Biostat 203B Homework 1

Due Jan 24, 2025 @ 11:59PM

AUTHOR

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Display machine information for reproducibility:

```
sessionInfo()
```

```
R version 4.3.2 (2023-10-31)
```

Platform: aarch64-apple-darwin20 (64-bit)

Running under: macOS Sonoma 14.0

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib

LAPACK: /Library/Frameworks/R.framework/Versions/4.3-

arm64/Resources/lib/libRlapack.dylib; LAPACK version 3.11.0

locale:

```
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

time zone: America/Los_Angeles

tzcode source: internal

attached base packages:

```
[1] stats graphics grDevices utils datasets methods base
```

loaded via a namespace (and not attached):

```
[1] htmlwidgets_1.6.4 compiler_4.3.2 fastmap_1.1.1 cli_3.6.2 [5] tools_4.3.2 htmltools_0.5.7 rstudioapi_0.15.0 yaml_2.3.8 [9] rmarkdown_2.29 knitr_1.45 jsonlite_1.8.8 xfun_0.50
```

[13] digest_0.6.33 rlang_1.1.2 evaluate_0.23

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 <u>Student Developer Pack</u> at GitHub using your UCLA email. You'll get GitHub Pro account for free (unlimited public and private repositories). **Completed.**
- 2. Create a **private** repository biostat-203b-2025-winter and add Hua-Zhou and TA team (Tomoki-0kuno for Lec 1; parsajamshidian and BowenZhang2001 for Lec 82) as your collaborators with write permission. **Completed.**

- 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. **Completed.**
- 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. **Completed.**
- 5. After this course, you can make this repository public and use it to demonstrate your skill sets on job market.

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 https://mimic.mit.edu/docs/gettingstarted/ 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: Here is the Completion Report of my CITI Training.

Here is the Completion Certification of my CITI Training.

Q3. Linux Shell Commands

- 1. 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).
- (3.1) Solution: I downloaded the MIMIC IV v3.1 data and it is available under `~/mimic' folder as requested.

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

```
total 35943120
```

```
-rw-r--r-@ 1 julielee staff 15199 Oct 10 16:29 CHANGELOG.txt
-rw-r--r-@ 1 julielee staff 2518 Oct 10 17:30 LICENSE.txt
-rw-r--r-@ 1 julielee staff 2884 Oct 11 17:55 SHA256SUMS.txt
drwxr-xr-x@ 24 julielee staff 768 Jan 23 17:49 hosp
drwxr-xr-x@ 11 julielee staff 352 Jan 16 00:51 icu
-rw-r--r- 1 julielee staff 18402851720 Jan 19 21:09 labevents.csv
```

Refer to the documentation https://physionet.org/content/mimiciv/3.1/ 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.

- 2. Display the contents in the folders hosp and icu using Bash command ls -l. 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.
- (3.2) **Solution:** Here is the content of 'hosp' folder:

```
ls -l ~/mimic/hosp/
```

```
total 12306248
-rw-r--r--@ 1 julielee
                              19928140 Jun 24 2024 admissions.csv.gz
                      staff
-rw-r--r--@ 1 julielee
                                427554 Apr 12 2024 d hcpcs.csv.gz
                     staff
-rw-r--r-@ 1 julielee staff
                                876360 Apr 12 2024 d_icd_diagnoses.csv.gz
-rw-r--r--@ 1 julielee
                     staff
                                589186 Apr 12 2024 d_icd_procedures.csv.gz
                                 13169 Oct 3 09:07 d_labitems.csv.gz
-rw-r--r-@ 1 julielee staff
-rw-r--r-@ 1 julielee staff
                              -rw-r--r--@ 1 julielee staff
                               9743908 Oct 3 09:07 drgcodes.csv.gz
-rw-r--r-@ 1 julielee staff
                             811305629 Apr 12 2024 emar.csv.gz
                             748158322 Apr 12 2024 emar_detail.csv.gz
-rw-r--r-@ 1 julielee staff
-rw-r--r-@ 1 julielee staff
                               2162335 Apr 12 2024 hcpcsevents.csv.gz
-rw-r--r-@ 1 julielee staff
                            2592909134 Oct 3 09:08 labevents.csv.gz
-rw-r--r-@ 1 julielee staff
                             117644075 Oct 3 09:08 microbiologyevents.csv.gz
-rw-r--r-@ 1 julielee staff
                              44069351 Oct 3 09:08 omr.csv.gz
                               -rw-r--r-@ 1 julielee staff
-rw-r--r-@ 1 julielee staff
                             525708076 Apr 12 2024 pharmacy.csv.gz
-rw-r--r-@ 1 julielee staff
                             666594177 Apr 12 2024 poe.csv.gz
-rw-r--r-@ 1 julielee staff
                              55267894 Apr 12 2024 poe_detail.csv.gz
-rw-r--r--@ 1 julielee staff
                             606298611 Apr 12 2024 prescriptions.csv.gz
-rw-r--r-@ 1 julielee staff
                               7777324 Apr 12 2024 procedures icd.csv.gz
-rw-r--r--@ 1 julielee
                     staff
                                127330 Apr 12 2024 provider.csv.gz
-rw-r--r-@ 1 julielee staff
                               8569241 Apr 12 2024 services.csv.gz
```

Here is the content of 'icu' folder:

-rw-r--r--@ 1 julielee

```
ls -l ~/mimic/icu/
```

46185771 Oct 3 09:08 transfers.csv.gz

```
total 8506784
-rw-r--r-@ 1 julielee staff 41566 Apr 12 2024 caregiver.csv.gz
-rw-r--r-@ 1 julielee staff 3502392765 Apr 12 2024 chartevents.csv.gz
-rw-r--r-@ 1 julielee staff 58741 Apr 12 2024 d_items.csv.gz
-rw-r--r-@ 1 julielee staff 63481196 Apr 12 2024 datetimeevents.csv.gz
-rw-r--r-@ 1 julielee staff 3342355 Oct 3 07:36 icustays.csv.gz
```

```
-rw-r--r-@ 1 julielee staff 311642048 Apr 12 2024 ingredientevents.csv.gz

-rw-r--r-@ 1 julielee staff 401088206 Apr 12 2024 inputevents.csv.gz

-rw-r--r-@ 1 julielee staff 49307639 Apr 12 2024 outputevents.csv.gz

-rw-r--r-@ 1 julielee staff 24096834 Apr 12 2024 procedureevents.csv.gz
```

These data were distributed as ".csv.gz" files instead of .csv files because the ".gz" extension insinuates that the CSV data has been compressed due to its large size. When compressing the CSV file, the underlying data format is still CSV but users are more easily able to open and the read the data in any CSV reader even after decompression. The data that we downloaded (Mimic) is an extremely large file and beig able to compress it using the Gzip algorithm reduces the file size and makes it more efficient to store.

- 3. Briefly describe what Bash commands zcat, zless, zmore, and zgrep do.
- **(3.3) Solution:** The Bash command zcat is equivalent to the cat for gzip-compressed files. It is used to output the contents of the .gz file without creating an uncompressed version of the file.

The Bash command zless is similar to the less command. It allows users to view the contents of the compressed files without having to decompress or extract them.

The Bash command zmore is used to display compressed or plan text files one screen at a time without first decompressing them.

The Bash command zgrep is used to search through a combination of uncompressed and compressed files without explicitly decompressing them first.

- 4. (Looping in Bash) What's the output of the following bash script?
- **(3.4) Solution:** The output of the following bash script is down below. It is a list of the compressed (.gz) files that start with "a", "l", and "pa" in ~/mimic/hosp/. More specifically, the compressed files listed correspond to admissions, labevents, and patients. Information regarding the compressed files correspond to the file permissions, file sizes, dates and times, and file paths.

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

```
-rw-r--r-@ 1 julielee staff 19928140 Jun 24 2024 /Users/julielee/mimic/hosp/admissions.csv.gz -rw-r--r-@ 1 julielee staff 2592909134 Oct 3 09:08 /Users/julielee/mimic/hosp/labevents.csv.gz -rw-r--r-@ 1 julielee staff 2835586 Apr 12 2024 /Users/julielee/mimic/hosp/patients.csv.gz
```

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

Solution: The number of lines in each data file for admission.csv.gv, labevents.csv.gz, and patients.csv.gz are as follows:

```
for datafile in ~/mimic/hosp/{a,l,pa}*.gz
do
    echo $datafile
    gzcat "$datafile" | wc -l
done
```

```
/Users/julielee/mimic/hosp/admissions.csv.gz
546029
/Users/julielee/mimic/hosp/labevents.csv.gz
158374765
/Users/julielee/mimic/hosp/patients.csv.gz
364628
```

In summary, there are 546029 lines in the file 'admissions.csv.gz", there are 158374765 lines in the file 'labevents.csv.gz', and there are 364628 lines in the 'patients.csv.gz' data file. In the following code, we iterate through all the .gz files in the ~/mimic/hosp directory that matches the "a, l, pa" prefixes. The "gzcat" command decompresses each file and outputs its content to standard output. Afterwards, the "wc -l" command prints the number of lines in each iterated file.

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 data 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.)

(3.5) Solution:

The first few lines of admissions.csv.gz are:

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

```
subject_id,hadm_id,admittime,dischtime,deathtime,admission_type,admit_provider_id,admissi
on_location,discharge_location,insurance,language,marital_status,race,edregtime,edouttime
,hospital_expire_flag
10000032,22595853,2180-05-06 22:23:00,2180-05-07 17:15:00,,URGENT,P49AFC,TRANSFER FROM
HOSPITAL, HOME, Medicaid, English, WIDOWED, WHITE, 2180-05-06 19:17:00, 2180-05-06 23:30:00, 0
10000032,22841357,2180-06-26 18:27:00,2180-06-27 18:49:00,,EW EMER.,P784FA,EMERGENCY
ROOM, HOME, Medicaid, English, WIDOWED, WHITE, 2180-06-26 15:54:00, 2180-06-26 21:31:00, 0
10000032,25742920,2180-08-05 23:44:00,2180-08-07 17:50:00,,EW EMER.,P19UTS,EMERGENCY
ROOM, HOSPICE, Medicaid, English, WIDOWED, WHITE, 2180-08-05 20:58:00, 2180-08-06 01:44:00, 0
10000032,29079034,2180-07-23 12:35:00,2180-07-25 17:55:00,,EW EMER.,P060TX,EMERGENCY
ROOM, HOME, Medicaid, English, WIDOWED, WHITE, 2180-07-23 05:54:00, 2180-07-23 14:00:00, 0
10000068,25022803,2160-03-03 23:16:00,2160-03-04 06:26:00,,EU
OBSERVATION, P39NWO, EMERGENCY ROOM, , , English, SINGLE, WHITE, 2160-03-03 21:55:00, 2160-03-04
06:26:00,0
10000084,23052089,2160-11-21 01:56:00,2160-11-25 14:52:00,,EW EMER.,P42H7G,WALK-IN/SELF
REFERRAL, HOME HEALTH CARE, Medicare, English, MARRIED, WHITE, 2160-11-20 20:36:00, 2160-11-21
03:20:00,0
```

```
10000084,29888819,2160-12-28 05:11:00,2160-12-28 16:07:00,,EU

0BSERVATION,P35NE4,PHYSICIAN REFERRAL,,Medicare,English,MARRIED,WHITE,2160-12-27

18:32:00,2160-12-28 16:07:00,0

10000108,27250926,2163-09-27 23:17:00,2163-09-28 09:04:00,,EU

0BSERVATION,P40JML,EMERGENCY ROOM,,,English,SINGLE,WHITE,2163-09-27 16:18:00,2163-09-28 09:04:00,0

10000117,22927623,2181-11-15 02:05:00,2181-11-15 14:52:00,,EU

0BSERVATION,P47EY8,EMERGENCY ROOM,,Medicaid,English,DIVORCED,WHITE,2181-11-14 21:51:00,2181-11-15 09:57:00,0
```

The number of rows in this data file, excluding the header line is:

```
zcat < ~/mimic/hosp/admissions.csv.gz |
tail -n +2 |
wc -l</pre>
```

546028

If each hadm_id identifies a hospitalization, the number of hospitalizations in this data file is the same as the number of rows in the file (546028). Therefore, we are able to conclude that each hospital admission is unique and independent as none of the entries repeat.

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

546028

The number of unique patients there are in this data file (admissions) is 223452 patients (identified by subject_id).

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

223452

Now, let's first peek the first few lines of the patient.csv.gz file:

```
zcat < ~/mimic/hosp/patients.csv.gz | head</pre>
```

```
subject_id,gender,anchor_age,anchor_year,anchor_year_group,dod
10000032,F,52,2180,2014 - 2016,2180-09-09
10000048,F,23,2126,2008 - 2010,
```

```
10000058,F,33,2168,2020 - 2022,

10000068,F,19,2160,2008 - 2010,

10000084,M,72,2160,2017 - 2019,2161-02-13

10000102,F,27,2136,2008 - 2010,

10000108,M,25,2163,2014 - 2016,

10000115,M,24,2154,2017 - 2019,

10000117,F,48,2174,2008 - 2010,
```

The number of patients listed in this patients.csv.gz file is 364627 patients. Recall that the number of unique patients that are in the admission.csv.gz file(identified by subject_id) is 223452 patients. These 2 numbers do not match as the number of patients listed in the patients.csv.gv file is greater than the number of unique patients in the admissions.csv.gz file.

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

364627

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.)

(3.6) Solution

Start with listing out all the variable names (header row):

```
zcat < ~/mimic/hosp/admissions.csv.gz | head -1</pre>
```

subject_id,hadm_id,admittime,dischtime,deathtime,admission_type,admit_provider_id,admissi
on_location,discharge_location,insurance,language,marital_status,race,edregtime,edouttime
,hospital_expire_flag

The possible unique values and their corresponding counts taken by the variable 'admission_type' are:

```
zcat < ~/mimic/hosp/admissions.csv.gz |
tail -n +2 |
awk -F, '{print $6}' |
sort |
uniq -c |
sort -nr</pre>
```

```
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
```

The possible unique values and their corresponding counts taken by the variable 'admission_location' are:

```
zcat < ~/mimic/hosp/admissions.csv.gz |
tail -n +2 |
awk -F, '{print $8}' |
sort |
uniq -c |
sort -nr</pre>
```

```
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
```

The possible unique values and their corresponding counts taken by the variable 'insurance' are:

```
zcat < ~/mimic/hosp/admissions.csv.gz |
tail -n +2 |
awk -F, '{print $10}' |
sort |
uniq -c |
sort -nr</pre>
```

```
244576 Medicare
173399 Private
104229 Medicaid
14006 Other
9355
463 No charge
```

The possible values taken by the varaible 'ethnicity' are:

```
zcat < ~/mimic/hosp/admissions.csv.gz |
tail -n +2 |
awk -F, '{print $13}' |</pre>
```

```
sort |
uniq -c |
sort -nr
```

1/23/25, 6:09 PM

```
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?

(3.7) Solution Let's first take a peek of the first few rows of the 'icusays.csv.gv'

```
zcat < ~/mimic/icu/icustays.csv.gz | head</pre>
```

```
subject_id,hadm_id,stay_id,first_careunit,last_careunit,intime,outtime,los 10000032,29079034,39553978,Medical Intensive Care Unit (MICU),Medical Intensive Care Unit (MICU),2180-07-23 14:00:00,2180-07-23 23:50:47,0.4102662037037037 10000690,25860671,37081114,Medical Intensive Care Unit (MICU),Medical Intensive Care Unit (MICU),2150-11-02 19:37:00,2150-11-06 17:03:17,3.8932523148148146 10000980,26913865,39765666,Medical Intensive Care Unit (MICU),Medical Intensive Care Unit
```

```
(MICU),2189-06-27 08:42:00,2189-06-27 20:38:27,0.4975347222222222
10001217,24597018,37067082,Surgical Intensive Care Unit (SICU),Surgical Intensive Care
Unit (SICU),2157-11-20 19:18:02,2157-11-21 22:08:00,1.1180324074074075
10001217,27703517,34592300,Surgical Intensive Care Unit (SICU),Surgical Intensive Care
Unit (SICU),2157-12-19 15:42:24,2157-12-20 14:27:41,0.948113425925926
10001725,25563031,31205490,Medical/Surgical Intensive Care Unit
(MICU/SICU), Medical/Surgical Intensive Care Unit (MICU/SICU), 2110-04-11 15:52:22, 2110-04-
12 23:59:56,1.338587962962963
10001843,26133978,39698942, Medical/Surgical Intensive Care Unit
(MICU/SICU), Medical/Surgical Intensive Care Unit (MICU/SICU), 2134-12-05 18:50:03, 2134-12-
06 14:38:26,0.8252662037037037
10001884,26184834,37510196,Medical Intensive Care Unit (MICU),Medical Intensive Care Unit
(MICU),2131-01-11 04:20:05,2131-01-20 08:27:30,9.17181712962963
10002013,23581541,39060235,Cardiac Vascular Intensive Care Unit (CVICU),Cardiac Vascular
Intensive Care Unit (CVICU),2160-05-18 10:00:53,2160-05-19 17:33:33,1.314351851852
The number of ICU stays (as identified by 'stay id') is in the data file is 94458 ICU stays.
```

```
zcat < ~/mimic/icu/icustays.csv.gz |
tail -n +2 |
awk -F, '{print $3}' |
sort |
uniq |
wc -l</pre>
```

94458

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The number of unique patients (identified by 'subject_id') in the data file is 65366 patients.

```
zcat < ~/mimic/icu/icustays.csv.gz |
tail -n +2 |
awk -F, '{print $1}' |
sort |
uniq |
wc -l</pre>
```

65366

- 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 -l versus wc -l 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.)
- (3.8) **Solution:** The compressed gz file (labevents.csv.gz) has a size of 2.4G. The uncompressed file ('labevents.csv') has a size of 17G.

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

```
-rw-r--re-@ 1 julielee staff 2.4G Oct 3 09:08 /Users/julielee/mimic/hosp/labevents.csv.gz
```

```
gzip -dk < ~/mimic/hosp/labevents.csv.gz > ~/mimic/hosp/labevents.csv
ls -lh ~/mimic/hosp/labevents.csv
```

```
-rw-r--r-- 1 julielee staff 17G Jan 23 17:54 /Users/julielee/mimic/hosp/labevents.csv
```

The run times of zcat $< \sim/\min(c/labevents.csv.gz \mid wc - l are displayed below:$

```
time zcat < ~/mimic/hosp/labevents.csv.gz | wc -l</pre>
```

158374765

```
real 0m41.934s
user 0m46.350s
sys 0m11.309s
```

The run time of wc -l labevents.csv are displayed below:

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

158374765 /Users/julielee/mimic/hosp/labevents.csv

```
real 0m39.056s
user 0m29.488s
sys 0m5.753s
```

From the outputs above, we observe that the compressed .gz file is significantly smaller in size compared to the uncompressed file. However, running the same command to count the number of lines takes longer on the compressed file than on the uncompressed file. This highlights the trade-offs between storage and speed: while compressed files are more efficient in saving disk space, they require decompression, which increases processing time and computational resource usage. For large datasets, operations like wc -l are slower on compressed files compared to uncompressed ones, due to the added overhead of decompression (computational effort and use of more system resources such as CPU and memory).

We erase the 'labevents.csv' file before proceeding on the next exercise.

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

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 http://www.gutenberg.org/cache/epub/42671/pg42671.txt and save to your local folder. **Done**

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

Explain what wget -nc does.

(4.1) Solution: The 'wget -nc' command is used to download a file from the internet, retrieving files using HTTP, HTTPS, and FTP protocols. The '-nc' flag is used to prevent the download of the file if it already exists in the current directory. If a file with the same name is already downloaded, then the wget command will skip downloading the file.

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.

Explanation of Code: By utilizing the grep -o, we are able to search for all the occurrences that the exact value of "\$char" takes on in the pg42671.txt file. Every time an occurrence (in this case, a specific name) is detected, it outputs the specific name on a new line. The wc -l counts the number of lines or number of occurrences (names) there are in the entire pg42671.txt file.

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

for char in Elizabeth Jane Lydia Darcy
do
    echo "Count of $char: "
    grep -o "$char" pg42671.txt | wc -l
done
```

```
Count of Elizabeth:
634
Count of Jane:
293
Count of Lydia:
170
Count of Darcy:
417
```

- 2. What's the difference between the following two commands?
- **(4.2) Solution:** The first command writes the string "hello, world" to the file test1.txt. If the file test1.txt already exists, then the contents of the existing file will be overwritten by the contents of the new text. However, if text1.txt file does not exist, then it will be created and the text will be written. The second command appends the string "hello, world" to the file test2.txt. In other words, if the file test2.txt already existed, the new string will be added to the end of the existing content. However, if the file test2.txt does not exist, it will be created and the text will be written to it. The >> operator is in indicator that the new content appends to the existing content in the file.

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

and

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

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

(4.3) Solution:

I manually created the middle.sh file using the text editor nano and included middle.sh in the submission folder on Git.

```
#!/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 the following command to test the script: (Note that instead of 20 5, I showcased the results for 18 6 to better understand the content of these lines)

```
chmod a+x middle.sh
./middle.sh pg42671.txt 18 6
```

Author: Jane Austen

Editor: R. W. Chapman

Release date: May 9, 2013 [eBook #42671]

Explain the output.

Solution: The output showcases that the author of the book "Price and Prejudice is Jane Austen, the Editor is R.W Chapman, and the release date was May 9, 2013 (eBook \$42671). We extracted lines 13-18 from the original text.

Explain the meaning of "\$1", "\$2", and "\$3" in this shell script.

Solution: In this shelll script, the "\$1" refers to the first argument passed to the script, which is the pg42671.txt file. The "\$2" refers to the second argument passed to the script, which is the ending line number (line number 18). The "\$3" refers to the third argument passed to the script, which is the num_lines or the number of lines to extract before and including the 18th line. In this case, we extract 6 lines from line number 18.

Why do we need the first line of the shell script?

Solution: The first line of the script is a shebang, which specifies the interpreter used to execute the script. It tells the system which shell or program should run the script. In this case, the shebang #!/bin/sh directs the system to use the Bourne shell as the interpreter.

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" The "cal" command showcases the calendar for the current month.

cal

The "cal 2025" command showcases the calendar for the year 2025 (for all 12 months).

cal 2025

2025 January February March 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 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 19 20 21 22 2 3 24 25 16 17 18 19 20 21 22 16 17 18 19 20 21 22 23 24 25 26 27 28 29 26 27 28 29 30 31 23 24 25 26 27 28 30 31

```
April
                      May
                                       June
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 5
                          1 2 3
                                  1 2 3 4 5 6 7
     8 9 10 11 12
                 4 5 6
                          8 9 10
                                  8
                                   9 10 11 12 13 14
13 14 15 16 17 18 19 11 12 13 14 15 16 17 15 16 17 18 19 20 21
27 28 29 30
                25 26 27 28 29 30 31 29 30
```

```
July
                           August
                                              September
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 5
                                             1 2 3 4
                                   1 2
  7 8 9 10 11 12
                           5
                              6 7 8 9
                                          7 8 9 10 11 12 13
                     3 4
13 14 15 16 17 18 19
                    10 11 12 13 14 15 16 14 15 16 17 18 19 20
20 21 22 23 24 25 26 17 18 19 20 21 22 23
                                         21 22 23 24 25 26 27
27 28 29 30 31
                    24 25 26 27 28 29 30 28 29 30
```

1/23/25, 6:09 PM 31

	October						November							December						
Su	Мо	Tu	We	Th	Fr	Sa	Su	Мо	Tu	We	Th	Fr	Sa	Su	Мо	Tu	We	Th	Fr	Sa
			1	2	3	4							1		1	2	3	4	5	6
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													

The "cal 9 1752" command showcases the calendar for the month of September in the year of 1752. However, there is unusual behavior in this command. We are able to see that the calendar is missing 11 days (September 3 -September 13, 1752.) This is because the Gregorian calendar was adopted in 1752 and the Julian calendar was replaced.

```
cal 9 1752
```

September 1752 Su Mo Tu We Th Fr Sa 1 2 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30

The "date" command showcases the current date and time in PST.

date

Thu Jan 23 17:55:23 PST 2025

The "hostname" command showcases the hostname of the current system.

hostname

Julies-Laptop-2.local

The "arch" command showcases the hardware architecture of the current system.

arch

arm64

The "uname -a" command showcases the kernel name/version, system information, hostname, architecture, and OS of the current machine.

```
uname -a
```

Darwin Julies-Laptop-2.local 23.0.0 Darwin Kernel Version 23.0.0: Fri Sep 15 14:42:57 PDT 2023; root:xnu-10002.1.13~1/RELEASE_ARM64_T8112 arm64

The uptime command showcases how long the machine has been running, system load averages, and the number of users logged in.

```
uptime
```

```
17:55 up 4 days, 3:47, 3 users, load averages: 5.74 5.18 5.35
```

The who am i command showcases the current user logged in (username) and login time.

```
who am i
```

```
julielee Jan 23 17:55
```

The who command showcases the list of all currently logged-in users.

```
who
```

```
julielee ttys000 Jan 23 17:11
julielee console Jan 19 23:57
julielee ttys001 Jan 23 17:11
```

The w command showcases information regarding the users who are currently logged into the system and their activities. It includes system information including the current time, how long the system has been running, and the number of users logged in. It includes user information including usernmae, terminal decive, login time, idle time, and current directory used.

```
W
```

```
17:55
       up 4 days,
                   3:47, 3 users, load averages: 5.74 5.18 5.35
USER
         TTY
                  FROM
                                     LOGIN@ IDLE WHAT
julielee s000
                                    17:11
                                               44 -zsh
julielee console
                                    Sun23
                                            3days -
julielee s001
                                    17:11
                                               24 -zsh
```

The id command showcases the user ID, groupID, user name, and the groups for the current user.

```
id
```

```
uid=501(julielee) gid=20(staff)
groups=20(staff),12(everyone),61(localaccounts),79(_appserverusr),80(admin),81(_appserver
adm),98(_lpadmin),701(com.apple.sharepoint.group.1),33(_appstore),100(_lpoperator),204(_d
```

1/23/25, 6:09 PM Biostat 203B Homework 1

eveloper),250(_analyticsusers),395(com.apple.access_ftp),398(com.apple.access_screensharing),399(com.apple.access_ssh),400(com.apple.access_remote_ae)

The last | head command showcases the most recent logins (first 10 logg-in users).

```
last | head
```

```
julielee
          ttys001
                                          Thu Jan 23 17:11
                                                            still logged in
                                                            still logged in
julielee ttys000
                                          Thu Jan 23 17:11
                                          Thu Jan 23 13:23 - 13:23 (00:00)
julielee
         ttys000
                                          Wed Jan 22 21:24 - 21:24 (00:00)
julielee ttys000
                                          Wed Jan 22 21:08 - 21:08 (00:00)
julielee
         ttys000
                                          Wed Jan 22 20:33 - 20:33 (00:00)
julielee ttys000
julielee ttys000
                                          Wed Jan 22 20:31 - 20:31 (00:00)
                                         Wed Jan 22 20:28 - 20:28 (00:00)
julielee
          ttys000
julielee
          ttys000
                                          Wed Jan 22 18:08 - 18:08 (00:00)
                                          Wed Jan 22 17:11 - 17:11 (00:00)
julielee
          ttys000
```

The echo {con, pre} {sent,fer}{s,ed} command showcases different combinations of words.

```
echo {con,pre}{sent,fer}{s,ed}
```

consents consented confers confered presents presented prefers prefered

The time sleep 5 command showcases how long the operation takes to execute after the system pasues for 5 seconds.

```
time sleep 5
```

```
real 0m5.009s
user 0m0.000s
sys 0m0.002s
```

The history | tail command showcases the last 10 commands that were executed in the terminal.

```
history | tail

#My following output for this command on my terminal:
    #158    date
    #159    hostname
    #160    arch
    #161    uname
    #162    uptime
    #163    who am i
    #164    history | tail
    #165    wget
    #166    wget -V
    #167    cal    9 1752
```

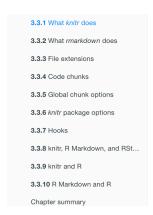
Q6. Book

- 1. Git clone the repository https://github.com/christophergandrud/Rep-Res-Book 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: 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.

This is the End of Homework #1