

Introduction to the *sampleClassifierData* Package

Khadija El Amrani

November 5, 2019

Contents

| | | |
|---|-------------------------------|---|
| 1 | Introduction | 1 |
| 2 | Data overview | 1 |
| 3 | Data pre-processing | 2 |

1 Introduction

sampleClassifierData contains a collection of publicly available microarray and RNA-seq datasets that have been pre-processed for use with the *sampleClassifier* package. These pre-processed datasets can be used as reference matrices for gene expression profile classification using *sampleClassifier*. This introduction contains a brief overview of the datasets included in the package. For more examples on how to use *sampleClassifier* and *sampleClassifierData*, please refer to the *sampleClassifier* Vignette.

2 Data overview

First, we load the package *sampleClassifierData*:

```
> library(sampleClassifierData)
```

The *sampleClassifierData* package contains two microarray datasets and two RNA-seq datasets that have been pre-processed for use with *sampleClassifier*.

The datasets are stored as `SummarizedExperiment` objects. The numeric matrices to use with the *sampleClassifier* can be extracted using the `assay()` function from *SummarizedExperiment* package.

The object `se_rnaseq_refmat` contains pre-processed RNA-seq data from the study E-MTAB-1733 [1]. The data are available from the ArrayExpress [2] (<http://www.ebi.ac.uk/arrayexpress/>) database. The provided dataset contains gene expression profiles from 24 tissue types. Each tissue is represented by 3 replicates, except ovary which is represented by 2 replicates.

To download and load this dataset, run the following code:

Introduction to the *sampleClassifierData* Package

```
> data("se_rnaseq_refmat")
> rnaseq_refmat <- assay(se_rnaseq_refmat)
> dim(rnaseq_refmat)

[1] 43819    71
```

The object *se_micro_refmat* contains normalized microarray data from the study GSE3526 [3]. The dataset is available from GEO [4] (<https://www.ncbi.nlm.nih.gov/geo/>). The provided dataset contains gene expression profiles from 26 tissues. Each tissue is represented by 3 replicates. To download and load this dataset, run the following code:

```
> data("se_micro_refmat")
> micro_refmat <- assay(se_micro_refmat)
> dim(micro_refmat)

[1] 54675    78
```

The object *se_rnaseq_testmat* contains pre-processed RNA-seq data derived from the study E-MTAB-513 [5]. The data are available from the ArrayExpress (<http://www.ebi.ac.uk/arrayexpress/>) database. The provided dataset contains gene expression profiles from 12 tissues. To download and load this dataset, run the following code:

```
> data("se_rnaseq_testmat")
> rnaseq_testmat <- assay(se_rnaseq_testmat)
> dim(rnaseq_testmat)

[1] 43819    12
```

The object *se_micro_testmat* contains normalized microarray data derived from the study GSE2361 [6]. The dataset is available from GEO. The provided dataset contains gene expression profiles from 16 tissues. To download and load this dataset, run the following code:

```
> data("se_micro_testmat")
> micro_testmat <- assay(se_micro_testmat)
> dim(micro_refmat)

[1] 54675    78
```

3 Data pre-processing

The reads from the studies E-MTAB-1733 and E-MTAB-513 were mapped to the GRCh37 version of the human genome with Tophat v2.1.0 [7]. FPKM (fragments per kilobase of exon model per million mapped reads) values were calculated using cuffnorm v2.2.1 [8]. The used data from E-MTAB-1733 were extracted after processing of all samples and averaging across technical replicates.

The microarray data from the studies GSE3526 and GSE2361 were normalized using YuGene [9].

References

- [1] Linn Fagerberg, Björn M Hallström, Per Oksvold, Caroline Kampf, Dijana Djureinovic, Jacob Odeberg, Masato Habuka, Simin Tahmasebpour, Angelika Danielsson, Karolina Edlund, Anna Asplund, Evelina Sjöstedt, Emma Lundberg, Cristina Al-Khalili Szigyarto, Marie Skogs, Jenny Ottosson Takanen, Holger Berling, Hanna Tegel, Jan Mulder, Peter Nilsson, Jochen M Schwenk, Cecilia Lindskog, Frida Danielsson, Adil Mardinoglu, Asa Sivertsson, Kalle von Feilitzen, Mattias Forsberg, Martin Zwahlen, IngMarie Olsson, Sanjay Navani, Mikael Huss, Jens Nielsen, Fredrik Ponten, and Mathias Uhlén. Analysis of the human tissue-specific expression by genome-wide integration of transcriptomics and antibody-based proteomics. *Molecular & cellular proteomics : MCP*, 13(2):397–406, feb 2014. URL: <http://www.ncbi.nlm.nih.gov/pubmed/24309898><http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC3916642>, doi:10.1074/mcp.M113.035600.
- [2] Alvis Brazma, Helen Parkinson, Ugis Sarkans, Mohammadreza Shojatalab, Jaak Vilo, Niran Abeygunawardena, Ele Holloway, Misha Kapushesky, Patrick Kemmeren, Gonzalo Garcia Lara, Ahmet Oezcimen, Philippe Rocca-Serra, and Susanna-Assunta Sansone. ArrayExpress—a public repository for microarray gene expression data at the EBI. *Nucleic acids research*, 31(1):68–71, jan 2003. URL: <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=165538&tool=pmcentrez&rendertype=abstract>.
- [3] Richard B Roth, Peter Hevezi, Jerry Lee, Dorian Willhite, Sandra M Lechner, Alan C Foster, and Albert Zlotnik. Gene expression analyses reveal molecular relationships among 20 regions of the human CNS. *Neurogenetics*, 7(2):67–80, may 2006. URL: <http://www.ncbi.nlm.nih.gov/pubmed/16572319>, doi:10.1007/s10048-006-0032-6.
- [4] Tanya Barrett, Dennis B Troup, Stephen E Wilhite, Pierre Ledoux, Dmitry Rudnev, Carlos Evangelista, Irene F Kim, Alexandra Soboleva, Maxim Tomashevsky, and Ron Edgar. NCBI GEO: mining tens of millions of expression profiles—database and tools update. *Nucleic acids research*, 35(Database issue):D760–5, jan 2007. URL: <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1669752&tool=pmcentrez&rendertype=abstract>, doi:10.1093/nar/gkl887.
- [5] The illumina body map 2.0 data. <https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-513/>.
- [6] Xijin Ge, Shogo Yamamoto, Shuichi Tsutsumi, Yutaka Midorikawa, Sigeo Ihara, San Ming Wang, and Hiroyuki Aburatani. Interpreting expression profiles of cancers by genome-wide survey of breadth of expression in normal tissues. *Genomics*, 86(2):127–41, aug 2005. URL: <http://www.sciencedirect.com/science/article/pii/S0888754305001114>, doi:10.1016/j.ygeno.2005.04.008.
- [7] Cole Trapnell, Lior Pachter, and Steven L Salzberg. TopHat: Discovering splice junctions with RNA-Seq. *Bioinformatics*, 25(9):1105–1111, may 2009. URL: <http://www.ncbi.nlm.nih.gov/pubmed/19289445><http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC2672628>, arXiv:9605103, doi:10.1093/bioinformatics/btp120.
- [8] Cole Trapnell, Brian A Williams, Geo Pertea, Ali Mortazavi, Gordon Kwan, Marijke J van Baren, Steven L Salzberg, Barbara J Wold, and Lior Pachter. Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. *Nature Biotechnology*, 28(5):511–515, may 2010. URL: <http://www.nature.com/doi/10.1038/nbt.1621><http://www.nature.com/doi/10.1038/nbt.1621>

Introduction to the *sampleClassifierData* Package

[//www.nature.com/nbt/journal/v28/n5/full/nbt.1621.html](http://www.nature.com/nbt/journal/v28/n5/full/nbt.1621.html){%}5Cnhttp:
[//www.nature.com/nbt/journal/v28/n5/pdf/nbt.1621.pdf](http://www.nature.com/nbt/journal/v28/n5/pdf/nbt.1621.pdf), arXiv:171,
doi:10.1038/nbt.1621.

- [9] Kim-Anh Lê Cao, Florian Rohart, Leo Mchugh, Othmar Korn, and Christine A Wells. YuGene: A simple approach to scale gene expression data derived from different platforms for integrated analyses. *Genomics*, 103:239–251, 2014.
doi:10.1016/j.ygeno.2014.03.001.