

Data Exploration and Preparation

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1 ndexr

Installation via Bioconductor:

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

library(ndexr)
```

2 RCX

For installing packages from github the `devtools` package is the most common approach. However, it requires XML libraries installed on the system which can cause problems while installation due to unmet dependencies. The `remotes` package covers the functionality to download and install R packages stored in 'GitHub', 'GitLab', 'Bitbucket', 'Bioconductor', or plain 'subversion' or 'git' repositories without depending on XML libraries. If `devtools` is already installed, of course it can be used, otherwise it is recommended to use the lightweight `remotes` package.

2.1 From Bioconductor:

```
if (!"BiocManager" %in% installed.packages()) {
  install.packages("BiocManager")
}
if (!"RCX" %in% installed.packages()) {
  BiocManager::install("RCX")
}
library(RCX)
```

2.2 From github using remotes:

```
if (!"remotes" %in% installed.packages()) {
  install.packages("remotes")
}
if (!"RCX" %in% installed.packages()) {
  remotes::install_github("frankkramer-lab/RCX")
}
library(RCX)
```

2.3 From github using devtools:

```
if (!"devtools" %in% installed.packages()) {
  install.packages("devtools")
}
if (!"RCX" %in% installed.packages()) {
  devtools::install_github("frankkramer-lab/RCX")
}
```

```
}
library(RCX)
```

3 Session info

```
sessionInfo()
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.3 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.9.0
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.9.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C              LC_TIME=de_DE.UTF-8      LC_COLLATE=en_US.UTF-8
##  [6] LC_MESSAGES=en_US.UTF-8   LC_PAPER=de_DE.UTF-8      LC_NAME=C                 LC_ADDRESS=C
## [11] LC_MEASUREMENT=de_DE.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
##  [1] XML_3.99-0.8      httr_1.4.2        RJSONIO_1.3-1.6    pacman_0.5.1      devtools_2.4.2
##  [8] timeDate_3043.102 pander_0.6.4      xtable_1.8-4       stringr_1.4.0     BiocStyle_2.18.1
## [15] igraph_1.2.7      gplots_3.1.1      dplyr_1.0.7        RColorBrewer_1.1-2 survival_3.2-7
##
## loaded via a namespace (and not attached):
##  [1] pkgload_1.2.3      jsonlite_1.7.2     splines_4.0.3      gtools_3.9.2      assertthat_0.2.1
##  [8] stats4_4.0.3       remotes_2.4.1      yaml_2.2.1         sessioninfo_1.1.1 pillar_1.6.4
## [15] digest_0.6.28      htmltools_0.5.2    Matrix_1.2-18      plyr_1.8.6        pkgconfig_2.0.3
## [22] webshot_0.5.2      processx_3.5.2     tibble_3.1.5       generics_0.1.1    ellipsis_0.3.2
## [29] cachem_1.0.6       BiocGenerics_0.36.1 cli_3.0.1          mime_0.12         magrittr_2.0.1
## [36] memoise_2.0.0      evaluate_0.14      fs_1.5.0           fansi_0.5.0       pkgbuild_1.2.0
## [43] tools_4.0.3        formatR_1.11       lifecycle_1.0.1    callr_3.7.0       compiler_4.0.3
## [50] tinytex_0.34       rlang_0.4.12       grid_4.0.3         htmlwidgets_1.5.4 crosstalk_1.1.1
## [57] testthat_3.1.0     DBI_1.1.1          curl_4.3.2         markdown_1.1      R6_2.5.1
## [64] utf8_1.2.2         rprojroot_2.0.2    desc_1.4.0         KernSmooth_2.23-17 stringi_1.7.5
## [71] vctrs_0.3.8        tidyrselect_1.1.1  xfun_0.27
```