# Biostat 203B Homework 1

Due Jan 24, 2025 @ 11:59PM

# Wenqiang Ge and 106371961

# Table of contents

Q1. Git/GitHub		
Display machine information for	reproducibility:	
sessionInfo()		
R version 4.4.2 (2024-10-31) Platform: x86_64-pc-linux-gr Running under: Ubuntu 24.04	nu	
Matrix products: default BLAS: /usr/lib/x86_64-line LAPACK: /usr/lib/x86_64-line	<u> </u>	
locale: [1] LC_CTYPE=C.UTF-8 [4] LC_COLLATE=C.UTF-8 [7] LC_PAPER=C.UTF-8 [10] LC_TELEPHONE=C	LC_MONETARY=C.UTF-8	LC_ADDRESS=C
time zone: America/Los_Angetzcode source: system (glibe		
attached base packages: [1] stats graphics grDe	evices utils datase	ts methods base
loaded via a namespace (and	not attached):	

```
[1] compiler_4.4.2 fastmap_1.2.0 cli_3.6.3 tools_4.4.2 [5] htmltools_0.5.8.1 rstudioapi_0.17.1 yaml_2.3.10 rmarkdown_2.29 [9] knitr_1.49 jsonlite_1.8.9 xfun_0.50 digest_0.6.37 [13] rlang_1.1.5 evaluate_1.0.3
```

# Q1. Git/GitHub

No handwritten homework reports are accepted for this course. We work with Git and GitHub. Efficient and abundant use of Git, e.g., frequent and well-documented commits, is an important criterion for grading your homework.

- 1. Apply for the Student Developer Pack at GitHub using your UCLA email. You'll get GitHub Pro account for free (unlimited public and private repositories).
- 2. Create a **private** repository biostat-203b-2025-winter and add Hua-Zhou and TA team (Tomoki-Okuno for Lec 1; parsajamshidian and BowenZhang2001 for Lec 82) as your collaborators with write permission.
- 3. Top directories of the repository should be hw1, hw2, ... Maintain two branches main and develop. The develop branch will be your main playground, the place where you develop solution (code) to homework problems and write up report. The main branch will be your presentation area. Submit your homework files (Quarto file qmd, html file converted by Quarto, all code and extra data sets to reproduce results) in the main branch.
- 4. After each homework due date, course reader and instructor will check out your main branch for grading. Tag each of your homework submissions with tag names hw1, hw2, ... Tagging time will be used as your submission time. That means if you tag your hw1 submission after deadline, penalty points will be deducted for late submission.
- 5. After this course, you can make this repository public and use it to demonstrate your skill sets on job market.

#### Solution:

Done!

## Q2. Data ethics training

This exercise (and later in this course) uses the MIMIC-IV data v3.1, a freely accessible critical care database developed by the MIT Lab for Computational Physiology. Follow the instructions at <a href="https://mimic.mit.edu/docs/gettingst">https://mimic.mit.edu/docs/gettingst</a> arted/ to (1) complete the CITI Data or Specimens Only Research course and (2) obtain the PhysioNet credential for using the MIMIC-IV data. Display the verification links to your completion report and completion certificate here. You must complete Q2 before working on the remaining questions.

(Hint: The CITI training takes a few hours and the PhysioNet credentialing takes a couple days; do not leave it to the last minute.)

#### **Solution:**

 $\label{lem:completion} Completion Report Link: $https://www.citiprogram.org/verify/?kcc436586-af5d-4128-bb91-ef37f2326698-67297842$ 

 $Completion\ Certificate\ Link: https://www.citiprogram.org/verify/?w7ddecc3c-d853-4bc4-95ec-c08cd3268665-67297842$ 

sessionInfo()

## Q3. Linux Shell Commands

Make the MIMIC-IV v3.1 data available at location ~/mimic. The output
of the ls -l ~/mimic command should be similar to the below (from my
laptop).

```
# content of mimic folder
ls -l ~/mimic/
```

### total 28

```
-rwxrwxrwx 1 gewenqiang gewenqiang 15199 Jan 16 19:00 CHANGELOG.txt
-rwxrwxrwx 1 gewenqiang gewenqiang 2518 Jan 16 19:00 LICENSE.txt
-rwxrwxrwx 1 gewenqiang gewenqiang 2884 Jan 16 19:00 SHA256SUMS.txt
drwxrwxrwx 1 gewenqiang gewenqiang 4096 Jan 23 15:28 hosp
drwxrwxrwx 1 gewenqiang gewenqiang 4096 Jan 16 19:00 index.html
```

Refer to the documentation <a href="https://physionet.org/content/mimiciv/3.1/">https://physionet.org/content/mimiciv/3.1/</a> for details of data files. Do **not** put these data files into Git; they are big. Do **not** copy them into your directory. Do **not** decompress the gz data files. These create unnecessary big files and are not big-data-friendly practices. Read from the data folder ~/mimic directly in following exercises.

Use Bash commands to answer following questions.

Display the contents in the folders hosp and icu using Bash command 1s -1. Why are these data files distributed as .csv.gz files instead of .csv (comma separated values) files? Read the page https://mimic.mit.edu/docs/iv/to understand what's in each folder.

## **Solution:**

```
ls -l ~/mimic/hosp

total 6153128
-rwxrwxrwx 1 gewenqiang 19928140 Jan 16 19:00 admissions.csv.gz
```

```
-rwxrwxrwx 1 gewengiang gewengiang
                                       427554 Jan 16 19:00 d_hcpcs.csv.gz
                                       876360 Jan 16 19:00 d_icd_diagnoses.csv.gz
-rwxrwxrwx 1 gewenqiang gewenqiang
-rwxrwxrwx 1 gewengiang gewengiang
                                       589186 Jan 16 19:00 d_icd_procedures.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                        13169 Jan 16 19:00 d_labitems.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                     33564802 Jan 16 19:00 diagnoses_icd.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                      9743908 Jan 16 19:00 drgcodes.csv.gz
-rwxrwxrwx 1 gewenqiang gewenqiang
                                    811305629 Jan 16 19:00 emar.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                    748158322 Jan 16 19:00 emar_detail.csv.gz
                                      2162335 Jan 16 19:00 hcpcsevents.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
-rwxrwxrwx 1 gewengiang gewengiang
                                         2907 Jan 16 19:00 index.html
-rwxrwxrwx 1 gewenqiang gewenqiang 2592909134 Jan 16 19:01 labevents.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                   117644075 Jan 16 19:01 microbiologyevents.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                     44069351 Jan 16 19:01 omr.csv.gz
                                      2835586 Jan 16 19:01 patients.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
-rwxrwxrwx 1 gewenqiang gewenqiang 525708076 Jan 16 19:01 pharmacy.csv.gz
                                    666594177 Jan 16 19:01 poe.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
-rwxrwxrwx 1 gewenqiang gewenqiang
                                     55267894 Jan 16 19:01 poe_detail.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                    606298611 Jan 16 19:01 prescriptions.csv.gz
                                      7777324 Jan 16 19:01 procedures_icd.csv.gz
-rwxrwxrwx 1 gewenqiang gewenqiang
-rwxrwxrwx 1 gewengiang gewengiang
                                       127330 Jan 16 19:01 provider.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                      8569241 Jan 16 19:01 services.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                     46185771 Jan 16 19:01 transfers.csv.gz
```

## ls -1 ~/mimic/icu

#### total 4253396

```
-rwxrwxrwx 1 gewengiang gewengiang
                                       41566 Jan 16 19:01 caregiver.csv.gz
-rwxrwxrwx 1 gewenqiang gewenqiang 3502392765 Jan 16 19:02 chartevents.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                        58741 Jan 16 19:02 d items.csv.gz
                                     63481196 Jan 16 19:02 datetimeevents.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
-rwxrwxrwx 1 gewengiang gewengiang
                                      3342355 Jan 16 19:02 icustavs.csv.gz
                                         1336 Jan 16 19:02 index.html
-rwxrwxrwx 1 gewenqiang gewenqiang
-rwxrwxrwx 1 gewenqiang gewenqiang 311642048 Jan 16 19:02 ingredientevents.csv.gz
-rwxrwxrwx 1 gewenqiang gewenqiang 401088206 Jan 16 19:02 inputevents.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                     49307639 Jan 16 19:02 outputevents.csv.gz
-rwxrwxrwx 1 gewengiang gewengiang
                                     24096834 Jan 16 19:02 procedureevents.csv.gz
```

Compressed files save disk space as .gz files are smaller than raw .csv files. This will help to reduce network bandwidth usage and time required to download or transfer files. In addition, compression ensures the original data remains unaltered.

3. Briefly describe what Bash commands zcat, zless, zmore, and zgrep do.

zcat: Outputs the contents of a compressed .gz file to the standard output without decompressing it to disk.

#### **Solution:**

zless: Allows you to view a compressed .gz file interactively, similar to less for uncompressed files.

zmore: Similar to zless, but works like more, showing the file in a paginated manner.

zgrep: Searches for a pattern inside a .gz compressed file, equivalent to grep for uncompressed files.

4. (Looping in Bash) What's the output of the following bash script?

```
for datafile in ~/mimic/hosp/{a,1,pa}*.gz
do
    ls -l $datafile
done
```

Display the number of lines in each data file using a similar loop. (Hint: combine linux commands zcat < and wc -1.)

### **Solution:**

```
for datafile in ~/mimic/hosp/*.gz
    echo "File: $datafile"
    zcat "$datafile" | wc -1
  done
File: /home/gewenqiang/mimic/hosp/admissions.csv.gz
546029
File: /home/gewenqiang/mimic/hosp/d_hcpcs.csv.gz
89209
File: /home/gewenqiang/mimic/hosp/d_icd_diagnoses.csv.gz
112108
File: /home/gewenqiang/mimic/hosp/d_icd_procedures.csv.gz
86424
File: /home/gewenqiang/mimic/hosp/d_labitems.csv.gz
1651
File: /home/gewenqiang/mimic/hosp/diagnoses_icd.csv.gz
6364489
File: /home/gewenqiang/mimic/hosp/drgcodes.csv.gz
761857
File: /home/gewenqiang/mimic/hosp/emar.csv.gz
42808594
File: /home/gewenqiang/mimic/hosp/emar_detail.csv.gz
File: /home/gewenqiang/mimic/hosp/hcpcsevents.csv.gz
```

```
186075
File: /home/gewenqiang/mimic/hosp/labevents.csv.gz
File: /home/gewenqiang/mimic/hosp/microbiologyevents.csv.gz
3988225
File: /home/gewenqiang/mimic/hosp/omr.csv.gz
7753028
File: /home/gewenqiang/mimic/hosp/patients.csv.gz
364628
File: /home/gewenqiang/mimic/hosp/pharmacy.csv.gz
17847568
File: /home/gewenqiang/mimic/hosp/poe.csv.gz
52212110
File: /home/gewenqiang/mimic/hosp/poe detail.csv.gz
8504983
File: /home/gewenqiang/mimic/hosp/prescriptions.csv.gz
20292612
File: /home/gewenqiang/mimic/hosp/procedures_icd.csv.gz
859656
File: /home/gewenqiang/mimic/hosp/provider.csv.gz
42245
File: /home/gewenqiang/mimic/hosp/services.csv.gz
593072
File: /home/gewenqiang/mimic/hosp/transfers.csv.gz
2413582
  for datafile in ~/mimic/icu/*.gz
    echo "File: $datafile"
    zcat "$datafile" | wc -1
  done
File: /home/gewenqiang/mimic/icu/caregiver.csv.gz
17985
File: /home/gewenqiang/mimic/icu/chartevents.csv.gz
432997492
File: /home/gewenqiang/mimic/icu/d_items.csv.gz
4096
File: /home/gewenqiang/mimic/icu/datetimeevents.csv.gz
9979762
File: /home/gewenqiang/mimic/icu/icustays.csv.gz
94459
File: /home/gewenqiang/mimic/icu/ingredientevents.csv.gz
14253481
File: /home/gewenqiang/mimic/icu/inputevents.csv.gz
```

10953714

File: /home/gewenqiang/mimic/icu/outputevents.csv.gz

5359396

File: /home/gewenqiang/mimic/icu/procedureevents.csv.gz 808707

5. Display the first few lines of admissions.csv.gz. How many rows are in this data file, excluding the header line? Each hadm\_id identifies a hospitalization. How many hospitalizations are in this data file? How many unique patients (identified by subject\_id) are in this da'ta file? Do they match the number of patients listed in the patients.csv.gz file? (Hint: combine Linux commands zcat <, head/tail, awk, sort, uniq, wc, and so on.)

## Solution:

```
zcat ~/mimic/hosp/admissions.csv.gz | head
```

subject\_id,hadm\_id,admittime,dischtime,deathtime,admission\_type,admit\_provider\_id,admission\_10000032,22595853,2180-05-06 22:23:00,2180-05-07 17:15:00,,URGENT,P49AFC,TRANSFER FROM HOSP:10000032,22841357,2180-06-26 18:27:00,2180-06-27 18:49:00,,EW EMER.,P784FA,EMERGENCY ROOM,H01000032,25742920,2180-08-05 23:44:00,2180-08-07 17:50:00,,EW EMER.,P19UTS,EMERGENCY ROOM,H01000032,29079034,2180-07-23 12:35:00,2180-07-25 17:55:00,,EW EMER.,P060TX,EMERGENCY ROOM,H01000068,25022803,2160-03-03 23:16:00,2160-03-04 06:26:00,,EU DBSERVATION,P39NWO,EMERGENCY ROOM,H01000084,23052089,2160-11-21 01:56:00,2160-11-25 14:52:00,,EW EMER.,P42H7G,WALK-IN/SELF REFI10000084,29888819,2160-12-28 05:11:00,2160-12-28 16:07:00,,EU DBSERVATION,P35NE4,PHYSICIAN ROOM,P1000108,27250926,2163-09-27 23:17:00,2163-09-28 09:04:00,,EU DBSERVATION,P40JML,EMERGENCY ROOM,P10000117,22927623,2181-11-15 02:05:00,2181-11-15 14:52:00,,EU DBSERVATION,P47EY8,EMERGENCY ROOM,P10000117,P47EY8,EMERGENCY ROOM,P10000117,P4

```
zcat ~/mimic/hosp/admissions.csv.gz | tail -n+2 | \
   awk -F, '{print $2}' | wc -l

zcat ~/mimic/hosp/admissions.csv.gz | tail -n+2 | \
   awk -F, '{print $2}' | sort | uniq | wc -l

zcat ~/mimic/hosp/admissions.csv.gz | tail -n+2 | \
   awk -F, '{print $1}' | sort | uniq | wc -l

zcat ~/mimic/hosp/patients.csv.gz | tail -n+2 | \
   awk -F, '{print $1}' | sort | uniq | wc -l
```

546028

546028

223452

364627

There are 546028 lines in the adimission.csv.gz.

546028 hospitalizations; 223452 unique patients.

There are 364627 unique patients listed in the patients.csv.gz file. They are not matched.

6. What are the possible values taken by each of the variable admission\_type, admission\_location, insurance, and ethnicity? Also report the count for each unique value of these variables in decreasing order. (Hint: combine Linux commands zcat, head/tail, awk, uniq -c, wc, sort, and so on; skip the header line.)

#### Solution:

```
zcat ~/mimic/hosp/admissions.csv.gz | head -n 1 | tr ',' '\n' | nl
   1 subject id
   2 hadm_id
   3 admittime
   4 dischtime
   5 deathtime
   6 admission_type
   7 admit_provider_id
   8 admission_location
   9 discharge_location
   10 insurance
   11 language
   12 marital_status
   13 race
   14 edregtime
  15 edouttime
   16 hospital_expire_flag
 zcat ~/mimic/hosp/admissions.csv.gz | tail -n+2 | \
   awk -F ',' '{print $6}' | sort | uniq -c | sort -nr
 zcat ~/mimic/hosp/admissions.csv.gz | tail -n+2 | \
   awk -F ',' '{print $8}' | sort | uniq -c | sort -nr
 zcat ~/mimic/hosp/admissions.csv.gz | tail -n+2 | \
   awk -F ',' '{print $10}' | sort | uniq -c | sort -nr
 zcat ~/mimic/hosp/admissions.csv.gz | tail -n+2 | \
   awk -F ',' '{print $13}' | sort | uniq -c | sort -nr
177459 EW EMER.
119456 EU OBSERVATION
```

84437 OBSERVATION ADMIT

```
54929 URGENT
```

42898 SURGICAL SAME DAY ADMISSION

24551 DIRECT OBSERVATION

21973 DIRECT EMER.

13130 ELECTIVE

7195 AMBULATORY OBSERVATION

244179 EMERGENCY ROOM

163228 PHYSICIAN REFERRAL

56227 TRANSFER FROM HOSPITAL

42365 WALK-IN/SELF REFERRAL

12965 CLINIC REFERRAL

8518 PROCEDURE SITE

6317 TRANSFER FROM SKILLED NURSING FACILITY

5837 INTERNAL TRANSFER TO OR FROM PSYCH

5734 PACU

402 INFORMATION NOT AVAILABLE

255 AMBULATORY SURGERY TRANSFER

1

244576 Medicare

173399 Private

104229 Medicaid

14006 Other

9355

463 No charge

336538 WHITE

75482 BLACK/AFRICAN AMERICAN

19788 OTHER

13972 WHITE - OTHER EUROPEAN

13870 UNKNOWN

10903 HISPANIC/LATINO - PUERTO RICAN

8287 HISPANIC OR LATINO

7809 ASIAN

7644 ASIAN - CHINESE

6597 WHITE - RUSSIAN

6205 BLACK/CAPE VERDEAN

6070 HISPANIC/LATINO - DOMINICAN

3875 BLACK/CARIBBEAN ISLAND

3495 BLACK/AFRICAN

3478 UNABLE TO OBTAIN

2162 PATIENT DECLINED TO ANSWER

2082 PORTUGUESE

1973 ASIAN - SOUTH EAST ASIAN

1886 WHITE - EASTERN EUROPEAN

1858 HISPANIC/LATINO - GUATEMALAN

1661 ASIAN - ASIAN INDIAN

1526 WHITE - BRAZILIAN

```
1320 HISPANIC/LATINO - SALVADORAN

1247 AMERICAN INDIAN/ALASKA NATIVE

920 HISPANIC/LATINO - COLUMBIAN

883 HISPANIC/LATINO - MEXICAN

774 SOUTH AMERICAN

725 HISPANIC/LATINO - HONDURAN

664 ASIAN - KOREAN

641 HISPANIC/LATINO - CUBAN

603 HISPANIC/LATINO - CENTRAL AMERICAN

596 MULTIPLE RACE/ETHNICITY

494 NATIVE HAWAIIAN OR OTHER PACIFIC ISLANDER
```

7. The icusays.csv.gz file contains all the ICU stays during the study period. How many ICU stays, identified by stay\_id, are in this data file? How many unique patients, identified by subject\_id, are in this data file?

#### Solution:

```
zcat ~/mimic/icu/icustays.csv.gz | head -n 1 | tr ',' '\n' |nl
     1 subject_id
     2 hadm_id
     3 stay_id
     4 first_careunit
     5 last_careunit
     6 intime
       outtime
    7
     8 los
  zcat ~/mimic/icu/icustays.csv.gz | tail -n+2 | \
    awk -F ',' '{print $1}' | wc -l
  zcat ~/mimic/icu/icustays.csv.gz | tail -n+2 | \
    awk -F ',' '{print $1}' | sort | uniq | wc -1
  zcat ~/mimic/icu/icustays.csv.gz | tail -n+2 | \
    awk -F ',' '{print $3}' | sort | uniq | wc -1
  zcat ~/mimic/icu/icustays.csv.gz | tail -n+2 | \
    awk -F ',' '{print $1}' | wc -l
94458
65366
94458
94458
```

There are 94458 ICU stays and 65366 unique patients in this data file.

8. To compress, or not to compress. That's the question. Let's focus on the big data file labevents.csv.gz. Compare compressed gz file size to the uncompressed file size. Compare the run times of zcat < ~/mimic/labevents.csv.gz | wc -1 versus wc -1 labevents.csv. Discuss the trade off between storage and speed for big data files. (Hint: gzip -dk < FILENAME.gz > ./FILENAME. Remember to delete the large labevents.csv file after the exercise.)

#### **Solution:**

Comparison of file size:

```
ls -lh ~/mimic/hosp/labevents.csv.gz
ls -lh ~/mimic/hosp/labevents.csv

-rwxrwxrwx 1 gewenqiang gewenqiang 2.5G Jan 16 19:01 /home/gewenqiang/mimic/hosp/labevents.cs
-rwxrwxrwx 1 gewenqiang gewenqiang 18G Jan 16 19:01 /home/gewenqiang/mimic/hosp/labevents.cs

Comparison of run times:

time zcat ~/mimic/hosp/labevents.csv.gz | wc -l

158374765

real 1m51.541s
user 1m17.670s
sys 0m25.059s

time wc -l ~/mimic/hosp/labevents.csv

rm ~/mimic/hosp/labevents.csv
```

gzip -dk ~/mimic/hosp/labevents.csv.gz

Trade off: Storage trade-off Compressing files can save a lot of disk space and reduce network transmission time when moving data. Uncompressed files require more disk space, which may not be feasible for very large datasets. Due to decompression overhead, reading compressed files (zcat) may be slightly slower. However, for linear operations such as counting lines (wc-l), this difference can usually be ignored. The operation of uncompressed files can be faster because there is no decompression step. For very large files, the speed improvement may be obvious, but the storage overhead may outweigh the benefits.

# Q4. Who's popular in Price and Prejudice

1. You and your friend just have finished reading *Pride and Prejudice* by Jane Austen. Among the four main characters in the book, Elizabeth, Jane, Lydia, and Darcy, your friend thinks that Darcy was the most mentioned. You, however, are certain it was Elizabeth. Obtain the full text of the novel from <a href="http://www.gutenberg.org/cache/epub/42671/pg42671.txt">http://www.gutenberg.org/cache/epub/42671/pg42671.txt</a> and save to your local folder.

```
wget -nc http://www.gutenberg.org/cache/epub/42671/pg42671.txt
```

system("quarto -version") Explain what wget -nc does. Do **not** put this text file pg42671.txt in Git. Complete the following loop to tabulate the number of times each of the four characters is mentioned using Linux commands.

```
wget -nc http://www.gutenberg.org/cache/epub/42671/pg42671.txt
for char in Elizabeth Jane Lydia Darcy
do
    echo $char:
    grep -ow "$char" pg42671.txt | wc -l
done
```

Solution:

wget is used to download files from the web.

2. What's the difference between the following two commands?

```
echo 'hello, world' > test1.txt
and
echo 'hello, world' >> test2.txt
```

#### Solution:

The first one creates a new file test1.txt (if it doesn't already exist) and writes 'hello, world' to it. If test1.txt already exists, this command overwrites the file, replacing its contents with 'hello, world'.

If test2.txt doesn't exist, the second command creates the file first and writes 'hello, world' to it. If test2.txt already exists, this command adds 'hello, world' to the end of the existing file without deleting its previous contents.

3. Using your favorite text editor (e.g., vi), type the following and save the file as middle.sh:

```
#!/bin/sh
# Select lines from the middle of a file.
# Usage: bash middle.sh filename end_line num_lines
head -n "$2" "$1" | tail -n "$3"
```

Using chmod to make the file executable by the owner, and run

```
chmod u+x middle.sh
./middle.sh pg42671.txt 20 5
```

Explain the output. Explain the meaning of "\$1", "\$2", and "\$3" in this shell script. Why do we need the first line of the shell script?

#### Solution:

head -n 20 pg42671.txt: Extracts the first 20 lines of the file pg42671.txt.

tail -n 5: From the 20 lines produced by head, it extracts the last 5 lines.

The command runs the shell script middle.sh on the file pg42671.txt, extracting 5 lines from the end of the first 20 lines of the file.

In shell scripting, \$1, \$2, \$3, etc., refer to the positional parameters.

\$1: The first argument, in this case, the file name (pg42671.txt). \$2: The second argument, representing the total number of lines to extract from the beginning of the file. \$3: The third argument, representing the number of lines to extract from the result of head.

The shebang ensures that the correct shell is used to interpret the script. If we don't use it, the script might default to another shell (e.g., bash, zsh), which could lead to unexpected behavior if the script uses syntax specific to sh.

# Q5. More fun with Linux

Try following commands in Bash and interpret the results: cal, cal 2025, cal 9 1752 (anything unusual?), date, hostname, arch, uname -a, uptime, who am i, who, w, id, last | head, echo {con,pre}{sent,fer}{s,ed}, time sleep 5, history | tail.

#### **Solution:**

```
cal
cal 2025
cal 9 1752
January 2025
Su Mo Tu We Th Fr Sa
1 2 3 4
```

5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31

2025

January February Su Mo Tu We Th Fr Sa Su Mo Tu We Th Fr Sa Su Mo Tu We Th Fr Sa 1 2 3 4 1 5 6 7 8 9 10 11 2 3 4 5 6 7 8 2 3 4 5 6 7 8 12 13 14 15 16 17 18 9 10 11 12 13 14 15 9 10 11 12 13 14 15 26 27 28 29 30 31 23 24 25 26 27 28 23 24 25 26 27 28 29 30 31

Su Mo Tu We Th Fr Sa Su Mo Tu

Su Mo Mo Tu We Th Fr Sa Su Mo

October November December Su Mo Tu We Th Fr Sa Su Mo Tu We Th Fr Sa Su Mo Tu We Th Fr Sa 1 2 3 4 1 2 3 4 5 6 1 5 6 7 8 9 10 11 2 3 4 5 6 7 8 7 8 9 10 11 12 13 12 13 14 15 16 17 18 9 10 11 12 13 14 15 14 15 16 17 18 19 20 19 20 21 22 23 24 25 16 17 18 19 20 21 22 21 22 23 24 25 26 27 26 27 28 29 30 31 23 24 25 26 27 28 29 28 29 30 31 30

```
date
  hostname
  arch
  uname -a
  uptime
Thu Jan 23 18:37:02 PST 2025
gewww
x86 64
Linux gewww 5.15.167.4-microsoft-standard-WSL2 #1 SMP Tue Nov 5 00:21:55 UTC 2024 x86_64 x86
 18:37:02 up 8:40, 1 user, load average: 1.09, 1.04, 0.71
  who am i
  who
  id
  last | head
  echo {con,pre}{sent,fer}{s,ed}
  time sleep 5
  history | tail
                        2025-01-23 14:06
gewenqiang pts/1
 18:37:02 up 8:40, 1 user, load average: 1.09, 1.04, 0.71
USER
        TTY
                  FROM
                                   LOGIN@
                                            IDLE
                                                   JCPU
                                                          PCPU WHAT
                                            4:30m 0.03s 0.02s -bash
gewengia pts/1
                                   14:06
uid=1000(gewenqiang) gid=1000(gewenqiang) groups=1000(gewenqiang),4(adm),20(dialout),24(cdro
         system boot 5.15.167.4-micro Thu Jan 23 14:06
                                                          still running
         system boot 5.15.167.4-micro Wed Jan 22 23:10
reboot
                                                          still running
reboot
         system boot 5.15.167.4-micro Wed Jan 22 21:56
                                                          still running
        system boot 5.15.167.4-micro Wed Jan 22 21:15
                                                          still running
reboot
         system boot 5.15.167.4-micro Wed Jan 22 20:31
                                                          still running
reboot
         system boot 5.15.167.4-micro Wed Jan 22 20:26
reboot
                                                          still running
reboot
         system boot 5.15.167.4-micro Wed Jan 22 18:39
                                                          still running
         system boot 5.15.167.4-micro Wed Jan 22 18:39
                                                          still running
reboot
         system boot 5.15.167.4-micro Wed Jan 22 18:38
                                                          still running
reboot
         system boot 5.15.167.4-micro Wed Jan 22 18:37
                                                          still running
reboot
consents consented confers confered presents presented prefers prefered
real
        0m5.003s
        0m0.001s
user
sys 0m0.000s
```

# Q6. Book

- 1. Git clone the repository <a href="https://github.com/christophergandrud/Rep-Res-Book">https://github.com/christophergandrud/Rep-Res-Book</a> for the book *Reproducible Research with R and RStudio* to your local machine. Do **not** put this repository within your homework repository biostat-203b-2025-winter.
- 2. Open the project by clicking rep-res-3rd-edition.Rproj and compile the book by clicking Build Book in the Build panel of RStudio. (Hint: I was able to build git\_book and epub\_book directly. For pdf\_book, I needed to add a line \usepackage{hyperref} to the file Rep-Res-Book/rep-res-3rd-edition/latex/preabmle.tex.)

The point of this exercise is (1) to obtain the book for free and (2) to see an example how a complicated project such as a book can be organized in a reproducible way. Use sudo apt install PKGNAME to install required Ubuntu packages and tlmgr install PKGNAME to install missing TexLive packages.

For grading purpose, include a screenshot of Section 4.1.5 of the book here.

### Solution:

I cloned the reporsitory and compiled the book. Here is the screenshot of Section 4.1.5 of the book.

#### 4.1.5 Spaces in directory and file names

It is good practice to avoid putting spaces in your file and directory names. For example, I called the example project parent directory in Figure 4.1 "example-project" rather than "Example Project". Spaces in file and directory names can sometimes create problems for computer programs trying to read the file path. The program may believe that the space indicates that the path name has ended. To make multi-word names easily readable without using spaces, adopt a consistent naming convention.

One approach is to use a convention that contrasts with the R object naming convention you are using. A contrasting convention helps make it clear if something is an R object or a file name. For example, if we adopt the underscore method for R object names used in Chapter 3 (e.g. health\_data) we could use hyphens (-) to separate words in file names. For example: example-source.R. This is sometimes called kebab-case.

#### 4.2 Organizing Your Research Project

Figure 4.1 gives an example of how the files in a simple reproducible research project could be organized. The project's parent directory is called example-project. Inside this directory are the primary knittable documents (paper.Rmd slideshow.Rmd, and website.Rmd). In addition, there is an analysis sub-directory with the R files to run the statistical analyses followed by a further data child directory.

The nested file structure allows you to use relative file paths. The knittable documents can call analysis-1.R with the relative path analysis/analysis-1.R.

In addition to the main files and sub-directories in example-project, you will notice files called README.md and example-project.Rproj. We'll discuss the example-project.Rproj file in the next section. The README.md file is a human readable overview of all the files in the project. It should briefly describe the project including things like its title, author(s), topic, any copyright information, and so on. It should also indicate how the folders in the project are organized and give instructions for how to reproduce the project. The README file should be in the main project folder—in our example this is called example-project—so that it is easy to find. If you are storing your project as a GitHub repository (see Chapter 5) and the file is called README, its contents will automatically be displayed on the repository's main page. If the README file is written using Markdown (c.g. README.md), it will also be properly formatted. Figure 5.2 shows an example of this.

It is good practice to dynamically include the system information for the R ses-