

StemnesScoRe: An R package to estimate the stemness of glioma cancer cells at single-cell resolution

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Cancer stem cells are one of these populations and the study of cancer stem cells, which are thought to play an active role in the growth and recurrence of tumor cells, is critical in understanding the initiation, development, and resistance to treatment of cancer. This R package was developed to estimate the stemness score specific to glioblastoma using scATAC-seq data. In this way, researchers will be able to investigate the cancer stemness of GBM cells using only accessible regions in chromatin (scATAC-seq data).

Installation

```
library(devtools)
```

```
## Loading required package: usethis
```

```
devtools::install_github("Necla/StemnesScoRe")
```

```
## Skipping install of 'StemnesScoRe' from a github remote, the SHA1 (c017a255) has not changed since 1.
```

```
## Use 'force = TRUE' to force installation
```

```
library(StemnesScoRe)
```

Dependencies for the StemnesScoRe package

While using R programming, we suggest you use Rstudio which is the R statistical computing environment to use. devtools is required to install StemnesScoRe. StemnesScoRe uses the following R packages which have to be installed before installing the StemnesScoRe package:

- Iranges
- GenomicRanges
- readr
- readxl
- dplyr
- Matrix
- tidyverse

For complete list of functions and instructions:

```
library(help = "StemnesScoRe")
```

Downloading GBM scATAC-seq data

To execute the `stemness.score()` function within the package, you can download the GBM scATAC-seq data from either of the following sources:

1. Download the data from the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (GEO) using the accession number GSE139136.
2. Access the data directly from the "DATA" folder included within the package.

Obtaining/Reading gene list, gene importance, and genomic region data

Download genes obtained from machine learning algorithms along with their respective importance values from the "DATA" folder within the package. One can use different gene lists and their associated importance scores for downstream analyses and applications.

Obtain promoter and enhancer regions associated with the genes identified through ML algorithms using the GeneAlaCart database (<https://genealacart.genecards.org/>).

Set the File Path

Before running the `stemness.score()` function, you need to specify the file path to the folder containing your data. Let's call this folder "GBM_Data." Now, you can proceed to run the `stemness.score()` function on the acquired dataset as follows:

```
stemness.score("GBM_Data", "GSM4131776_4218_matrix.mtx.gz",  
"GSM4131776_4218_peaks.bed.gz", "GSM4131776_4218_barcodes.tsv.gz",  
"genelist.csv", "Classification_feature_Importance_RF.tsv", genomic.regions)
```

Session Info

```
sessionInfo()
```

```
## R version 4.2.1 (2022-06-23)  
## Platform: x86_64-apple-darwin17.0 (64-bit)  
## Running under: macOS Big Sur ... 10.16  
##  
## 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] StemnesScore_0.0.0.9000 devtools_2.4.5 usethis_2.1.6  
##  
## loaded via a namespace (and not attached):  
## [1] Rcpp_1.0.10 urlchecker_1.0.1 compiler_4.2.1 later_1.3.0  
## [5] remotes_2.4.2 prettyunits_1.1.1 profvis_0.3.7 tools_4.2.1
```

## [9] digest_0.6.31	pkgbuild_1.4.0	pkgload_1.3.2	evaluate_0.20
## [13] memoise_2.0.1	lifecycle_1.0.3	rlang_1.0.6	shiny_1.7.4
## [17] cli_3.6.0	rstudioapi_0.14	curl_5.0.0	yaml_2.3.7
## [21] xfun_0.39	fastmap_1.1.0	stringr_1.5.0	knitr_1.42
## [25] fs_1.6.1	vctr_0.5.2	htmlwidgets_1.6.1	glue_1.6.2
## [29] R6_2.5.1	processx_3.8.0	rmarkdown_2.20	sessioninfo_1.2.2
## [33] purrr_1.0.1	callr_3.7.3	magrittr_2.0.3	promises_1.2.0.1
## [37] ps_1.7.2	ellipsis_0.3.2	htmltools_0.5.4	mime_0.12
## [41] xtable_1.8-4	httpuv_1.6.8	stringi_1.7.12	miniUI_0.1.1.1
## [45] cachem_1.0.6	crayon_1.5.2		