Fração de Linfócitos

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Contexto

Fração de linfócitos

```
# pacotes  necessarios
library(UCSCXenaTools)
```

```
================================================================================
UCSCXenaTools version 1.4.8
Project URL: https://github.com/ropensci/UCSCXenaTools
Usages: https://cran.r-project.org/web/packages/UCSCXenaTools/vignettes/USCSXenaTools.html

If you use it in published research, please cite:
Wang et al., (2019). The UCSCXenaTools R package: a toolkit for accessing genomics data
  from UCSC Xena platform, from cancer multi-omics to single-cell RNA-seq.
  Journal of Open Source Software, 4(40), 1627, https://doi.org/10.21105/joss.01627
================================================================================
                              --Enjoy it--
```

```
library(IOBR)
```

```
Loading required package: tibble
```

```
Loading required package: dplyr
```

```
Attaching package: 'dplyr'
```

```
The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union

Loading required package: ggplot2

Loading required package: ggpubr

Loading required package: survival

Loading required package: ComplexHeatmap

Loading required package: grid

========================================
ComplexHeatmap version 2.18.0
Bioconductor page: http://bioconductor.org/packages/ComplexHeatmap/
Github page: https://github.com/jokergoo/ComplexHeatmap
Documentation: http://jokergoo.github.io/ComplexHeatmap-reference

If you use it in published research, please cite either one:
- Gu, Z. Complex Heatmap Visualization. iMeta 2022.
- Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional
    genomic data. Bioinformatics 2016.


The new InteractiveComplexHeatmap package can directly export static
complex heatmaps into an interactive Shiny app with zero effort. Have a try!

This message can be suppressed by:
  suppressPackageStartupMessages(library(ComplexHeatmap))
========================================

Loading required package: tidyHeatmap
```

```
======================================
tidyHeatmap version 1.8.1
If you use tidyHeatmap in published research, please cite:
1) Mangiola et al. tidyHeatmap: an R package for modular heatmap production
  based on tidy principles. JOSS 2020.
2) Gu, Z. Complex heatmaps reveal patterns and correlations in multidimensional
  genomic data. Bioinformatics 2016.
This message can be suppressed by:
  suppressPackageStartupMessages(library(tidyHeatmap))
======================================


Attaching package: 'tidyHeatmap'

The following object is masked from 'package:stats':

    heatmap

Loading required package: clusterProfiler



clusterProfiler v4.10.1  For help: https://yulab-smu.top/biomedical-knowledge-mining-book/

If you use clusterProfiler in published research, please cite:
T Wu, E Hu, S Xu, M Chen, P Guo, Z Dai, T Feng, L Zhou, W Tang, L Zhan, X Fu, S Liu, X Bo, a


Attaching package: 'clusterProfiler'

The following object is masked from 'package:stats':

    filter

Loading required package: patchwork

Loading required package: survminer


Attaching package: 'survminer'
```

```
The following object is masked from 'package:survival':

    myeloma

========================================================================
  IOBR v0.99.8  Immuno-Oncology Biological Research
  For Tutorial: https://iobr.github.io/book/
  For Help: https://github.com/IOBR/IOBR/issues

 If you use IOBR in published research, please cite:
 DQ Zeng, YR Fang, WJ Qiu, ..., GC Yu*, WJ Liao*, (2024)
 IOBR2: Multidimensional Decoding Tumor Microenvironment for Immuno-Oncology Research.
 bioRxiv, 2024.01. 13.575484;
 https://www.biorxiv.org/content/10.1101/2024.01.13.575484v2.full.pdf
========================================================================
 DQ Zeng, ZL Ye, RF Sheng, GC Yu, Y Xiong, ..., WJ Liao*.
 IOBR: Multi-omics Immuno-Oncology Biological Research to decode
  tumor microenvironment and signatures. Frontiers in Immunology. 12:687975,(2021).
 DOI: 10.3389/fimmu.2021.687975
 Higly Cited Paper and Hot Paper of WOS
========================================================================
```

```r
## -- download da matriz de expressao genica atraves do xenabrowser
eset_acc<-XenaGenerate(subset = XenaCohorts =="GDC TCGA Adrenocortical Cancer (ACC)") %>%
  XenaFilter(filterDatasets    = "TCGA-ACC.htseq_counts.tsv") %>%
  XenaQuery() %>%
  XenaDownload() %>%
  XenaPrepare()
```

```
This will check url status, please be patient.

All downloaded files will under directory /tmp/Rtmp8rnMUG.

The 'trans_slash' option is FALSE, keep same directory structure as Xena.

Creating directories for datasets...

Downloading TCGA-ACC.htseq_counts.tsv.gz
```

```
## -- anotacao e normalizacao em TPM
eset_acc$Ensembl_ID <- gsub("\\..*","",eset_acc$Ensembl_ID) # remocao da versao
eset_acc <- column_to_rownames(eset_acc, var = "Ensembl_ID")
eset_acc <- (2^eset_acc)+1 # revertendo para a contagem original (pois estao em log2)
eset_acc <- count2tpm(countMat = eset_acc, idType = "Ensembl") # normalizacao em TPM
```

```
>>>--- Using variables (anno_grch38) and gene lengths (eff_length)  built into the IOBR packa

>>>--- The gene lengths (eff_length) was estimated by function `getGeneLengthAndGCContent` fi

Warning in count2tpm(countMat = eset_acc, idType = "Ensembl"): >>>--- Omit 3985
genes of which length is not available !
```

```
epic <- deconvo_tme(eset = log2(eset_acc+1), method = "epic", arrays = FALSE)
```

```
>>> Running EPIC

Warning in IOBR::EPIC(bulk = eset, reference = ref, mRNA_cell = NULL, scaleExprs = TRUE): The
TCGA-OR-A5JR-01A; TCGA-OR-A5JW-01A; TCGA-PA-A5YG-01A; TCGA-OR-A5L8-01A; TCGA-OR-A5JM-01A; TC
 - check fit.gof for the convergeCode and convergeMessage

Warning in IOBR::EPIC(bulk = eset, reference = ref, mRNA_cell = NULL,
scaleExprs = TRUE): mRNA_cell value unknown for some cell types: CAFs,
Endothelial - using the default value of 0.4 for these but this might bias the
true cell proportions from all cell types.
```

```
head(epic)
```

```
# A tibble: 6 x 9
  ID      Bcells_EPIC CAFs_EPIC CD4_Tcells_EPIC CD8_Tcells_EPIC Endothelial_EPIC
  <chr>         <dbl>     <dbl>           <dbl>           <dbl>            <dbl>
1 TCGA-O~     0.00927   0.0144            0.149         0.0155             0.125
2 TCGA-O~     0.00638   0.0126            0.154         0.00438            0.124
3 TCGA-O~     0.0183    0.0100            0.147         0.0248             0.172
4 TCGA-O~     0.0125    0.00681           0.118         0.0379             0.129
```

```
5 TCGA-O~     0.0116    0.0104            0.111         0.0268            0.0854
6 TCGA-O~     0.0124    0.0109            0.137         0.0238            0.138
# i 3 more variables: Macrophages_EPIC <dbl>, NKcells_EPIC <dbl>,
#   otherCells_EPIC <dbl>
```

```r
xcell <- deconvo_tme(eset = log2(eset_acc+1), method = "xcell", arrays = FALSE)
```

```
>>> Running xCell

[1] "Num. of genes: 10773"

Warning: Calling gsva(expr=., gset.idx.list=., method=., ...) is deprecated;
use a method-specific parameter object (see '?gsva').

Estimating ssGSEA scores for 489 gene sets.
[1] "Calculating ranks..."
[1] "Calculating absolute values from ranks..."

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```
head(xcell)
```

```
# A tibble: 6 x 68
  ID               aDC_xCell Adipocytes_xCell Astrocytes_xCell `B-cells_xCell`
  <chr>                <dbl>            <dbl>            <dbl>           <dbl>
1 TCGA-OR-A5JP-01A   0.0341          0                7.12e- 2        2.49e-18
2 TCGA-OR-A5JG-01A   0.0789          1.48e-19         3.74e-18        2.24e- 2
3 TCGA-OR-A5K1-01A   0.0485          4.96e- 3         4.65e-18        0
4 TCGA-OR-A5JR-01A   0.0502          1.25e-18         0               6.35e- 3
5 TCGA-OR-A5KU-01A   0.00250         1.27e-20         0               1.08e- 2
6 TCGA-OR-A5L9-01A   0.290           3.39e- 3         2.45e-18        0
# i 63 more variables: Basophils_xCell <dbl>,
#   `CD4+_memory_T-cells_xCell` <dbl>, `CD4+_naive_T-cells_xCell` <dbl>,
#   `CD4+_T-cells_xCell` <dbl>, `CD4+_Tcm_xCell` <dbl>, `CD4+_Tem_xCell` <dbl>,
#   `CD8+_naive_T-cells_xCell` <dbl>, `CD8+_T-cells_xCell` <dbl>,
#   `CD8+_Tcm_xCell` <dbl>, `CD8+_Tem_xCell` <dbl>, cDC_xCell <dbl>,
#   Chondrocytes_xCell <dbl>, `Class-switched_memory_B-cells_xCell` <dbl>,
#   CLP_xCell <dbl>, CMP_xCell <dbl>, DC_xCell <dbl>, ...
```

```
mcp <- deconvo_tme(eset = log2(eset_acc+1), method = "mcpcounter", arrays = FALSE)
```

```
>>> Running MCP-counter
```

```
head(mcp)
```

```
# A tibble: 6 x 11
  ID            T_cells_MCPcounter CD8_T_cells_MCPcounter Cytotoxic_lymphocyte~1
  <chr>                      <dbl>                  <dbl>                  <dbl>
1 TCGA-OR-A5JP~              0.404                 0.0611                  0.337
2 TCGA-OR-A5JG~              0.314                 0.0706                  0.373
3 TCGA-OR-A5K1~              0.536                 0.189                   0.676
4 TCGA-OR-A5JR~              0.580                 0.442                   0.984
5 TCGA-OR-A5KU~              0.653                 0.0605                  0.349
6 TCGA-OR-A5L9~              0.300                 0.146                   0.320
# i abbreviated name: 1: Cytotoxic_lymphocytes_MCPcounter
# i 7 more variables: B_lineage_MCPcounter <dbl>, NK_cells_MCPcounter <dbl>,
#   Monocytic_lineage_MCPcounter <dbl>,
#   Myeloid_dendritic_cells_MCPcounter <dbl>, Neutrophils_MCPcounter <dbl>,
#   Endothelial_cells_MCPcounter <dbl>, Fibroblasts_MCPcounter <dbl>
```

```
estimate <- deconvo_tme(eset = log2(eset_acc+1), method = "estimate", arrays = FALSE)
```

```
>>> Running ESTIMATE
```

```
[1] "Merged dataset includes 10158 genes (254 mismatched)."
[1] "1 gene set: StromalSignature  overlap= 138"
[1] "2 gene set: ImmuneSignature  overlap= 133"
```

```
head(estimate)
```

```
# A tibble: 6 x 5
  ID           StromalScore_estimate ImmuneScore_estimate ESTIMATEScore_estimate
  <chr>                        <dbl>                <dbl>                   <dbl>
1 TCGA-OR-A5J~                 -687.                -962.                  -1649.
2 TCGA-OR-A5J~                 -746.                -439.                  -1185.
3 TCGA-OR-A5K~                 -603.                -175.                   -778.
4 TCGA-OR-A5J~                 -858.                 -48.9                  -906.
5 TCGA-OR-A5K~                 -947.               -1110.                  -2057.
6 TCGA-OR-A5L~                 -195.                 830.                    635.
# i 1 more variable: TumorPurity_estimate <dbl>
```

```r
timer <- deconvo_tme(eset = log2(eset_acc+1),
                     method = "timer",
                     group_list = rep("acc",ncol(eset_acc)),
                     arrays = FALSE)
```

```
## Enter batch mode

## Loading immune gene expression

[1] "Outlier genes: APOE CYP17A1 FTL MT.ATP6 MT.CO1 MT.CO2 MT.CO3 MT.CYB MT.ND1 MT.ND2 MT.ND3

## Removing the batch effect of /tmp/Rtmp8rnMUG/file68b4484cc87a

Found2batches

Adjusting for0covariate(s) or covariate level(s)

Standardizing Data across genes

Fitting L/S model and finding priors

Finding parametric adjustments

Adjusting the Data
```

```r
head(timer)
```

```
# A tibble: 6 x 7
  ID             B_cell_TIMER T_cell_CD4_TIMER T_cell_CD8_TIMER Neutrophil_TIMER
  <chr>                 <dbl>            <dbl>            <dbl>             <dbl>
1 TCGA-OR-A5JP-~        0.114            0.101            0.219             0.111
2 TCGA-OR-A5JG-~        0.110            0.104            0.212             0.108
3 TCGA-OR-A5K1-~        0.112            0.106            0.233             0.110
4 TCGA-OR-A5JR-~        0.113            0.106            0.233             0.112
5 TCGA-OR-A5KU-~        0.109            0.108            0.213             0.106
6 TCGA-OR-A5L9-~        0.107            0.103            0.213             0.103
# i 2 more variables: Macrophage_TIMER <dbl>, DC_TIMER <dbl>
```

```r
save(epic, file = "epic.RData")
save(eset_acc, file = "eset_acc_xenabrowser.RData")
```