PatientGeneSets package

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Contents

1 Overview

Patient-oriented methods are a novel approach to gene-set analysis which calculate gene-set scores for each sample, then combine them across samples. By comparison, gene-oriented methods calculate a score for each gene across all samples, then combine them into gene-set scores. We find that for cancer mutation data, patient-oriented methods often perform better on both real and simulated data.

The PatientGeneSets package has functions which perform gene-set analyses for cancer mutation data. It can be used to compute p-values and q-values for 4 patient-oriented methods described in [2], as well as the gene-oriented method described in [10] (see also [8]), which is in the limma package and performs a Wilcoxon test. It can also be used to do the simulations described in [2]. The user has a choice between calculating q-values based on the FDR-control method in [1] or [11]. This package is closely related to the CancerMutationAnalysis package, available at http://bcb.dfci.harvard.edu/~gp/software/CancerMutationAnalysis/cma.htm ([6]), which provides methods for gene-level analysis of cancer mutation data. In particular, the cma.scores function and the data format are nearly identical, but the PatientGeneSets package does not consider the two-phase design when performing gene-set analysis.

This vignette represents an introduction on the PatientGeneSets package. The primary function do.gene.set.analysis, which implements the gene-set analysis methods. The function

sim.data.p.values performs simulations using either the permutation null or the passenger null (see [2]). The function cma.data calculates scores for each gene across all samples, as in [9] and [12]. The functions extract.sims.method and combine.sims are used to manipulate the objects resulting from sim.data.p.values.

2 Glioblastoma dataset

We use the glioblastoma dataset from [7]. When typing data(Parsons), 4 objects are loaded: CoverageBrain, EventsBySampleBrain, GeneSizes08 and MutationsBrain. For this example, we use KEGG annotations ([3], [5], [4]). from the Bioconductor package KEGG.db by using the KEGGPATHID2EXTID object.

```
> library(PatientGeneSets)
> data(Parsons)
> ls()

[1] "CoverageBrain"       "EventsBySampleBrain" "GeneSizes08"
[4] "MutationsBrain"

> library(KEGG.db)
> KEGGPATHID2EXTID

PATHID2EXTID map for KEGG (object of class "AnnDbBimap")
```

Since the genes in the glioblastoma dataset are annotated by gene-names, while KEGGPATHID2EXTID uses EntrezGene identifiers, we also provide a vector mapping the identifiers to the names, which we obtained by using the biomaRt package.

```
> data(ID2name)
> head(ID2name)

     10      100     1000    10000    10007     1001
 "NAT2"    "ADA"   "CDH2"   "AKT3" "GNPDA1"   "CDH3"
```

3 Implementing the gene-set analysis methods

The function do.gene.set.analysis returns a data-frame with p-values and q-values for all the methods selected. By default, all the methods are implemented; however this takes several minutes. Setting the gene.method parameter to TRUE implements the gene-oriented method. The other method parameters refer to the patient-oriented methods: perm.null.method refers to the permutation null without heterogeneity, perm.null.het.method to the permutation null with heterogeneity, pass.null.method to the passenger null without heterogeneity, and pass.null.het.method to the passenger null with heterogeneity. See [2] for more details on all these methods.
The gene-sets we use correspond to the KEGG annotations for endometrial cancer, non-small cell lung cancer, and alanine, aspartate and glutamate metabolism i.e. hsa05213, hsa05223, and hsa00250:

```
> as.character(KEGGPATHNAME2ID[c("Endometrial cancer",
+                                "Non-small cell lung cancer",
+                                "Alanine, aspartate and glutamate metabolism")])
```

```
Alanine, aspartate and glutamate metabolism
                                    "00250"
                           Endometrial cancer
                                    "05213"
                  Non-small cell lung cancer
                                    "05223"
```

```
> resultsBrain <-
+     do.gene.set.analysis(EventsBySample = EventsBySampleBrain,
+                          GeneSizes = GeneSizes08,
+                          GeneSets = KEGGPATHID2EXTID[c("hsa05213",
+                          "hsa05223",  "hsa00250")],
+                          Coverage = CoverageBrain,
+                          ID2name = ID2name,
+                          gene.method = FALSE,
+                          perm.null.method = TRUE,
+                          perm.null.het.method = FALSE,
+                          pass.null.method = TRUE,
+                          pass.null.het.method = FALSE)
```

```
[1] "Permutation null w/o heterogeneity"
[1] "Mon Oct 31 23:01:35 2011"
[1] "Passenger null w/o heterogeneity"
[1] "Mon Oct 31 23:01:35 2011"
[1] "Mon Oct 31 23:01:39 2011"
```

The resulting object is a data-frame, with NAs for the methods which were not implemented:

```
> resultsBrain
```

```
         p.values.gene q.values.gene p.values.perm.null q.values.perm.null
hsa05213            NA             1       9.019202e-16       2.705761e-15
hsa05223            NA             1       1.644843e-15       2.467264e-15
hsa00250            NA             1       3.105934e-01       3.105934e-01
         p.values.perm.null.het q.values.perm.null.het p.values.pass.null
hsa05213                     NA                      1       2.108377e-10
hsa05223                     NA                      1       2.735935e-11
hsa00250                     NA                      1       6.340137e-01
         q.values.pass.null p.values.pass.null.het q.values.pass.null.het
hsa05213      3.162565e-10                     NA                      1
hsa05223      8.207804e-11                     NA                      1
hsa00250      6.340137e-01                     NA                      1
```

3.1 Calculating gene scores

In order to implement the gene-oriented method, we need to have gene-level scores. We can obtain a variety of scores using the `cma.scores` function. The functions in this package are designed to use the `logLRT` scores.

```
> GeneScores <- cma.scores(cma.data = MutationsBrain,
+                          number.genes = nrow(GeneSizes08))
> head(GeneScores)

                   CaMP neglogPg   logLRT logitBinomialPosteriorDriver
A2M@@408      0.7113996 2.279349 1.845074                          NA
A4GALT@@21470 1.2286366 3.232244 2.798146                          NA
ABCA10@@388   0.9279687 2.597908 2.163654                          NA
ABCA4@@140    0.5650629 2.097952 1.663669                          NA
ABCA7@@194    0.9745022 2.673914 2.239663                          NA
ABCB6@@2071   1.2044322 3.146882 2.712739                          NA
              PoissonlogBF PoissonPosterior Poissonlmlik0 Poissonlmlik1
A2M@@408                NA               NA            NA            NA
A4GALT@@21470           NA               NA            NA            NA
ABCA10@@388             NA               NA            NA            NA
ABCA4@@140              NA               NA            NA            NA
ABCA7@@194              NA               NA            NA            NA
ABCB6@@2071             NA               NA            NA            NA
```

4 Simulating data

We now demonstrate the use of the `sim.data.p.values` function, which simulates datasets under either the permutation or passenger null (see [2]), depending on whether `pass.null` is set to `TRUE` or `FALSE`, and calculates the p-values and q-values for those datasets for the selected methods. The simulations may also include spiked-in gene-sets, by using the `perc.samples` and `spiked.set.sizes` options. For example, if one desires to have two spiked-in gene-sets, both having 50 genes, but one having the probability of being altered in any given sample of 0.75 and the other of 0.95, then these parameters should be set to `perc.samples = c(75, 90)` and `spiked.set.sizes = 50`. The spiked-in gene-sets are artificially created with hypothetical genes (for more details on how they are generated, see [2]. To simulate the data without spiked-in sets, under the permutation or passenger null hypotheses, the parameters should be set as following: `perc.samples = NULL, spiked.set.sizes = NULL`. The object outputted by `sim.data.p.values` is of the class `SetMethodsSims`. Note that this code takes several minutes to run:

```
> set.seed(831984)
> resultsSim <-
+     sim.data.p.values(EventsBySample = EventsBySampleBrain,
+                       Mutations = MutationsBrain,
+                       GeneSizes = GeneSizes08,
+                       Coverage = CoverageBrain,
+                       GeneSets = KEGGPATHID2EXTID[c("hsa05213",
+                       "hsa05223", "hsa00250")],
+                       ID2name = ID2name,
+                       nr.iter = 2,
+                       pass.null = TRUE,
+                       perc.samples = c(75, 95),
+                       spiked.set.sizes = c(50),
+                       show.iter = TRUE,
```

```
+                       gene.method = FALSE,
+                       perm.null.method = TRUE,
+                       perm.null.het.method = FALSE,
+                       pass.null.method = TRUE,
+                       pass.null.het.method = FALSE)

[1] "Currently simulating data: Iteration #1"
[1] "Mon Oct 31 23:01:40 2011"
[1] "Currently simulating data: Iteration #2"
[1] "Mon Oct 31 23:02:31 2011"
[1] ""
[1] "Implement methods: Iteration #1"
[1] "Permutation null w/o heterogeneity"
[1] "Mon Oct 31 23:03:18 2011"
[1] "Passenger null w/o heterogeneity"
[1] "Mon Oct 31 23:03:18 2011"
[1] "Mon Oct 31 23:03:20 2011"
[1] ""
[1] "Implement methods: Iteration #2"
[1] "Permutation null w/o heterogeneity"
[1] "Mon Oct 31 23:03:20 2011"
[1] "Passenger null w/o heterogeneity"
[1] "Mon Oct 31 23:03:20 2011"
[1] "Mon Oct 31 23:03:22 2011"

> resultsSim

Simulation results for gene-set analysis of mutations
  Data-generating mechanism : Passenger null
  Number of simulations     : 2
  Number of gene-sets       : 5
     Original  : 3
     Spiked-in : 2
  Spiked-in sets            :
     Probability of being mutated in a set : 0.75 0.95
     Length (as number of genes)           : 50

> slotNames(resultsSim)

 [1] "null.dist"        "perc.samples"     "spiked.set.sizes" "GeneSizes"
 [5] "GeneSets"         "Coverage"         "EventsBySample"   "Mutations"
 [9] "Scores"           "results"

> resultsSim@null.dist

[1] "Passenger null"
```

4.1 Manipulating the `SetMethodsSims` objects

We provide 2 functions to help manipulate the `SetMethodsSims` objects which result from the `sim.data.p.values` function: `extract.sims.method` and `combine.sims`. The `extract.sims.method`

function is used to obtain a single data frame with the p-values or q-values from one of the specific methods. For instance, the command to get the p-values for the permutation null with no heterogeneity method is:

```
> extract.sims.method(resultsSim,
+                     "p.values.perm.null")

                       [,1]         [,2]
hsa05213       1.628379e-02 3.150681e-01
hsa05223       1.951091e-02 5.847419e-01
hsa00250       5.545376e-01 2.693547e-01
gene.set.50.75 6.645712e-10 2.550107e-14
gene.set.50.95 7.502657e-18 4.783445e-16

>
```

The function `combine.sims` may be used to combine 2 simulations:

```
> combine.sims(resultsSim, resultsSim)

Simulation results for gene-set analysis of mutations
  Data-generating mechanism : Passenger null
  Number of simulations     : 4
  Number of gene-sets       : 5
     Original  : 3
     Spiked-in : 2
  Spiked-in sets            :
     Probability of being mutated in a set : 0.75 0.95
     Length (as number of genes)           : 50
```

References

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