

Session info

Here, we import the libraries used and then show the session info for reference

```
### From CRAN
library(RColorBrewer)
library(corr)
library(dplyr)
library(ggbeeswarm)
library(ggplot2)
library(ggrepel)
library(here)
library(pheatmap)
library(tidyr)

### From Bioconductor
library(biobroom)

### From Github
library(camprotR)

sessionInfo()

## R version 4.1.2 (2021-11-01)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] camprotR_0.0.0.9000 biobroom_1.26.0    broom_0.7.12
## [4] tidyr_1.2.0          pheatmap_1.0.12    here_1.0.1
## [7] ggrepel_0.9.1        ggbeeswarm_0.7.2   ggplot2_3.4.2
## [10] dplyr_1.1.4          corrr_0.4.4        RColorBrewer_1.1-3
##
## loaded via a namespace (and not attached):
## [1] Biobase_2.54.0      vsn_3.62.0          foreach_1.5.2
## [4] BiocManager_1.30.16 affy_1.72.0          stats4_4.1.2
## [7] vipor_0.4.5         robustbase_0.93-9    yaml_2.3.5
## [10] impute_1.68.0       pillar_1.9.0         backports_1.4.1
## [13] lattice_0.20-45     glue_1.6.2           limma_3.50.1
```

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## [16] digest_0.6.29      colorspace_2.1-0    htmltools_0.5.7
## [19] preprocessCore_1.56.0 plyr_1.8.6          MALDIquant_1.21
## [22] XML_3.99-0.9        pkgconfig_2.0.3     zlibbioc_1.40.0
## [25] purrr_0.3.4         scales_1.2.1        affyio_1.64.0
## [28] BiocParallel_1.28.3 tibble_3.2.1        IRanges_2.28.0
## [31] generics_0.1.2      withr_2.5.0         BiocGenerics_0.40.0
## [34] cli_3.6.1           magrittr_2.0.3      evaluate_0.15
## [37] ncd4_1.19           fansi_1.0.4         doParallel_1.0.17
## [40] MASS_7.3-55         beeswarm_0.4.0      mzR_2.28.0
## [43] tools_4.1.2         lifecycle_1.0.3     stringr_1.5.0
## [46] MSnbase_2.20.4      S4Vectors_0.32.3    munsell_0.5.0
## [49] cluster_2.1.2       pcaMethods_1.86.0   compiler_4.1.2
## [52] mzID_1.32.0         rlang_1.1.1         grid_4.1.2
## [55] iterators_1.0.14    rstudioapi_0.13     MsCoreUtils_1.6.2
## [58] rmarkdown_2.12      gtable_0.3.3        codetools_0.2-18
## [61] DBI_1.1.2           R6_2.5.1            knitr_1.37
## [64] fastmap_1.1.0       utf8_1.2.3          clue_0.3-60
## [67] rprojroot_2.0.2     ProtGenerics_1.26.0 stringi_1.7.6
## [70] parallel_4.1.2      Rcpp_1.0.8.3        vctrs_0.6.5
## [73] DEoptimR_1.0-10     tidyselect_1.2.0    xfun_0.41

```