

NetBoxR Tutorial

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Overview

The **netboxr** package composes a number of functions to retrieve and process genetic data from large-scale genomics projects (e.g. TCGA projects) including from mutations, copy number alterations, gene expression and DNA methylation. The netboxr package implements NetBox algorithm in R package. NetBox algorithm integrates genetic alterations with literature-curated pathway knowledge to identify pathway modules in cancer. NetBox algorithm uses (1) global network null model and (2) local network null model to assess the statistic significance of the discovered pathway modules.

Basics

Installation

References

- Cerami E, Demir E, Schultz N, Taylor BS, Sander C (2010) Automated Network Analysis Identifies Core Pathways in Glioblastoma. PLoS ONE 5(2): e8918. doi:10.1371/journal.pone.0008918
- Cerami EG, Gross BE, Demir E, Rodchenkov I, Babur O, Anwar N, Schultz N, Bader GD, Sander C. Pathway Commons, a web resource for biological pathway data. Nucleic Acids Res. 2011 Jan;39(Database issue):D685-90. doi:10.1093/nar/gkq1039. Epub 2010 Nov 10.

Session Information

```
sessionInfo()
```

```
## R version 3.6.1 (2019-07-05)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.5
##
## Matrix products: default
```

```

## BLAS: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] parallel stats4 stats graphics grDevices utils datasets
## [8] methods base
##
## other attached packages:
## [1] BiocStyle_2.12.0 knitr_1.25 netboxr_0.99.6
## [4] org.Hs.eg.db_3.8.2 AnnotationDbi_1.46.1 IRanges_2.18.3
## [7] S4Vectors_0.22.1 Biobase_2.44.0 BiocGenerics_0.30.0
## [10] clusterProfiler_3.12.0 paxtoolsr_1.18.0 XML_3.98-1.20
## [13] rJava_0.9-11 igraph_1.2.4.1
##
## loaded via a namespace (and not attached):
## [1] fgsea_1.10.1 colorspace_1.4-1 rjson_0.2.20
## [4] gggridges_0.5.1 rprojroot_1.3-2 qvalue_2.16.0
## [7] rstudioapi_0.10 roxygen2_6.1.1 farver_1.1.0
## [10] urltools_1.7.3 graphlayouts_0.5.0 ggrepel_0.8.1
## [13] bit64_0.9-7 xml2_1.2.2 splines_3.6.1
## [16] R.methodsS3_1.7.1 GOSemSim_2.10.0 polyclip_1.10-0
## [19] pkgload_1.0.2 zeallot_0.1.0 jsonlite_1.6
## [22] GO.db_3.8.2 R.oo_1.22.0 ggforce_0.3.1
## [25] BiocManager_1.30.4 readr_1.3.1 compiler_3.6.1
## [28] httr_1.4.1 rvcheck_0.1.3 backports_1.1.4
## [31] assertthat_0.2.1 Matrix_1.2-17 lazyeval_0.2.2
## [34] formatR_1.7 tweenr_1.0.1 htmltools_0.3.6
## [37] prettyunits_1.0.2 tools_3.6.1 gtable_0.3.0
## [40] glue_1.3.1 reshape2_1.4.3 DO.db_2.9
## [43] dplyr_0.8.3 fastmatch_1.1-0 Rcpp_1.0.2
## [46] enrichplot_1.4.0 vctr_0.2.0 gdata_2.18.0
## [49] ggraph_2.0.0 xfun_0.9 stringr_1.4.0
## [52] testthat_2.2.1 lifecycle_0.1.0 gtools_3.8.1
## [55] DOSE_3.10.2 europepmc_0.3 MASS_7.3-51.4
## [58] scales_1.0.0 tidygraph_1.1.2 hms_0.5.1
## [61] RColorBrewer_1.1-2 yaml_2.2.0 memoise_1.1.0
## [64] gridExtra_2.3 ggplot2_3.2.1 UpSetR_1.4.0
## [67] triebeard_0.3.0 stringi_1.4.3 RSQLite_2.1.2
## [70] desc_1.2.0 caTools_1.17.1.2 BiocParallel_1.18.1
## [73] rlang_0.4.0 pkgconfig_2.0.3 commonmark_1.7
## [76] bitops_1.0-6 evaluate_0.14 lattice_0.20-38
## [79] purrr_0.3.2 cowplot_1.0.0 bit_1.1-14
## [82] tidyselect_0.2.5 plyr_1.8.4 magrittr_1.5
## [85] R6_2.4.0 gplots_3.0.1.1 DBI_1.0.0
## [88] pillar_1.4.2 withr_2.1.2 tibble_2.1.3
## [91] crayon_1.3.4 KernSmooth_2.23-15 rmarkdown_1.15
## [94] viridis_0.5.1 progress_1.2.2 grid_3.6.1
## [97] data.table_1.12.2 blob_1.2.0 digest_0.6.21
## [100] tidyr_1.0.0 gridGraphics_0.4-1 R.utils_2.9.0
## [103] munsell_0.5.0 viridisLite_0.3.0 ggplotify_0.0.4

```