main_r

September 18, 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   3.1.4       dplyr   1.0.7
  tidyr    1.1.3       stringr 1.4.0
  readr    2.0.1       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'= '../../../_m/genes/diffExpr_szVctl_full.txt',
               'dlpfc'= '/ceph/projects/v4_phase3_paper/inputs/public_data/_m/
↪phase2/dlpfc_diffExpr_szVctl_full.txt',
               'hippo'= '/ceph/projects/v4_phase3_paper/inputs/public_data/_m/
↪phase2/hippo_diffExpr_szVctl_full.txt',
               'cmc'=paste0("/ceph/projects/v4_phase3_paper/inputs/public_data/
↪_m/cmc/CMC_MSSM-Penn-Pitt_DLPFC_mRNA_",
                                        ␣
↪"IlluminaHiSeq2500_gene-adjustedSVA-differentialExpression-includeAncestry-DxSCZ-DE.
↪tsv"),
               'cmc_noSVA'=paste0("/ceph/projects/v4_phase3_paper/inputs/
↪public_data/_m/cmc/CMC_MSSM-Penn-Pitt_DLPFC_mRNA_",
                                              ␣
↪"IlluminaHiSeq2500_gene-adjustedNoSVA-differentialExpression-includeAncestry-DxSCZ-DE.
↪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 ('gencodeID' %in% colnames(dft)){
             dft <- dft %>%
                 mutate(Feature=gencodeID, Dir=sign(t)) %>%
                 select("Feature", "ensemblID", "adj.P.Val", "logFC", "t", "Dir")
         } else if ('MAPPED_genes' %in% colnames(dft)){
             dft <- dft %>%
                 mutate(Feature=genes, ensemblID=genes, Dir=sign(t)) %>%
                 select("Feature", "ensemblID", "adj.P.Val", "logFC", "t", "Dir")
         } else {
             dft <- dft %>%
                 mutate(Feature=V1, Dir=sign(dft$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='ensemblID', suffixes=c(paste0('_',tissue1),␣
      ↪paste0('_',tissue2))))
     }

     merge_dataframes_sig <- function(tissue1, tissue2){
         fdr1 = ifelse(tissue1 != 'dlpfc', 0.05, 0.05)
         fdr2 = ifelse(tissue2 != 'dlpfc', 0.05, 0.05)
         return(merge(get_deg_sig(config[[tissue1]], fdr1),␣
      ↪get_deg_sig(config[[tissue2]], fdr2),
                      by='ensemblID', suffixes=c(paste0('_',tissue1),␣
      ↪paste0('_',tissue2))))
     }

     tissue_annotation <- function(tissue){
         return(list('dlpfc'='DLPFC', 'hippo'='Hippocampus',
                     'caudate'='Caudate', 'cmc'="CMC DLPFC",
                     "cmc_noSVA"="CMC DLPFC [no SVA]")[[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=TRUE,
                        cor.method="pearson", cor.coef=FALSE, cor.coef.size=7,
                        cor.coeff.args=list(label.sep="\n"), ylim=c(-6,8),
                        ggtheme=theme_pubr(base_size=20)) +
             stat_cor(aes(label=..rr.label..), label.sep='\n', size=8,
                      method="spearman",  label.x=-8, label.y=7) +
             font("xylab", face='bold')
         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)
         }
     }
```

1.1 BrainSeq Comparison

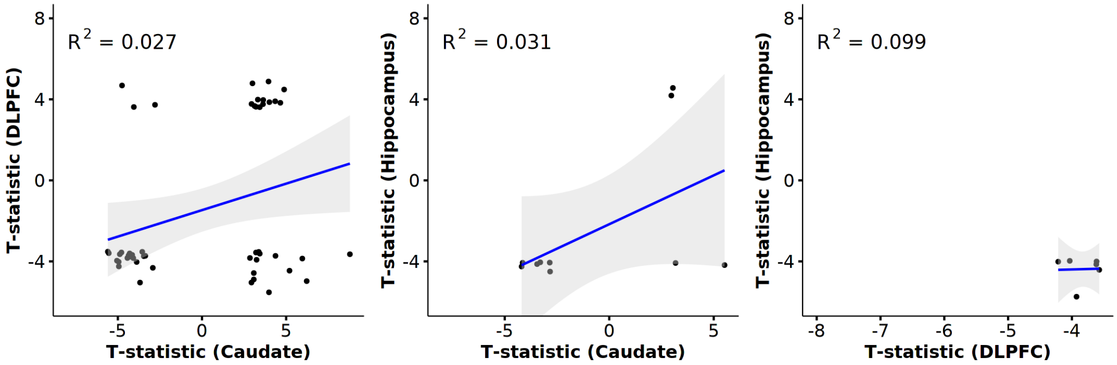
[4]:

```
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, nrow=1, align='v')
print(fig1)
```

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

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

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



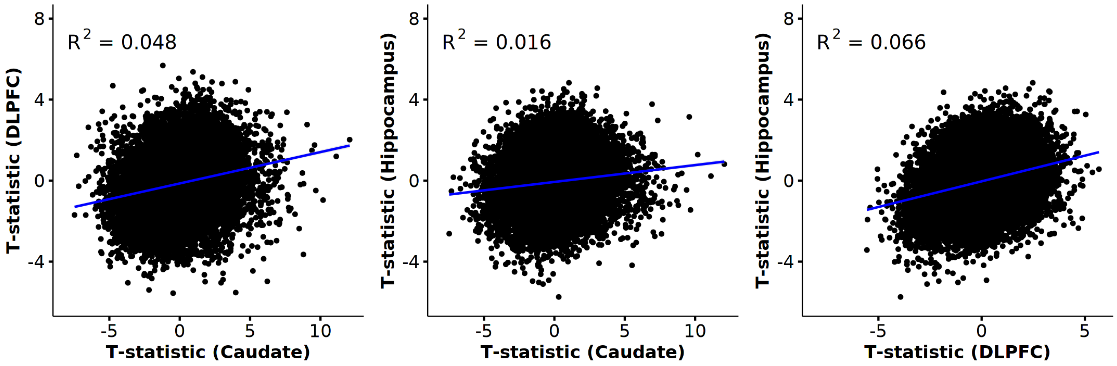
```
[5]: save_ggplots("tstatistic_corr_sig", fig1, 18, 6)
```

```
[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, nrow=1, 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)
```

1.2 CMC Comparison

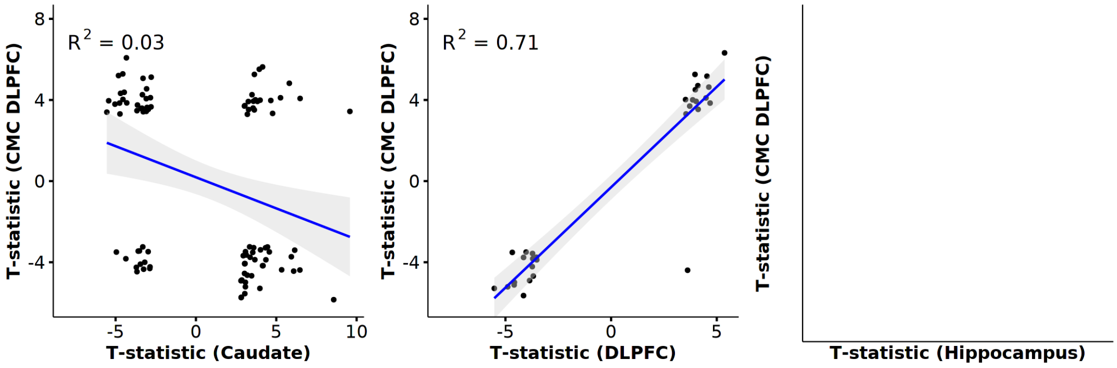
1.2.1 SVA correction

[8]:

```
options(repr.plot.width=18, repr.plot.height=6)
sp1_sig = get_scatter_plot('caudate', 'cmc', merge_dataframes_sig, c(-110, 85))
sp2_sig = get_scatter_plot('dlpfc', 'cmc', merge_dataframes_sig, c(-110, 85))
sp3_sig = get_scatter_plot('hippo', 'cmc', merge_dataframes_sig, c(-110, 85))
fig1 = ggarrange(sp1_sig, sp2_sig, sp3_sig, ncol=3, nrow=1, align='v')
print(fig1)
```

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

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



[9]:

```
save_ggplots("cmc_tstatistic_corr_sig", fig1, 18, 6)
```

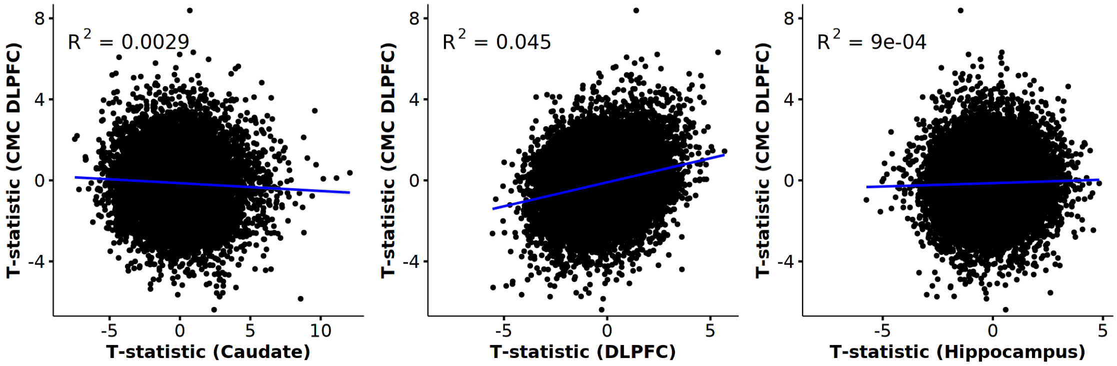
[10]:

```
sp1 = get_scatter_plot('caudate', 'cmc', merge_dataframe, c(-110, 85))
sp2 = get_scatter_plot('dlpfc', 'cmc', merge_dataframe, c(-110, 85))
sp3 = get_scatter_plot('hippo', 'cmc', merge_dataframe, c(-110, 85))
fig2 = ggarrange(sp1, sp2, sp3, ncol=3, nrow=1, align='v')
print(fig2)
```

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

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

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



```
[11]: save_ggplots("cmc_tstatistic_corr", fig2, 18, 6)
```

1.2.2 No SVA correction

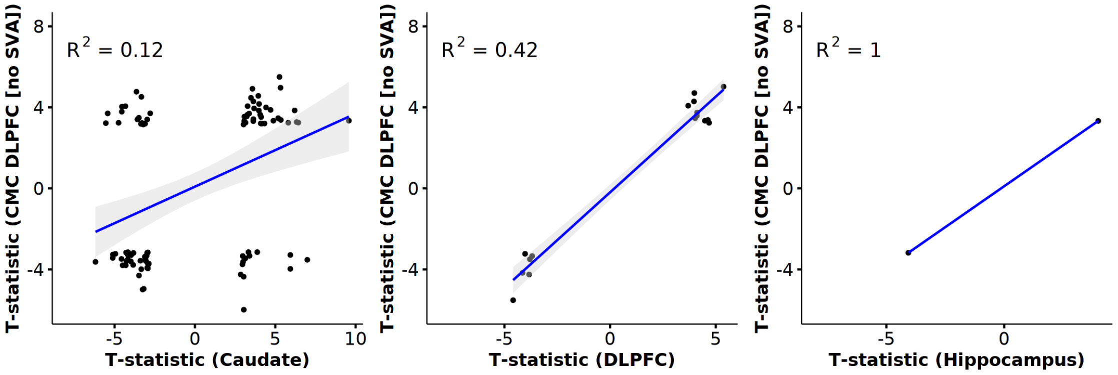
```
[12]: options(repr.plot.width=18, repr.plot.height=6)
      sp1_sig = get_scatter_plot('caudate', 'cmc_noSVA', merge_dataframes_sig,␣
       ↪c(-110, 85))
      sp2_sig = get_scatter_plot('dlpfc', 'cmc_noSVA', merge_dataframes_sig, c(-110,␣
       ↪85))
      sp3_sig = get_scatter_plot('hippo', 'cmc_noSVA', merge_dataframes_sig, c(-110,␣
       ↪85))
      fig1 = ggarrange(sp1_sig, sp2_sig, sp3_sig, ncol=3, nrow=1, align='v')
      print(fig1)
```

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

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

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

Warning message in qt((1 - level)/2, df):
"NaNs produced"
Warning message in max(ids, na.rm = TRUE):
"no non-missing arguments to max; returning -Inf"
```



[13]:

```
save_ggplots("cmc_noSVA_tstatistic_corr_sig", fig1, 18, 6)
```

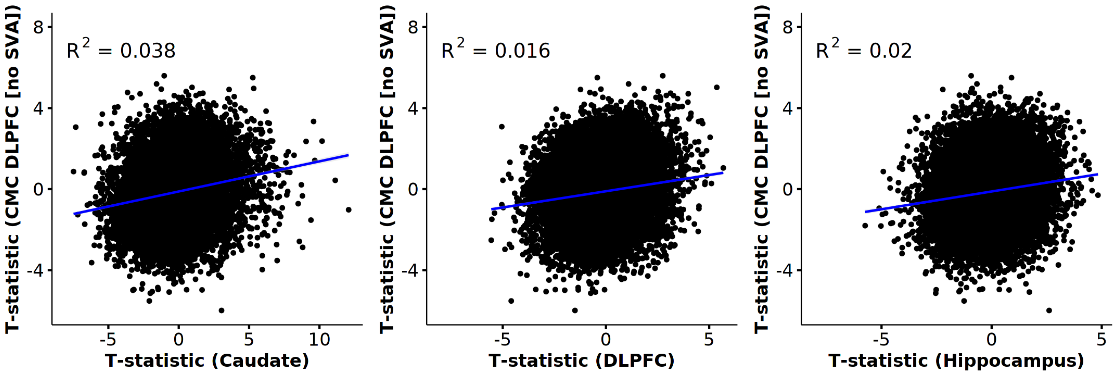
[14]:

```
sp1 = get_scatter_plot('caudate', 'cmc_noSVA', merge_dataframe, c(-110, 85))
sp2 = get_scatter_plot('dlpfc', 'cmc_noSVA', merge_dataframe, c(-110, 85))
sp3 = get_scatter_plot('hippo', 'cmc_noSVA', merge_dataframe, c(-110, 85))
fig2 = ggarrange(sp1, sp2, sp3, ncol=3, nrow=1, align='v')
print(fig2)
```

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

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

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



[15]:

```
save_ggplots("cmc_noSVA_tstatistic_corr", fig2, 18, 6)
```

1.3 Reproducibility Information

[16]:

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

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

```
[1] "2021-09-18 17:46:13 EDT"
```

```
   user  system elapsed 
 68.803   1.748  45.483 
```

```
 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     2021-09-18

 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)
 bit            4.0.4    2020-08-04 [1] CRAN (R 4.0.2)
 bit64          4.0.5    2020-08-30 [1] CRAN (R 4.0.2)
 broom          0.7.9    2021-07-27 [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            3.0.1    2021-07-17 [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)
fastmap        1.1.0    2021-01-25 [1] CRAN (R 4.0.2)
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          2.4.3    2021-08-04 [1] CRAN (R 4.0.3)
hms            1.1.0    2021-05-17 [1] CRAN (R 4.0.3)
htmltools      0.5.2    2021-08-25 [1] CRAN (R 4.0.3)
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         1.6.2    2021-07-29 [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             2.5.1    2021-08-19 [1] CRAN (R 4.0.3)
Rcpp           1.0.7    2021-07-07 [1] CRAN (R 4.0.3)
readr        * 2.0.1    2021-08-10 [1] CRAN (R 4.0.3)
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         2.0.1    2021-08-05 [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          1.0.1    2021-07-26 [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       1.7.4   2021-08-25 [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      * 3.1.4   2021-08-25 [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)
 tzdb          0.1.2   2021-07-20 [1] CRAN (R 4.0.3)
 utf8          1.2.2   2021-07-24 [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
```