Last login: Mon Feb 26 18:40:19 on ttys001

The default interactive shell is now zsh.

To update your account to use zsh, please run `chsh -s /bin/zsh`.

For more details, please visit https://support.apple.com/kb/HT208050.

(base) a-10-27-23-46:∼ zoehaskellcraig\$ gcloud auth login --no-launch-browser

Go to the following link in your browser:

Enter authorization code: ERROR: There was a problem with web authentication.

ERROR: (gcloud.auth.login) Please supply either code or authorization_response parameters.
(base) a-10-27-23-46:~ zoehaskellcraig\$ 4/0AeaYSHAB-tu1utUER_1Y1aR1f5E5UIMWIptdA-lZLHeE4DPqdgJeesDP75DF2z2Jclltjg
-bash: 4/0AeaYSHAB-tu1utUER_1Y1aR1f5E5UIMWIptdA-lZLHeE4DPqdgJeesDP75DF2z2Jclltjg: No such file or directory
(base) a-10-27-23-46:~ zoehaskellcraig\$ gcloud auth login --no-launch-browser
Go to the following link in your browser:

https://accounts.google.com/o/oauth2/auth?response_type=code&client_id=32555940559.apps.googleusercontent.com&redirect_uri=https%3A%2F%2Fsdk.cloud.google.com%2Fauthcode.html&scope=openid+https%3A%2F%2Fwww.googleapis.com%2Fauth%2Fcloud-platform+https%3A%2F%2Fwww.googleapis.com%2Fauth%2Fcloud-platform+https%3A%2F%2Fwww.googleapis.com%2Fauth%2Fcppengine.admin+https%3A%2F%2Fwww.googleapis.com%2Fauth%2Fsqlservice.login+https%3A%2F%2Fwww.googleapis.com%2Fauth%2Fsqlservice.login+https%3A%2F%2Fwww.googleapis.com%2Fauth%2Faccounts.reauth&state=FX3Q0zB6XYz9sYYIrK8wmkJx35Xe24&prompt=consent&access_type=offline&code_challenge=ynT7Jr_2EFK80pE3TaC8oo@951j0pu0coahBRIPZ3B4&code_challenge_method=5256

Enter authorization code: 4/0AeaYSHBLhM3uafypdUI_-JefOnAsgp-Yd7uRSxygq-mzuY6y6A0iKvABxpnc8S1Jdt8HBQ

You are now logged in as [zjh235@nyu.edu].
Your current project is [premier-data-bastion-1999]. You can change this setting by running:
\$ gcloud config set project PROJECT_ID
(base) a-10-27-23-46:~ zoehaskellcraig\$ eval `ssh-agent -s`
Agent pid 69557
(base) a-10-27-23-46:~ zoehaskellcraig\$
(base) a-10-27-23-46:~ zoehaskellcraig\$ ssh-add ~/.ssh/google_compute_engine
Identity added: /Users/zoehaskellcraig/.ssh/google_compute_engine (zoehaskellcraig@10-18-235-29.dynapool.wireless.nyu.edu)
(base) a-10-27-23-46:~ zoehaskellcraig\$ gcloud compute ssh bastion-vm --ssh-flag="-A" --tunnel-through-iap --project=premier-data-bastion-1999

To increase the performance of the tunnel, consider installing NumPy. For instructions, please see https://cloud.google.com/iap/docs/using-tcp-forwarding#increasing_the_tcp_upload_bandwidth

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Activate the web console with: systemctl enable --now cockpit.socket

Register this system with Red Hat Insights: insights-client --register Create an account or view all your systems at https://red.ht/insights-dashboard Last login: Mon Feb 26 18:47:55 2024 from 35.235.241.32 -bash-4.4\$ ssh 10.0.0.2

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ANYONE USING THIS SYSTEM EXPRESSLY CONSENTS TO SUCH MONITORING

Activate the web console with: systemctl enable --now cockpit.socket

Register this system with Red Hat Insights: insights-client --register Create an account or view all your systems at https://red.ht/insights-dashboard Last login: Mon Feb 26 18:48:02 2024 from 11.0.0.2 [zjh235_nyu_edu@workspace-vm ~]\$ cd /scratch/ [zjh235_nyu_edu@workspace-vm scratch]\$ # Merging for respiratory distress dataset [zjh235_nyu_edu@workspace-vm scratch]\$ [zjh235_nyu_edu@workspace-vm scratch]\$ setwd("/scratch/Premier/Raw_Data")
-bash: syntax error near unexpected token `"/scratch/Premier/Raw_Data"' [zjh235_nyu_edu@workspace-vm scratch]\$ [zjh235_nyu_edu@workspace-vm scratch]\$ library(haven) -bash: syntax error near unexpected token `haven' [zjh235_nyu_edu@workspace-vm scratch]\$ library(dplyr) -bash: syntax error near unexpected token `dplyr' [zjh235_nyu_edu@workspace-vm scratch]\$ library(tidyr) -bash: syntax error near unexpected token `tidyr [zjh235_nyu_edu@workspace-vm scratch]\$ [zjh235_nyu_edu@workspace-vm scratch]\$ # load file [zjh235_nyu_edu@workspace-vm scratch]\$ print("loading files...") -bash: syntax error near unexpected token `"loading files..." [zjh235_nyu_edu@workspace-vm scratch]\$ print("demo:") -bash: syntax error near unexpected token `"demo:"'
[zjh235_nyu_edu@workspace-vm scratch]\$ t1 <- Sys.time()</pre> -bash: syntax error near unexpected token `('

```
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$ t2 <- Sys.time()</pre>
-bash: syntax error near unexpected token `('
[zjh235_nyu_edu@workspace-vm scratch]$ print("Total time:", t2-t1)
 -bash: syntax error near unexpected token `"Total time:",'
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$
Lejhas5_nyu_edu@workspace-vm scratch]$ setwd("/scratch/Premier/Raw_Data/_paticd_diag")
-bash: syntax error near unexpected token `"/scratch/Premier/Raw_Data/_paticd_diag"'
[zjh235_nyu_edu@workspace-vm scratch]$ print("diagnosis:")
-bash: syntax error near unexpected token `"diagnosis:""
[zjh235_nyu_edu@workspace-vm scratch]$ t1 <- Sys.time()
-bash: syntax error near unexpected token `('
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$ files <- list.files()</pre>
-bash: syntax error near unexpected token `('
[zjh235_nyu_edu@workspace-vm scratch]$ dta_files <- files[grep("\\.dta$", files)]</pre>
-bash: syntax error near unexpected token `('
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$ data <- NA
-bash: -: No such file or directory
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$ for (f in dta_files){
-bash: syntax error near unexpected token `('
[zjh235_nyu_edu@workspace-vm scratch]$ if (stringr::str_detect(f, "wide_")){
-bash: syntax error near unexpected token `f,'
[zjh235_nyu_edu@workspace-vm scratch]$
[zih235 nvu edu@workspace-vm scratch]$
                                                 temp <- read.dta(f)
 -bash: syntax error near unexpected token `(
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$
                                                 if (is.na(data)) { #first file
-bash: syntax error near unexpected token `data'
[zjh235_nyu_edu@workspace-vm scratch]$
                                                  data <- temp
-bash: -: No such file or directory
[zjh235_nyu_edu@workspace-vm scratch]$
                                                 } else {
-bash: syntax error near unexpected token `}'
[zjh235_nyu_edu@workspace-vm scratch]$
                                                  data <- rbind(data, temp)
 -bash: syntax error near unexpected token `('
[zjh235_nyu_edu@workspace-vm scratch]$
-bash: syntax error near unexpected token `}'
[zjh235_nyu_edu@workspace-vm scratch]$
[zih235 nvu edu@workspace-vm scratch]$
-bash: syntax error near unexpected token `}'
[zjh235_nyu_edu@workspace-vm scratch]$ }
 -bash: syntax error near unexpected token `}'
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$ save(data, file = "nyu_allyears_diagnosis.RData")
-bash: syntax error near unexpected token `data,
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235_nyu_edu@workspace-vm scratch]$
[zjh235\_nyu\_edu@workspace-vm scratch] t2 <- Sys.time()
-bash: syntax error near unexpected token `('
[zjh235_nyu_edu@workspace-vm scratch]$ print("Total time:", t2-t1)
-bash: syntax error near unexpected token `"Total time:",
[zjh235_nyu_edu@workspace-vm scratch] $ R
R version 4.3.2 (2023-10-31) -- "Eye Holes"
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'citation()' on how to cite R or R packages in publications.
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
> # Merging for respiratory distress dataset
setwd("/scratch/Premier/Raw Data")
library(haven)
library(dplyr)
library(tidyr)
# load file
print("loading files...")
print("demo:")
t1 <- Sys.time()
t2 <- Sys.time()
print("Total time:", t2-t1)
```

[zjh235_nyu_edu@workspace-vm scratch]\$

```
setwd("/scratch/Premier/Raw_Data/_paticd_diag")
print("diagnosis:")
t1 <- Svs.time()
files <- list.files()</pre>
dta_files <- files[grep("\\.dta$", files)]</pre>
data <- NA
for (f in dta_files){
  if (stringr::str_detect(f, "wide_")){
    temp <- read.dta(f)</pre>
    if (is.na(data)) { #first file
      data <- temp
    } else {
      data <- rbind(data, temp)</pre>
print("Total time:", t2-t1)ears_diagnosis.RData")
Attaching package: 'dplyr'
The following objects are masked from 'package:stats':
    filter, lag
The following objects are masked from 'package:base':
    intersect, setdiff, setequal, union
[1] "loading files..."
[1] "demo:"
Error in print.default("Total time:", t2 - t1) :
invalid printing digits 0
> library(haven)
library(dplyr)
library(tidyr)
> setwd("/scratch/Premier/Raw_Data/_paticd_diag")
print("diagnosis:")
t1 <- Sys.time()
files <- list.files()</pre>
dta_files <- files[grep("\\.dta$", files)]</pre>
data <- NA
for (f in dta_files){
  if (stringr::str_detect(f, "wide_")){
    temp <- read.dta(f)
    if (is.na(data)) { #first file
    data <- temp
} else {</pre>
      data <- rbind(data, temp)</pre>
    }
  }
}
save(data, file = "nyu_allyears_diagnosis.RData")
t2 <- Sys.time()
print("Total time:", t2-t1)
[1] "diagnosis:"
Error in read.dta(f) : could not find function "read.dta"
> setwd("/scratch/Premier/Raw_Data/_paticd_diag")
print("diagnosis:")
t1 <- Sys.time()
files <- list.files()</pre>
dta_files <- files[grep("\\.dta$", files)]</pre>
data <- NA
for (f in dta_files){
  if (stringr::str_detect(f, "wide_")){
    temp <- read_dta(f)</pre>
    if (is.na(data)) { #first file
      data <- temp
    } else {
       data <- rbind(data, temp)</pre>
  }
```

```
save(data, file = "nyu_allyears_diagnosis.RData")
t2 <- Sys.time()
print("Total time:", t2-t1)
[1] "diagnosis:"
Error in if (is.na(data)) { : the condition has length > 1
> setwd("/scratch/Premier/Raw_Data/_paticd_diag")
print("diagnosis:")
t1 <- Sys.time()
files <- list.files()
dta_files <- files[grep("\\.dta$", files)]</pre>
for (f in dta_files){
   if (stringr::str_detect(f, "wide_")){
     print(f)
     temp <- read_dta(f)
     if (init == 1) { #first file
        data <- temp
        init = 0
     } else {
       data <- rbind(data, temp)</pre>
  }
}
save(data, file = "nyu_allyears_diagnosis.RData")
[1] "diagnosis:"
[1] "wide_nyu_20171_paticd_diag.dta"
[1] "wide_nyu_20172_paticd_diag.dta"
[1] "wide_nyu_20173_paticd_diag.dta"
[1] "wide_nyu_20174_paticd_diag.dta"
[1] "wide_nyu_20181_paticd_diag.dta"
 [1] "wide_nyu_20182_paticd_diag.dta"
[1] "wide_nyu_20183_paticd_diag.dta"
[1] "wide_nyu_20184_paticd_diag.dta"
[1] "wide_nyu_20191_paticd_diag.dta"
[1] "wide_nyu_20192_paticd_diag.dta"
[1] "wide_nyu_20193_paticd_diag.dta"
 [1] "wide_nyu_20194_paticd_diag.dta"
[1] "wide_nyu_20201_paticd_diag.dta"
[1] "wide_nyu_20202_paticd_diag.dta"
 [1] "wide_nyu_20203_paticd_diag.dta"
 [1] "wide_nyu_20204_paticd_diag.dta"
 [1] "wide_nyu_20211_paticd_diag.dta"
 [1] "wide_nyu_20212_paticd_diag.dta"
[1] "wide_nyu_20213_paticd_diag.dta"
[zjh235_nyu_edu@workspace-vm scratch]$ R
R version 4.3.2 (2023-10-31) -- "Eye Holes"
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Platform: x86_64-pc-linux-gnu (64-bit)
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R is a collaborative project with many contributors. Type 'contributors()' for more information and
 'citation()' on how to cite R or R packages in publications.
Type 'demo()' for some demos, 'help()' for on-line help, or 'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
> load(file = "nyu_allyears_diagnosis.RData") 
 Error in readChar(con, 5L, useBytes = TRUE) : cannot open the connection
In addition: Warning message:
In readChar(con, 5L, useBytes = TRUE) :
   cannot\ open\ compressed\ file\ 'nyu\_allyears\_diagnosis. RData',\ probable\ reason\ 'No\ such\ file\ or\ directory'
> getwd()
[1] "/scratch"
> setwd("/scratch/Premier/Raw_Data/_paticd_diag")
> load(file = "nyu_allyears_diagnosis.RData")
> setwd("/scratch/Premier/Raw_Data/_patcpt")
library(dplyr)
library(tidyr)
library(haven)
```

```
print("cpt files..")
files <- list.files()</pre>
dta_files <- files[grep("\\.dta$", files)]</pre>
for (f in dta_files){
  if (stringr::str_detect(f, "wide_")){
    print(f)
    temp <- read_dta(f)
    if (init == 1) { #first file
      all_cpt <- temp
      init = 0
    } else {
      all_cpt <- rbind(all_cpt, temp)</pre>
 }
save(all_cpt, file = "nyu_allyears_cpt.RData")
Attaching package: 'dplyr'
The following objects are masked from 'package:stats':
    filter, lag
The following objects are masked from 'package:base':
    intersect, setdiff, setequal, union
[1] "cpt files.."
[1] "wide_nyu_20171_patcpt.dta"
[1] "wide_nyu_20172_patcpt.dta"
[1] "wide_nyu_20173_patcpt.dta"
[1] "wide_nyu_20174_patcpt.dta"
[1] "wide_nyu_20181_patcpt.dta"
[1] "wide_nyu_20182_patcpt.dta"
[1] "wide_nyu_20183_patcpt.dta"
[1] "wide_nyu_20184_patcpt.dta"
[1] "wide_nyu_20191_patcpt.dta"
[1] "wide_nyu_20192_patcpt.dta"
[1] "wide_nyu_20193_patcpt.dta"
[1] "wide_nyu_20194_patcpt.dta"
[1] "wide_nyu_20201_patcpt.dta"
[1] "wide_nyu_20202_patcpt.dta"
[1] "wide_nyu_20203_patcpt.dta"
[1] "wide_nyu_20204_patcpt.dta"
[1] "wide_nyu_20211_patcpt.dta"
[1] "wide_nyu_20212_patcpt.dta"
[1] "wide_nyu_20213_patcpt.dta"
> setwd("/scratch/Premier/Raw_Data/_paticd_proc")
library(dplyr)
library(tidyr)
library(haven)
print("proc files..")
files <- list.files()</pre>
dta_files <- files[grep("\\.dta$", files)]</pre>
init <- 1
for (f in dta_files){
  if (stringr::str_detect(f, "wide_")){
    print(f)
    temp <- read_dta(f)
    if (init == 1) { #first file
      all_proc <- temp
      init = 0
    } else {
      all_proc <- rbind(all_proc, temp)</pre>
 }
save(all_proc, file = "nyu_allyears_proc.RData")
[1] "proc files..."
[1] "wide_nyu_20171_paticd_proc.dta"
[1] "wide_nyu_20172_paticd_proc.dta"
[1] "wide_nyu_20173_paticd_proc.dta"
[1] "wide_nyu_20174_paticd_proc.dta"
[1] "wide_nyu_20181_paticd_proc.dta"
```

```
[1] "wide_nyu_20182_paticd_proc.dta"
[1] "wide_nyu_20183_paticd_proc.dta"
[1] "wide_nyu_20184_paticd_proc.dta"
[1] "wide_nyu_20191_paticd_proc.dta"
[1] "wide_nyu_20192_paticd_proc.dta"
[1] "wide_nyu_20193_paticd_proc.dta"
[1] "wide_nyu_20194_paticd_proc.dta"
[1] "wide_nyu_20201_paticd_proc.dta"
[1] "wide_nyu_20202_paticd_proc.dta"
    "wide_nyu_20203_paticd_proc.dta"
[1]
    "wide_nyu_20204_paticd_proc.dta"
[1] "wide_nyu_20211_paticd_proc.dta"
    "wide_nyu_20212_paticd_proc.dta"
[1] "wide_nyu_20213_paticd_proc.dta"
> a()
\label{lem:continuous} $$[z]h235_nyu_edu@workspace-vm scratch] $ cd /scratch/Premier/Raw_Data/[z]h235_nyu_edu@workspace-vm Raw_Data] $ ls
Copyright.txt
                              nyu_aprdrg.txt
                                                    nyu_de_admin.txt nyu_icdpoa.txt
                                                                                               nyu_pattype.txt nyu_poorigin.txt _patcpt
                                                                                                                                                         _paticd_proc
                                                                                              nyu_payor.txt __pataprdrg
nyu_physpec.txt __patbill
                               nyu_chgmstr.txt nyu_disstat.txt nyu_msdrgmdc.txt nyu_payor.txt
nyu_cptcode.txt nyu_icdcode.txt nyu_msdrg.txt nyu_physpec.tx
                                                                                                                                        _patdemo
manifest_data_extract.txt nyu_chgmstr.txt
                                                                                                                                                         _paticd_proc.zip
nyu_admtype.txt nyu_cptcode.txt nyu_icdc
[zjh235_nyu_edu@workspace-vm Raw_Data]$ cd _patdemo/
                                                                                                                                        _paticd_diag _readmit
[zjh235_nyu_edu@workspace-vm _patdemo]$ ls
nyu_20171_patdemo.dta nyu_20181_patdemo.txt nyu_20192_patdemo.dta nyu_20202_patdemo.txt nyu_20213_patdemo.dta
nyu_20171_patdemo.txt nyu_20182_patdemo.dta nyu_20192_patdemo.txt nyu_20203_patdemo.dta nyu_20213_patdemo.txt
nyu_20172_patdemo.dta nyu_20182_patdemo.txt
                                                      nyu_20193_patdemo.dta nyu_20203_patdemo.txt
                                                                                                             nyu_allyears_patdemo.dta
                                                                                                             nyu_allyears_patdemo_INPATIENT_ONLY.dta
nyu_allyears_patdemo_OUTPATIENT_ONLY.dta
                                                      nyu_20193_patdemo.txt nyu_20204_patdemo.dta
nyu 20172 patdemo.txt nyu 20183 patdemo.dta
nyu_20173_patdemo.dta nyu_20183_patdemo.txt
                                                       nyu_20194_patdemo.dta nyu_20204_patdemo.txt
nyu_20173_patdemo.txt nyu_20184_patdemo.dta
                                                       nyu_20194_patdemo.txt nyu_20211_patdemo.dta
nyu_20174_patdemo.dta nyu_20184_patdemo.txt
                                                       nyu_20201_patdemo.dta nyu_20211_patdemo.txt
nyu_20174_patdemo.txt nyu_20191_patdemo.dta nyu_20201_patdemo.txt nyu_20212_patdemo.dta nyu_20181_patdemo.dta nyu_20191_patdemo.txt nyu_20202_patdemo.dta nyu_20212_patdemo.txt
                                                      nyu_20201_patdemo.txt nyu_20212_patdemo.dta
[zjh235_nyu_edu@workspace-vm _patdemo]$
[zjh235_nyu_edu@workspace-vm _patdemo]$
[zjh235_nyu_edu@workspace-vm _patdemo]$ R
R version 4.3.2 (2023-10-31) -- "Eye Holes"
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Platform: x86_64-pc-linux-gnu (64-bit)
R is free software and comes with ABSOLUTELY NO WARRANTY. You are welcome to redistribute it under certain conditions. Type 'license()' or 'licence()' for distribution details.
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R is a collaborative project with many contributors. Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
> setwd("/scratch/Premier/Raw_Data")
library(haven)
library(dplyr)
library(tidyr)
print("loading .... demo")
print(Sys.time())
demo <- read_dta("/_patdemo/nyu_allyears_patdemo.dta")</pre>
print(Sys.time())
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
[1] "loading .... demo" [1] "2024-02-26 20:01:16 EST"
Error: '/_patdemo/nyu_allyears_patdemo.dta' does not exist.
> setwd("/scratch/Premier/Raw_Data")
library(haven)
library(dplyr)
library(tidyr)
print("loading .... demo")
print(Sys.time())
demo <- read_dta("_patdemo/nyu_allyears_patdemo.dta")</pre>
print(Sys.time())
[1] "loading .... demo"
[1] "2024-02-26 20:01:54 EST"
[1] "2024-02-26 20:06:41 EST"
```

```
> names(demo)
 [1] "pat_key"
                          "medrec_key"
                                              "disc_mon"
                                                                   "disc_mon_seq"
 [5] "adm_mon"
                          "prov_id"
                                               "i_o_ind"
                                                                   "pat_type'
     "ms_drg"
                           'ms_drg_mdc"
                                                                   "adm_type"
 [9]
                                               "point_of_origin'
[13] "disc_status'
                           'mart_status"
                                               .
'age"
                                                                   "gender
[17] "race"
                          "hispanic_ind"
                                               "admphy_spec"
                                                                   "adm_phy"
[21] "attphy_spec"
                          "att_phy"
                                               "std_payor"
                                                                   "los"
                          "pat_cost"
[25] "pat_charges"
                                              "pat_fix_cost"
                                                                   "pat_var_cost"
[29] "publish_type"
> print("loading ... diagnosis")
setwd("/scratch/Premier/Raw_Data/_paticd_diag")
print(Sys.time())
load(file = "nyu_allyears_diagnosis.RData")
print(Sys.time())
print("merging")
merged_data <- left_join(demo, data, by = "pat_key")</pre>
print(Sys.time())
[1] "loading .... diagnosis"
[1] "2024-02-26 20:10:46 EST"
[1] "2024-02-26 20:11:57 EST"
[1] "merging"
[1] "2024-02-26 20:12:40 EST" > print("loading ... proc")
setwd("/scratch/Premier/Raw_Data/_paticd_proc")
print(Sys.time())
load(file = "nyu_allyears_proc.RData")
print(Sys.time())
print("merging")
merged_data <- left_join(merged_data, all_proc, by = "pat_key")</pre>
print(Sys.time())
[1] "loading .... proc" [1] "2024-02-26 20:15:23 EST"
[1] "2024-02-26 20:15:29 EST"
[1] "merging"
[1] "2024-02-26 20:16:13 EST"
> colnames(merged_data)
 [1] "pat key"
                          "medrec_key"
                                                                   "disc_mon_seq"
                                              "disc mon"
 [5] "adm_mon"
                          "prov_id"
                                                                   "pat_type
                                              "i o ind"
 [9] "ms_drg"
                          "ms_drg_mdc"
                                               "point_of_origin"
                                                                   "adm_type"
[13] "disc_status"
                          "mart_status"
                                               "age"
                                                                   "gender"
[17] "race"
                          "hispanic_ind"
                                              "admphy_spec"
                                                                   "adm_phy"
                                                                   "los"
[21] "attphy_spec"
                                               "std_payor"
                          "att_phy"
[25] "pat_charges"
                          "pat_cost"
                                               "pat_fix_cost"
                                                                   "pat_var_cost"
[29] "publish_type"
                          "all_diagnoses"
                                              "all_proc_codes"
> head(merged_data)
# A tibble: 6 x 31
    \verb"pat_key medrec_key disc_mon_seq adm_mon prov_id i\_o\_ind pat\_type \\
                                            <dbl>
   26<u>527</u>999
               31<u>687</u>923 2<u>017</u>102
                                                1 2017102
                                                               <u>2</u>330 0
  741<u>707</u>753 424<u>745</u>332
                          2<u>017</u>101
                                                 1 2<u>017</u>101
                                                                 27 0
                                                                                     30
 741<u>709</u>880 307<u>441</u>050 2<u>017</u>101
                                                1 2016412
                                                                 27 I
                                                                                     8
                                                                272 0
  741710545
               91939687
                           2017101
                                                1 2017101
                                                                                     30
  741<u>710</u>661
              224<u>810</u>373 2<u>017</u>101
                                                1 2017101
  741<u>713</u>693 866<u>425</u>808 2<u>017</u>101
                                                2 2017101
                                                                272 0
# i 23 more variables: ms_drg <dbl>, ms_drg_mdc <dbl>,
                                                              point_of_origin <chr>,
    adm_type <dbl>, disc_status <dbl>, mart_status <chr>, age <dbl>,
    gender <chr>, race <chr>, hispanic ind <chr>, admphy spec <dbl>,
    adm_phy dbl>, attphy_spec dbl>, att_phy dbl>, std_payor dbl>, los dbl>, pat_charges dbl>, pat_cost dbl>, pat_fix_cost dbl>,
    pat_var_cost <dbl>, publish_type <chr>, all_diagnoses <chr>,
    all proc codes <chr>
> head(merged_data$all_diagnoses)
[1]
[2] "C79.51, C79.51, C64.9, G89.3"
    "K81.0, R10.13, D68.61, E66.9, E87.6, G43.909, I10, K29.00, N39.0, Z68.26, Z86.718, Z89.512"
[4] "[42.9"
    "I48.91, Z00.00"
[5]
[6] "R06.00, D64.9, Z95.4"
> merged data <- merged data %>%
  mutate(ARDS = if_else(stringr::str_detect(all_diagnoses, "J80"), 1, 0))
 colnames(merged_data)
 [1] "pat_key"
                          "medrec_key"
                                              "disc_mon"
                                                                   "disc_mon_seq"
 [5] "adm_mon"
                          "prov_id"
                                               "i_o_ind"
                                                                   "pat_type"
 [9] "ms_drg"
                          "ms_drg_mdc"
                                               "point_of_origin"
                                                                   "adm_type"
[13] "disc_status"
                          "mart_status"
                                               .
'age"
                                                                   "gender
[17] "race"
                          "hispanic_ind"
                                              "admphy_spec"
                                                                   "adm_phy"
[21] "attphy_spec"
                          "att_phy"
                                               "std_payor"
                                                                   "los"
                          "pat_cost"
[25] "pat_charges"
                                              "pat_fix_cost"
                                                                   "pat_var_cost"
                                              "all_proc_codes"
                                                                   "ARDS"
[29] "publish_type"
                          "all diagnoses"
```

```
> head(merged_data$ARDS)
[1] 0 0 0 0 0 0
> sum(merged_data$ARDS == 1)
[1] NA
> sum(merged data$ARDS)
[1] NA
> sum(merged_data$ARDS, na.rm = TRUE)
[1] 99165
> length(merged data$ARDS)
[1] 39482050
> merged_data <- merged_data %>%
 mutate(J96 = if_else(stringr::str_detect(all_diagnoses, "J96"), 1, 0))
  sum(merged_data$J96)
[1] NA
> sum(merged data$J96, na.rm = TRUE)
[1] 4761493
> sum(is.na(merged_data$ARDS))
[1] 9
> sum(is.na(merged_data$J96))
[1] 9
[zjh235_nyu_edu@workspace-vm _patdemo]$ ls
nyu_20171_patdemo.txt nyu_20181_patdemo.txt nyu_20192_patdemo.txt nyu_20202_patdemo.txt nyu_20213_patdemo.txt nyu_20171_patdemo.txt nyu_20182_patdemo.dta nyu_20192_patdemo.txt nyu_20203_patdemo.dta nyu_20203_patdemo.txt
nyu_20172_patdemo.dta nyu_20182_patdemo.txt
                                                 nyu_20193_patdemo.dta nyu_20203_patdemo.txt
                                                                                                  nyu_allyears_patdemo.dta
nyu_20172_patdemo.txt nyu_20183_patdemo.dta
                                                 nyu_20193_patdemo.txt
                                                                         nyu_20204_patdemo.dta
                                                                                                  nyu_allyears_patdemo_INPATIENT_ONLY.dta
nyu_20173_patdemo.dta nyu_20183_patdemo.txt
                                                 nyu_20194_patdemo.dta nyu_20204_patdemo.txt nyu_allyears_patdemo_OUTPATIENT_ONLY.dta
nyu 20173 patdemo.txt nyu 20184 patdemo.dta
                                                 nvu 20194 patdemo.txt
                                                                         nyu 20211 patdemo.dta
nyu_20174_patdemo.dta nyu_20184_patdemo.txt
                                                 nyu_20201_patdemo.dta nyu_20211_patdemo.txt
nyu_20174_patdemo.txt nyu_20191_patdemo.dta
                                                 nyu_20201_patdemo.txt nyu_20212_patdemo.dta
nyu_20181_patdemo.dta nyu_20191_patdemo.txt nyu_20202_patdemo.dta nyu_20212_patdemo.txt
[zjh235_nyu_edu@workspace-vm _patdemo]$ cd ..
[zjh235_nyu_edu@workspace-vm Raw_Data]$ ls
Copyright.txt
                            nyu_aprdrg.txt nyu_de_admin.txt nyu_icdpoa.txt
                                                                                     nyu_pattype.txt nyu_poorigin.txt _patcpt
                                                                                                                                          _paticd_proc
_paticd_diag _readmit
                                                                                     nyu_payor.txt _pataprdrg nyu_physpec.txt _patbill
                                                                                                                          _patdemo
nyu_admtype.txt
[zjh235_nyu_edu@workspace-vm Raw_Data]$ cd _pataprdrg/
[zjh235_nyu_edu@workspace-vm _pataprdrg]$ ls
nyu_20171_pataprdrg.dta nyu_20174_pataprdrg.txt nyu_20184_pataprdrg.dta nyu_20193_pataprdrg.txt nyu_20203_pataprdrg.dta nyu_20212_pataprdrg.txt
nýu_20171_pataprdrg.txt nýu_20181_pataprdrg.dta nýu_20184_pataprdrg.txt nýu_20194_pataprdrg.dta nýu_20203_pataprdrg.txt nýu_20213_pataprdrg.dta
nyu_20172_pataprdrg.dta nyu_20181_pataprdrg.txt
                                                     nyu_20191_pataprdrg.dta nyu_20194_pataprdrg.txt nyu_20204_pataprdrg.dta
                                                                                                                                     nyu_20213_pataprdrg.txt
nyu_20172_pataprdrg.txt nyu_20182_pataprdrg.dta nyu_20191_pataprdrg.txt nyu_20201_pataprdrg.dta nyu_20204_pataprdrg.txt nyu_20173_pataprdrg.dta nyu_20182_pataprdrg.txt nyu_20192_pataprdrg.dta nyu_20201_pataprdrg.txt nyu_20211_pataprdrg.dta
                                                                                nyu_20201_pataprdrg.dta nyu_20204_pataprdrg.txt
                                                                                                                                     nyu allyears pataprdrq.dta
nyu_20173_pataprdrg.txt nyu_20183_pataprdrg.dta nyu_20192_pataprdrg.txt nyu_20202_pataprdrg.dta nyu_20211_pataprdrg.txt
nyu_20174_pataprdrg.dta nyu_20183_pataprdrg.txt nyu_20193_pataprdrg.dta nyu_20202_pataprdrg.txt nyu_20212_pataprdrg.dta
[zjh235_nyu_edu@workspace-vm _pataprdrg]$ cd /scratch/Premier/Merged_Data/
[zjh235_nyu_edu@workspace-vm Merged_Data]$ cd /scratch/Premier/Raw_Data/
[zjh235_nyu_edu@workspace-vm Raw_Data]$ ls
                            nyu_aprdrg.txt
Copyright.txt
                                              nyu de admin.txt nyu icdpoa.txt
                                                                                     nyu pattype.txt nyu poorigin.txt patcpt
                                                                                                                                          paticd proc
manifest_data_extract.txt nyu_chgmstr.txt nyu_disstat.txt nyu_msdrgmdc.txt nyu_payor.txt
                                                                                                                                          _paticd_proc.zip
                            nyu_cptcode.txt nyu_icdcode.txt
                                                                  nyu_msdrg.txt
                                                                                     nyu_physpec.txt
                                                                                                       _patbill
                                                                                                                           _paticd_diag _readmit
nyu_admtype.txt
[zjh235_nyu_edu@workspace-vm Raw_Data]$ cd /scratch/Premier/Merged_Data/
[zjh235_nyu_edu@workspace-vm Merged_Data]$ ls
nyu_allyears_demo+aprdrg_IP.dta nyu_allyears_INPATIENT_demo+aprdrg+diag+cpt.dta nyu_allyears_INPATIENT_demo+aprdrg+diag.dta
[zjh235_nyu_edu@workspace-vm Merged_Data]$ R
R version 4.3.2 (2023-10-31) -- "Eve Holes"
Copyright (C) 2023 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)
\ensuremath{\mathsf{R}} is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions. Type 'license()' or 'licence()' for distribution details.
  Natural language support but running in an English locale
R is a collaborative project with many contributors. Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
# PATAPR files
setwd("/scratch/Premier/Raw_Data/_pataprdrg")
library(dplyr)
library(tidyr)
library(haven)
print("demographic files..")
files <- list.files()
dta_files <- files[grep("\\.dta$", files)]</pre>
for (f in dta files){
  if (!stringr::str_detect(f, "nyu_allyears")){
```

```
print(f)
     temp <- read_dta(f)
     if (init == 1) { #first file
        all_aprdrg <- temp
     } else {
        all_aprdrg <- rbind(all_aprdrg, temp)</pre>
}
save(all_aprdrg, file = "nyu_allyears_aprdrg.RData")
## Merge all files
setwd("/scratch/Premier/Raw_Data")
save(respiratory_demo_aprdrg_diag, file = "respiratory_demo_aprdrg_diag.RData")
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
 [1] "demographic files.."
 [1] "nyu_20171_pataprdrg.dta"
[1] "nyu_20172_pataprdrg.dta"
[1] "nyu_20173_pataprdrg.dta"
[1] "nyu_20173_pataprdrg.dta"
[1] "nyu_20174_pataprdrg.dta"
[1] "nyu_20181_pataprdrg.dta"
 [1] "nyu_20182_pataprdrg.dta"
 [1] "nyu_20183_pataprdrg.dta"
[1] "nyu_20184_pataprdrg.dta"
[1] "nyu_20191_pataprdrg.dta"
 [1] "nyu_20192_pataprdrg.dta"
 [1] "nyu_20193_pataprdrg.dta"
 [1] "nyu_20194_pataprdrg.dta"
[1] "nyu_20201_pataprdrg.dta"
[1] "nyu_20202_pataprdrg.dta"
 [1] "nyu_20203_pataprdrg.dta"
 [1] "nyu_20204_pataprdrg.dta"
 [1] "nyu_20211_pataprdrg.dta"
[1] "nyu_20211_pataprdrg.dta"

[1] "nyu_20212_pataprdrg.dta"

[1] "nyu_20213_pataprdrg.dta"

[1] "loading ... demo"

[1] "2024-02-26 20:42:00 EST"
 [1] "2024-02-26 20:46:44 EST"
[1] "loading .... diagnosis"
[1] "2024-02-26 20:46:44 EST"
 [1] "2024-02-26 20:47:52 EST"
 [1] "merging"
 [1] "2024-02-26 20:48:27 EST"
[1] "loading .... aprdrg"
[1] "2024-02-26 20:48:27 EST"
 [1] "2024-02-26 20:48:44 EST"
 [1] "merging"
[1] "2024-02-26 20:49:22 EST"
[1] "creating ARDS"
[1] "creating J96"
 [1] "saving respiratory dataset"
```