## Installation

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## **Dependencies**

KEGGREST Seurat SeuratObject sp dplyr Matrix

If not installed already, we recommend to first install the latest version of Seurat and SeuratObject.

```
# we remove the last version to demonstrate installation
remove.packages("CellSpectra")

## Removing package from '/Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/library'
## (as 'lib' is unspecified)

#time stamp
start.time <- Sys.time()

# download the .tar.gz file and change to the respective path</pre>
```

install.packages("/Users/konstantin/Documents/GitHub/CellSpectra\_0.1.0.tar.gz", repos = NULL, type = "s

## Load

Check if we can load CellSpectra

```
end.time <- Sys.time()
execution_time <- end.time - start.time
print(execution_time)</pre>
```

## Time difference of 10.72674 secs

```
sessionInfo()
```

```
## R version 4.2.2 (2022-10-31)
## Platform: aarch64-apple-darwin20 (64-bit)
## Running under: macOS 15.1.1
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/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] CellSpectra_0.1.0
##
## loaded via a namespace (and not attached):
## [1] compiler_4.2.2
                               pillar_1.9.0
                                                      GenomeInfoDb_1.34.9
## [4] XVector_0.38.0
                               bitops_1.0-7
                                                      tools_4.2.2
## [7] zlibbioc_1.44.0
                               digest_0.6.31
                                                      lattice_0.20-45
## [10] evaluate_0.20
                               lifecycle_1.0.4
                                                      tibble_3.2.1
## [13] pkgconfig_2.0.3
                               png_0.1-8
                                                      rlang_1.1.4
## [16] Matrix_1.6-5
                               cli_3.6.3
                                                      rstudioapi_0.14
## [19] yaml 2.3.7
                               xfun 0.42
                                                      fastmap_1.1.1
## [22] GenomeInfoDbData_1.2.9 httr_1.4.5
                                                      dplyr_1.1.4
                               Biostrings_2.66.0
                                                       generics_0.1.3
## [25] knitr 1.45
## [28] S4Vectors_0.36.1
                               vctrs_0.6.5
                                                       IRanges_2.32.0
## [31] grid_4.2.2
                               tidyselect_1.2.1
                                                       stats4_4.2.2
                                                      fansi_1.0.6
## [34] glue_1.8.0
                               R6_2.5.1
## [37] rmarkdown 2.20
                               purrr_1.0.2
                                                      tidyr_1.3.1
## [40] magrittr_2.0.3
                                                      BiocGenerics_0.44.0
                               htmltools_0.5.4
## [43] KEGGREST_1.38.0
                               utf8_1.2.4
                                                      RCurl_1.98-1.10
## [46] crayon_1.5.2
```