230510_rstudio_sex_bias_drugs_info

Jennifer Fisher

2022-12-21

```
System which operations were done on:
my laptop

GitHub Repo:
230321_JLF_Sex_bias_adverse_events

Docker:
jenfisher7/rstudio_sex_bias_drugs

Directory of operations:
~/Documents/230321_JLF_Sex_bias_adverse_events

Scripts being edited for operations:
NA

Data being used:
```

sessionInfo()

```
## R version 4.2.2 (2022-10-31)
## Platform: x86 64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 22.04.1 LTS
##
## Matrix products: default
## BLAS:
           /usr/lib/x86 64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86 64-linux-gnu/openblas-pthread/libopenblasp-r0.3.20.so
##
## locale:
##
   [1] LC CTYPE=en US.UTF-8
                                   LC NUMERIC=C
   [3] LC_TIME=en_US.UTF-8
                                   LC_COLLATE=en_US.UTF-8
##
   [5] LC MONETARY=en US.UTF-8
                                   LC_MESSAGES=en_US.UTF-8
##
   [7] LC_PAPER=en_US.UTF-8
                                   LC_NAME=C
  [9] LC ADDRESS=C
                                   LC TELEPHONE=C
## [11] LC MEASUREMENT=en US.UTF-8 LC IDENTIFICATION=C
##
## attached base packages:
## [1] stats
                graphics grDevices utils
                                              datasets methods
                                                                   base
##
## loaded via a namespace (and not attached):
   [1] digest 0.6.31
                       R6 2.5.1
                                        lifecycle 1.0.3 jsonlite 1.8.4
##
  [5] magrittr_2.0.3 evaluate 0.19
                                        stringi 1.7.8
                                                       cachem 1.0.6
## [9] rlang 1.0.6
                       cli 3.5.0
                                       rstudioapi_0.14 jquerylib_0.1.4
## [13] bslib_0.4.2
                   vctrs_0.5.1
                                       rmarkdown_2.19 tools_4.2.2
## [17] stringr 1.5.0 glue 1.6.2
                                       xfun 0.36
                                                        yaml 2.3.6
## [21] fastmap 1.1.0
                       compiler 4.2.2 htmltools 0.5.4 knitr 1.41
## [25] sass 0.4.4
```

```
# Listing packages
installed.packages()[,c(1,3)]
```

##	Package	Version
## abind	"abind"	"1.4-5"
## affy	"affy"	"1.76.0"
## affyio	"affyio"	"1.68.0"
## amap	"amap"	"0.8-19"
## annotate	"annotate"	"1.76.0"
## AnnotationDbi	"AnnotationDbi"	"1.60.0"
## AnnotationFilter	"AnnotationFilter"	"1.22.0"
## AnnotationForge	"AnnotationForge"	"1.40.0"
## AnnotationHub	"AnnotationHub"	"3.6.0"
## apcluster	"apcluster"	"1.4.10"
## ape	"ape"	"5.6-2"
## aplot	"aplot"	"0.1.9"
## ashr	"ashr"	"2.2-54"
## askpass	"askpass"	"1.1"
## assertthat	"assertthat"	"0.2.1"
## backports	"backports"	"1.4.1"
## base64	"base64"	"2.0.1"
## base64enc	"base64enc"	"0.1-3"
## base64url	"base64url"	"1.4"
## bayestestR	"bayestestR"	"0.13.0"
## beanplot	"beanplot"	"1.3.1"
## bench	"bench"	"1.1.2"
## BgeeDB	"BgeeDB"	"2.24.0"
## BH	"BH"	"1.78.0-0"
## Biobase	"Biobase"	"2.58.0"
## BiocBaseUtils	"BiocBaseUtils"	"1.0.0"
## BiocFileCache	"BiocFileCache"	"2.6.0"
## BiocGenerics	"BiocGenerics"	"0.44.0"
## BiocIO	"BiocIO"	"1.8.0"
## BiocManager	"BiocManager"	"1.30.19"
## BiocParallel	"BiocParallel"	"1.32.5"
## BiocVersion	"BiocVersion"	"3.16.0"
## biomaRt	"biomaRt"	"2.54.0"
## Biostrings	"Biostrings"	"2.66.0"
## bit	"bit"	"4.0.5"
## bit64	"bit64"	"4.0.5"
## bitops	"bitops"	"1.0-7"
## biwt	"biwt"	"1.0.1"
## blob	"blob"	"1.2.3"
## brew	"brew"	"1.0-8"
## brio	"brio"	"1.1.3"
## broom	"broom"	"1.0.2"
## broom.mixed	"broom.mixed"	"0.2.9.4"
## bslib	"bslib"	"0.4.2"
## bumphunter	"bumphunter"	"1.40.0"
## BumpyMatrix	"BumpyMatrix"	"1.6.0"
## cachem	"cachem"	"1.0.6"
## callr	"callr"	"3.7.3"
## car	"car"	"3.1-1"
## carData	"carData"	"3.0-5"
## caret	"caret"	"6.0-93"

2/23, 11:23/1111	250510_1310	dio_sex_bias_drags_i
## Category	"Category"	"2.64.0"
## caTools	"caTools"	"1.18.2"
## celestial	"celestial"	"1.4.6"
## cellranger	"cellranger"	"1.1.0"
## checkmate	"checkmate"	"2.1.0"
## ChemmineR	"ChemmineR"	"3.50.0"
## chron	"chron"	"2.3-58"
## circlize	"circlize"	"0.4.15"
## classInt	"classInt"	"0.4-8"
## cli	"cli"	"3.5.0"
## clipr	"clipr"	"0.8.0"
## clock	"clock"	"0.6.1"
## clue	"clue"	"0.3-63"
## clusterProfiler	"clusterProfiler"	"4.6.0"
## coda	"coda"	"0.19-4"
## CoGAPS	"CoGAPS"	"3.18.0"
## cogena	"cogena"	"1.32.0"
## colorspace	"colorspace"	"2.0-3"
## combinat	"combinat"	"0.0-8"
## commonmark	"commonmark"	"1.8.1"
## ComplexHeatmap	"ComplexHeatmap"	"2.14.0"
## ComplexUpset	"ComplexUpset"	"1.3.3"
## conflicted	"conflicted"	"1.1.0"
## coop	"coop"	"0.6-3"
## CoreGx	"CoreGx"	"2.2.0"
## corrplot	"corrplot"	"0.92"
## cowplot	"cowplot"	"1.1.1"
## cowplot ## cpp11	"cpp11"	"0.4.3"
## crayon	"crayon"	"1.5.2"
## credentials	"credentials"	"1.3.2"
## crosstalk	"crosstalk"	"1.2.0"
## curl	"curl"	"4.3.3"
## customCMPdb	"customCMPdb"	"1.8.0"
## data.table	"data.table"	"1.14.6"
## data.table ## datawizard	"datawizard"	"0.6.5"
## datawizaid	"DBI"	"1.1.3"
## dbplyr		"2.2.1"
	"dbplyr"	"0.24.0"
## DelayedArray	"DelayedArray" "DelayedMatrixStats"	"1.20.0"
## DelayedMatrixStats	<u>=</u>	
## dendextend	"dendextend"	"1.16.0"
## DEoptimR	"DEoptimR"	"1.0-11"
## desc	"desc"	"1.4.2"
## DESeq2	"DESeq2"	"1.38.2"
## devtools	"devtools"	"2.4.5"
## DEXSeq	"DEXSeq"	"1.44.0"
## dials	"dials"	"1.1.0"
## DiceDesign	"DiceDesign"	"1.9"
## diffobj	"diffobj"	"0.3.5"
## digest	"digest"	"0.6.31"
## discrim	"discrim"	"1.0.0"
## docopt	"docopt"	"0.7.1"
## doParallel	"doParallel"	"1.0.17"

## doRNG	dorng"	"1.8.3"
## DOSE	"DOSE"	"3.24.2"
## dotwhisker	"dotwhisker"	"0.7.4"
## downlit	"downlit"	"0.4.2"
## downloader	"downloader"	"0.4"
## downroader ## dplyr	"dplyr"	"1.0.10"
## drugbankR	"drugbankR"	"1.5"
## DT	"DT"	"0.26"
## dtplyr	"dtplyr"	"1.2.2"
## e1071	"e1071"	"1.7-12"
## e10/1 ## earth	"earth"	"5.3.1"
## edgeR	"edgeR"	"3.40.1"
## ellipse	"ellipse"	"0.4.3"
## ellipse ## ellipsis	"ellipsis"	"0.3.2"
## emmeans	"emmeans"	"1.8.3"
## enrichplot	"enrichplot"	"1.18.3"
## EnsDb.Hsapiens.v75	"EnsDb.Hsapiens.v75"	"2.99.0"
## ensembldb	"ensembldb"	"2.22.0"
## ensemblub ## estimability	"estimability"	"1.4.1"
## etrunct	"etrunct"	"0.1"
## evaluate	"evaluate"	"0.19"
## ExperimentHub	"ExperimentHub"	"2.6.0"
## factoextra	"factoextra"	"1.0.7"
## FactoMineR	"FactoMineR"	"2.7"
## fansi	"fansi"	"1.0.3"
## farver	"farver"	"2.1.1"
## fastcluster	"fastcluster"	"1.2.3"
## fastmap	"fastmap"	"1.1.0"
## fastmatch	"fastmatch"	"1.1-3"
## fgsea	"fgsea"	"1.24.0"
## filelock	"filelock"	"1.0.2"
## flashClust	"flashClust"	"1.01-2"
## fmcsR	"fmcsR"	"1.40.0"
## fontawesome	"fontawesome"	"0.4.0"
## forcats	"forcats"	"0.5.2"
## foreach	"foreach"	"1.5.2"
## formatR	"formatR"	"1.13"
## Formula	"Formula"	"1.2-4"
## fs	"fs"	"1.5.2"
## furrr	"furrr"	"0.3.1"
## futile.logger	"futile.logger"	"1.4.3"
## futile.options	"futile.options"	"1.0.1"
## future	"future"	"1.30.0"
## future.apply	"future.apply"	"1.10.0"
## gargle	"gargle"	"1.2.1"
## gbm	"gbm"	"2.1.8.1"
## genefilter	"genefilter"	"1.80.2"
## geneplotter	"geneplotter"	"1.76.0"
## generics	"generics"	"0.1.3"
## GenomeInfoDb	"GenomeInfoDb"	"1.34.4"
## GenomeInfoDbData	"GenomeInfoDbData"	"1.2.9"
## GenomicAlignments	"GenomicAlignments"	"1.34.0"
	3	-

	-	8 _
## GenomicFeatures	"GenomicFeatures"	"1.50.3"
## GenomicRanges	"GenomicRanges"	"1.50.2"
## GEOquery	"GEOquery"	"2.66.0"
## gert	"gert"	"1.9.1"
## GetoptLong	"GetoptLong"	"1.0.5"
## ggalluvial	"ggalluvial"	"0.12.3"
## ggdendro	"ggdendro"	"0.1.23"
## ggforce	"ggforce"	"0.4.1"
## ggfun	"ggfun"	"0.0.9"
## ggnewscale	"ggnewscale"	"0.4.8"
## ggplot2	"ggplot2"	"3.4.0"
## ggplotify	"ggplotify"	"0.1.0"
## ggpubr	"ggpubr"	"0.5.0"
## ggraph	"ggraph"	"2.1.0"
## ggrepel	"ggrepel"	"0.9.2"
## ggsci	"ggsci"	"2.9"
## ggsignif	"ggsignif"	"0.6.4"
## ggstance	"ggstance"	"0.3.6"
## ggtree	"ggtree"	"3.6.2"
## gh	"gh"	"1.3.1"
## gitcreds	"gitcreds"	"0.1.2"
## glmnet	"glmnet"	"4.1-6"
## GlobalOptions	"GlobalOptions"	"0.1.2"
## globals	"globals"	"0.16.2"
## glue	"glue"	"1.6.2"
## GO.db	"GO.db"	"3.16.0"
## googledrive	"googledrive"	"2.0.0"
## googlesheets4	"googlesheets4"	"1.0.1"
## GOSemSim	"GOSemSim"	"2.24.0"
## GOstats	"GOstats"	"2.64.0"
## gower	"gower"	"1.0.1"
## GPfit	"GPfit"	"1.0-8"
## gplots	"gplots"	"3.1.3"
## gprofiler2	"gprofiler2"	"0.2.1"
## graph	"graph"	"1.76.0"
## graphlayouts	"graphlayouts"	"0.8.4"
## gridBase	"gridBase"	"0.4-7"
## gridExtra	"gridExtra"	"2.3"
## gridGraphics	"gridGraphics"	"0.5-1"
## GSEABase	"GSEABase"	"1.60.0"
## gson	"gson"	"0.0.9"
## gsubfn	"gsubfn"	"0.7"
## gtable	"gtable"	"0.3.1"
## gtools	"gtools"	"3.9.4"
## hardhat	"hardhat"	"1.2.0"
## hash	"hash"	"2.2.6.2"
## haven	"haven"	"2.5.1"
## HDF5Array	"HDF5Array"	"1.26.0"
## HDO.db	"HDO.db"	"0.99.1"
## here	"here"	"1.0.1"
## hexbin	"hexbin"	"1.28.2"
## highr	"highr"	"0.10"

_,	23, 11	.23 / 1111	250510_1studio	_sex_olas_arags_n
l	##	hms	"hms"	"1.1.2"
	##	htmltools	"htmltools"	"0.5.4"
	##	htmlwidgets	"htmlwidgets"	"1.6.0"
	##	httpuv	"httpuv"	"1.6.7"
	##	httr	"httr"	"1.4.4"
	##	hwriter	"hwriter"	"1.3.2.1"
	##	ids	"ids"	"1.0.1"
	##	igraph	"igraph"	"1.3.5"
	##	illuminaio	"illuminaio"	"0.40.0"
	##	infer	"infer"	"1.0.4"
	##	ini	"ini"	"0.3.1"
	##	insight	"insight"	"0.18.8"
	##	$\verb interactiveDisplayBase \\$		
	##	inum	"inum"	"1.0-4"
		invgamma	"invgamma"	"1.1"
	##	ipred	"ipred"	"0.9-13"
		IRanges	"IRanges"	"2.32.0"
	##	IRdisplay	"IRdisplay"	"1.1"
	##	IRkernel	"IRkernel"	"1.3.1"
	##	irlba	"irlba"	"2.3.5.1"
	##	isoband	"isoband"	"0.2.7"
	##	iterators	"iterators"	"1.0.14"
	##	jquerylib	"jquerylib"	"0.1.4"
	##	jsonlite	"jsonlite"	"1.8.4"
	##	KEGGREST	"KEGGREST"	"1.38.0"
	##	kernlab	"kernlab"	"0.9-31"
		klaR	"klaR"	"1.7-1"
		knitr	"knitr"	"1.41"
		kohonen	"kohonen"	"3.0.11"
		labeling	"labeling"	"0.4.2"
		labelled	"labelled"	"2.10.0"
		lambda.r	"lambda.r"	"1.2.4"
		later	"later"	"1.3.0"
		lava	"lava"	"1.7.0"
		lazyeval	"lazyeval"	"0.2.2"
		leaps	"leaps"	"3.1"
		lhs	"lhs"	"1.1.6"
		libcoin	"libcoin"	"1.0-9"
		LiblineaR	"LiblineaR"	"2.10-22"
		lifecycle	"lifecycle"	"1.0.3"
		limma	"limma"	"3.54.0"
		listenv	"listenv"	"0.9.0"
		littler	"littler"	"0.3.17"
		lme4	"lme4"	"1.1-31"
		locfit	"locfit"	"1.5-9.7"
		lsa	"lsa"	"0.73.3"
		lubridate	"lubridate"	"1.9.0"
		magicaxis	"magicaxis"	"2.2.14"
		magrittr	"magrittr"	"2.0.3"
		mapproj	"mapproj"	"1.2.9" "3.4.1"
		maps margins	"maps" "margins"	"0.3.26"
	<i>π1</i>	шат утпа	margina	0.3.20
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2/23, 11.23/1111	250510_1stad	io_sex_blas_drugs_info
## markdown	"markdown"	"1.4"
## marray	"marray"	"1.76.0"
## mashr	"mashr"	"0.2.69"
## MASS	"MASS"	"7.3-58.1"
## matrixcalc	"matrixcalc"	"1.0-6"
## MatrixGenerics	"MatrixGenerics"	"1.10.0"
## MatrixModels	"MatrixModels"	"0.5-1"
## matrixStats	"matrixStats"	"0.63.0"
## mclust	"mclust"	"6.0.0"
## memoise	"memoise"	"2.0.1"
## mime	"mime"	"0.12"
## minfi	"minfi"	"1.44.0"
## miniUI	"miniUI"	"0.1.1.1"
## minqa	"minqa"	"1.2.5"
## mixsqp	"mixsqp"	"0.3-48"
## modeldata	"modeldata"	"1.0.1"
## modelenv	"modelenv"	"0.1.0"
## ModelMetrics	"ModelMetrics"	"1.2.2.2"
## modelr	"modelr"	"0.1.10"
## multcompView	"multcompView"	"0.1-8"
## MultiAssayExperiment	"MultiAssayExperiment"	"1.24.0"
## multtest	"multtest"	"2.54.0"
## munsell	"munsell"	"0.5.0"
## mvtnorm	"mvtnorm"	"1.1-3"
## naivebayes	"naivebayes"	"0.9.7"
## netZooR	"netZooR"	"1.2.1"
## NISTunits	"NISTunits"	"1.0.1"
## nloptr	"nloptr"	"2.0.3"
## NMF	"NMF"	"0.25"
## nnet	"nnet"	"7.3-18"
## nor1mix	"nor1mix"	"1.3-0"
## numDeriv	"numDeriv"	"2016.8-1.1"
## openssl	"openssl"	"2.0.5"
## org.Hs.eg.db	"org.Hs.eg.db"	"3.16.0"
## pamr	"pamr"	"1.56.1"
## pandaR	"pandaR"	"1.30.0"
## parallelly	"parallelly"	"1.33.0"
## parameters	"parameters"	"0.20.0"
## parsnip	"parsnip"	"1.0.3"
## partykit	"partykit"	"1.2-16"
## pasilla	"pasilla"	"1.26.0"
## patchwork	"patchwork"	"1.1.2"
## pbdZMQ	"pbdZMQ"	"0.3-8"
## pbkrtest	"pbkrtest"	"0.5.1"
## penalized	"penalized"	"0.9-52"
## permute	"permute"	"0.9-7"
## PharmacoGx	"PharmacoGx"	"3.2.0"
## pheatmap	"pheatmap"	"1.0.12"
## piano	"piano"	"2.14.0"
## pillar	"pillar"	"1.8.1"
## pkgbuild	"pkgbuild"	"1.3.1"
## pkgconfig	"pkgconfig"	"2.0.3"

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## pkgdown	"pkgdown"	"2.0.6"
## pkgload	"pkgload"	"1.3.1"
## PLIER	"PLIER"	"0.99.0"
## plogr	"plogr"	"0.2.0"
## plotly	"plotly"	"4.10.1"
## plotmo	"plotmo"	"3.6.2"
## plotrix	"plotrix"	"3.8-2"
## plyr	"plyr"	"1.8.8"
## png	"png"	"0.1-8"
## polyclip	"polyclip"	"1.10-4"
## polynom	"polynom"	"1.4-1"
## pracma	"pracma"	"2.4.2"
## praise	"praise"	"1.0.0"
## prediction	"prediction"	"0.3.14"
## preprocessCore	"preprocessCore"	"1.60.1"
## prettyunits	"prettyunits"	"1.1.1"
## pROC	"pROC"	"1.18.0"
## processx	"processx"	"3.8.0"
## prodlim	"prodlim"	"2019.11.13"
## profmem	"profmem"	"0.6.0"
## profvis	"profvis"	"0.3.7"
## progress	"progress"	"1.2.2"
## progressr	"progressr"	"0.12.0"
## projectR	"projectR"	"1.14.0"
## ProliferativeIndex	"ProliferativeIndex"	"1.0.1"
## promises	"promises"	"1.2.0.1"
## ProtGenerics	"ProtGenerics"	"1.30.0"
## proto	"proto"	"1.0.0"
## proxy	"proxy"	"0.4-27"
## ps	"ps"	"1.7.2"
## purrr	"purrr"	"1.0.0"
## quadprog	"quadprog"	"1.5-8"
## quantreg	"quantreg"	"5.94"
## quantro	"quantro"	"1.32.0"
## questionr	"questionr"	"0.7.7"
## qvalue	- "qvalue"	"2.30.0"
## R.cache	"R.cache"	"0.16.0"
## R.methodsS3	"R.methodsS3"	"1.8.2"
## R.00	"R.00"	"1.25.0"
## R.utils	"R.utils"	"2.12.2"
## R6	"R6"	"2.5.1"
## ragg	"ragg"	"1.2.4"
## randomForest	"randomForest"	"4.7-1.1"
## ranger	"ranger"	"0.14.1"
## RANN	"RANN"	"2.6.1"
## rappdirs	"rappdirs"	"0.3.3"
## RBGL	"RBGL"	"1.74.0"
## rcmdcheck	"rcmdcheck"	"1.4.0"
## RColorBrewer	"RColorBrewer"	"1.1-3"
## Rcpp	"Rcpp"	"1.0.9"
## RcppArmadillo	"RcppArmadillo"	"0.11.4.2.1"
## RcppEigen	"RcppEigen"	"0.3.3.9.3"
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## RcppGSL	"RcppGSL"	"0.3.12"
## RcppTOML	"RcppTOML"	"0.1.7"
## RCurl	"RCurl"	"1.98-1.9"
## RCy3	"RCy3"	"2.18.0"
## reactome.db	"reactome.db"	"1.82.0"
## readr	"readr"	"2.1.3"
## readxl	"readxl"	"1.4.1"
## recipes	"recipes"	"1.0.3"
## recount3	"recount3"	"1.8.0"
## registry	"registry"	"0.5-1"
## relations	"relations"	"0.6-12"
## rematch	"rematch"	"1.0.1"
## rematch2	"rematch2"	"2.1.2"
## remotes	"remotes"	"2.4.2"
## repr	"repr"	"1.1.4"
## reprex	"reprex"	"2.0.2"
## reshape	"reshape"	"0.8.9"
## reshape2	"reshape2"	"1.4.4"
## restfulr	"restfulr"	"0.0.15"
## reticulate	"reticulate"	"1.26"
## Rgraphviz	"Rgraphviz"	"2.42.0"
## rhdf5	"rhdf5"	"2.42.0"
## rhdf5filters	"rhdf5filters"	"1.10.0"
## Rhdf5lib	"Rhdf5lib"	"1.20.0"
## Rhtslib	"Rhtslib"	"2.0.0"
## rJava	"rJava"	"1.0-6"
## rjson	"rjson"	"0.2.21"
## RJSONIO	"RJSONIO"	"1.3-1.6"
## rlang	"rlang"	"1.0.6"
## rmarkdown	"rmarkdown"	"2.19"
## rmeta	"rmeta"	"3.0"
## rngtools	"rngtools"	"1.5.2"
## robustbase	"robustbase"	"0.95-0"
## ROCR	"ROCR"	"1.0-11"
## roxygen2	"roxygen2"	"7.2.1"
## rpart	"rpart"	"4.1.19"
## rprojroot	"rprojroot"	"2.0.3"
## rsample	"rsample"	"1.1.1"
## Rsamtools	"Rsamtools"	"2.14.0"
## RSQLite	"RSQLite"	"2.2.20"
## rstatix	"rstatix"	"0.7.1"
## rstudioapi	"rstudioapi"	"0.14"
## rsvd	"rsvd"	"1.0.5"
## rsvg	"rsvg"	"2.4.0"
## rtracklayer	"rtracklayer"	"1.58.0"
## RUnit	"RUnit"	"0.4.32"
## rversions	"rversions"	"2.1.2"
## rvest	"rvest"	"1.0.3"
## RWeka	"RWeka"	"0.4-44"
## RWekajars ## S4Vectors	"RWekajars" "S4Vectors"	"3.9.3-2" "0.36.1"
		"0.4.4"
## sass	"sass"	0.4.4

,	_	
## scales	"scales"	"1.2.1"
## scatterpie	"scatterpie"	"0.1.8"
## scatterplot3d	"scatterplot3d"	"0.3-42"
## scrime	"scrime"	"1.3.5"
## selectr	"selectr"	"0.4-2"
## sessioninfo	"sessioninfo"	"1.2.2"
## sets	"sets"	"1.0-21"
## shadowtext	"shadowtext"	"0.1.2"
## shape	"shape"	"1.4.6"
## shiny	"shiny"	"1.7.4"
## shinydashboard	"shinydashboard"	"0.7.2"
## shinyjs	"shinyjs"	"2.1.0"
## siggenes	"siggenes"	"1.72.0"
## signatureSearch	"signatureSearch"	"1.11.1"
## signatureSearchData	"signatureSearchData"	"1.12.0"
## SingleCellExperiment	"SingleCellExperiment"	"1.20.0"
## skimr	"skimr"	"2.1.5"
## slam	"slam"	"0.1-50"
## slider	"slider"	"0.3.0"
## sm	"sm"	"2.2-5.7.1"
## snow	"snow"	"0.4-4"
## SnowballC	"SnowballC"	"0.7.0"
## softImpute	"softImpute"	"1.4-1"
## sourcetools	"sourcetools"	"0.1.7"
## SparseM	"SparseM"	"1.81"
## sparseMatrixStats	"sparseMatrixStats"	"1.10.0"
## sqldf	"sqldf"	"0.4-11"
## SQUAREM	"SQUAREM"	"2021.1"
## statmod	"statmod"	"1.4.37"
## STRINGdb	"STRINGdb"	"2.10.0"
## stringi	"stringi"	"1.7.8"
## stringr	"stringr"	"1.5.0"
## styler	"styler"	"1.8.1"
## SummarizedExperiment	"SummarizedExperiment"	"1.28.0"
## sys	"sys"	"3.4.1"
## systemfonts	"systemfonts"	"1.0.4"
## TeachingDemos	"TeachingDemos"	"2.12"
## testthat	"testthat"	"3.1.5"
## textshaping	"textshaping"	"0.3.6"
## TFEA.ChIP	"TFEA.ChIP"	"1.18.0"
## tibble	"tibble"	"3.1.8"
## tidygraph	"tidygraph"	"1.2.2"
## tidymodels	"tidymodels"	"1.0.0"
## tidyr	"tidyr"	"1.2.1"
## tidyselect	"tidyselect"	"1.2.0"
## tidytree	"tidytree"	"0.4.2"
## tidyverse	"tidyverse"	"1.3.2"
## timechange	"timechange"	"0.1.1"
## timeDate	"timeDate"	"4021.107"
## tinytex	"tinytex"	"0.43"
## topGO	"topGO"	"2.50.0"
## treeio	"treeio"	"1.22.0"

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## truncnorm	"truncnorm"	"1.0-8"
## tune	"tune"	"1.0.1"
## tweenr	"tweenr"	"2.0.2"
## tzdb	"tzdb"	"0.3.0"
## uchardet	"uchardet"	"1.1.1"
## urlchecker	"urlchecker"	"1.0.1"
## usethis	"usethis"	"2.1.6"
## utf8	"utf8"	"1.2.2"
## uuid	"uuid"	"1.1-0"
## vctrs	"vctrs"	"0.5.1"
## vegan	"vegan"	"2.6-4"
## VennDiagram	"VennDiagram"	"1.7.3"
## viridis	"viridis"	"0.6.2"
## viridisLite	"viridisLite"	"0.4.1"
## visNetwork	"visNetwork"	"2.1.2"
## vroom	"vroom"	"1.6.0"
## waldo	"waldo"	"0.4.0"
## warp	"warp"	"0.2.0"
## whisker	"whisker"	"0.4"
## withr	"withr"	"2.5.0"
## workflows	"workflows"	"1.1.2"
## workflowsets	"workflowsets"	"1.0.0"
## xfun	"xfun"	"0.36"
## xgboost	"xgboost"	"1.6.0.1"
## XML	"XML"	"3.99-0.13"
## xml2	"xml2"	"1.3.3"
## xopen	"xopen"	"1.0.0"
## xtable	"xtable"	"1.8-4"
## XVector	"XVector"	"0.38.0"
## yaml	"yaml"	"2.3.6"
## yardstick	"yardstick"	"1.1.0"
## yarn	"yarn"	"1.24.0"
## yulab.utils	"yulab.utils"	"0.0.6"
- ## zip	zip"	"2.2.2"
## zlibbioc	"zlibbioc"	"1.44.0"
## base	"base"	"4.2.2"
## boot	"boot"	"1.3-28"
## class	"class"	"7.3-20"
## cluster	"cluster"	"2.1.4"
## codetools	"codetools"	"0.2-18"
## compiler	"compiler"	"4.2.2"
## datasets	"datasets"	"4.2.2"
## foreign	"foreign"	"0.8-83"
## graphics	"graphics"	"4.2.2"
## grDevices	"grDevices"	"4.2.2"
## grid	"grid"	"4.2.2"
## KernSmooth	"KernSmooth"	"2.23-20"
## lattice	"lattice"	"0.20-45"
## MASS	"MASS"	"7.3-58.1"
## Matrix	"Matrix"	"1.5-1"
## methods	"methods"	"4.2.2"
## mgcv	"mgcv"	"1.8-41"

## nlme	"nlme"	"3.1-160"	
## nnet	"nnet"	"7.3-18"	
## parallel	"parallel"	"4.2.2"	
## rpart	"rpart"	"4.1.19"	
## spatial	"spatial"	"7.3-15"	
## splines	"splines"	"4.2.2"	
## stats	"stats"	"4.2.2"	
## stats4	"stats4"	"4.2.2"	
## survival	"survival"	"3.4-0"	
## tcltk	"tcltk"	"4.2.2"	
## tools	"tools"	"4.2.2"	
## utils	"utils"	"4.2.2"	

230510_rstudio_sex_bias_drugs_singularity

Jennifer Fisher

05/10/2023

```
System which operations were done on:
cheaha

GitHub Repo:
230321_JLF_Sex_bias_adverse_events

Directory of operations:
/data/project/lasseigne_lab/JLF_scratch/230321_JLF_Sex_bias_adverse_events

GitHub Repo:
230321_JLF_Sex_bias_adverse_events

Docker:
rstudio_sex_bias_drugs (singularity)
```

```
sessionInfo()
```

```
## R version 4.2.2 (2022-10-31)
## Platform: x86 64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 22.04.1 LTS
##
## Matrix products: default
          /usr/lib/x86 64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86 64-linux-gnu/openblas-pthread/libopenblasp-r0.3.20.so
##
## locale:
## [1] LC_CTYPE=en_US.UTF-8
                                  LC NUMERIC=C
## [3] LC TIME=en US.UTF-8
                                  LC COLLATE=en US.UTF-8
## [5] LC_MONETARY=en_US.UTF-8
                                  LC MESSAGES=en US.UTF-8
  [7] LC PAPER=en US.UTF-8
                                  LC NAME=C
## [9] LC ADDRESS=C
                                  LC TELEPHONE=C
## [11] LC MEASUREMENT=en US.UTF-8 LC IDENTIFICATION=C
## attached base packages:
## [1] stats
                graphics grDevices utils
                                              datasets methods
                                                                  base
##
## loaded via a namespace (and not attached):
## [1] digest 0.6.31
                       R6 2.5.1
                                       lifecycle 1.0.3 jsonlite 1.8.4
## [5] magrittr 2.0.3 evaluate 0.19 stringi 1.7.8
                                                       cachem 1.0.6
## [9] rlang_1.0.6
                       cli 3.5.0
                                       rstudioapi_0.14 jquerylib_0.1.4
## [13] bslib 0.4.2
                       vctrs 0.5.1
                                       rmarkdown 2.19 tools 4.2.2
## [17] stringr 1.5.0
                       glue 1.6.2
                                       xfun 0.36
                                                       yaml 2.3.6
## [21] fastmap_1.1.0
                       compiler_4.2.2 htmltools_0.5.4 knitr_1.41
## [25] sass 0.4.4
```

Listing packages
installed.packages()[,c(1,3)]

##	Package	Version
## abind	"abind"	"1.4-5"
## affy	"affy"	"1.76.0"
## affyio	"affyio"	"1.68.0"
## amap	"amap"	"0.8-19"
## annotate	"annotate"	"1.76.0"
## AnnotationDbi	"AnnotationDbi"	"1.60.0"
## AnnotationFilter	"AnnotationFilter"	"1.22.0"
## AnnotationForge	"AnnotationForge"	"1.40.0"
## AnnotationHub	"AnnotationHub"	"3.6.0"
## apcluster	"apcluster"	"1.4.10"
## ape	"ape"	"5.6-2"
## aplot	"aplot"	"0.1.9"
## ashr	"ashr"	"2.2-54"
## askpass	"askpass"	"1.1"
## assertthat	"assertthat"	"0.2.1"
## backports	"backports"	"1.4.1"
## base64	"base64"	"2.0.1"
## base64enc	"base64enc"	"0.1-3"
## base64url	"base64url"	"1.4"
## bayestestR	"bayestestR"	"0.13.0"
## beanplot	"beanplot"	"1.3.1"
## bench	"bench"	"1.1.2"
## BgeeDB	"BgeeDB"	"2.24.0"
## BH	"BH"	"1.78.0-0"
## Biobase	"Biobase"	"2.58.0"
## BiocBaseUtils	"BiocBaseUtils"	"1.0.0"
## BiocFileCache	"BiocFileCache"	"2.6.0"
## BiocGenerics	"BiocGenerics"	"0.44.0"
## BiocIO	"BiocIO"	"1.8.0"
## BiocManager	"BiocManager"	"1.30.19"
## BiocParallel	"BiocParallel"	"1.32.5"
## BiocVersion	"BiocVersion"	"3.16.0"
## biomaRt	"biomaRt"	"2.54.0"
## Biostrings	"Biostrings"	"2.66.0"
## bit	"bit"	"4.0.5"
## bit64	"bit64"	"4.0.5" "1.0-7"
## bitops	"bitops"	
## biwt ## blob	"biwt" "blob"	"1.0.1" "1.2.3"
## brew	"brew"	"1.0-8"
## brew ## brio	"brio"	"1.1.3"
## broom	"broom"	"1.0.2"
## broom.mixed	"broom.mixed"	"0.2.9.4"
## bslib	"bslib"	"0.4.2"
## bumphunter	"bumphunter"	"1.40.0"
## BumpyMatrix	"BumpyMatrix"	"1.6.0"
## cachem	"cachem"	"1.0.6"
## callr	"callr"	"3.7.3"
## car	"car"	"3.1-1"
## carData	"carData"	"3.0-5"
## caret	"caret"	"6.0-93"
## Category	"Category"	"2.64.0"
## caTools	"caTools"	"1.18.2"

/23, 1	1:23 AM	230510_rstudio	_sex_bias_drug
##	celestial	"celestial"	"1.4.6"
##	cellranger	"cellranger"	"1.1.0"
##	checkmate	"checkmate"	"2.1.0"
##	ChemmineR	"ChemmineR"	"3.50.0"
	chron	"chron"	"2.3-58"
	circlize	"circlize"	"0.4.15"
	classInt	"classInt"	"0.4-8"
	cli	"cli"	"3.5.0"
	clipr	"clipr"	"0.8.0"
	clock	"clock"	"0.6.1"
	clue	"clue"	"0.3-63"
	clusterProfiler	"clusterProfiler"	"4.6.0"
	coda	"coda"	"0.19-4"
	COGAPS	"COGAPS"	"3.18.0"
	cogena	"cogena"	"1.32.0"
	colorspace	"colorspace"	"2.0-3"
	combinat	"combinat"	"0.0-8"
	commonmark	"commonmark"	"1.8.1"
	ComplexHeatmap	"ComplexHeatmap"	"2.14.0"
	ComplexUpset	"ComplexUpset"	"1.3.3"
	conflicted	"conflicted"	"1.1.0"
	coop	"coop"	"0.6-3"
	CoreGx	"CoreGx"	"2.2.0" "0.92"
	corrplot	"corrplot"	"1.1.1"
	cowplot cpp11	"cowplot" "cpp11"	"0.4.3"
	crayon	"crayon"	"1.5.2"
	credentials	"credentials"	"1.3.2"
	crosstalk	"crosstalk"	"1.2.0"
	curl	"curl"	"4.3.3"
	customCMPdb	"customCMPdb"	"1.8.0"
	data.table	"data.table"	"1.14.6"
	datawizard	"datawizard"	"0.6.5"
##	DBI	"DBI"	"1.1.3"
##	dbplyr	"dbplyr"	"2.2.1"
	DelayedArray	"DelayedArray"	"0.24.0"
	DelayedMatrixStats	"DelayedMatrixStats"	"1.20.0"
##	dendextend	"dendextend"	"1.16.0"
##	DEoptimR	"DEoptimR"	"1.0-11"
##	desc	"desc"	"1.4.2"
##	DESeq2	"DESeq2"	"1.38.2"
##	devtools	"devtools"	"2.4.5"
##	DEXSeq	"DEXSeq"	"1.44.0"
##	dials	"dials"	"1.1.0"
	DiceDesign	"DiceDesign"	"1.9"
	diffobj	"diffobj"	"0.3.5"
	digest	"digest"	"0.6.31"
	discrim	"discrim"	"1.0.0"
	docopt	"docopt"	"0.7.1"
	doParallel	"doParallel"	"1.0.17"
	doRNG	"doRNG"	"1.8.3"
	DOSE	"DOSE"	"3.24.2"
	dotwhisker	"dotwhisker"	"0.7.4"
	downlit	"downlit"	"0.4.2"
##	downloader	"downloader"	"0.4"

2/23, 11.23/111	250510_1stac	iio_sex_bias_drags
## dplyr	"dplyr"	"1.0.10"
## drugbankR	"drugbankR"	"1.5"
## DT	"DT"	"0.26"
## dtplyr	"dtplyr"	"1.2.2"
## e1071	"e1071"	"1.7-12"
## earth	"earth"	"5.3.1"
## edgeR	"edgeR"	"3.40.1"
## ellipse	"ellipse"	"0.4.3"
## ellipsis	"ellipsis"	"0.3.2"
## emmeans	"emmeans"	"1.8.3"
## enrichplot	"enrichplot"	"1.18.3"
## EnsDb.Hsapiens.v75	"EnsDb.Hsapiens.v75"	"2.99.0"
## ensembldb	"ensembldb"	"2.22.0"
## estimability	"estimability"	"1.4.1"
## etrunct	"etrunct"	"0.1"
## evaluate	"evaluate"	"0.19"
## ExperimentHub	"ExperimentHub"	"2.6.0"
## factoextra	"factoextra"	"1.0.7"
## FactoMineR	"FactoMineR"	"2.7"
## fansi	"fansi"	"1.0.3"
## farver	"farver"	"2.1.1"
## fastcluster	"fastcluster"	"1.2.3"
## fastmap	"fastmap"	"1.1.0"
## fastmatch	"fastmatch"	"1.1-3"
## fgsea	"fgsea"	"1.24.0"
## filelock	"filelock"	"1.0.2"
## flashClust	"flashClust"	"1.01-2"
## fmcsR	"fmcsR"	"1.40.0"
## fontawesome	"fontawesome"	"0.4.0"
## forcats	"forcats"	"0.5.2"
## foreach	"foreach"	"1.5.2"
## formatR	"formatR"	"1.13"
## Formula	"Formula"	"1.2-4"
## fs	"fs"	"1.5.2"
## furrr	"furrr"	"0.3.1"
## futile.logger	"futile.logger"	"1.4.3"
## futile.options	"futile.options"	"1.0.1"
## future	"future"	"1.30.0"
## future.apply	"future.apply"	"1.10.0"
## gargle	"gargle"	"1.2.1"
## gbm	"gbm"	"2.1.8.1"
## genefilter	"genefilter"	"1.80.2"
## geneplotter	"geneplotter"	"1.76.0"
## generics	"generics"	"0.1.3"
## GenomeInfoDb	"GenomeInfoDb"	"1.34.4"
## GenomeInfoDbData	"GenomeInfoDbData"	"1.2.9"
## GenomicAlignments	"GenomicAlignments"	"1.34.0"
## GenomicFeatures	"GenomicFeatures"	"1.50.3"
## GenomicRanges	"GenomicRanges"	"1.50.2"
## GEOquery	"GEOquery"	"2.66.0"
## gert	"gert"	"1.9.1"
## GetoptLong	"GetoptLong"	"1.0.5"
## ggalluvial	"ggalluvial"	"0.12.3"
## ggdendro	"ggdendro"	"0.1.23"
## ggforce	"ggforce"	"0.4.1"

2/25, 11:25 AM		250510_fstudio_sex_blas_drugs_
## ggfun	"ggfun"	"0.0.9"
## ggnewscale	"ggnewscale"	"0.4.8"
## ggplot2	"ggplot2"	"3.4.0"
## ggplotify	"ggplotify"	"0.1.0"
## ggpubr	"ggpubr"	"0.5.0"
## ggraph	"ggraph"	"2.1.0"
## ggrepel	"ggrepel"	"0.9.2"
## ggsci	"ggsci"	"2.9"
## ggsignif	"ggsignif"	"0.6.4"
## ggstance	"ggstance"	"0.3.6"
## ggtree	"ggtree"	"3.6.2"
## gh	"gh"	"1.3.1"
## gitcreds	"gitcreds"	"0.1.2"
## glmnet	"glmnet"	"4.1-6"
## GlobalOptions	"GlobalOptions"	"0.1.2"
## globals	"globals"	"0.16.2"
## glue	"glue"	"1.6.2"
## GO.db	"GO.db"	"3.16.0"
## googledrive	"googledrive"	"2.0.0"
## googlesheets4	"googlesheets4"	"1.0.1"
## GOSemSim	"GOSemSim"	"2.24.0"
## GOstats	"GOstats"	"2.64.0"
## gower	"gower"	"1.0.1"
## GPfit	"GPfit"	"1.0-8"
## gplots	"gplots"	"3.1.3"
## gprofiler2	"gprofiler2"	"0.2.1"
## graph	"graph"	"1.76.0"
## graphlayouts	"graphlayouts"	"0.8.4"
## gridBase	"gridBase"	"0.4-7"
## gridExtra	"gridExtra"	"2.3"
## gridGraphics	"gridGraphics"	"0.5-1"
## GSEABase	"GSEABase"	"1.60.0"
## gson	"gson"	"0.0.9"
## gsubfn	"gsubfn"	"0.7"
## gtable	"gtable"	"0.3.1"
## gtools	"gtools"	"3.9.4"
## hardhat	"hardhat"	"1.2.0"
## hash	"hash"	"2.2.6.2"
## haven	"haven"	"2.5.1"
## HDF5Array	"HDF5Array"	"1.26.0"
## HDO.db	"HDO.db"	"0.99.1"
## here	"here"	"1.0.1"
## hexbin	"hexbin"	"1.28.2"
## highr	"highr"	"0.10"
## hms	"hms"	"1.1.2"
## htmltools	"htmltools"	"0.5.4"
## htmlwidgets	"htmlwidgets"	"1.6.0"
## httpuv	"httpuv"	"1.6.7"
## httr	"httr"	"1.4.4"
## hwriter	"hwriter"	"1.3.2.1"
## ids	"ids"	"1.0.1"
## igraph	"igraph"	"1.3.5"
<pre>## illuminaio ## infer</pre>	"illuminaio" "infer"	"0.40.0"
## inier ## ini	"ini"	"1.0.4" "0.3.1"
<i>ππ</i> 1111	TIIT	0.3.1

_	23, 11	1:25 AIVI	250510_Istudio	_sex_blas_drugs_s
	##	insight	"insight"	"0.18.8"
l	##	$\verb interactiveDisplayBase \\$	"interactiveDisplayBase"	"1.36.0"
	##	inum	"inum"	"1.0-4"
l	##	invgamma	"invgamma"	"1.1"
l	##	ipred	"ipred"	"0.9-13"
	##	IRanges	"IRanges"	"2.32.0"
l	##	IRdisplay	"IRdisplay"	"1.1"
	##	IRkernel	"IRkernel"	"1.3.1"
	##	irlba	"irlba"	"2.3.5.1"
	##	isoband	"isoband"	"0.2.7"
	##	iterators	"iterators"	"1.0.14"
	##	jquerylib	"jquerylib"	"0.1.4"
	##	jsonlite	"jsonlite"	"1.8.4"
	##	KEGGREST	"KEGGREST"	"1.38.0"
	##	kernlab	"kernlab"	"0.9-31"
	##	klaR	"klaR"	"1.7-1"
	##	knitr	"knitr"	"1.41"
l	##	kohonen	"kohonen"	"3.0.11"
	##	labeling	"labeling"	"0.4.2"
l	##	labelled	"labelled"	"2.10.0"
l	##	lambda.r	"lambda.r"	"1.2.4"
	##	later	"later"	"1.3.0"
	##	lava	"lava"	"1.7.0"
		lazyeval	"lazyeval"	"0.2.2"
	##	leaps	"leaps"	"3.1"
		lhs	"lhs"	"1.1.6"
		libcoin	"libcoin"	"1.0-9"
		LiblineaR	"LiblineaR"	"2.10-22"
		lifecycle	"lifecycle"	"1.0.3"
		limma	"limma"	"3.54.0"
		listenv	"listenv"	"0.9.0"
		littler	"littler"	"0.3.17"
		lme4	"lme4"	"1.1-31"
		locfit	"locfit"	"1.5-9.7"
		lsa	"lsa"	"0.73.3"
		lubridate	"lubridate"	"1.9.0"
		magicaxis	"magicaxis"	"2.2.14"
		magrittr	"magrittr"	"2.0.3"
		mapproj	"mapproj"	"1.2.9"
		maps .	"maps"	"3.4.1"
		margins	"margins"	"0.3.26"
		markdown	"markdown"	"1.4"
		marray	"marray"	"1.76.0"
		mashr	"mashr"	"0.2.69"
		MASS	"MASS"	"7.3-58.1" "1.0-6"
		matrixcalc	"matrixcalc"	
		MatrixGenerics MatrixModels	"MatrixGenerics" "MatrixModels"	"1.10.0" "0.5-1"
		matrixModels matrixStats	<pre>matrixModels "matrixStats"</pre>	"0.63.0"
		mclust memoise	"mclust" "memoise"	"6.0.0" "2.0.1"
		memoise	memoise "mime"	
		mime	"mime" "minfi"	"0.12" "1.44.0"
		miniUI	miniu"	"0.1.1.1"
		minqa	minioi "minqa"	"1.2.5"
	##	mrnqa	mrnya	1.2.5

2/23, 1	1:25 AM	250510_Istudi	o_sex_bias_drugs_sing
##	mixsqp	"mixsqp"	"0.3-48"
##	modeldata	"modeldata"	"1.0.1"
##	modelenv	"modelenv"	"0.1.0"
##	ModelMetrics	"ModelMetrics"	"1.2.2.2"
##	modelr	"modelr"	"0.1.10"
	multcompView	"multcompView"	"0.1-8"
##	MultiAssayExperiment	"MultiAssayExperiment"	"1.24.0"
##	multtest	"multtest"	"2.54.0"
##	munsell	"munsell"	"0.5.0"
	mvtnorm	"mvtnorm"	"1.1-3"
##	naivebayes	"naivebayes"	"0.9.7"
##	netZooR	"netZooR"	"1.2.1"
	NISTunits	"NISTunits"	"1.0.1"
##	nloptr	"nloptr"	"2.0.3"
	NMF	"NMF"	"0.25"
##	nnet	"nnet"	"7.3-18"
##	nor1mix	"nor1mix"	"1.3-0"
	numDeriv	"numDeriv"	"2016.8-1.1"
	openssl	"openssl"	"2.0.5"
##	org.Hs.eg.db	"org.Hs.eg.db"	"3.16.0"
##	pamr	"pamr"	"1.56.1"
	pandaR	"pandaR"	"1.30.0"
##	parallelly	"parallelly"	"1.33.0"
	parameters	"parameters"	"0.20.0"
##	parsnip	"parsnip"	"1.0.3"
##	partykit	"partykit"	"1.2-16"
	pasilla	"pasilla"	"1.26.0"
	patchwork	"patchwork"	"1.1.2"
	pbdZMQ	"pbdZMQ"	"0.3-8"
	pbkrtest	"pbkrtest"	"0.5.1"
	penalized	"penalized"	"0.9-52"
	permute	"permute"	"0.9-7"
	PharmacoGx	"PharmacoGx"	"3.2.0"
	pheatmap	"pheatmap"	"1.0.12"
	piano	"piano"	"2.14.0"
	pillar	"pillar"	"1.8.1"
	pkgbuild	"pkgbuild"	"1.3.1"
	pkgconfig	"pkgconfig"	"2.0.3"
	pkgdown	"pkgdown"	"2.0.6"
	pkgload	"pkgload"	"1.3.1"
	PLIER	"PLIER"	"0.99.0"
	plogr	"plogr"	"0.2.0"
	plotly	"plotly"	"4.10.1"
	plotmo	"plotmo"	"3.6.2"
	plotrix	"plotrix"	"3.8-2" "1.8.8"
	plyr	"plyr"	
	png	"png"	"0.1-8"
	polyclip	"polyclip" "nolynom"	"1.10-4" "1.4-1"
	polynom	"polynom"	
	pracma	"pracma"	"2.4.2" "1.0.0"
	praise	"praise"	"0.3.14"
	prediction	"prediction"	"1.60.1"
	preprocessCore prettyunits	"preprocessCore" "prettyunits"	"1.1.1"
	pROC	"pROC"	"1.18.0"
7777	proc	proc	1.10.0

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## processx	"processx"	"3.8.0"
## prodlim	"prodlim"	"2019.11.13"
## profmem	"profmem"	"0.6.0"
## profvis	"profvis"	"0.3.7"
## progress	"progress"	"1.2.2"
## progressr	"progressr"	"0.12.0"
## projectR	"projectR"	"1.14.0"
## ProliferativeIndex	"ProliferativeIndex"	"1.0.1"
## promises	"promises"	"1.2.0.1"
## ProtGenerics	"ProtGenerics"	"1.30.0"
## proto	"proto"	"1.0.0"
## proxy	"proxy"	"0.4-27"
## ps	"ps"	"1.7.2"
## purrr	"purrr"	"1.0.0"
## quadprog	"quadprog"	"1.5-8"
## quantreg	"quantreg"	"5.94"
## quantro	"quantro"	"1.32.0"
## questionr	"questionr"	"0.7.7"
## qvalue	"qvalue"	"2.30.0"
## R.cache	"R.cache"	"0.16.0"
## R.methodsS3	"R.methodsS3"	"1.8.2"
## R.00	"R.00"	"1.25.0"
## R.utils	"R.utils"	"2.12.2"
## R6	"R6"	"2.5.1"
## ragg	"ragg"	"1.2.4"
## randomForest	"randomForest"	"4.7-1.1"
## ranger	"ranger"	"0.14.1"
## RANN	"RANN"	"2.6.1"
## rappdirs	"rappdirs"	"0.3.3"
## RBGL	"RBGL"	"1.74.0"
## rcmdcheck	"rcmdcheck"	"1.4.0"
## RColorBrewer	"RColorBrewer"	"1.1-3"
## Rcpp	"Rcpp"	"1.0.9"
## RcppArmadillo	"RcppArmadillo"	"0.11.4.2.1"
## RcppEigen	"RcppEigen"	"0.3.3.9.3"
## RcppGSL	"RcppGSL"	"0.3.12"
## RcppTOML	"RcppTOML"	"0.1.7"
## RCurl	"RCurl"	"1.98-1.9"
## RCy3	"RCy3"	"2.18.0"
## reactome.db	"reactome.db"	"1.82.0"
## readr	"readr"	"2.1.3"
## readxl	"readxl"	"1.4.1"
## recipes	"recipes"	"1.0.3"
## recount3	"recount3"	"1.8.0"
## registry	"registry"	"0.5-1"
## relations	"relations"	"0.6-12"
## rematch	"rematch"	"1.0.1"
## rematch2	"rematch2"	"2.1.2"
## remotes	"remotes"	"2.4.2"
## repr	"repr"	"1.1.4"
## reprex	"reprex"	"2.0.2"
## reshape	"reshape"	"0.8.9"
## reshape2	"reshape2"	"1.4.4"
## restfulr	"restfulr"	"0.0.15"
## reticulate	"reticulate"	"1.26"

2/23, 11.23 / 1111	250510_15tac	no_sex_ons_urugs_sm
## Rgraphviz	"Rgraphviz"	"2.42.0"
## rhdf5	"rhdf5"	"2.42.0"
## rhdf5filters	"rhdf5filters"	"1.10.0"
## Rhdf5lib	"Rhdf5lib"	"1.20.0"
## Rhtslib	"Rhtslib"	"2.0.0"
## rJava	"rJava"	"1.0-6"
## rjson	"rjson"	"0.2.21"
## RJSONIO	"RJSONIO"	"1.3-1.6"
## rlang	"rlang"	"1.0.6"
## rmarkdown	"rmarkdown"	"2.19"
## rmeta	"rmeta"	"3.0"
## rngtools	"rngtools"	"1.5.2"
## robustbase	"robustbase"	"0.95-0"
## ROCR	"ROCR"	"1.0-11"
## roxygen2	"roxygen2"	"7.2.1"
## rpart	"rpart"	"4.1.19"
## rprojroot	"rprojroot"	"2.0.3"
## rsample	"rsample"	"1.1.1"
## Rsamtools	"Rsamtools"	"2.14.0"
## RSQLite	"RSQLite"	"2.2.20"
## rstatix	"rstatix"	"0.7.1"
## rstudioapi	"rstudioapi"	"0.14"
## rsvd	"rsvd"	"1.0.5"
## rsvg	"rsvg"	"2.4.0"
## rtracklayer	"rtracklayer"	"1.58.0"
## RUnit	"RUnit"	"0.4.32"
## rversions	"rversions"	"2.1.2"
## rvest	"rvest"	"1.0.3"
## RWeka	"RWeka"	"0.4-44"
## RWekajars	"RWekajars"	"3.9.3-2"
## S4Vectors	"S4Vectors"	"0.36.1"
## sass	"sass"	"0.4.4"
## scales	"scales"	"1.2.1" "0.1.8"
## scatterpie	"scatterpie"	
## scatterplot3d	"scatterplot3d" "scrime"	"0.3-42" "1.3.5"
<pre>## scrime ## selectr</pre>	"selectr"	"0.4-2"
## serectr ## sessioninfo	"sessioninfo"	"1.2.2"
## sets	"sets"	"1.0-21"
## shadowtext	"shadowtext"	"0.1.2"
## shape	"shape"	"1.4.6"
## shape ## shiny	"shiny"	"1.7.4"
## shinydashboard	"shinydashboard"	"0.7.2"
## shinydashboard ## shinyjs	"shinyjs"	"2.1.0"
## siggenes	"siggenes"	"1.72.0"
## signatureSearch	"signatureSearch"	"1.11.1"
## signatureSearchData	"signatureSearchData"	"1.12.0"
## SingleCellExperiment	"SingleCellExperiment"	"1.20.0"
## skimr	"skimr"	"2.1.5"
## slam	"slam"	"0.1-50"
## slider	"slider"	"0.3.0"
## sm	"sm"	"2.2-5.7.1"
## snow	"snow"	"0.4-4"
## SnowballC	"SnowballC"	"0.7.0"
## softImpute	"softImpute"	"1.4-1"
1	-	

223, 11.23 1111	250510_15tac	iio_sex_bias_arags_sing
## sourcetools	"sourcetools"	"0.1.7"
## SparseM	"SparseM"	"1.81"
## sparseMatrixStats	"sparseMatrixStats"	"1.10.0"
## sqldf	"sqldf"	"0.4-11"
## SQUAREM	"SQUAREM"	"2021.1"
## statmod	"statmod"	"1.4.37"
## STRINGdb	"STRINGdb"	"2.10.0"
## stringi	"stringi"	"1.7.8"
## stringr	"stringr"	"1.5.0"
## styler	"styler"	"1.8.1"
## SummarizedExperiment	"SummarizedExperiment"	"1.28.0"
## sys	"sys"	"3.4.1"
## systemfonts	"systemfonts"	"1.0.4"
## TeachingDemos	"TeachingDemos"	"2.12"
## testthat	"testthat"	"3.1.5"
## textshaping	"textshaping"	"0.3.6"
## TFEA.ChIP	"TFEA.ChIP"	"1.18.0"
## tibble	"tibble"	"3.1.8"
## tidygraph	"tidygraph"	"1.2.2"
## tidymodels	"tidymodels"	"1.0.0"
## tidyr	"tidyr"	"1.2.1"
## tidyselect	"tidyselect"	"1.2.0"
## tidytree	"tidytree"	"0.4.2"
## tidyverse	"tidyverse"	"1.3.2"
## timechange	"timechange"	"0.1.1"
## timeDate	"timeDate"	"4021.107"
## tinytex	"tinytex"	"0.43"
## topGO	"topGO"	"2.50.0"
## treeio	"treeio"	"1.22.0"
## truncnorm	"truncnorm"	"1.0-8"
## tune	"tune"	"1.0.1"
## tweenr	"tweenr"	"2.0.2"
## tzdb	"tzdb"	"0.3.0"
## uchardet	"uchardet"	"1.1.1"
## urlchecker	"urlchecker"	"1.0.1"
## usethis	"usethis"	"2.1.6"
## utf8	"utf8"	"1.2.2"
## uuid	"uuid"	"1.1-0"
## vctrs	"vctrs"	"0.5.1"
## vegan	"vegan"	"2.6-4"
## VennDiagram	"VennDiagram"	"1.7.3"
<pre>## viridis ## viridisLite</pre>	"viridis"	"0.6.2"
"" '	"viridisLite"	"0.4.1"
## visNetwork	"visNetwork" "vroom"	"2.1.2"
## vroom ## waldo	vroom "waldo"	"1.6.0" "0.4.0"
		"0.2.0"
## warp ## whisker	"warp" "whisker"	"0.4"
## whisker ## withr	"withr"	"2.5.0"
## withi	"workflows"	"1.1.2"
## workflowsets	workflows "workflowsets"	"1.0.0"
## workflowsets ## xfun	"xfun"	"0.36"
## xgboost	"xgboost"	"1.6.0.1"
## XML	"XML"	"3.99-0.13"
## xml2	"xml2"	"1.3.3"
,,,, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		1.0.0

2/23, 11:23 AM	2305	10_rstudio_sex_bias_drugs_singularity	
## xopen	"xopen"	"1.0.0"	
## xtable	"xtable"	"1.8-4"	
## XVector	"XVector"	"0.38.0"	
## yaml	"yaml"	"2.3.6"	
## yardstick	"yardstick"	"1.1.0"	
## yarn	"yarn"	"1.24.0"	
## yulab.utils	"yulab.utils"	"0.0.6"	
## zip	"zip"	"2.2.2"	
## zlibbioc	"zlibbioc"	"1.44.0"	
## base	"base"	"4.2.2"	
## boot	"boot"	"1.3-28"	
## class	"class"	"7.3-20"	
## cluster	"cluster"	"2.1.4"	
## codetools	"codetools"	"0.2-18"	
## compiler	"compiler"	"4.2.2"	
## datasets	"datasets"	"4.2.2"	
## foreign	"foreign"	"0.8-83"	
## graphics	"graphics"	"4.2.2"	
## grDevices	"grDevices"	"4.2.2"	
## grid	"grid"	"4.2.2"	
## KernSmooth	"KernSmooth"	"2.23-20"	
## lattice	"lattice"	"0.20-45"	
## MASS	"MASS"	"7.3-58.1"	
## Matrix	"Matrix"	"1.5-1"	
## methods	"methods"	"4.2.2"	
## mgcv	"mgcv"	"1.8-41"	
## nlme	"nlme"	"3.1-160"	
## nnet	"nnet"	"7.3-18"	
## parallel	"parallel"	"4.2.2"	
## rpart	"rpart"	"4.1.19"	
## spatial	"spatial"	"7.3-15"	
## splines	"splines"	"4.2.2"	
## stats	"stats"	"4.2.2"	
## stats4	"stats4"	"4.2.2"	
## survival	"survival"	"3.4-0"	
## tcltk	"tcltk"	"4.2.2"	
## tools	"tools"	"4.2.2"	
## utils	"utils"	"4.2.2"	

R version 4.0.5 (2021-03-31)

Platform: x86_64-conda-linux-gnu (64-bit) Running under: Red Hat Enterprise Linux

Matrix products: default

BLAS/LAPACK: /data/user/jfisher7/.conda/envs/SR_TAU_CELL/lib/

libopenblasp-r0.3.18.so

locale: [1] C

attached base packages:

[1] stats graphics grDevices utils datasets methods base

Version

loaded via a namespace (and not attached):

Package

[1] compiler_4.0.5

[1] "Listing packages"

	rackage	VCISION
AnnotationDbi	"AnnotationDbi"	"1.52.0"
AnnotationHub	"AnnotationHub"	"2.22.1"
ВН	"BH"	"1.78.0-0"
Biobase	"Biobase"	"2.50.0"
BiocFileCache	"BiocFileCache"	"1.14.0"
BiocGenerics	"BiocGenerics"	"0.36.1"
BiocManager	"BiocManager"	"1.30.16"
BiocParallel	"BiocParallel"	"1.24.1"
BiocVersion	"BiocVersion"	"3.12.0"
DBI	"DBI"	"1.1.2"
DO.db	"D0.db"	"2.9"
DOSE	"DOSE"	"3.16.0"
DT	"DT"	"0.20"
DelayedArray	"DelayedArray"	"0.16.3"
ExperimentHub	"ExperimentHub"	"1.16.1"
GO. db	"G0. db"	"3.12.1"
GOSemSim	"GOSemSim"	"2.16.1"
GSEABase	"GSEABase"	"1.52.1"
GenomeInfoDb	"GenomeInfoDb"	"1.26.7"
GenomeInfoDbData	"GenomeInfoDbData"	"1.2.4"
GenomicRanges	"GenomicRanges"	"1.42.0"
HDF5Array	"HDF5Array"	"1.18.1"
IRanges	"IRanges"	"2.24.1"
MASS	"MASS"	"7 . 3-55"
Matrix	"Matrix"	"1.4-0"
MatrixGenerics	"MatrixGenerics"	"1.2.1"
R.methodsS3	"R.methodsS3"	"1.8.1"
R. 00	"R.oo"	"1.24.0"
R.utils	"R.utils"	"2.11.0"
R6	"R6"	"2.5.1"
RColorBrewer	"RColorBrewer"	"1.1-2"
RCurl	"RCurl"	"1.98-1.5"

RSQLite	"RSQLite"	"2.2.9"
Rcpp	"Rcpp"	"1.0.8"
RcppArmadillo	"RcppArmadillo"	"0.10.8.1.0"
RcppEigen	"RcppEigen"	"0.3.3.9.1"
Rhdf5lib	"Rhdf5lib"	"1.12.1"
S4Vectors	"S4Vectors"	"0.28.1"
SummarizedExperiment	"SummarizedExperiment"	"1.20.0"
XML	"XML"	"3.99-0.8"
XVector	"XVector"	"0.30.0"
affy	"affy"	"1.68.0"
affyio	"affyio"	"1.60.0"
annotate	"annotate"	"1.68.0"
askpass	"askpass"	"1.1"
assertthat	"assertthat"	"0.2.1"
backports	"backports"	"1.4.1"
base	"base ['] '	"4.0.5"
base64enc	"base64enc"	"0.1-3"
bit	"bit"	"4.0.4"
bit64	"bit64"	"4.0.5"
bitops	"bitops"	"1.0-7"
blob	"blob"	"1.2.2"
brio	"brio"	"1.1.3"
broom	"broom"	"0.7.12"
bslib	"bslib"	"0.3.1"
cachem	"cachem"	"1.0.6"
callr	"callr"	"3.7.0"
cellranger	"cellranger"	"1.1.0"
cli	"cli"	"3.1.1"
clipr	"clipr"	"0.7.1"
clusterProfiler	"clusterProfiler"	"3.18.1"
colorspace	"colorspace"	"2.0-2"
commonmark	"commonmark"	"1.7"
compiler	"compiler"	"4.0.5"
cowplot	"cowplot"	"1.1.1"
cpp11	"cpp11"	"0.4.2"
crayon	"crayon"	"1.4.2"
crosstalk	"crosstalk"	"1.2.0"
curl	"curl"	"4.3.2"
data.table	"data.table"	"1.14.2"
datasets	"datasets"	"4.0.5"
dbplyr	"dbplyr"	"2.1.1"
desc	"desc"	"1.4.0"
diffobj	"diffobj"	"0.3.5"
digest	"digest ["]	"0.6.29"
downloader	"downloader"	"0.4"
dplyr	"dplyr"	"1.0.7"
dtplyr	"dtplyr"	"1.2.1"
ellipsis	"ellipsis"	"0.3.2"
enrichplot	"enrichplot"	"1.10.2"
evaluate	"evaluate"	"0.14"

fansi	"fansi"	"1.0.2"
farver	"farver"	"2.1.0"
fastmap	"fastmap"	"1.1.0"
fastmatch	"fastmatch"	"1.1-3"
fgsea	"fgsea"	"1.16.0"
fontawesome	"fontawesome"	"0.2.2"
forcats	"forcats"	"0.5.1"
formatR	"formatR"	"1.11"
fs	"fs"	"1.5.2"
futile.logger	"futile.logger"	"1.4.3"
futile.options	"futile.options"	"1.0.1"
gargle	"gargle"	"1.2.0"
generics	"generics"	"0.1.2"
ggforce	"ggforce"	"0.3.3"
ggfun	"ggfun"	"0.0.5"
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lubridate	"lubridate"	T.O.A

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withr	"withr"	"2.4.3"
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