main_r

July 13, 2021

1 Generate a prettier plot with statistics on the plot

[1]:
```
library(repr)
library(ggpubr)
library(tidyverse)
```

```
Loading required package: ggplot2

  Attaching packages                                    tidyverse
1.3.1

  tibble  3.1.2      dplyr   1.0.7
  tidyr   1.1.3      stringr 1.4.0
  readr   1.4.0      forcats 0.5.1
  purrr   0.3.4

  Conflicts
tidyverse_conflicts()
  dplyr::filter() masks stats::filter()
  dplyr::lag()    masks stats::lag()
```

[2]:
```
config <- list('caudate'= '../../../caudate/_m/genes/diffExpr_maleVfemale_full.
 ↪txt',
               'dlpfc'= '../../../dlpfc/_m/genes/diffExpr_maleVfemale_full.txt',
               'hippo'= '../../../hippocampus/_m/genes/
 ↪diffExpr_maleVfemale_full.txt',
               'cmc_dlpfc'= '../../../cmc_dlpfc/_m/mssm_penn_pitt_maleVfemale.
 ↪tsv',
               'cmc_hbcc'= '../../../cmc_dlpfc/_m/nimh_hbcc_maleVfemale.tsv')
```

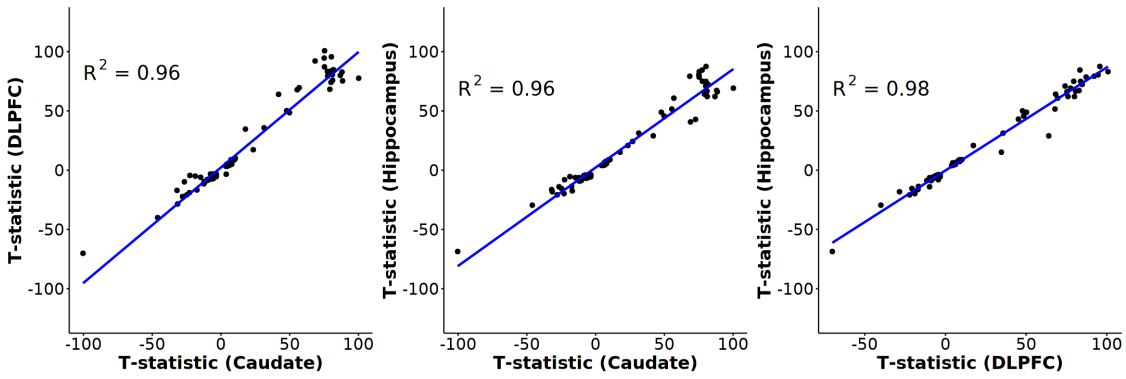
[3]:
```
get_deg <- function(fn){
    dft <- data.table::fread(fn)
    if('gene_id' %in% colnames(dft)){
        dft <- dft %>%
            mutate(Feature=gene_id, Dir=sign(t)) %>%
            rename(ensemblID=ensembl_gene_id) %>%
            select('Feature', 'ensemblID', 'adj.P.Val', 'logFC', 't', 'Dir')
```

```
    } else if('Geneid' %in% colnames(dft)) {
        dft <- dft %>%
            mutate(Feature=Geneid, Dir=sign(t),
                   ensemblID=str_replace(Geneid, "\\..*", "")) %>%
            select('Feature', 'ensemblID', 'adj.P.Val', 'logFC', 't', 'Dir')
    } else {
        dft <- dft %>%
            mutate(Feature=V1, Dir=sign(t)) %>%
            select('Feature', 'ensemblID', 'adj.P.Val', 'logFC', 't', 'Dir')
    }
    return(dft)
}

get_deg_sig <- function(fn, fdr){
    dft <- get_deg(fn)
    return(subset(dft, adj.P.Val < fdr))
}

merge_dataframe <- function(tissue1, tissue2){
    return(merge(get_deg(config[[tissue1]]), get_deg(config[[tissue2]]),
                 by='Feature', suffixes=c(paste0('_',tissue1),␣
 ↪paste0('_',tissue2))))
}

merge_dataframes_sig <- function(tissue1, tissue2){
    fdr = 0.05
    return(merge(get_deg_sig(config[[tissue1]], fdr),␣
 ↪get_deg_sig(config[[tissue2]], fdr),
                 by='Feature', suffixes=c(paste0('_',tissue1),␣
 ↪paste0('_',tissue2))))
}

tissue_annotation <- function(tissue){
    return(list('dlpfc'='DLPFC', 'hippo'='Hippocampus',
                'caudate'='Caudate', 'cmc_dlpfc'='CMC DLPFC',
                'cmc_hbcc'='CMC DLPFC: HBCC')[[tissue]])
}

get_scatter_plot <- function(tissue1, tissue2, merge_fnc, coords){
    dft <- merge_fnc(tissue1, tissue2)
    sp = ggscatter(dft, x=paste0('t_', tissue1), y=paste0('t_', tissue2),␣
 ↪add="reg.line",
                   xlab=paste0('T-statistic (',tissue_annotation(tissue1), ')'),
                   ylab=paste0('T-statistic (',tissue_annotation(tissue2), ')'),
                   add.params = list(color = "blue", fill = "lightgray"), conf.
 ↪int = FALSE,
                   cor.method = "pearson", cor.coef = FALSE, cor.coef.size = 7,
```

```
                    cor.coeff.args = list(label.sep = "\n"),  #cor.coef.coord =␣
 ↪coords,
                    ylim=c(-125, 125)) +
    stat_cor(aes(label = paste0(..rr.label..)), size=8, method = "pearson") +
    font("xylab", size = 20, face='bold') + font("xy.text", size = 18)
    return(sp)
}


save_ggplots <- function(fn, p, w, h){
    for(ext in c('.pdf', '.png', '.svg')){
        ggsave(paste0(fn, ext), plot=p, width=w, height=h)
    }
}
```

[4]:
```
options(repr.plot.width=18, repr.plot.height=6)
sp1_sig = get_scatter_plot('caudate', 'dlpfc', merge_dataframes_sig, c(-110,␣
 ↪85))
sp2_sig = get_scatter_plot('caudate', 'hippo', merge_dataframes_sig, c(-110,␣
 ↪85))
sp3_sig = get_scatter_plot('dlpfc', 'hippo', merge_dataframes_sig, c(-110, 85))
fig1 = ggarrange(sp1_sig, sp2_sig, sp3_sig, ncol=3, align='v')
print(fig1)
```

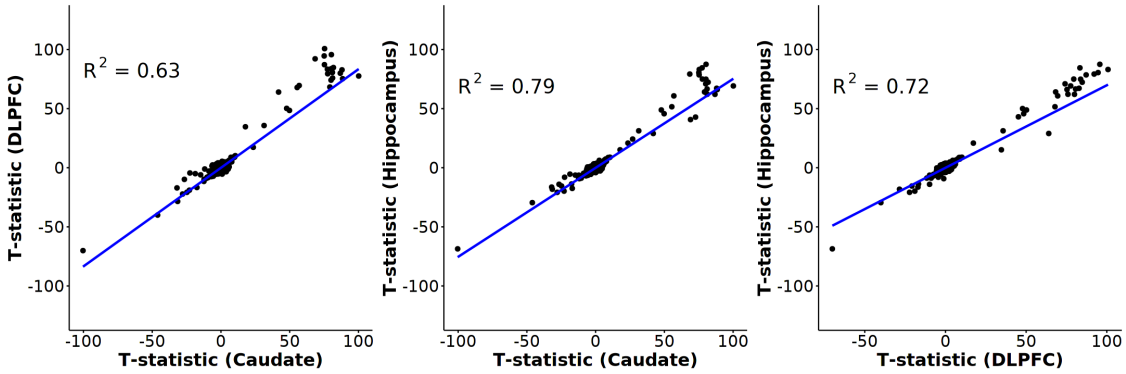
```
`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'
```



[5]:
```
save_ggplots("tstatistic_corr_sig", fig1, 18, 6)
```

[6]:
```
sp1 = get_scatter_plot('caudate', 'dlpfc', merge_dataframe, c(-110, 85))
sp2 = get_scatter_plot('caudate', 'hippo', merge_dataframe, c(-110, 85))
sp3 = get_scatter_plot('dlpfc', 'hippo', merge_dataframe, c(-110, 85))
fig2 = ggarrange(sp1, sp2, sp3, ncol=3, align='v')
print(fig2)
```

```
`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'
```

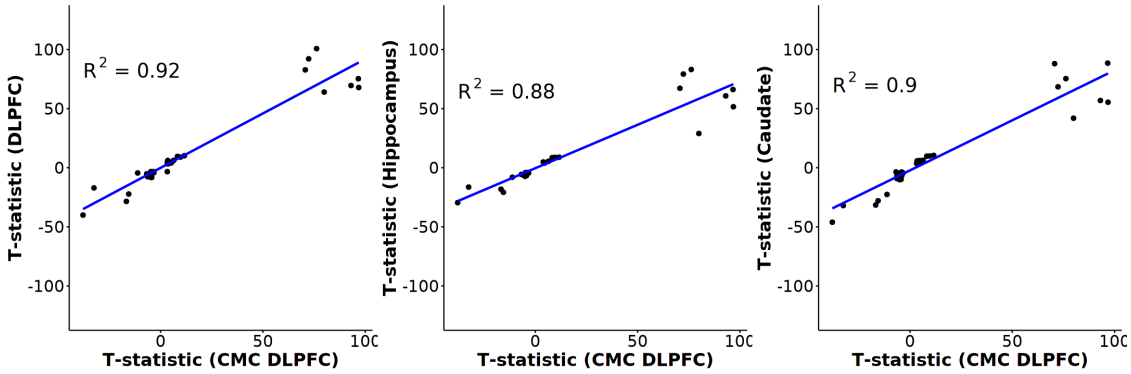


[7]:
```
save_ggplots("tstatistic_corr", fig2, 18, 6)
```

1.1 CommonMind comparison: MSSM Penn Pitt

[8]:
```
sp4_sig = get_scatter_plot('cmc_dlpfc', 'dlpfc', merge_dataframes_sig, c(-55,␣
↪85))
sp5_sig = get_scatter_plot('cmc_dlpfc', 'hippo', merge_dataframes_sig, c(-55,␣
↪85))
sp6_sig = get_scatter_plot('cmc_dlpfc', 'caudate', merge_dataframes_sig, c(-55,␣
↪85))
fig3 = ggarrange(sp4_sig, sp5_sig, sp6_sig, ncol=3, align='v')
print(fig3)
```

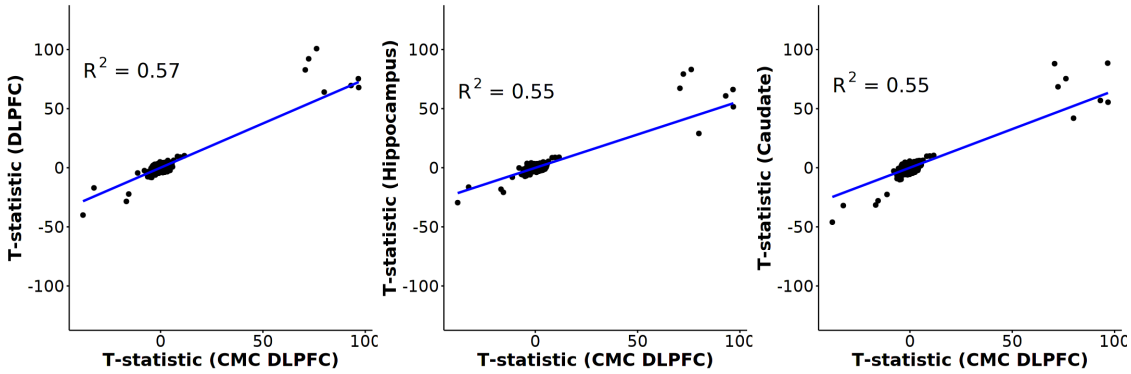
```
`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'
```



[9]:
```
save_ggplots("cmc_tstatistic_corr_sig", fig3, 18, 6)
```

[10]:
```
sp4 = get_scatter_plot('cmc_dlpfc', 'dlpfc', merge_dataframe, c(-55, 85))
sp5 = get_scatter_plot('cmc_dlpfc', 'hippo', merge_dataframe, c(-55, 85))
sp6 = get_scatter_plot('cmc_dlpfc', 'caudate', merge_dataframe, c(-55, 85))
fig4 = ggarrange(sp4, sp5, sp6, ncol=3)
print(fig4)
```

```
`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'
```

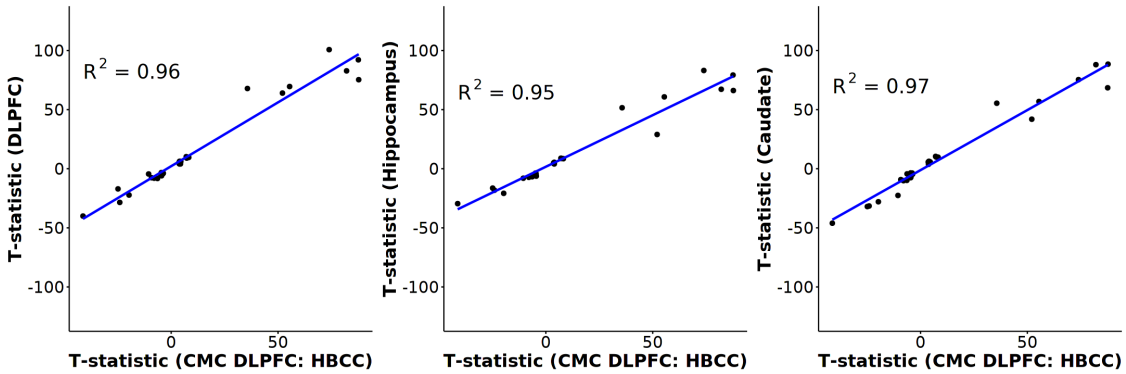


[11]:
```
save_ggplots("cmc_tstatistic_corr", fig4, 18, 6)
```

1.2 CommonMind comparison: NIMH HBCC

[12]:
```
sp4_sig = get_scatter_plot('cmc_hbcc', 'dlpfc', merge_dataframes_sig, c(-55,␣
↪85))
sp5_sig = get_scatter_plot('cmc_hbcc', 'hippo', merge_dataframes_sig, c(-55,␣
↪85))
sp6_sig = get_scatter_plot('cmc_hbcc', 'caudate', merge_dataframes_sig, c(-55,␣
↪85))
fig3 = ggarrange(sp4_sig, sp5_sig, sp6_sig, ncol=3, align='v')
print(fig3)
```

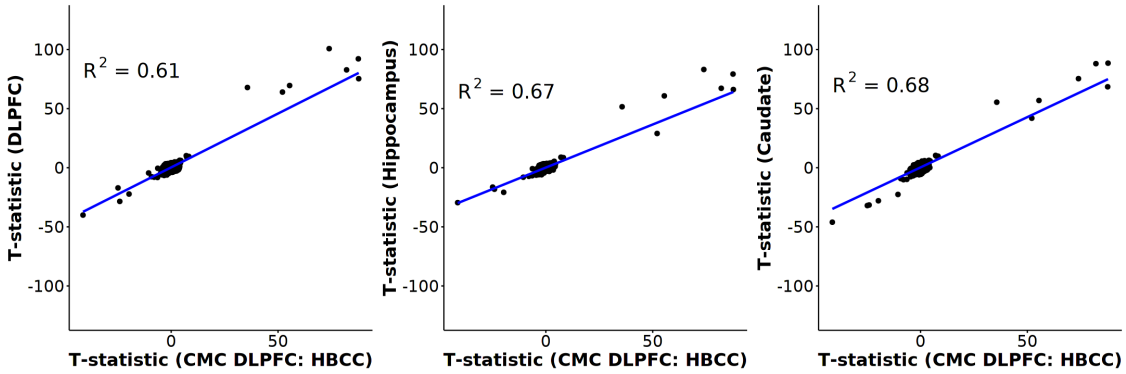
```
`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'
```



[13]:
```
save_ggplots("cmc_hbcc_tstatistic_corr_sig", fig3, 18, 6)
```

[14]:
```
sp4 = get_scatter_plot('cmc_hbcc', 'dlpfc', merge_dataframe, c(-55, 85))
sp5 = get_scatter_plot('cmc_hbcc', 'hippo', merge_dataframe, c(-55, 85))
sp6 = get_scatter_plot('cmc_hbcc', 'caudate', merge_dataframe, c(-55, 85))
fig4 = ggarrange(sp4, sp5, sp6, ncol=3)
print(fig4)
```

```
`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'

`geom_smooth()` using formula 'y ~ x'
```



[15]:
```
save_ggplots("cmc_hbcc_tstatistic_corr", fig4, 18, 6)
```

1.3 Reproducibility Information

[16]:
```
print("Reproducibility Information:")
Sys.time()
proc.time()
options(width=120)
sessioninfo::session_info()
```

```
[1] "Reproducibility Information:"
```

```
[1] "2021-07-13 11:01:42 EDT"
```

```
   user  system elapsed
 53.615   1.402  38.393
```

```
 Session info
setting  value
version  R version 4.0.3 (2020-10-10)
os       Arch Linux
system   x86_64, linux-gnu
ui       X11
language (EN)
collate  en_US.UTF-8
ctype    en_US.UTF-8
tz       America/New_York
date     2021-07-13

 Packages
package     * version  date       lib source
abind         1.4-5    2016-07-21 [1] CRAN (R 4.0.2)
assertthat    0.2.1    2019-03-21 [1] CRAN (R 4.0.2)
backports     1.2.1    2020-12-09 [1] CRAN (R 4.0.2)
base64enc     0.1-3    2015-07-28 [1] CRAN (R 4.0.2)
```

```
broom         0.7.8    2021-06-24 [1] CRAN (R 4.0.3)
Cairo         1.5-12.2 2020-07-07 [1] CRAN (R 4.0.2)
car           3.0-11   2021-06-27 [1] CRAN (R 4.0.3)
carData       3.0-4    2020-05-22 [1] CRAN (R 4.0.2)
cellranger    1.1.0    2016-07-27 [1] CRAN (R 4.0.2)
cli           3.0.0    2021-06-30 [1] CRAN (R 4.0.3)
colorspace    2.0-2    2021-06-24 [1] CRAN (R 4.0.3)
cowplot       1.1.1    2020-12-30 [1] CRAN (R 4.0.2)
crayon        1.4.1    2021-02-08 [1] CRAN (R 4.0.3)
curl          4.3.2    2021-06-23 [1] CRAN (R 4.0.3)
data.table    1.14.0   2021-02-21 [1] CRAN (R 4.0.3)
DBI           1.1.1    2021-01-15 [1] CRAN (R 4.0.2)
dbplyr        2.1.1    2021-04-06 [1] CRAN (R 4.0.3)
digest        0.6.27   2020-10-24 [1] CRAN (R 4.0.2)
dplyr       * 1.0.7    2021-06-18 [1] CRAN (R 4.0.3)
ellipsis      0.3.2    2021-04-29 [1] CRAN (R 4.0.3)
evaluate      0.14     2019-05-28 [1] CRAN (R 4.0.2)
fansi         0.5.0    2021-05-25 [1] CRAN (R 4.0.3)
farver        2.1.0    2021-02-28 [1] CRAN (R 4.0.3)
forcats     * 0.5.1    2021-01-27 [1] CRAN (R 4.0.2)
foreign       0.8-80   2020-05-24 [2] CRAN (R 4.0.3)
fs            1.5.0    2020-07-31 [1] CRAN (R 4.0.2)
generics      0.1.0    2020-10-31 [1] CRAN (R 4.0.2)
ggplot2     * 3.3.5    2021-06-25 [1] CRAN (R 4.0.3)
ggpubr      * 0.4.0    2020-06-27 [1] CRAN (R 4.0.2)
ggsignif      0.6.2    2021-06-14 [1] CRAN (R 4.0.3)
glue          1.4.2    2020-08-27 [1] CRAN (R 4.0.2)
gtable        0.3.0    2019-03-25 [1] CRAN (R 4.0.2)
haven         2.4.1    2021-04-23 [1] CRAN (R 4.0.3)
hms           1.1.0    2021-05-17 [1] CRAN (R 4.0.3)
htmltools     0.5.1.1  2021-01-22 [1] CRAN (R 4.0.2)
httr          1.4.2    2020-07-20 [1] CRAN (R 4.0.2)
IRdisplay     1.0      2021-01-20 [1] CRAN (R 4.0.2)
IRkernel      1.2      2021-05-11 [1] CRAN (R 4.0.3)
jsonlite      1.7.2    2020-12-09 [1] CRAN (R 4.0.2)
labeling      0.4.2    2020-10-20 [1] CRAN (R 4.0.2)
lattice       0.20-41  2020-04-02 [2] CRAN (R 4.0.3)
lifecycle     1.0.0    2021-02-15 [1] CRAN (R 4.0.3)
lubridate     1.7.10   2021-02-26 [1] CRAN (R 4.0.3)
magrittr      2.0.1    2020-11-17 [1] CRAN (R 4.0.2)
Matrix        1.3-4    2021-06-01 [1] CRAN (R 4.0.3)
mgcv          1.8-33   2020-08-27 [2] CRAN (R 4.0.3)
modelr        0.1.8    2020-05-19 [1] CRAN (R 4.0.2)
munsell       0.5.0    2018-06-12 [1] CRAN (R 4.0.2)
nlme          3.1-152  2021-02-04 [1] CRAN (R 4.0.3)
openxlsx      4.2.4    2021-06-16 [1] CRAN (R 4.0.3)
pbdZMQ        0.3-5    2021-02-10 [1] CRAN (R 4.0.3)
pillar        1.6.1    2021-05-16 [1] CRAN (R 4.0.3)
```

```
 pkgconfig     2.0.3    2019-09-22 [1] CRAN (R 4.0.2)
 purrr       * 0.3.4    2020-04-17 [1] CRAN (R 4.0.2)
 R6            2.5.0    2020-10-28 [1] CRAN (R 4.0.2)
 Rcpp          1.0.7    2021-07-07 [1] CRAN (R 4.0.3)
 readr       * 1.4.0    2020-10-05 [1] CRAN (R 4.0.2)
 readxl        1.3.1    2019-03-13 [1] CRAN (R 4.0.2)
 repr        * 1.1.3    2021-01-21 [1] CRAN (R 4.0.2)
 reprex        2.0.0    2021-04-02 [1] CRAN (R 4.0.3)
 rio           0.5.27   2021-06-21 [1] CRAN (R 4.0.3)
 rlang         0.4.11   2021-04-30 [1] CRAN (R 4.0.3)
 rstatix       0.7.0    2021-02-13 [1] CRAN (R 4.0.3)
 rstudioapi    0.13     2020-11-12 [1] CRAN (R 4.0.2)
 rvest         1.0.0    2021-03-09 [1] CRAN (R 4.0.3)
 scales        1.1.1    2020-05-11 [1] CRAN (R 4.0.2)
 sessioninfo   1.1.1    2018-11-05 [1] CRAN (R 4.0.2)
 stringi       1.6.2    2021-05-17 [1] CRAN (R 4.0.3)
 stringr     * 1.4.0    2019-02-10 [1] CRAN (R 4.0.2)
 svglite       2.0.0    2021-02-20 [1] CRAN (R 4.0.3)
 systemfonts   1.0.2    2021-05-11 [1] CRAN (R 4.0.3)
 tibble      * 3.1.2    2021-05-16 [1] CRAN (R 4.0.3)
 tidyr       * 1.1.3    2021-03-03 [1] CRAN (R 4.0.3)
 tidyselect    1.1.1    2021-04-30 [1] CRAN (R 4.0.3)
 tidyverse   * 1.3.1    2021-04-15 [1] CRAN (R 4.0.3)
 utf8          1.2.1    2021-03-12 [1] CRAN (R 4.0.3)
 uuid          0.1-4    2020-02-26 [1] CRAN (R 4.0.2)
 vctrs         0.3.8    2021-04-29 [1] CRAN (R 4.0.3)
 withr         2.4.2    2021-04-18 [1] CRAN (R 4.0.3)
 xml2          1.3.2    2020-04-23 [1] CRAN (R 4.0.2)
 zip           2.2.0    2021-05-31 [1] CRAN (R 4.0.3)

[1] /home/jbenja13/R/x86_64-pc-linux-gnu-library/4.0
[2] /usr/lib/R/library
```