Biostat 203B Homework 1

Due Jan 24, 2025 @ 11:59PM

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Display machine information for reproducibility:										
sessionInfo()										
R version 4.3.0 (2023-04-21) Platform: aarch64-apple-darwin20 (64-bit) Running under: macOS 14.4.1										
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;										
locale: [1] 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] compiler_4.3.0 fastmap_1.1.1 cli_3.6.2 tools_4.3.0

[5] htmltools_0.5.7 rstudioapi_0.14 yaml_2.3.8 rmarkdown_2.29

[9] knitr_1.45 jsonlite_1.8.8 xfun_0.50 digest_0.6.34

[13] rlang 1.1.3 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 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 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 and Completion Certificate 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).

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

```
total 48
-rw-r--r-@ 1 kiananik staff 15199 Oct 10 17:29 CHANGELOG.txt
-rw-r--r-@ 1 kiananik staff 2518 Oct 10 18:30 LICENSE.txt
-rw-r--r-@ 1 kiananik staff 2884 Oct 11 18:55 SHA256SUMS.txt
drwxr-xr-x@ 24 kiananik staff 768 Jan 24 22:09 hosp
drwxr-xr-x@ 11 kiananik staff 352 Jan 21 06:28 icu
```

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.

Solution: I downloaded the MIMIC IV v3.1 data and it's available under ~/mimic folder as requested.

2. 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: Here is the content of hosp folder

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

```
total 12328176
-rw-r--r--@ 1 kiananik
                       staff
                                19928140 Jun 24
                                                2024 admissions.csv.gz
-rw-r--r--@ 1 kiananik
                      staff
                                  427554 Apr 12
                                                2024 d_hcpcs.csv.gz
                                                2024 d_icd_diagnoses.csv.gz
-rw-r--r-0 1 kiananik staff
                                  876360 Apr 12
-rw-r--r-0 1 kiananik staff
                                  589186 Apr 12
                                                2024 d icd procedures.csv.gz
-rw-r--r-0 1 kiananik staff
                                   13169 Oct 3 10:07 d_labitems.csv.gz
-rw-r--r-0 1 kiananik staff
                                33564802 Oct 3 10:07 diagnoses icd.csv.gz
-rw-r--r-0 1 kiananik staff
                                 9743908 Oct 3 10:07 drgcodes.csv.gz
-rw-r--r-0 1 kiananik staff
                               811305629 Apr 12
                                                2024 emar.csv.gz
-rw-r--r-0 1 kiananik staff
                               748158322 Apr 13
                                                2024 emar_detail.csv.gz
                                                2024 hcpcsevents.csv.gz
-rw-r--r-0 1 kiananik staff
                                 2162335 Apr 12
-rw-r--r-0 1 kiananik staff
                              2592909134 Oct 3 10:08 labevents.csv.gz
                               117644075 Oct 3 10:08 microbiologyevents.csv.gz
-rw-r--r-0 1 kiananik staff
-rw-r--r-0 1 kiananik staff
                                44069351 Oct 3 10:08 omr.csv.gz
-rw-r--r-0 1 kiananik
                      staff
                                 2835586 Apr 12
                                                2024 patients.csv.gz
-rw-r--r-0 1 kiananik staff
                               525708076 Apr 12
                                                2024 pharmacy.csv.gz
-rw-r--r-0 1 kiananik staff
                               666594177 Apr 12
                                                2024 poe.csv.gz
-rw-r--r-0 1 kiananik staff
                                55267894 Apr 12
                                                2024 poe_detail.csv.gz
-rw-r--r-0 1 kiananik staff
                               606298611 Apr 12
                                                2024 prescriptions.csv.gz
                                                2024 procedures icd.csv.gz
-rw-r--r-0 1 kiananik staff
                                 7777324 Apr 12
-rw-r--r-0 1 kiananik staff
                                  127330 Apr 12
                                                2024 provider.csv.gz
-rw-r--r-0 1 kiananik staff
                                 8569241 Apr 12 2024 services.csv.gz
-rw-r--r-0 1 kiananik staff
                                46185771 Oct 3 10:08 transfers.csv.gz
```

and content of the icu folder

ls -l ~/mimic/icu/

```
total 8506784
-rw-r--r-0 1 kiananik staff
                                   41566 Apr 13
                                                 2024 caregiver.csv.gz
-rw-r--r-0 1 kiananik staff
                              3502392765 Apr 13
                                                 2024 chartevents.csv.gz
-rw-r--r-0 1 kiananik
                                   58741 Apr 13
                                                 2024 d_items.csv.gz
                       staff
                                                 2024 datetimeevents.csv.gz
-rw-r--r-0 1 kiananik staff
                                63481196 Apr 13
-rw-r--r-0 1 kiananik staff
                                 3342355 Oct 3 08:36 icustays.csv.gz
-rw-r--r--@ 1 kiananik staff
                               311642048 Apr 13
                                                 2024 ingredientevents.csv.gz
-rw-r--r-0 1 kiananik staff
                               401088206 Apr 13
                                                 2024 inputevents.csv.gz
-rw-r--r-0 1 kiananik staff
                                49307639 Apr 13
                                                 2024 outputevents.csv.gz
-rw-r--r-0 1 kiananik staff
                                24096834 Apr 13
                                                 2024 procedureevents.csv.gz
```

These data were distributed as gz file because .csv.gz files effectively compress big data files such as this and reduce storage space needed for them by decreasing the file size.

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

Solution: zcat is used to view the contents of a compressed file without having to uncompress the file. zless allows us to view the contents of compressed files withouth having to decompress them first. zmore uncompresses files and displays them one screenful at a time. zgrep command is used to search within compressed files without explicitly decompressing them first.

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

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

```
-rw-r--r-@ 1 kiananik staff 19928140 Jun 24 2024 /Users/kiananik/mimic/hosp/admissions.com-rw-r--r-@ 1 kiananik staff 2592909134 Oct 3 10:08 /Users/kiananik/mimic/hosp/labevents.com-rw-r--r--@ 1 kiananik staff 2835586 Apr 12 2024 /Users/kiananik/mimic/hosp/patients.com/scales/
```

Solution: This loop iterates through all files in the ~/mimic/hosp/ directory that start with a, 1, or pa and end with .gz and list the details such as size and permissions of each file that matches. In this scenario, the output turned out to be the admissions, labevents, and patients files that matched and their details were listed.

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

Displaying the number of lines in each data file

```
for datafile in ~/mimic/hosp/{a,l,pa}*.gz
do
    echo -n "$datafile: "
    zcat < "$datafile" | wc -l
done</pre>
```

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

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.)

Solution: Here's the first few lines of admissions.csv.gz

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

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

```
zcat < ~/mimic/hosp/admissions.csv.gz | tail -n +2 | wc -1</pre>
```

546028

The number of hospitalizations in this data file is

```
zcat < ~/mimic/hosp/admissions.csv.gz |
tail -n +2 |
cut -d, -f2 |
sort |
uniq |
wc -l</pre>
```

546028

the same as the number of rows in the file.

Peek the first few lines of patients.csv.gz:

```
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 unique patients in this data file is

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

223452

which is less than the number of paients listed in the patients.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.)

Solution:

Figuring out the column number for each variable

```
zcat < ~/mimic/hosp/admissions.csv.gz |
head -n 1 |
tr ',' '\n' |
nl</pre>
```

```
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
```

The count for each unique value of admission_type in decreasing order

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

The count for each unique value of admission_location in decreasing order

```
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
```

5837 INTERNAL TRANSFER TO OR FROM PSYCH

5734 PACU

402 INFORMATION NOT AVAILABLE

255 AMBULATORY SURGERY TRANSFER

6317 TRANSFER FROM SKILLED NURSING FACILITY

1

The count for each unique value of insurance in decreasing order

```
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 count for each unique value of ethnicity in decreasing order

```
tail -n +2
awk -F, '{print $13}' |
sort
uniq -c |
sort -nr
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
```

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

7. The icustays.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: Figuring out the column number for stay_id and subject_id

```
zcat < ~/mimic/icu/icustays.csv.gz |
head -n 1 |
tr ',' '\n' |
nl</pre>
```

```
1 subject_id
2 hadm_id
3 stay_id
4 first_careunit
5 last_careunit
6 intime
7 outtime
8 los
```

The number of ICU stays identified by stay_id

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

94458

The number of unique patients identified by subject_id

```
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.)

Solution:

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

```
-rw-r--r--@ 1 kiananik staff 2.4G Oct 3 10:08 /Users/kiananik/mimic/hosp/labevents.csv.gr-rw-r--r-- 1 kiananik staff 17G Oct 3 10:08 /Users/kiananik/mimic/hosp/labevents.csv
```

The runtime for zcat < ~/mimic/labevents.csv.gz | wc -l is

```
time zcat < ~/mimic/hosp/labevents.csv.gz | wc -1
```

158374765

```
real 0m18.726s
user 0m28.806s
sys 0m2.004s
```

The runtime for wc -1 labevents.csv

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

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

```
real 0m19.731s
user 0m17.318s
sys 0m1.580s
```

Deleting the labevents.csv file

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

The difference between the two runtimes shows that even though compressed files save significant storage space, they also require decompression for usage which can be slower than a regular file that doesn't need decompression.

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.

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

```
File 'pg42671.txt' already there; not retrieving.
```

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.

Solution: wget -nc has two parts where wget is used to download files from the web and -nc which stands for no-clobber prevents the code from overwriting an already existing file by not allowing it to download again if the file already exists.

```
wget -nc http://www.gutenberg.org/cache/epub/42671/pg42671.txt
for char in Elizabeth Jane Lydia Darcy
do
    echo $char:
    # some bash commands here
done
```

File 'pg42671.txt' already there; not retrieving.

Elizabeth:

Jane:

Lydia:

Darcy:

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

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

and

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

Solution: the command with > operator overwrites the file test1.txt with the text hello, world while the command with the >> appends the given text hello, world to the file test2.txt. With the >> operator, if the file test2.txt already exists, the text hello, world will be added to the end of the file instead of overwriting it.

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

```
./middle.sh pg42671.txt 20 5
```

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

Language: English

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: The output shows the date May 9, 2013, the format of the ebook, and it also shows that the language of ht ebook is English. "\$1" refers to the first argument which is the filename. "\$2" refers to the second argument which is the number of lines from the start. "\$3" refers to the third argument which is the number of lines to extract from the end of the previously selected lines. This resulted in the last 5 lines from the first 20 lines in the Pride and Prejudice text to be extracted. We need the first line in the shell script because it specifies which interpreter to use when executing the script and without it the script might not run properly.

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

 January 2025

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cal 2025

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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	23	24	25	16	17	18	19	20	21	22	16	17	18	19	20	21	22
26	27	28	29	30	31		23	24	25	26	27	28		23	24	25	26	27	28	29
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Su	Мо	Tu	We	Th	Fr	Sa	Su	Мо	Tu	We	Th	Fr	Sa	Su	Мо	Tu	We	Th	Fr	Sa
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13	14	15	16	17	18	19	11	12	13	14	15	16	17	15	16	17	18	19	20	21
20	21	22	23	24	25	26	18	19	20	21	22	23	24	22	23	24	25	26	27	28
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
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20 21 22 23 24 25 26
                     17 18 19 20 21 22 23
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                     24 25 26 27 28 29 30 28 29 30
                     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
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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													

cal 9 1752

The unusual occurance in the ouput for cal 9 1752 is that the calender skips sept 3-13 in 1752. Upon further research, I found the reason for this is that 1752 was the year that in the British Empire adopted the Gregorian calendar and 11 days were dropped.

date

Fri Jan 24 22:12:21 PST 2025

hostname

Kianas-MBP-2.lan

```
arch

arm64

uname -a

Darwin Kianas-MBP-2.lan 23.4.0 Darwin Kernel Version 23.4.0: Fri Mar 15 00:10:42 PDT 2024; ruptime

22:12 up 20 days, 8:08, 1 user, load averages: 3.77 3.53 2.83

who am i

kiananik Jan 24 22:12

who
```

22:12 up 20 days, 8:08, 1 user, load averages: 3.77 3.53 2.83
USER TTY FROM LOGIN@ IDLE WHAT
kiananik console - Thu15 30:48 -

kiananik console - Thu15 30:48 -

id

uid=501(kiananik) gid=20(staff) groups=20(staff),12(everyone),61(localaccounts),79(_appserve

last | head

kiananik	ttys000	Fri Jan 24 13:36 - 13:36 (00:00)
kiananik	ttys000	Fri Jan 24 12:51 - 12:51 (00:00)
kiananik	ttys000	Fri Jan 24 01:45 - 01:45 (00:00)
kiananik	ttys000	Thu Jan 23 15:23 - 15:23 (00:00)
kiananik	console	Thu Jan 23 15:23 still logged in
kiananik	ttys000	Thu Jan 23 15:23 - 15:23 (00:00)
kiananik	ttys000	Wed Jan 22 01:30 - 01:30 (00:00)
kiananik	ttys001	Tue Jan 21 15:32 - 15:32 (00:00)
kiananik	ttys001	Tue Jan 21 15:29 - 15:29 (00:00)
kiananik	ttys000	Tue Jan 21 15:20 - 15:20 (00:00)

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

consents consented confers confered presents presented prefers prefered

time sleep 5

real 0m5.009s user 0m0.000s sys 0m0.001s

history | tail

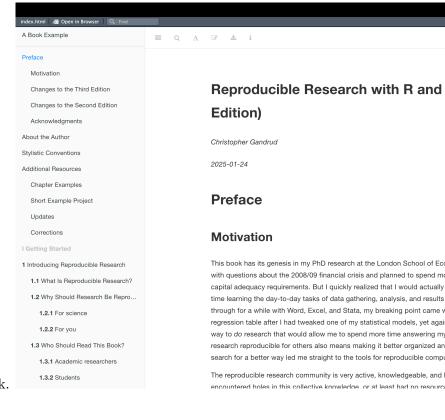
Done.

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 a screenshot of the book.