

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],

Melanoma [4], Prostate [5], Sarcoma [6], Head and neck cancer [7], response to breast cancer treatment [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 Leukemia 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 dangerous 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 variable 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 Sm",
    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 3.3.1 (2016-06-21), 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
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: GSBenchmark 0.108.0
- Loaded via a namespace (and not attached): tools 3.3.1

4 Literature Cited

References

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