```
* sessionInfo()


R version 3.4.0 (2017-04-21)

Platform: x86_64-apple-darwin15.6.0 (64-bit)

Running under: macOS Sierra 10.12.6


Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRblas.0.dylib

LAPACK: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRlapack.dylib


locale:

[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8


attached base packages:

[1] parallel  stats4    stats     graphics  grDevices utils     datasets  methods   base


other attached packages:

[1] BiocInstaller_1.26.0     ggthemes_3.4.0          tidyr_0.7.0          reshape2_1.4.2        genefilter_1.58.1

[6] PoiClaClu_1.0.2          RColorBrewer_1.1-2      pheatmap_1.0.8       ggplot2_2.2.1         DESeq2_1.16.1

[11] SummarizedExperiment_1.6.3 DelayedArray_0.2.7      matrixStats_0.52.2   Biobase_2.36.2        GenomicRanges_1.28.4

[16] GenomeInfoDb_1.12.2      IRanges_2.10.2          S4Vectors_0.14.3     BiocGenerics_0.22.0   ciiDE_1.0.0

[21] devtools_1.13.3


loaded via a namespace (and not attached):

[1] bit64_0.9-7           splines_3.4.0        Formula_1.2-2        assertthat_0.2.0     latticeExtra_0.6-28   blob_1.1.0

[7] GenomeInfoDbData_0.99.0 RSQLite_2.0          backports_1.1.0      lattice_0.20-35      glue_1.1.1            digest_0.6.1

[13] XVector_0.16.0        checkmate_1.8.3      colorspace_1.3-2     htmltools_0.3.6      Matrix_1.2-11         plyr_1.8.4

[19] XML_3.98-1.9          zlibbioc_1.22.0      purrr_0.2.3          xtable_1.8-2         scales_0.5.0          BioCParalle

[25] git2r_0.19.0          htmlTable_1.9        tibble_1.3.4         annotate_1.54.0      withr_2.0.0           nnet_7.3-12

[31] lazyeval_0.2.0        survival_2.41-3      magrittr_1.5         crayon_1.3.2         memoise_1.1.0         xml2_1.1.1

[37] foreign_0.8-69        tools_3.4.0          data.table_1.10.4    stringr_1.2.0        munsell_0.4.3         locfit_1.5-9

[43] cluster_2.0.6         AnnotationDbi_1.38.2 compiler_3.4.0       rlang_0.1.2          grid_3.4.0            RCurl_1.95-4

[49] htmlwidgets_0.9       bitops_1.0-6         base64enc_0.1-3      gtable_0.2.0         DBI_0.7               roxygen2_6.0

[55] R6_2.2.2              gridExtra_2.2.1      knitr_1.17           bit_1.1-12           commonmark_1.2        Hmisc_4.0-3

[61] rprojroot_1.2         desc_1.1.1           stringi_1.1.5        Rcpp_0.12.12         geneplotter_1.54.0    rpart_4.1-11

[67] acepack_1.4.1


* Out-of-date packages
```

	Package	LibPath	Installed	Built	Repos'
backports	"backports"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.1.0"	"3.4.0"	"1.1.1

BiocInstaller	"BiocInstaller"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.26.0"	"3.4.0"	"1.26
BSgenome	"BSgenome"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.44.1"	"3.4.1"	"1.44
caret	"caret"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"6.0-76"	"3.4.0"	"6.0-
checkmate	"checkmate"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.8.3"	"3.4.1"	"1.8.
commonmark	"commonmark"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.2"	"3.4.0"	"1.4"
crayon	"crayon"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.3.2"	"3.4.0"	"1.3.
doParallel	"doParallel"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.0.10"	"3.4.0"	"1.0.
dplyr	"dplyr"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.7.2"	"3.4.1"	"0.7.
energy	"energy"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.7-0"	"3.4.0"	"1.7-
gdtools	"gdtools"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.1.5"	"3.4.1"	"0.1.
GenomicFeatures	"GenomicFeatures"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.28.4"	"3.4.0"	"1.28
GenomicRanges	"GenomicRanges"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.28.4"	"3.4.1"	"1.28
ggjoy	"ggjoy"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.3.0"	"3.4.1"	"0.4.
glmnet	"glmnet"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"2.0-10"	"3.4.0"	"2.0-
gridExtra	"gridExtra"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"2.2.1"	"3.4.0"	"2.3"
IRanges	"IRanges"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"2.10.2"	"3.4.0"	"2.10
lambda.r	"lambda.r"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.1.9"	"3.4.0"	"1.2"
lava	"lava"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.5"	"3.4.0"	"1.5.
limma	"limma"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"3.32.5"	"3.4.1"	"3.32
lme4	"lme4"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.1-13"	"3.4.0"	"1.1-
multcomp	"multcomp"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.4-6"	"3.4.0"	"1.4-
openssl	"openssl"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.9.6"	"3.4.0"	"0.9.
psych	"psych"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.7.5"	"3.4.0"	"1.7.
Rcpp	"Rcpp"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.12.12"	"3.4.1"	"0.12
RcppArmadillo	"RcppArmadillo"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.7.900.2.0"	"3.4.0"	"0.7.
rstudioapi	"rstudioapi"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.6"	"3.4.0"	"0.7"
S4Vectors	"S4Vectors"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.14.3"	"3.4.0"	"0.14
segmented	"segmented"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.5-2.1"	"3.4.0"	"0.5-
SummarizedExperiment	"SummarizedExperiment"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.6.3"	"3.4.0"	"1.6.
svglite	"svglite"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"1.2.0"	"3.4.0"	"1.2.
tidyr	"tidyr"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.7.0"	"3.4.1"	"0.7.
tidyselect	"tidyselect"	"/Library/Frameworks/R.framework/Versions/3.4/Resources/library"	"0.1.1"	"3.4.1"	"0.2.

	Repository
backports	"https://cran.rstudio.com/src/contrib"
BiocInstaller	"https://bioconductor.org/packages/3.5/bioc/src/contrib"
BSgenome	"https://bioconductor.org/packages/3.5/bioc/src/contrib"
caret	"https://cran.rstudio.com/src/contrib"
checkmate	"https://cran.rstudio.com/src/contrib"
commonmark	"https://cran.rstudio.com/src/contrib"
crayon	"https://cran.rstudio.com/src/contrib"
doParallel	"https://cran.rstudio.com/src/contrib"
dplyr	"https://cran.rstudio.com/src/contrib"

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energy              "https://cran.rstudio.com/src/contrib"

gdtools             "https://cran.rstudio.com/src/contrib"

GenomicFeatures     "https://bioconductor.org/packages/3.5/bioc/src/contrib"

GenomicRanges       "https://bioconductor.org/packages/3.5/bioc/src/contrib"

ggjoy               "https://cran.rstudio.com/src/contrib"

glmnet              "https://cran.rstudio.com/src/contrib"

gridExtra           "https://cran.rstudio.com/src/contrib"

IRanges             "https://bioconductor.org/packages/3.5/bioc/src/contrib"

lambda.r            "https://cran.rstudio.com/src/contrib"

lava                "https://cran.rstudio.com/src/contrib"

limma               "https://bioconductor.org/packages/3.5/bioc/src/contrib"

lme4                "https://cran.rstudio.com/src/contrib"

multcomp            "https://cran.rstudio.com/src/contrib"

openssl             "https://cran.rstudio.com/src/contrib"

psych               "https://cran.rstudio.com/src/contrib"

Rcpp                "https://cran.rstudio.com/src/contrib"

RcppArmadillo       "https://cran.rstudio.com/src/contrib"

rstudioapi          "https://cran.rstudio.com/src/contrib"

S4Vectors           "https://bioconductor.org/packages/3.5/bioc/src/contrib"

segmented           "https://cran.rstudio.com/src/contrib"

SummarizedExperiment "https://bioconductor.org/packages/3.5/bioc/src/contrib"

svglite             "https://cran.rstudio.com/src/contrib"

tidyr               "https://cran.rstudio.com/src/contrib"

tidyselect          "https://cran.rstudio.com/src/contrib"


update with biocLite()


* Packages too new for Bioconductor version '3.5'


        Version     LibPath

roxygen2 "6.0.1.9000" "/Library/Frameworks/R.framework/Versions/3.4/Resources/library"


downgrade with biocLite("roxygen2")


Error: 33 package(s) out of date; 1 package(s) too new
```