

main_hippocampus

September 14, 2021

1 eQTL boxplot

This is script ported from python to fix unknown plotting error.

```
[1]: suppressPackageStartupMessages({  
      library(tidyverse)  
      library(ggpubr)  
    })
```

1.1 Functions

```
[2]: tissue = "Hippocampus"
```

1.1.1 Cached functions

```
[3]: get_residualized_df <- function(){  
      expr_file = "../_m/genes_residualized_expression.csv"  
      return(data.table::fread(expr_file) %>% column_to_rownames("gene_id"))  
    }  
    memRES <- memoise::memoise(get_residualized_df)  
  
    get_biomart_df <- function(){  
      biomart = data.table::fread("../_h/biomart.csv")  
    }  
    memMART <- memoise::memoise(get_biomart_df)  
  
    get_pheno_df <- function(){  
      phenotype_file = paste0('/ceph/projects/v4_phase3_paper/inputs/',  
                              'phenotypes/_m/merged_phenotypes.csv')  
      return(data.table::fread(phenotype_file))  
    }  
    memPHENO <- memoise::memoise(get_pheno_df)  
  
    get_genotypes <- function(){  
      traw_file = paste0("/ceph/projects/brainseq/genotype/download/topmed/  
      ↪convert2plink/",  
                        "filter_maf_01/a_transpose/_m/LIBD_Brain_TopMed.traw")  
      traw = data.table::fread(traw_file) %>% rename_with(~ gsub('\\_.*', '', .x))
```

```

    return(traw)
}
memSNPs <- memoise::memoise(get_genotypes)

get_tissue_eqtls <- function(){
  mashr_file = paste0("../.../mashr/summary_table/_m/",
    "BrainSeq_sexGenotypes_4features_3regions.txt.gz")
  dt = data.table::fread(mashr_file) %>% filter(Type == "Gene")
  cc = dt %>% filter(Tissue == "Caudate")
  dd = dt %>% filter(Tissue == "DLPFC")
  hh = dt %>% filter(Tissue == "Hippocampus")
  geneids = setdiff(setdiff(unique(hh$gene_id), unique(dd$gene_id)),
    unique(cc$gene_id))
  return(data.table::fread(mashr_file) %>%
    filter(Type == "Gene", gene_id %in% geneids) %>%
    select(gene_id, variant_id))
}
memTISSUE <- memoise::memoise(get_tissue_eqtls)

get_eqtl_df <- function(){
  fastqtl_file = paste0("../.../.../prep_eqtl_analysis/", tolower(tissue),
    "/genes/prepare_expression/fastqtl_nominal/",
    "multiple_corrections/_m/Brainseq_LIBD.txt.gz")
  eqtl_df = data.table::fread(fastqtl_file) %>%
    filter(gene_id %in% unique(memTISSUE()$gene_id)) %>%
    arrange(BF)
  return(eqtl_df)
}
memEQTL <- memoise::memoise(get_eqtl_df)

get_snp_df <- function(variant_id, gene_id){
  zz = get_genos_annot() %>% filter(SNP == variant_id)
  xx = get_snps_df() %>% filter(SNP == variant_id) %>%
    column_to_rownames("SNP") %>% t %>% as.data.frame %>%
    rownames_to_column("BrNum") %>% mutate(COUNTED=zz$COUNTED, ALT=zz$ALT)
  → %>%
    rename("SNP"=all_of(variant_id))
  yy = memRES()[gene_id, ] %>% t %>% as.data.frame %>%
    rownames_to_column("RNum") %>% inner_join(memPHENO(), by="RNum")
  ## Annotated SNPs
  letters = c()
  for(ii in seq_along(xx$COUNTED)){
    a0 = xx$COUNTED[ii]; a1 = xx$ALT[ii]; number = xx$SNP[ii]
    letters <- append(letters, letter_snp(number, a0, a1))
  }
  xx = xx %>% mutate(LETTER=letters, ID=paste(SNP, LETTER, sep="\n"))
  df = inner_join(xx, yy, by="BrNum") %>% mutate_if(is.character, as.factor)
}

```

```

    return(df)
}
memDF <- memoise::memoise(get_snp_df)

```

1.1.2 Simple functions

```

[4]: get_genotype_annot <- function(){
    return(memSNPs() %>% select(CHR, SNP, POS, COUNTED, ALT))
}

get_snps_df <- function(){
    return(memSNPs() %>% select("SNP", starts_with("Br")))
}

letter_snp <- function(number, a0, a1){
    if(is.na(number)){ return(NA) }
    if( length(a0) == 1 & length(a1) == 1){
        seps = ""; collapse=""
    } else {
        seps = " "; collapse=NULL
    }
    return(paste(paste0(rep(a0, number), collapse = collapse),
                paste0(rep(a1, (2-number)), collapse = collapse), sep=seps))
}

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

get_gene_symbol <- function(gene_id){
    ensemblID = gsub("\\\\.*", "", gene_id)
    geneid = memMART() %>% filter(ensembl_gene_id == gsub("\\\\.*", "", gene_id))
    if(dim(geneid)[1] == 0){
        return("")
    } else {
        return(geneid$external_gene_name)
    }
}

plot_simple_eqtl <- function(fn, gene_id, variant_id){
    bxp = memDF(variant_id, gene_id) %>%
        mutate(Region=gsb("HIPPO", "Hippocampus", Region)) %>%
        ggboxplot(x="ID", y=gene_id, fill="Sex", color="Sex", add="jitter",
                facet.by="Region", panel.labs.font=list(face='bold'),

```

```

    xlab=variant_id, ylab="Residualized Expression", outlier.
↪shape=NA,

    add.params=list(alpha=0.5), alpha=0.4, legend="bottom",
    palette="npg", ggtheme=theme_pubr(base_size=20, border=TRUE))
↪+

    font("xy.title", face="bold") +
    ggtitle(paste(get_gene_symbol(gene_id), gene_id, sep='\n')) +
    theme(plot.title = element_text(hjust = 0.5, face="bold"))
print(bxp)
save_ggplots(fn, bxp, 10, 7)
}

```

1.2 Plot eQTL

```

[5]: eqtl_df = memEQTL()
eqtl_df %>% head(5)

```

	variant_id <chr>	gene_id <chr>	slope <dbl>	statistic <dbl>	pval_nominal <dbl>	fdr <dbl>
A data.table: 4 × 9	chr17:74622043:T:A	ENSG00000167862.9	0.449442	18.49751	2.82313e-07	0.0005
	chr18:80244356:T:C	ENSG00000267251.2	-0.591417	-13.13001	9.31740e-07	0.0008
	chr9:98263839:C:T	ENSG00000106789.12	-0.631614	-8.40021	9.21420e-05	0.0767
	chr22:50563003:G:C	ENSG00000185386.14	0.187462	10.48293	2.55136e-04	0.3671

1.2.1 Top 5 eQTLs

```

[6]: dir.create(tolower(tissue))

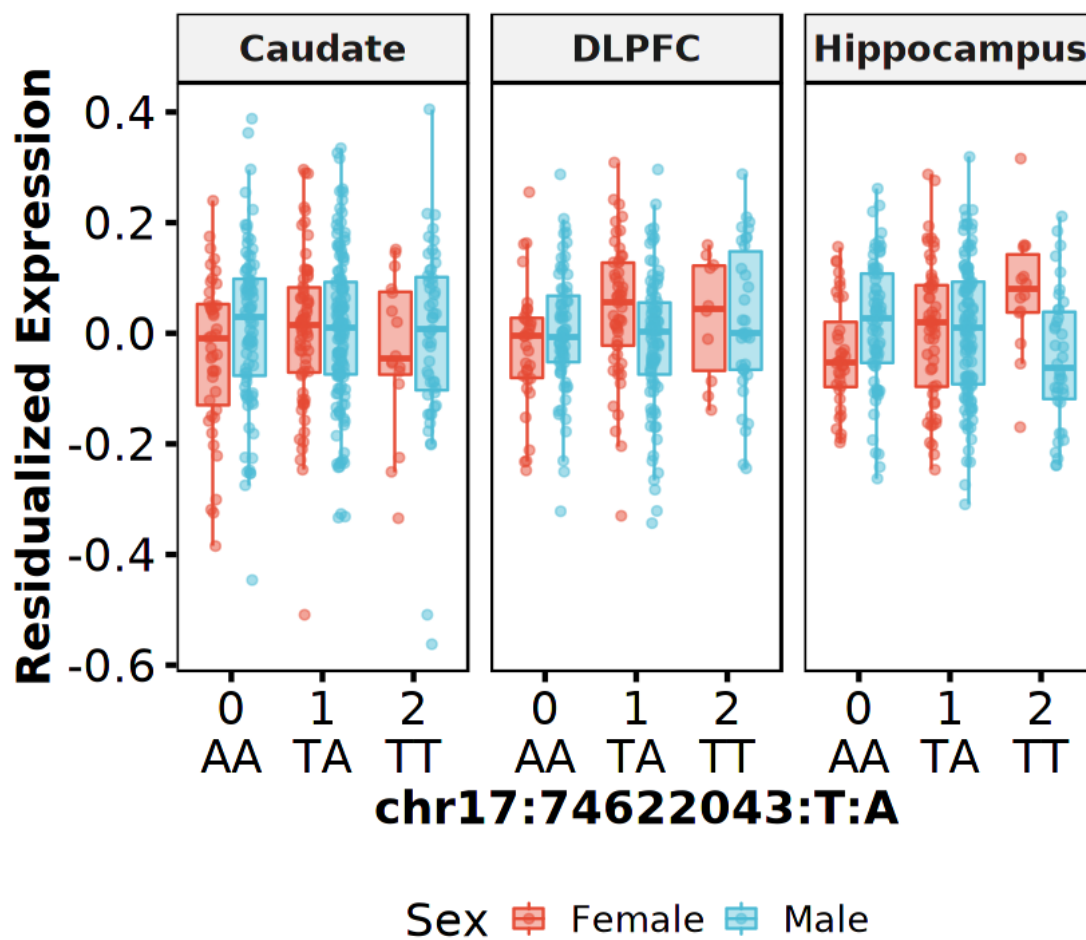
```

```

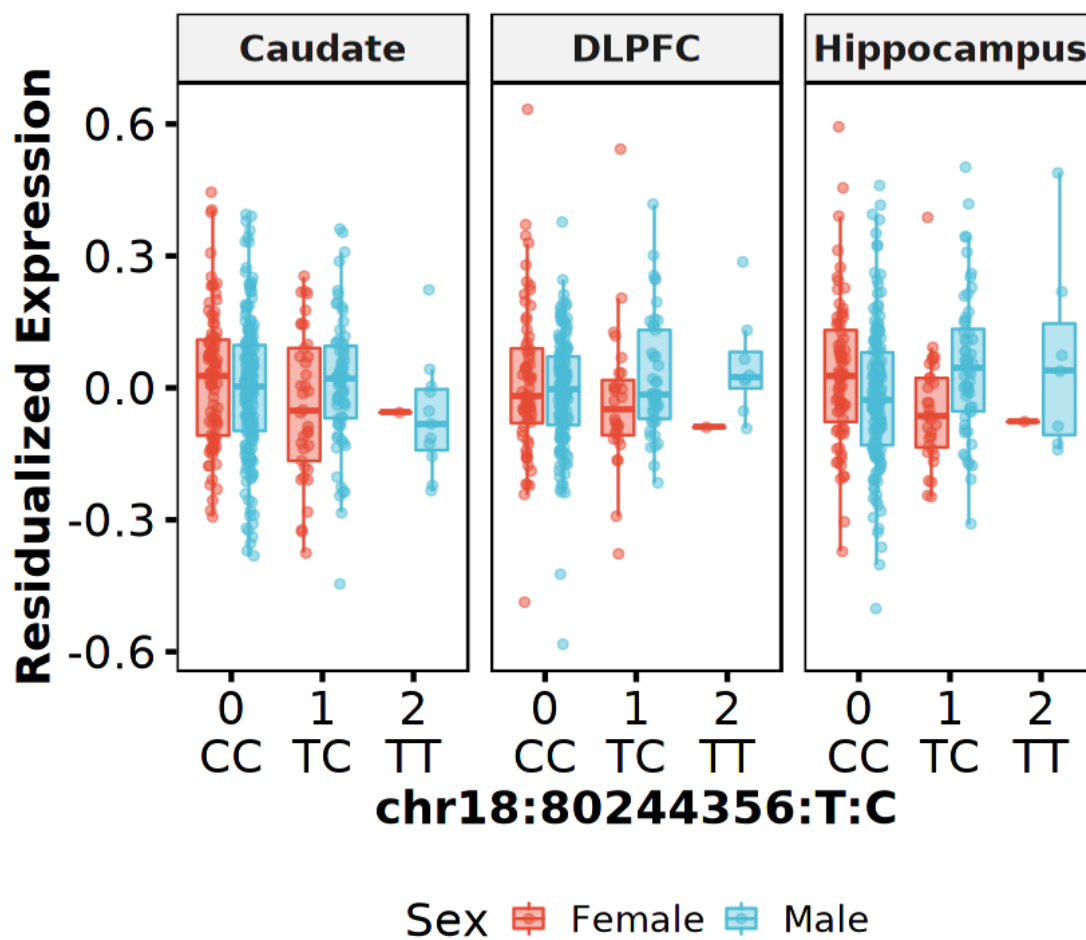
[7]: for(num in seq_along(eqtl_df$gene_id)){
  variant_id = memEQTL()$variant_id[num]
  gene_id = memEQTL()$gene_id[num]
  #eqtl_annot = paste("eQTL q-value:", signif(memEQTL()$BF[num], 2))
  fn = paste0(tolower(tissue), "/top_", num, "_interacting_eqtl")
  plot_simple_eqtl(fn, gene_id, variant_id)
}

```

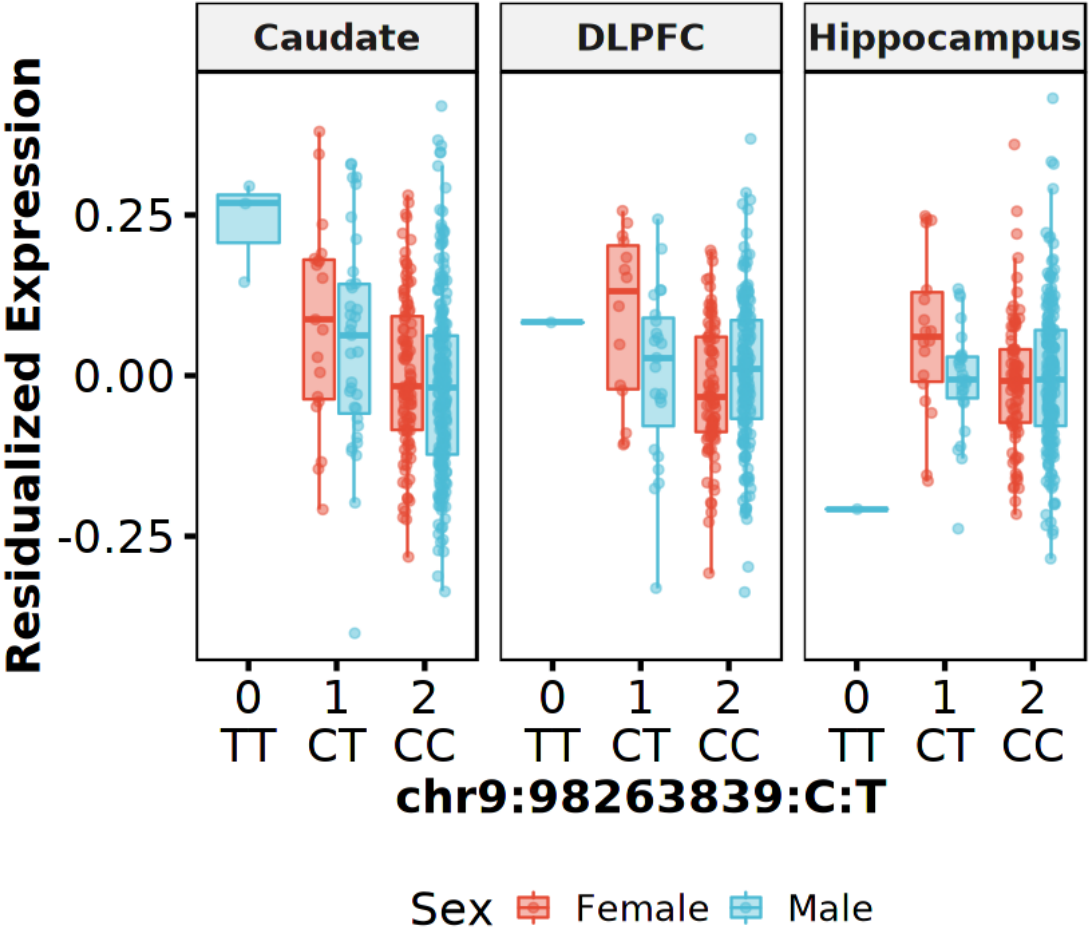
MRPL58 ENSG00000167862.9



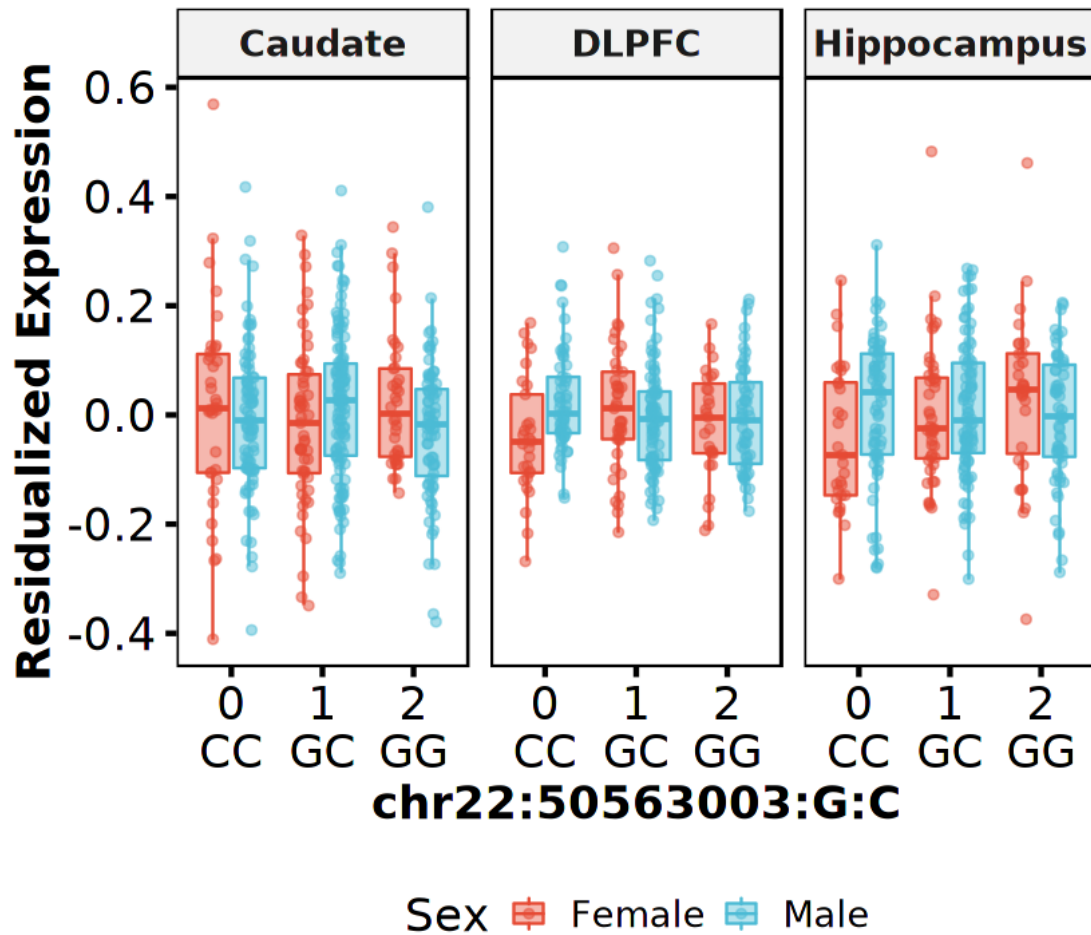
AC139100.1 ENSG00000267251.2



CORO2A
ENSG00000106789.12



MAPK11 ENSG00000185386.14



1.3 Session Info

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

```
[1] "2021-09-14 08:49:56 EDT"
```

```
      user   system elapsed
1867.527   340.905   360.260
```

```
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    2021-09-14

```

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	0.7.9	2021-07-27	[1]	CRAN (R 4.0.3)
cachem	1.0.6	2021-08-19	[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)
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)
ggsci	2.9	2018-05-14	[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)
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)
memoise	2.0.0	2021-01-26	[1]	CRAN	(R 4.0.2)
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)
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)
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	2.5.1	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
```