Package: SingscoreAMLMutations (via r-universe)

October 8, 2026

Title Using singscore to predict mutations in AML from transcriptomic signatures

Version 1.29.0

Description This workflow package shows how transcriptomic signatures can be used to infer phenotypes. The workflow begins by showing how the TCGA AML transcriptomic data can be downloaded and processed using the TCGAbiolinks packages. It then shows how samples can be scored using the singscore package and signatures from the MSigDB. Finally, the predictive capacity of scores in the context of predicting a specific mutation in AML is shown.The workflow exhibits the interplay of Bioconductor packages to achieve a gene-set level analysis.

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Encoding UTF-8

LazyData true

Workflow True

biocViews GeneExpressionWorkflow, GenomicVariantsWorkflow, ImmunoOncologyWorkflow, Workflow

VignetteBuilder knitr

Depends R (>= 4.1.0)

Imports dcanr, edgeR, ggplot2, gridExtra, GSEABase, mclust, org.Hs.eg.db, plyr, reshape2, rtracklayer, singscore, SummarizedExperiment, TCGAbiolinks, BiocFileCache

Suggests knitr, rmarkdown, BiocStyle, BiocWorkflowTools, spelling

RoxygenNote 7.2.0

Language en-US

URL https://github.com/DavisLaboratory/SingscoreAMLMutations

BugReports https://github.com/DavisLaboratory/SingscoreAMLMutations/issues

Config/pak/sysreqs cmake libglpk-dev make libbz2-dev libicu-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

Repository https://bioc.r-universe.dev

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RemoteUrl https://github.com/bioc/SingscoreAMLMutations

RemoteRef HEAD

RemoteSha 933e8dab832779fa56b129b43399f4105fb43b40

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`SingscoreAMLMutations-package`
SingscoreAMLMutations: Using singscore to predict mutations in AML from transcriptomic signatures

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Description

This workflow package shows how transcriptomic signatures can be used to infer phenotypes. The workflow begins by showing how the TCGA AML transcriptomic data can be downloaded and processed using the TCGAbiolinks packages. It then shows how samples can be scored using the singscore package and signatures from the MSigDB. Finally, the predictive capacity of scores in the context of predicting a specific mutation in AML is shown.The workflow exhibits the interplay of Bioconductor packages to achieve a gene-set level analysis.

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See Also

Useful links:

- https://github.com/DavisLaboratory/SingscoreAMLMutations
- Report bugs at https://github.com/DavisLaboratory/SingscoreAMLMutations/issues

AMLPatientMutationsTCGA

Mutation data for 4 genes for the TCGA AML patients

Description

This is the processed version of the mutation data available from the TCGA AML patients. The data set

Usage

```
AMLPatientMutationsTCGA
```

Format

A data.frame with 151 samples (rows) and mutation annotations for 4 genes:

NPM1c.Mut Mutations in the *NPM1* gene that result in a frame shit, also known as the NPM1c mutation (TRUE if mutated)

KMT2A.Fusion Fusion products of the *KMT2A* gene, also commonly known as *MLL* (TRUE if a fusion product exists)

KMT2A.PTD Partial tandem duplication of the *KMT2A* gene (TRUE if PTD observed)

PML.RARA Fusion of the *PML* and *RARA* gene (TRUE for fusions)

Source

(https://tcga-data.nci.nih.gov/docs/publications/aml_2012/SupplementalTable01.xlsx)

References

Cancer Genome Atlas Research Network, 2013. Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. New England Journal of Medicine, 368(22), pp.2059-2074.

Examples

```
data(AMLPatientMutationsTCGA)
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