Gene Set BenchMark

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1 Introduction

The `GSBenchMark` contains eleven expression datasets representative of different diseases. The package also contains a list of pathways and their associated gene targets. Together with these datasets and the pathways provide a benchmark for machine learning and pathway analyses, most of them used previously in [1].

2 Datasets

Benchmark datasets and pathway targets were downloaded from supplemental files and sources cited in [1]. These datasets covers different diseases: Leukaemia [2], Marfan [3],

1

Melanoma [4], Prostate [5], Sarcoma [6], Head and neck cancer [7], response to breast cancer treatmetn [8], Bipolar disorder [9]. We also added datasets for two new diseases: Parkinson's disease [10], and Melanoma cancer[4]. We did not include two of the datasets mentioned in [1]: First, the famous Leaukemia data set in [11] which is available through package **golubEsets**. Secondly, the data presented in paper [12] because the data were not available to us. These data were converted from Matlab to R for this package.

First, we load the library:

```
> require(GSBenchMark)
```

2.1 Pathway Data

GSBenchMark contains a list of the pathways.

```
> data(diracpathways)
> class(diracpathways)

[1] "list"

> names(diracpathways)[1:5]

[1] "DEATHPATHWAY"       "TCAPOPTOSISPATHWAY" "CCR3PATHWAY"
[4] "NEUTROPHILPATHWAY"  "ALTERNATIVEPATHWAY"

> class(diracpathways[[1]])

[1] "character"

> diracpathways[[1]]

      "BID"     "TRAF2" "TNFRSF25"   "NFKBIA"     "NFKB1" "TNFSF12"     "CASP6"

    "CASP3"     "CASP9"    "CASP7"     "BCL2"     "CASP8"    "CHUK"     "CFLAR"

     "DFFA"      "DFFB"     "RELA"     "CYCS"     "LMNA"     "GAS2"      "FADD"

    "BIRC4"     "BIRC3"    "BIRC2"    "TRADD" "TNFRSF10A"   "CASP10"  "TNFSF10"

"TNFRSF10B"     "RIPK1"    "APAF1"  "MAP3K14"   "SPTAN1"

> pathways = diracpathways;
```

The variable `diracpathways` contains the pathways genes. It is a list. Each element represents a pathway with its name. Each elements contains a list of characters which represent the genes in the pathway.

2.2 Gene Expression Datasets

Now, we load the datasets names:

```
> data(GSBenchMarkDatasets)
> print(GSBenchMark.Dataset.names)

 [1] "leukemia_GSEA"        "marfan_GDS2960"       "melanoma_GDS2735"
 [4] "parkinsons_GDS2519"   "prostate_GDS2545_m_nf" "prostate_GDS2545_m_p"
 [7] "prostate_GDS2545_p_nf" "sarcoma_data"         "squamous_GDS2520"
[10] "breast_GDS807"        "bipolar_GDS2190"
```

Here is a summary of the datasets:

```
> for(i in 1: length(GSBenchMark.Dataset.names))
 {
   DataSetStudy = GSBenchMark.Dataset.names[[i]]
   data(list=DataSetStudy)
   cat("Data Set",DataSetStudy,"\n")
   print(phenotypesLevels)
   print(table(phenotypes))
 }
Data Set leukemia_GSEA
     0     1
"AML" "ALL"
phenotypes
 0  1
24 24
Data Set marfan_GDS2960
         0         1
"non-MFS"     "MFS"
phenotypes
 0  1
41 60
Data Set melanoma_GDS2735
          0           1
    "Normal" "metastasis"
phenotypes
 0  1
23 23
Data Set parkinsons_GDS2519
          0           1
    "Normal" "Parkinson's"
phenotypes
 0  1
22 50
Data Set prostate_GDS2545_m_nf
          0           1
    "normal" "metastasis"
phenotypes
 0  1
```

```
18 25
Data Set prostate_GDS2545_m_p
             0              1
    "primary" "metastasis"
phenotypes
 0  1
65 25
Data Set prostate_GDS2545_p_nf
         0           1
 "normal" "primary"
phenotypes
 0  1
18 65
Data Set sarcoma_data
      0       1
 "LMS" "GIST"
phenotypes
 0  1
31 37
Data Set squamous_GDS2520
        0         1
"Normal"   "HNSCC"
phenotypes
 0  1
22 22
Data Set breast_GDS807
               0                1
    "Responsive" "Non-responsive"
phenotypes
 0  1
32 28
Data Set bipolar_GDS2190
        0         1
 "Normal" "Bipolar"
phenotypes
 0  1
31 30
```

The data consist of three variables: `exprsdata`, `phenotypes`, and `phenotypesLevels`. `exprsdata` consists of gene expressions. `phenotypes` contains the sample labels: "0" indicates less dangarous and "1" more dangerous phenotype. `phenotypesLevels` makes the connection between "0" and "1" with the real label names e.g. "Normal" and "Parkinson's". `GSBenchMark` requires the rownames of gene expression varaible represent the gene names, *i.e.* they are represented in the pathway information variable.

2.3   Matching pathway targets to gene expression datasets

One can extract the gene names by:

```
> genenames = rownames(exprsdata);
> genenames[1:10]

 [1] "DDR1"    "RFC2"    "HSPA6"   "PAX8"    "GUCA1A" "UBA7"    "THRA"    "PTPN21" "CCL5"
[10] "CYP2E1"
```

Also, it is possible that some of the genes in a pathway are not represented in the expression data. We prune them as the following:

```
> prunedpathways = lapply(pathways, function(x) intersect(x, genenames))
> emptypathways = which(sapply(prunedpathways, length) < 2)
> if (length(emptypathways) > 0) {
        warning(paste("After pruning the pathways, there exist pathways with zero or one gene!\n Sma
            paste(names(emptypathways), collapse = ","), "\n"))
        diracpathwayPruned= prunedpathways[-emptypathways]
 }else {
        diracpathwayPruned = prunedpathways
 }
> cat("Number of pathways before pruning ",length(pathways),"\n")

Number of pathways before pruning  249

> cat("Number of pathways after pruning ",length(diracpathwayPruned))

Number of pathways after pruning  249
```

phenotypes is a factor with with levels ("0","1") where "1" indicates more dangerous phenotype. For real labels, one can look at **phenotypesLevels**

```
> summary(phenotypes)

 0  1
31 30

> phenotypesLevels

        0         1
 "Normal" "Bipolar"
```

3   System Information

Session information:

```
> toLatex(sessionInfo())
```

- R version 3.5.0 (2018-04-23), `x86_64-pc-linux-gnu`

- Locale: `LC_CTYPE=en_US.UTF-8`, `LC_NUMERIC=C`, `LC_TIME=en_US.UTF-8`,
  `LC_COLLATE=C`, `LC_MONETARY=en_US.UTF-8`, `LC_MESSAGES=en_US.UTF-8`,
  `LC_PAPER=en_US.UTF-8`, `LC_NAME=C`, `LC_ADDRESS=C`, `LC_TELEPHONE=C`,
  `LC_MEASUREMENT=en_US.UTF-8`, `LC_IDENTIFICATION=C`

- Running under: `Ubuntu 16.04.4 LTS`

- Matrix products: default

- BLAS: `/home/biocbuild/bbs-3.7-bioc/R/lib/libRblas.so`

- LAPACK: `/home/biocbuild/bbs-3.7-bioc/R/lib/libRlapack.so`

- Base packages: base, datasets, grDevices, graphics, methods, stats, utils

- Other packages: GSBenchMark 0.114.0

- Loaded via a namespace (and not attached): compiler 3.5.0, tools 3.5.0

4   Literature Cited

References

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