Installing the crisprVerse and packages necessary for the tutorials

Jean-Philippe Fortin, Luke Hoberecht

Installation

We show in this tutorial how to install the crisprVerse packages, as well as other packages necessary for some of the crisprVerse tutorials.

Requirements

The crisprVerse is supported for macOS, Linux and Windows machines. It requires R version >=4.2.1. Some of the third-party functionalities are not available for Windows machines (BWA alignment, and some of the scoring functions). To download and install R, see the R-project website.

Bioconductor versions

The Bioconductor project has 2 concurrent versions: `release` and `devel`. Currently (August 2022), the release version is `3.15`, and the devel version is `3.16`. Release versions are created twice a year.

The current version of the crisprVerse was developed on the devel version of Bioconductor (`3.16`) to make sure it accesses all of the latest developments. Earlier versions of some of our packages are available on the release version, but we do not recommend using the release version as most of the functionalities described in the tutorials require devel functionalities.

See the Bioconductor install page for more information re. Bioconductor.

Installing the core crisprVerse packages

The crisprVerse package installs the core crisprVerse packages in a single command from Bioconductor. Simply type in the following commands in an R session:

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

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

Note that we specify the devel branch of Bioconductor so that we can use the latest functionalities.

This will install the following packages:

- 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.
- crisprScoreData to use pre-trained models for the `crisprScore` package.

The following command will load all of those packages in an R session:

```r
library(crisprVerse)
```

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

```
crisprVerse_update()
```

Installing data packages

The following genome data packages from Bioconductor are required for several of the tutorials:

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

BiocManager::install(version="devel")
BiocManager::install("BSgenome.Mmusculus.UCSC.mm10")
BiocManager::install("BSgenome.Hsapiens.UCSC.hg38")
BiocManager::install("BSgenome.Hsapiens.UCSC.hg38.dbSNP151.major")
BiocManager::install("BSgenome.Hsapiens.UCSC.hg38.dbSNP151.minor")
```

The crisrpDesignData package is also required for most of the tutorials and can be installed directly from our GitHub page using the `devtools` package:

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

devtools::install.packages("crisprVerse/crisprDesignData")
```

Installing optional packages

For maxOS and Linux users, the crisprBwa can be installed from Bioconductor using the following:

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

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

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] stats4    stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
```

```
##  [1] readxl_1.4.1
##  [2] BSgenome.Hsapiens.UCSC.hg38.dbSNP151.minor_0.0.9999
##  [3] BSgenome.Hsapiens.UCSC.hg38.dbSNP151.major_0.0.9999
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.4.3
##  [5] BSgenome.Hsapiens.UCSC.hg38_1.4.4
##  [6] BSgenome_1.65.2
##  [7] rtracklayer_1.57.0
##  [8] Biostrings_2.65.2
##  [9] XVector_0.37.0
## [10] GenomicRanges_1.49.1
## [11] GenomeInfoDb_1.33.5
## [12] IRanges_2.31.2
## [13] S4Vectors_0.35.1
## [14] crisprDesignData_0.99.17
## [15] crisprDesign_0.99.133
## [16] crisprScore_1.1.14
## [17] crisprScoreData_1.1.3
## [18] ExperimentHub_2.5.0
## [19] AnnotationHub_3.5.0
## [20] BiocFileCache_2.5.0
## [21] dbplyr_2.2.1
## [22] BiocGenerics_0.43.1
## [23] crisprBowtie_1.1.1
## [24] crisprBase_1.1.5
## [25] crisprVerse_0.99.8
## [26] rmarkdown_2.15.2
##
## loaded via a namespace (and not attached):
##  [1] rjson_0.2.21              ellipsis_0.3.2
##  [3] Rbowtie_1.37.0            bit64_4.0.5
##  [5] lubridate_1.8.0           interactiveDisplayBase_1.35.0
##  [7] AnnotationDbi_1.59.1      fansi_1.0.3
##  [9] xml2_1.3.3                codetools_0.2-18
## [11] cachem_1.0.6             knitr_1.40
## [13] jsonlite_1.8.0           Rsamtools_2.13.4
## [15] png_0.1-7                shiny_1.7.2
## [17] BiocManager_1.30.18      readr_2.1.2
## [19] compiler_4.2.1           httr_1.4.4
## [21] basilisk_1.9.2           assertthat_0.2.1
## [23] Matrix_1.4-1             fastmap_1.1.0
## [25] cli_3.3.0                later_1.3.0
## [27] htmltools_0.5.3          prettyunits_1.1.1
## [29] tools_4.2.1              glue_1.6.2
## [31] GenomeInfoDbData_1.2.8   dplyr_1.0.9
## [33] rappdirs_0.3.3           tinytex_0.41
## [35] Rcpp_1.0.9               Biobase_2.57.1
## [37] cellranger_1.1.0         vctrs_0.4.1
## [39] crisprBwa_1.1.3          xfun_0.32
## [41] stringr_1.4.1            mime_0.12
## [43] lifecycle_1.0.1          restfulr_0.0.15
## [45] XML_3.99-0.10            zlibbioc_1.43.0
## [47] basilisk.utils_1.9.1     vroom_1.5.7
## [49] VariantAnnotation_1.43.3 hms_1.1.2
## [51] promises_1.2.0.1         MatrixGenerics_1.9.1
```

```
## [53] parallel_4.2.1                 SummarizedExperiment_1.27.1
## [55] RMariaDB_1.2.2                 yaml_2.3.5
## [57] curl_4.3.2                     memoise_2.0.1
## [59] reticulate_1.25               biomaRt_2.53.2
## [61] stringi_1.7.8                 RSQLite_2.2.16
## [63] BiocVersion_3.16.0            highr_0.9
## [65] BiocIO_1.7.1                  randomForest_4.7-1.1
## [67] GenomicFeatures_1.49.6        filelock_1.0.2
## [69] BiocParallel_1.31.12          rlang_1.0.4
## [71] pkgconfig_2.0.3               matrixStats_0.62.0
## [73] bitops_1.0-7                  evaluate_0.16
## [75] lattice_0.20-45               purrr_0.3.4
## [77] GenomicAlignments_1.33.1      bit_4.0.4
## [79] tidyselect_1.1.2              magrittr_2.0.3
## [81] R6_2.5.1                      generics_0.1.3
## [83] DelayedArray_0.23.1           DBI_1.1.3
## [85] pillar_1.8.1                  KEGGREST_1.37.3
## [87] RCurl_1.98-1.8                tibble_3.1.8
## [89] dir.expiry_1.5.0              crayon_1.5.1
## [91] utf8_1.2.2                    tzdb_0.3.0
## [93] progress_1.2.2                grid_4.2.1
## [95] blob_1.2.3                    digest_0.6.29
## [97] xtable_1.8-4                  httpuv_1.6.5
## [99] Rbwa_1.1.0
```

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] stats4    stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] readxl_1.4.1
##  [2] BSgenome.Hsapiens.UCSC.hg38.dbSNP151.minor_0.0.9999
##  [3] BSgenome.Hsapiens.UCSC.hg38.dbSNP151.major_0.0.9999
##  [4] BSgenome.Mmusculus.UCSC.mm10_1.4.3
##  [5] BSgenome.Hsapiens.UCSC.hg38_1.4.4
##  [6] BSgenome_1.65.2
##  [7] rtracklayer_1.57.0
##  [8] Biostrings_2.65.2
```

```
##  [9] XVector_0.37.0
## [10] GenomicRanges_1.49.1
## [11] GenomeInfoDb_1.33.5
## [12] IRanges_2.31.2
## [13] S4Vectors_0.35.1
## [14] crisprDesignData_0.99.17
## [15] crisprDesign_0.99.133
## [16] crisprScore_1.1.14
## [17] crisprScoreData_1.1.3
## [18] ExperimentHub_2.5.0
## [19] AnnotationHub_3.5.0
## [20] BiocFileCache_2.5.0
## [21] dbplyr_2.2.1
## [22] BiocGenerics_0.43.1
## [23] crisprBowtie_1.1.1
## [24] crisprBase_1.1.5
## [25] crisprVerse_0.99.8
## [26] rmarkdown_2.15.2
##
## loaded via a namespace (and not attached):
##  [1] rjson_0.2.21               ellipsis_0.3.2
##  [3] Rbowtie_1.37.0            bit64_4.0.5
##  [5] lubridate_1.8.0          interactiveDisplayBase_1.35.0
##  [7] AnnotationDbi_1.59.1     fansi_1.0.3
##  [9] xml2_1.3.3               codetools_0.2-18
## [11] cachem_1.0.6             knitr_1.40
## [13] jsonlite_1.8.0           Rsamtools_2.13.4
## [15] png_0.1-7                shiny_1.7.2
## [17] BiocManager_1.30.18      readr_2.1.2
## [19] compiler_4.2.1           httr_1.4.4
## [21] basilisk_1.9.2           assertthat_0.2.1
## [23] Matrix_1.4-1             fastmap_1.1.0
## [25] cli_3.3.0                later_1.3.0
## [27] htmltools_0.5.3          prettyunits_1.1.1
## [29] tools_4.2.1              glue_1.6.2
## [31] GenomeInfoDbData_1.2.8   dplyr_1.0.9
## [33] rappdirs_0.3.3           tinytex_0.41
## [35] Rcpp_1.0.9               Biobase_2.57.1
## [37] cellranger_1.1.0         vctrs_0.4.1
## [39] crisprBwa_1.1.3          xfun_0.32
## [41] stringr_1.4.1            mime_0.12
## [43] lifecycle_1.0.1          restfulr_0.0.15
## [45] XML_3.99-0.10            zlibbioc_1.43.0
## [47] basilisk.utils_1.9.1     vroom_1.5.7
## [49] VariantAnnotation_1.43.3 hms_1.1.2
## [51] promises_1.2.0.1         MatrixGenerics_1.9.1
## [53] parallel_4.2.1           SummarizedExperiment_1.27.1
## [55] RMariaDB_1.2.2           yaml_2.3.5
## [57] curl_4.3.2               memoise_2.0.1
## [59] reticulate_1.25          biomaRt_2.53.2
## [61] stringi_1.7.8            RSQLite_2.2.16
## [63] BiocVersion_3.16.0       highr_0.9
## [65] BiocIO_1.7.1             randomForest_4.7-1.1
## [67] GenomicFeatures_1.49.6   filelock_1.0.2
```

```
## [69] BiocParallel_1.31.12        rlang_1.0.4
## [71] pkgconfig_2.0.3            matrixStats_0.62.0
## [73] bitops_1.0-7              evaluate_0.16
## [75] lattice_0.20-45           purrr_0.3.4
## [77] GenomicAlignments_1.33.1  bit_4.0.4
## [79] tidyselect_1.1.2          magrittr_2.0.3
## [81] R6_2.5.1                  generics_0.1.3
## [83] DelayedArray_0.23.1       DBI_1.1.3
## [85] pillar_1.8.1              KEGGREST_1.37.3
## [87] RCurl_1.98-1.8            tibble_3.1.8
## [89] dir.expiry_1.5.0          crayon_1.5.1
## [91] utf8_1.2.2                tzdb_0.3.0
## [93] progress_1.2.2            grid_4.2.1
## [95] blob_1.2.3                digest_0.6.29
## [97] xtable_1.8-4              httpuv_1.6.5
## [99] Rbwa_1.1.0
```

References