

crisprVerse: ecosystem of R packages for CRISPR gRNA design

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1 Installation and getting started

The `crisprVerse` is a collection of packages for CRISPR guide RNA (gRNA) design that can easily be installed with the `crisprVerse` package. This provides a convenient way of downloading and installing all `crisprVerse` packages with a single R command.

The package can be installed from the Bioconductor devel branch using the following commands in an R session:

```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")

BiocManager::install(version="devel")
BiocManager::install("crisprVerse")
```

The core `crisprVerse` includes the packages that are commonly used for gRNA design, and are attached when you attach the `crisprVerse` package:

```
library(crisprVerse)
```

You can check that all `crisprVerse` packages are up-to-date with the function `crisprVerse_update()`.

2 Components

The following packages are installed and loaded with the `crisprVerse` package:

- *crisprBase* to specify and manipulate CRISPR nucleases.
- *crisprBowtie* to perform gRNA spacer sequence alignment with Bowtie.
- *crisprScore* to annotate gRNAs with on-target and off-target scores.
- *crisprDesign* to design and manipulate gRNAs with `GuideSet` objects.

3 Reproducibility

```
sessionInfo()

## R version 4.2.1 (2022-06-23)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Catalina 10.15.7
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2/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] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] crisprDesign_0.99.134 crisprScore_1.1.14   crisprScoreData_1.1.3
## [4] ExperimentHub_2.5.0   AnnotationHub_3.5.0   BiocFileCache_2.5.0
## [7] dbplyr_2.2.1          BiocGenerics_0.43.1   crisprBowtie_1.1.1
## [10] crisprBase_1.1.5      crisprVerse_0.99.8
##
## loaded via a namespace (and not attached):
## [1] bitops_1.0-7           matrixStats_0.62.0
## [3] bit64_4.0.5           filelock_1.0.2
## [5] progress_1.2.2        httr_1.4.4
## [7] GenomeInfoDb_1.33.5   tools_4.2.1
## [9] utf8_1.2.2            R6_2.5.1
## [11] DBI_1.1.3             tidyselect_1.1.2
## [13] prettyunits_1.1.1     bit_4.0.4
## [15] curl_4.3.2            compiler_4.2.1
## [17] cli_3.3.0             Biobase_2.57.1
## [19] basilisk.utils_1.9.1   xml2_1.3.3
## [21] DelayedArray_0.23.1    rtracklayer_1.57.0
## [23] randomForest_4.7-1.1   readr_2.1.2
## [25] rappdirs_0.3.3        stringr_1.4.1
## [27] digest_0.6.29         Rsamtools_2.13.4
## [29] rmarkdown_2.15.2      basilisk_1.9.3
## [31] XVector_0.37.0        pkgconfig_2.0.3
## [33] htmltools_0.5.3       MatrixGenerics_1.9.1
## [35] fastmap_1.1.0         BSgenome_1.65.2
## [37] rlang_1.0.4           rstudioapi_0.14
## [39] RSQLite_2.2.16        shiny_1.7.2
## [41] BiocIO_1.7.1          generics_0.1.3
## [43] jsonlite_1.8.0        BiocParallel_1.31.12
## [45] dplyr_1.0.9           VariantAnnotation_1.43.3
## [47] RCurl_1.98-1.8        magrittr_2.0.3
## [49] GenomeInfoDbData_1.2.8 Matrix_1.4-1
## [51] Rcpp_1.0.9            S4Vectors_0.35.1
## [53] fansi_1.0.3           reticulate_1.25
## [55] Rbowtie_1.37.0        lifecycle_1.0.1
## [57] stringi_1.7.8         yaml_2.3.5
## [59] SummarizedExperiment_1.27.1 zlibbioc_1.43.0
## [61] grid_4.2.1           blob_1.2.3
## [63] promises_1.2.0.1      parallel_4.2.1
## [65] crayon_1.5.1          dir.expiry_1.5.0
## [67] lattice_0.20-45       Biostings_2.65.2
## [69] GenomicFeatures_1.49.6 hms_1.1.2
## [71] KEGGREST_1.37.3       knitr_1.40
## [73] pillar_1.8.1          GenomicRanges_1.49.1
## [75] rjson_0.2.21          codetools_0.2-18
## [77] biomaRt_2.53.2        stats4_4.2.1
## [79] BiocVersion_3.16.0    XML_3.99-0.10
## [81] glue_1.6.2            evaluate_0.16

```

```

## [83] BiocManager_1.30.18      httpuv_1.6.5
## [85] png_0.1-7                 vctrs_0.4.1
## [87] tzdb_0.3.0               purrr_0.3.4
## [89] assertthat_0.2.1         cachem_1.0.6
## [91] xfun_0.32                mime_0.12
## [93] xtable_1.8-4             restfulr_0.0.15
## [95] later_1.3.0              tibble_3.1.8
## [97] GenomicAlignments_1.33.1 AnnotationDbi_1.59.1
## [99] memoise_2.0.1            IRanges_2.31.2
## [101] interactiveDisplayBase_1.35.0 ellipsis_0.3.2
## [103] BiocStyle_2.25.0

```