

main

August 6, 2021

1 Generate Rank-Rank Hypergeometric Overlap (RRHO) plots

```
[1]: library(RRHO)
library(dplyr)
library(lattice)
```

Loading required package: grid

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

```
[2]: get_deg_df <- function(sex, tissue){
  if(tolower(sex) == 'female'){
    fn = paste0(".././.././", tolower(tissue), "/female_analysis/_m/genes/
    ↪diffExpr_szVctl_full.txt")
  } else {
    fn = paste0(".././.././", tolower(tissue), "/male_analysis/_m/genes/
    ↪diffExpr_szVctl_full.txt")
  }
  if(tolower(tissue) == 'cmc_dlpfc'){
    df = data.table::fread(fn) %>% mutate(metric=-log10(P.Value)*sign(t),
    ↪gencodeID=gene_id) %>%
      select('gencodeID', 'metric')
  } else {
```

```

    df = data.table::fread(fn) %>% mutate(metric=-log10(P.Value)*sign(t))
    ↪%>%
        select('gencodeID', 'metric')
    }
    return(df)
}

within_tissue_rrho_plot <- function(tissue){
  defaultW <- getOption("warn")
  options(warn = -1)
  f.list = get_deg_df('female', tolower(tissue)) %>% distinct(gencodeID, .
    ↪keep_all = TRUE)
  m.list = get_deg_df('male', tolower(tissue)) %>% distinct(gencodeID, .
    ↪keep_all = TRUE)
  rrho_df <- RRHO(f.list, m.list, BY=TRUE, labels=c("Female", "Male"),
    alternative='enrichment', log10.ind=TRUE)
  rrho_df$hypermat[is.na(rrho_df$hypermat)] <- 0 # for NA, correct to 0
  options(warn = defaultW)
  plt = levelplot(rrho_df$hypermat, col.regions=viridis::viridis(100),
    xlab="Female", ylab="Male", at=seq(0, 1000, 100))
  print(plt)
  label = paste("rrho_sex_compare", tolower(tissue), sep='_')
  R.devices::devEval(c("pdf", "png"), name=label, print(plt))
  #return(rrho_df)
}

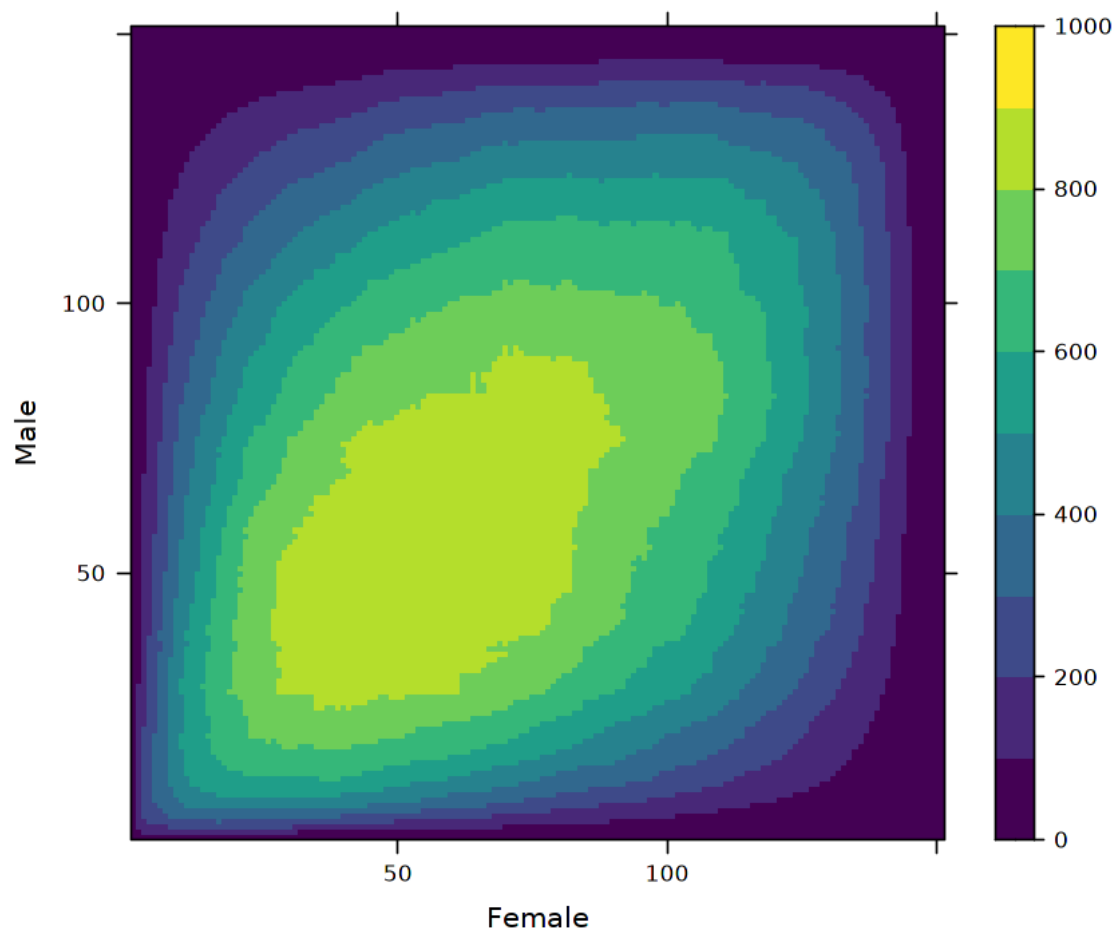
```

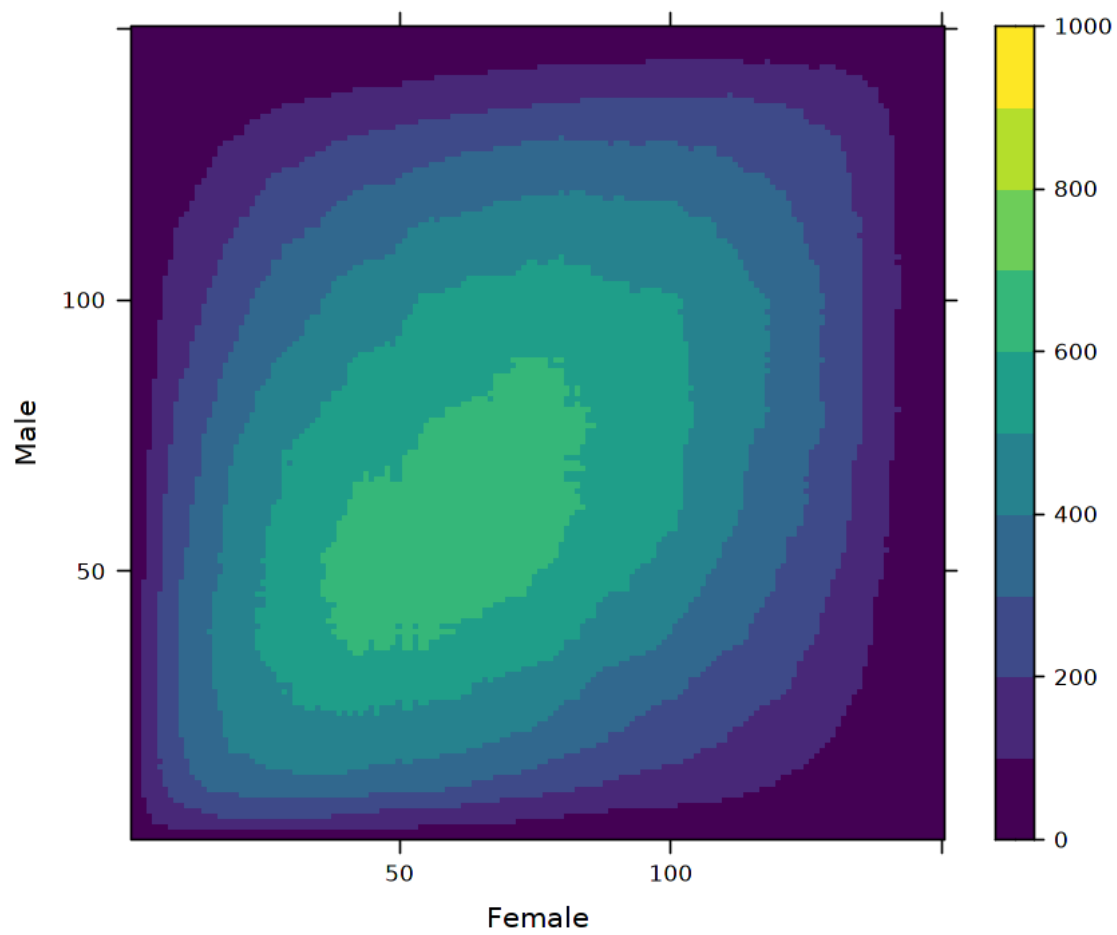
1.1 Within tissue comparison

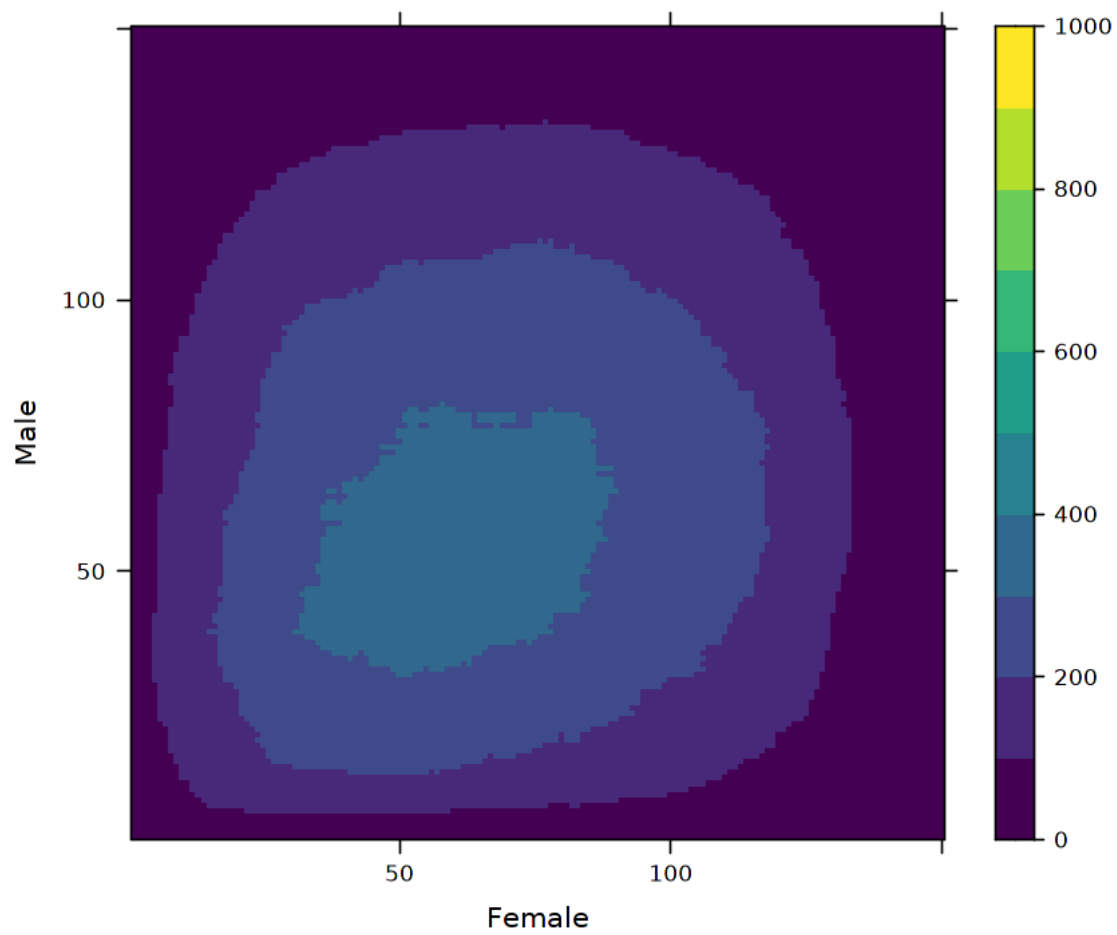
```

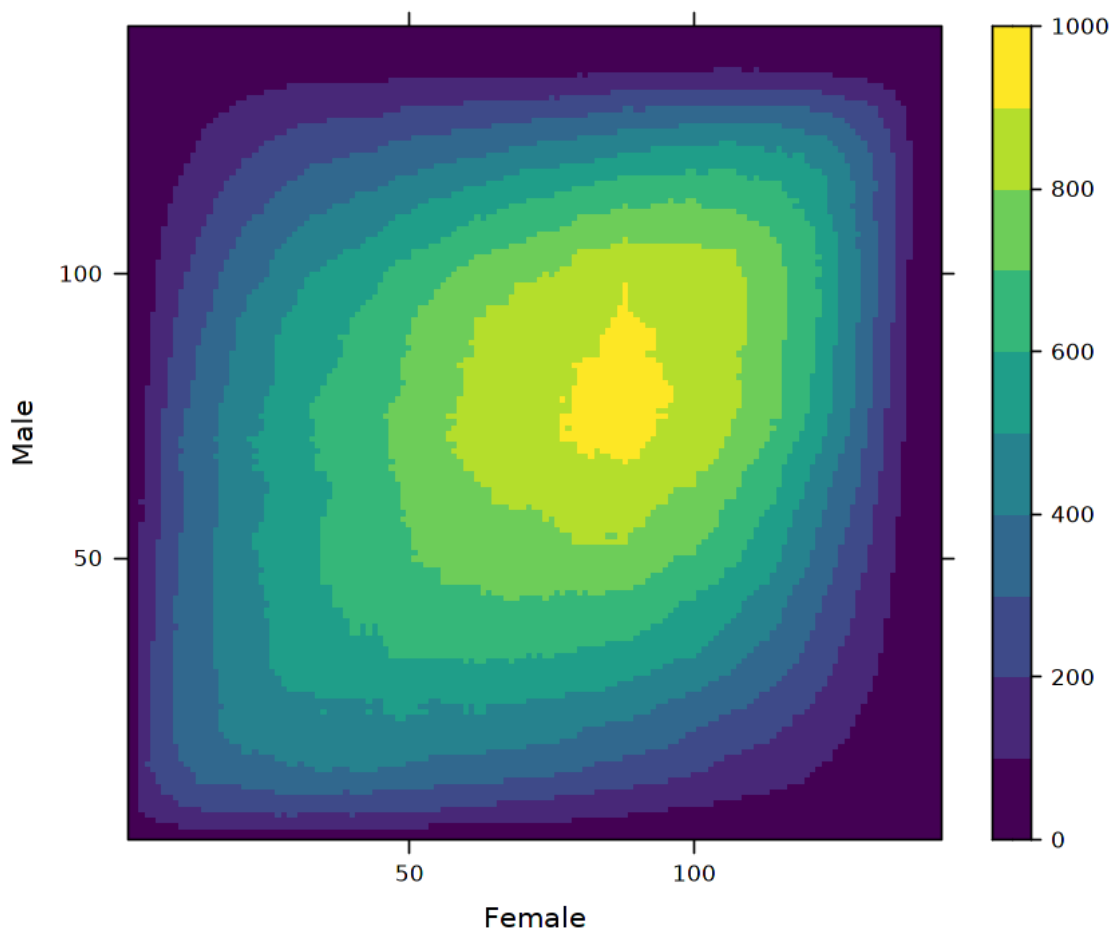
[3]: for(tissue in c('caudate', 'dlpfc', 'hippocampus', 'cmc_dlpfc')){
      within_tissue_rrho_plot(tissue)
    }

```









1.2 Female comparison across tissues

```
[4]: compare_tissue_plot <- function(sex, tissue1, tissue2){
  list1 = get_deg_df(sex, tissue1) %>% distinct(gencodeID, .keep_all = TRUE)
  list2 = get_deg_df(sex, tissue2) %>% distinct(gencodeID, .keep_all = TRUE)
  gene_overlap = intersect(list1$gencodeID, list2$gencodeID)
  list1 = list1 %>% filter(gencodeID %in% gene_overlap)
  list2 = list2 %>% filter(gencodeID %in% gene_overlap)
  rrho_df <- RRHO(list1, list2, BY=TRUE, labels=c(tissue1, tissue2),
    alternative='enrichment', log10.ind=TRUE)
  rrho_df$hypermat[is.na(rrho_df$hypermat)] <- 0 # for NA, correct to 0
  rrho_plot = levelplot(rrho_df$hypermat, col.regions=viridis::viridis,
    xlab=tissue1, ylab=tissue2, at=seq(0, 800, 100))
}
```

```

R.devices::devEval(c("pdf", "png"),
                    name=paste("rrho",sex,tissue1,tissue2, sep='_'),
                    print(rrho_plot))
}

```

1.2.1 Female

```

[5]: compare_tissue_plot("female", "Caudate", "DLPFC")
      compare_tissue_plot("female", "Caudate", "Hippocampus")
      compare_tissue_plot("female", "DLPFC", "Hippocampus")

```

\$pdf 'figures/rrho_female_Caudate_DLPFC.pdf'

\$png 'figures/rrho_female_Caudate_DLPFC.png'

\$pdf 'figures/rrho_female_Caudate_Hippocampus.pdf'

\$png 'figures/rrho_female_Caudate_Hippocampus.png'

\$pdf 'figures/rrho_female_DLPFC_Hippocampus.pdf'

\$png 'figures/rrho_female_DLPFC_Hippocampus.png'

```

[6]: compare_tissue_plot("female", "CMC_DLPFC", "Caudate")
      compare_tissue_plot("female", "CMC_DLPFC", "DLPFC")
      compare_tissue_plot("female", "CMC_DLPFC", "Hippocampus")

```

\$pdf 'figures/rrho_female_CMC_DLPFC_Caudate.pdf'

\$png 'figures/rrho_female_CMC_DLPFC_Caudate.png'

\$pdf 'figures/rrho_female_CMC_DLPFC_DLPFC.pdf'

\$png 'figures/rrho_female_CMC_DLPFC_DLPFC.png'

\$pdf 'figures/rrho_female_CMC_DLPFC_Hippocampus.pdf'

\$png 'figures/rrho_female_CMC_DLPFC_Hippocampus.png'

1.2.2 Male

```

[7]: compare_tissue_plot("male", "Caudate", "DLPFC")
      compare_tissue_plot("male", "Caudate", "Hippocampus")
      compare_tissue_plot("male", "DLPFC", "Hippocampus")

```

\$pdf 'figures/rrho_male_Caudate_DLPFC.pdf'

\$png 'figures/rrho_male_Caudate_DLPFC.png'

\$pdf 'figures/rrho_male_Caudate_Hippocampus.pdf'

\$png 'figures/rrho_male_Caudate_Hippocampus.png'

\$pdf 'figures/rrho_male_DLPFC_Hippocampus.pdf'

\$png 'figures/rrho_male_DLPFC_Hippocampus.png'

```
[8]: compare_tissue_plot("male", "CMC_DLPFC", "Caudate")
      compare_tissue_plot("male", "CMC_DLPFC", "DLPFC")
      compare_tissue_plot("male", "CMC_DLPFC", "Hippocampus")
```

```
$pdf 'figures/rrho_male_CMC_DLPFC_Caudate.pdf'
```

```
$png 'figures/rrho_male_CMC_DLPFC_Caudate.png'
```

```
$pdf 'figures/rrho_male_CMC_DLPFC_DLPFC.pdf'
```

```
$png 'figures/rrho_male_CMC_DLPFC_DLPFC.png'
```

```
$pdf 'figures/rrho_male_CMC_DLPFC_Hippocampus.pdf'
```

```
$png 'figures/rrho_male_CMC_DLPFC_Hippocampus.png'
```

1.3 Reproducibility Information

```
[9]: Sys.time()
      proc.time()
      options(width = 120)
      sessioninfo::session_info()
```

```
[1] "2021-08-06 10:21:03 EDT"
```

```
      user  system elapsed
291.148    1.320   298.800
```

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     2021-08-06
```

Packages

package	* version	date	lib	source
assertthat	0.2.1	2019-03-21	[1]	CRAN (R 4.0.2)
base64enc	0.1-3	2015-07-28	[1]	CRAN (R 4.0.2)
Cairo	1.5-12.2	2020-07-07	[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)
crayon	1.4.1	2021-02-08	[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)
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)
formatR	1.11	2021-06-01	[1]	CRAN	(R 4.0.3)
futile.logger	1.4.3	2016-07-10	[1]	CRAN	(R 4.0.2)
futile.options	1.0.1	2018-04-20	[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)
glue	1.4.2	2020-08-27	[1]	CRAN	(R 4.0.2)
gridExtra	2.3	2017-09-09	[1]	CRAN	(R 4.0.2)
gtable	0.3.0	2019-03-25	[1]	CRAN	(R 4.0.2)
htmltools	0.5.1.1	2021-01-22	[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)
lambda.r	1.2.4	2019-09-18	[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)
magrittr	2.0.1	2020-11-17	[1]	CRAN	(R 4.0.2)
munsell	0.5.0	2018-06-12	[1]	CRAN	(R 4.0.2)
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)
R.devices	2.17.0	2021-01-19	[1]	CRAN	(R 4.0.3)
R.methodsS3	1.8.1	2020-08-26	[1]	CRAN	(R 4.0.3)
R.oo	1.24.0	2020-08-26	[1]	CRAN	(R 4.0.3)
R.utils	2.10.1	2020-08-26	[1]	CRAN	(R 4.0.3)
R6	2.5.0	2020-10-28	[1]	CRAN	(R 4.0.2)
repr	1.1.3	2021-01-21	[1]	CRAN	(R 4.0.2)
rlang	0.4.11	2021-04-30	[1]	CRAN	(R 4.0.3)
RRHO	* 1.30.0	2020-10-27	[1]	Bioconductor	
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)
tibble	3.1.2	2021-05-16	[1]	CRAN	(R 4.0.3)
tidyselect	1.1.1	2021-04-30	[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)
VennDiagram	1.6.20	2018-03-28	[1]	CRAN	(R 4.0.3)
viridis	0.6.1	2021-05-11	[1]	CRAN	(R 4.0.3)
viridisLite	0.4.0	2021-04-13	[1]	CRAN	(R 4.0.3)
withr	2.4.2	2021-04-18	[1]	CRAN	(R 4.0.3)

[1] /home/jbenja13/R/x86_64-pc-linux-gnu-library/4.0

[2] /usr/lib/R/library

[]: