|  |
| --- |
| Figure 1: Impact of sex differences on the immune response to Mtb and their influence disease outcome. |

## 3.2 Data import and cleaning

*Write code that reads in the file and cleans it so it’s ready for analysis. Since this will be fairly long code for most datasets, it might be a good idea to have it in one or several R scripts. If that is the case, explain here briefly what kind of cleaning/processing you do, and provide more details and well documented code somewhere (e.g. as supplement in a paper). All materials, including files that contain code, should be commented well so everyone can follow along.*

We imported the data from MS Excel to R. We explored the data and found some missing values for some variables. We decided to drop one observation since the person lacked the primary exposure and did not have most of the details we needed for our final analysis. We categorized the participants age into four categories. That is 17-<28, 28-<40, 40-<60 and >=60.

## 3.3 Statistical analysis

*Explain anything related to your statistical analyses.*

# 4. Results

## 4.1 Exploratory/Descriptive analysis

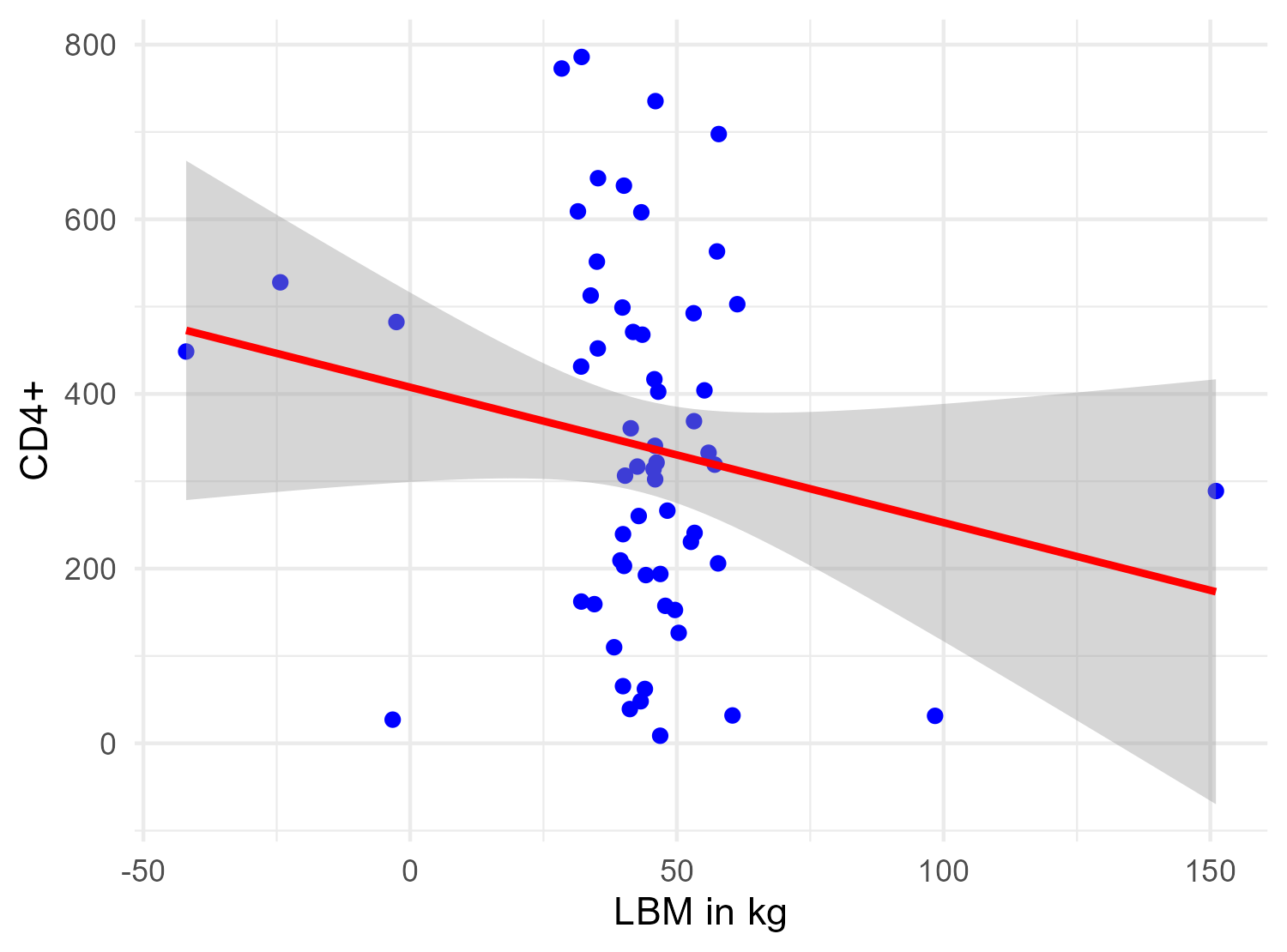
*Use a combination of text/tables/figures to explore and describe your data. Show the most important descriptive results here. Additional ones should go in the supplement. Even more can be in the R and Quarto files that are part of your project.* [Table 1](#tbl-TABLE1) shows a summary of the data

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table 1: Data descriptive summary table.   |  | F | M | Overall | | --- | --- | --- | --- | |  | (N=30) | (N=30) | (N=60) | | CD4+ |  |  |  | | Mean (SD) | 394 (217) | 289 (181) | 341 (205) | | Median [Min, Max] | 449 [27.0, 786] | 278 [8.64, 735] | 319 [8.64, 786] | | Missing | 1 (3.3%) | 0 (0%) | 1 (1.7%) | | CD4 Immune activation count |  |  |  | | Mean (SD) | 1750 (1340) | 2160 (3170) | 1960 (2430) | | Median [Min, Max] | 1520 [94.0, 7350] | 1210 [84.0, 17900] | 1380 [84.0, 17900] | | Missing | 1 (3.3%) | 0 (0%) | 1 (1.7%) | | Participant age |  |  |  | | Mean (SD) | 29.9 (12.8) | 30.2 (6.83) | 30.0 (10.1) | | Median [Min, Max] | 26.0 [17.0, 70.0] | 28.5 [19.0, 48.0] | 28.0 [17.0, 70.0] | | Fat in kg |  |  |  | | Mean (SD) | 18.9 (22.4) | 0.348 (21.9) | 9.62 (23.8) | | Median [Min, Max] | 10.9 [-0.192, 81.0] | 4.37 [-96.6, 21.3] | 8.70 [-96.6, 81.0] | | LBM in kg |  |  |  | | Mean (SD) | 31.1 (21.0) | 54.9 (21.1) | 43.0 (24.1) | | Median [Min, Max] | 39.6 [-42.0, 45.9] | 50.0 [38.2, 151] | 43.4 [-42.0, 151] | |

## 4.2 Basic statistical analysis

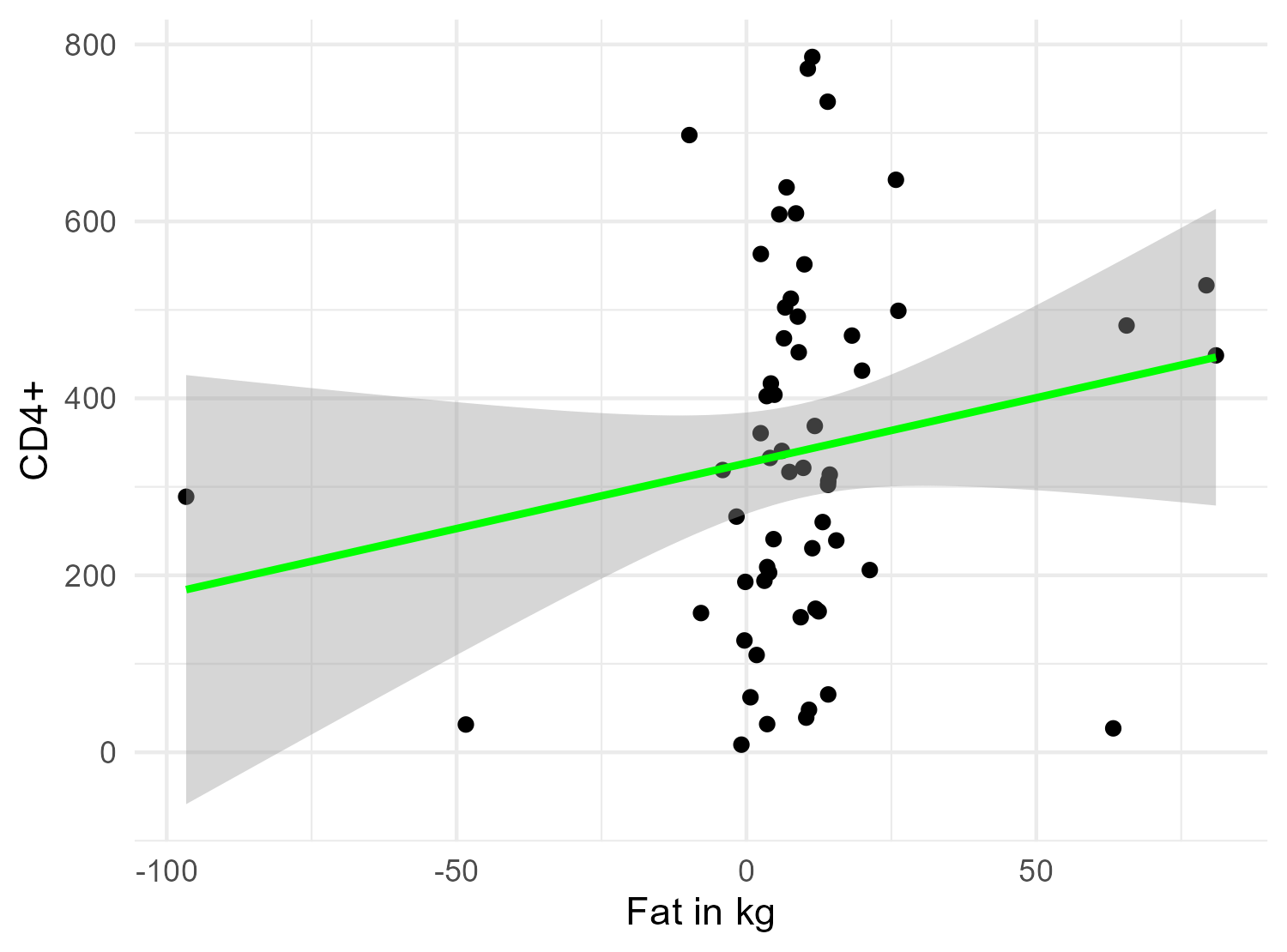
*To get some further insight into your data, if reasonable you could compute simple statistics (e.g. simple models with 1 predictor) to look for associations between your outcome(s) and each individual predictor variable. Though note that unless you pre-specified the outcome and main exposure, any “p<0.05 means statistical significance” interpretation is not valid.*

(**fig1-result?**) shows a scatter plot of lean body mass in kg and CD4



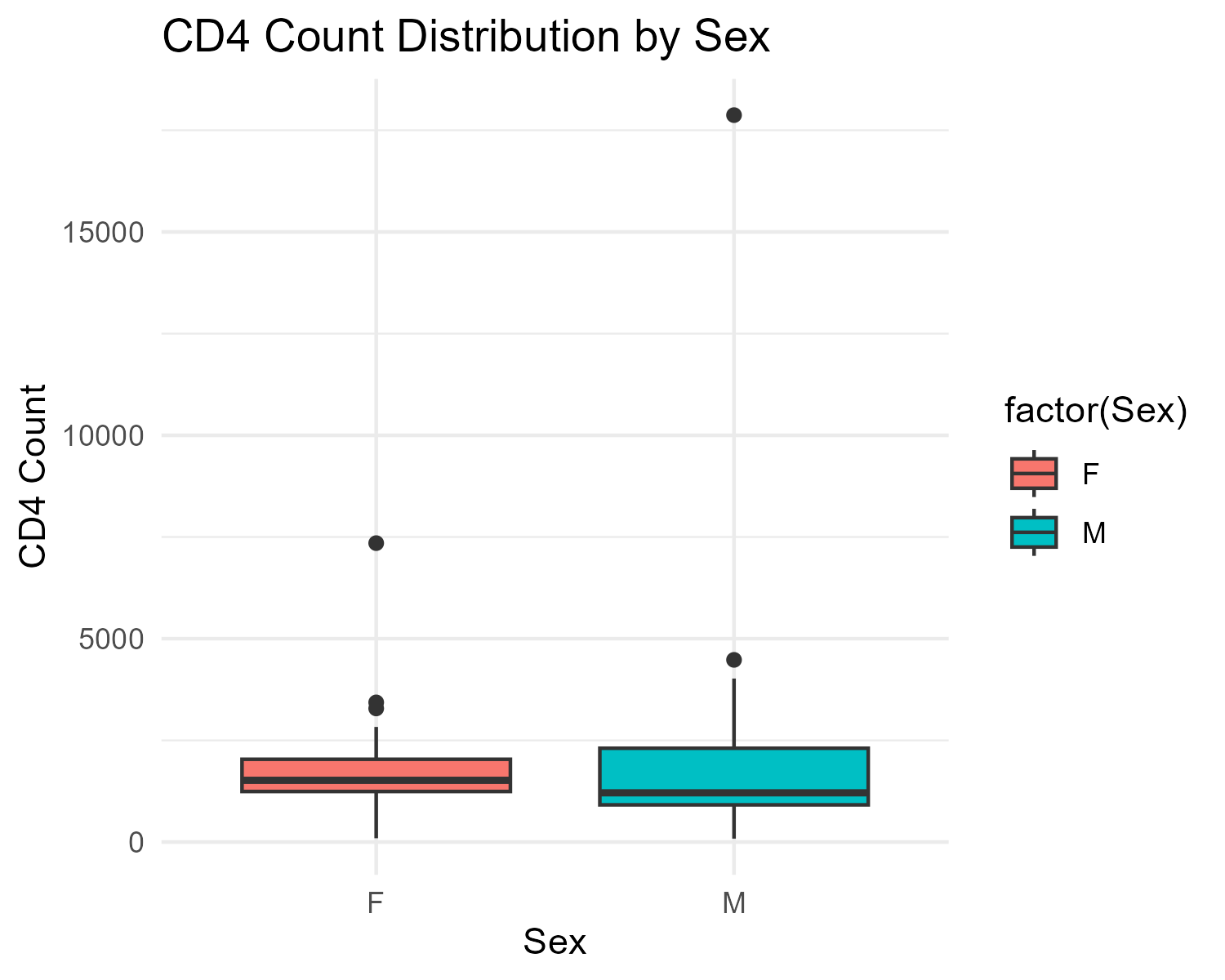
Scatter plot of CD4+ cells versus LBM in kg.

(**fig2-result?**) shows a scatter plot of CD4 vs Fat in kg.



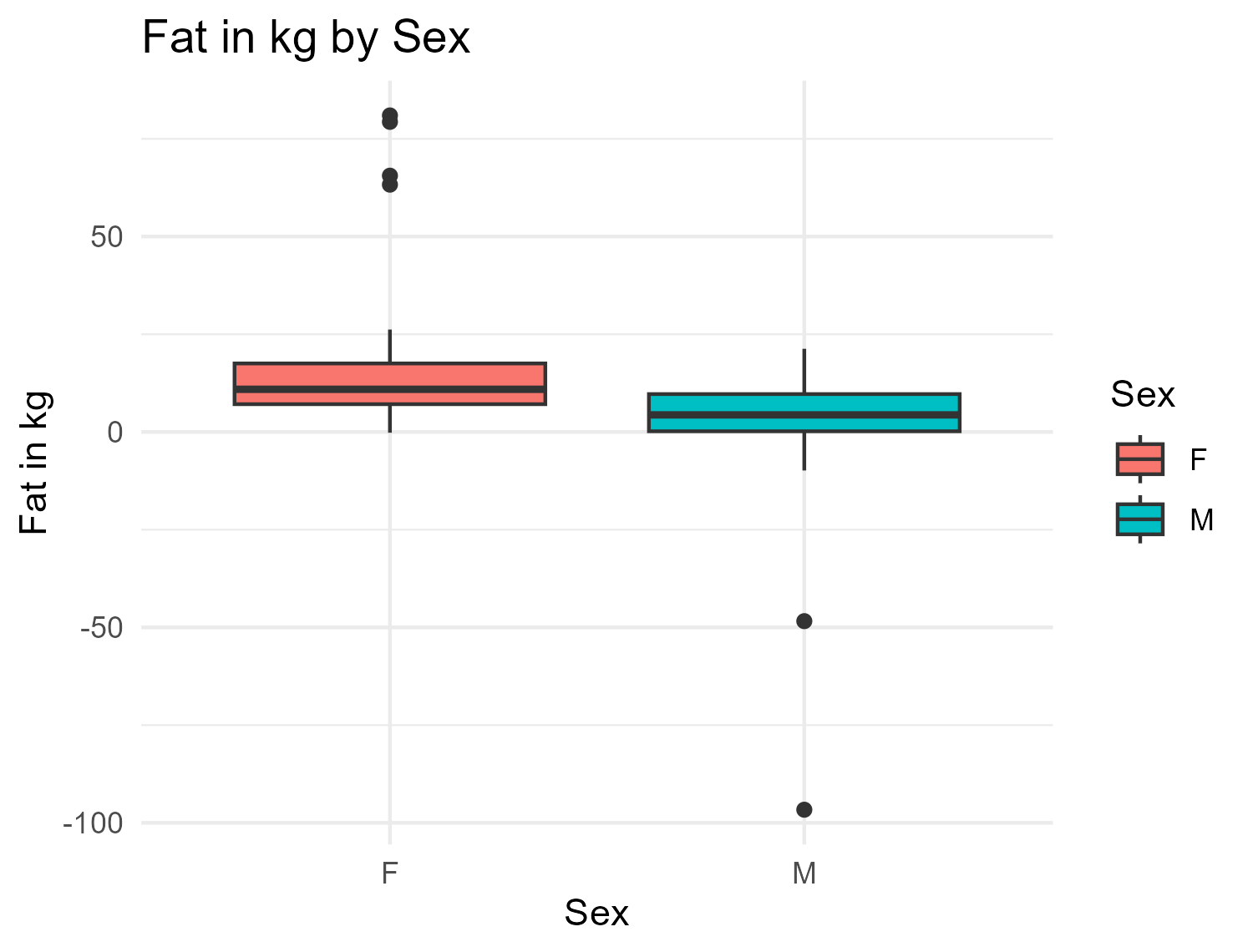
Scatter plot of CD4+ cells versus Fat in kg.

(**plot1-result?**) a boxplot of the cd4 immune activation count by sex.



Box plot to show the distribution of cd4 count immune activation counts among males and females.

(**plot2-result?**) a boxplot to show the distributions of fat in kilograms among males females.



Box plot showing Fat in kg among males and females.

## 4.3 Full analysis

*Use one or several suitable statistical/machine learning methods to analyze your data and to produce meaningful figures, tables, etc. This might again be code that is best placed in one or several separate R scripts that need to be well documented. You want the code to produce figures and data ready for display as tables, and save those. Then you load them here.*

Example [Table 2](#tbl-resulttable2) shows a summary of a linear model fit.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table 2: Linear model fit table.   | term | estimate | std.error | statistic | p.value | | --- | --- | --- | --- | --- | | (Intercept) | 149.2726967 | 23.3823360 | 6.3839942 | 0.0013962 | | Weight | 0.2623972 | 0.3512436 | 0.7470519 | 0.4886517 | | GenderM | -2.1244913 | 15.5488953 | -0.1366329 | 0.8966520 | | GenderO | -4.7644739 | 19.0114155 | -0.2506112 | 0.8120871 | |

# 5. Discussion

## 5.1 Summary and Interpretation

*Summarize what you did, what you found and what it means.*

## 5.2 Strengths and Limitations

*Discuss what you perceive as strengths and limitations of your analysis.*

## 5.3 Conclusions

*What are the main take-home messages?*

*Include citations in your Rmd file using bibtex, the list of references will automatically be placed at the end*

This paper (7) discusses types of analyses.

These papers (8,9) are good examples of papers published using a fully reproducible setup similar to the one shown in this template.

Note that this cited reference will show up at the end of the document, the reference formatting is determined by the CSL file specified in the YAML header. Many more style files for almost any journal [are available](https://www.zotero.org/styles). You also specify the location of your bibtex reference file in the YAML. You can call your reference file anything you like.

# 6. References

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