

CancerMutationAnalysis package

Giovanni Parmigiani
Dana-Farber Cancer Institute and
Harvard School of Public Health
email: `gp@jimmy.harvard.edu`,

Simina M. Boca
National Cancer Institute
email: `simina.boca@nih.gov`

March 31, 2012

Contents

1 Overview	1
2 Data objects	2
3 Calculating gene scores	3
4 Estimating passenger probabilities	3
5 Performing gene-set analyses	4
6 Simulating data for gene-sets	6
6.1 Manipulating the <code>SetMethodsSims</code> objects	8
7 Acknowledgments	9

1 Overview

This package contains software which implements a variety of methods for gene and gene-set level analysis in somatic mutation studies of cancer. The methods implemented are described in [12] and [8], for the gene level analysis, and [1], for the gene-set level analysis. The gene level methods considered were developed to distinguish between “driver genes” and “passenger genes;” the former play an active role in tumorigenesis, having mutations which are selected for in cancer, while the latter are mutated in tumor samples, but have no role in tumorigenesis. They incorporate the study design used in [12, 13, 4, 9, 10]: The complete collection of coding exons (the exome) was sequenced in several “discovery samples,” with a smaller number of genes being further sequenced in a larger number of “prevalence samples,” based on the results of the discovery screen, and possibly, on prior knowledge about their role in cancer.

The gene-set methods implemented carry out the “patient-oriented” approach, which calculates gene-set scores for each sample, then combines them across samples. By comparison, gene-oriented

methods calculate a score for each gene across all samples, then combine them into gene-set scores. The four patient-oriented methods described in [1] are included, as well as the gene-oriented method described in [7] (see also [11]), which is in the `limma` package and performs a Wilcoxon test. Data from several comprehensive studies are also distributed with this package [12, 13, 4, 9, 10].

This vignette represents an introduction to the `CancerMutationAnalysis` package. The primary functions are: `cma.scores`, which calculates a variety of gene scores; `cma.fdr`, which estimates passenger probabilities and false discovery rates; and `cma.set.stat`, which implements a number of gene-set level methods. The function `cma.set.sim` performs gene-set simulations using either the permutation null or the passenger null (see [1]). The functions `extract.sims.method` and `combine.sims` are used to manipulate the objects resulting from `cma.set.sim`.

2 Data objects

We first load the data and look at them:

```
> library(CancerMutationAnalysis)
> data(WoodBreast07)
> data(WoodColon07)
> data(JonesPancreas08)
> data(ParsonsGBM08)
> data(ParsonsMB11)
```

The datasets are labelled according to the publication year of the study and the tumor type. Thus, data is available for studies of breast cancer, colon cancer, pancreatic cancer, glioblastoma multiforme (GBM), and medulloblastoma (MB).

The objects containing information on the somatic mutations are labelled `GeneAlter*`. As an example, consider the `GeneAlterGBM` object:

```
> head(GeneAlterGBM)
```

	Gene	Type	Sample	Screen	WTNuc	Context	MutNuc
1	MRPL55@015731	Mut	BR11P	Disc	C	CpG	T
2	USH2A@045	Mut	BR20P	Disc	G	GpA	T
3	KCNH1@06084	Mut	BR09P	Disc	G		T
4	LAMB3@01338	Mut	BR17X	Disc	G		A
5	PIGR@07060	Mut	BR08X	Disc	G	CpG	A
6	REN@07303	Mut	BR20P	Disc	G	CpG	A

The columns represent the transcript, mutation type (`Mut`, `Amp`, `Del`, for point mutations, amplifications, and deletions, respectively), sample ID, screen (`Disc` or `Prev` for “Discovery” or “Prevalence”), wild type nucleotide, context, and nucleotide after mutation. Only point mutations are used to calculate gene scores, estimate passenger probabilities, and perform gene-set level analyses. Only discovery samples are used to perform the set analyses.

The `GeneCov*` objects contain data on the number of nucleotides of each type successfully sequenced for each transcript:

```
> head(GeneCovGBM)
```

	Gene	Screen	WtNuc	Context	Coverage
1	15E1.2@013849	Disc	C	CpG	387.0147

2	15E1.2@@13849	Prev	C	CpG	0.0000
3	15E1.2@@13849	Disc	G	CpG	465.2525
4	15E1.2@@13849	Prev	G	CpG	0.0000
5	15E1.2@@13849	Disc	G	GpA	470.0150
6	15E1.2@@13849	Prev	G	GpA	0.0000

The `GeneSamp*` objects store the number of discovery and prevalence samples for each transcript:

```
> head(GeneSampGBM)
```

	Gene	Screen	NrSamp
1	15E1.2@@13849	Disc	21
2	15E1.2@@13849	Prev	0
3	2'-PDE@@16564	Disc	21
4	2'-PDE@@16564	Prev	0
5	3'HEXO@@9816	Disc	21
6	3'HEXO@@9816	Prev	0

The `BackRates*` objects contain estimated passenger probabilities used in the original studies.

3 Calculating gene scores

Gene scores are obtained using the `cma.scores` function. These scores include the Cancer Mutation Prevalence (CaMP) score [8] and the log Likelihood Ratio (logLRT) score [3]. They take into account the mutation profile and the total number of nucleotides successfully sequenced for each gene, as well as an estimated “background passenger rate” of mutation:

```
> ScoresGBM <- cma.scores(cma.alter = GeneAlterGBM,
+                         cma.cov = GeneCovGBM,
+                         cma.samp = GeneSampGBM,
+                         passenger.rates = BackRatesGBM["MedianRates",])
> head(ScoresGBM)
```

	CaMP	logLRT
A2M@@408	0.9028709	2.158645
A4GALT@@21470	0.5706862	1.678895
ABCA10@@388	1.0423011	2.575103
ABCA4@@140	0.7044877	1.853172
ABCA7@@194	0.1076564	1.157538
ABCB6@@2071	0.5499152	1.655159

4 Estimating passenger probabilities

Passenger probabilities for individual genes are estimated using the `cma.fdr` function, which performs an empirical Bayes (EB) analysis. The output of this function is a list, each score having an entry which, for each gene, gives the corresponding score, the number of genes with scores greater or equal in the dataset (F), the average number of genes with scores greater or equal in the simulated datasets (F0), the estimated false discovery rate (Fdr), the estimated local false discovery

rate (`fdr`), and the estimated value of the prior probability of the gene being null (`p0`). The estimated passenger probabilities for individual genes are the estimate local false discovery rates. If `showFigure=TRUE`, a plot is also generated for each score, displaying the right tail of the density of null scores and a 1-D “rug plot” histogram of the observed scores. A cutoff is chosen so that the false discovery rate has the largest possible value below it. See Figure 1 for an example.

```
> set.seed(188310)
> FdrGBM <- cma.fdr(cma.alter = GeneAlterGBM,
+                  cma.cov = GeneCovGBM,
+                  cma.samp = GeneSampGBM,
+                  scores = "logLRT",
+                  passenger.rates = BackRatesGBM["MedianRates",],
+                  showFigure=TRUE,
+                  cutoffFdr=0.1,
+                  M = 5)
```

Score: logLRT.

```
> head(FdrGBM[["logLRT"]])
```

	Score	F	F0	Fdr	fdr	p0
PCOTH0018196	5.837195e-05	20671	20671	1	1	1
PMS2L3009470	9.693291e-05	20670	20670	1	1	1
ENST000003602160016327	1.011182e-04	20669	20669	1	1	1
CCL4L20014948	1.029200e-04	20668	20668	1	1	1
Q6PDB4_HUMAN0017521	1.036599e-04	20667	20667	1	1	1
LOC1496430015875	1.085358e-04	20666	20666	1	1	1

5 Performing gene-set analyses

The function `cma.set.stat` 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 [1] for more details on all these methods and [6] for a related method.

We use gene-sets from KEGG [5] in this example through the `KEGG.db` package [?]:

```
> library(KEGG.db)
> KEGGPATHID2EXTID
```

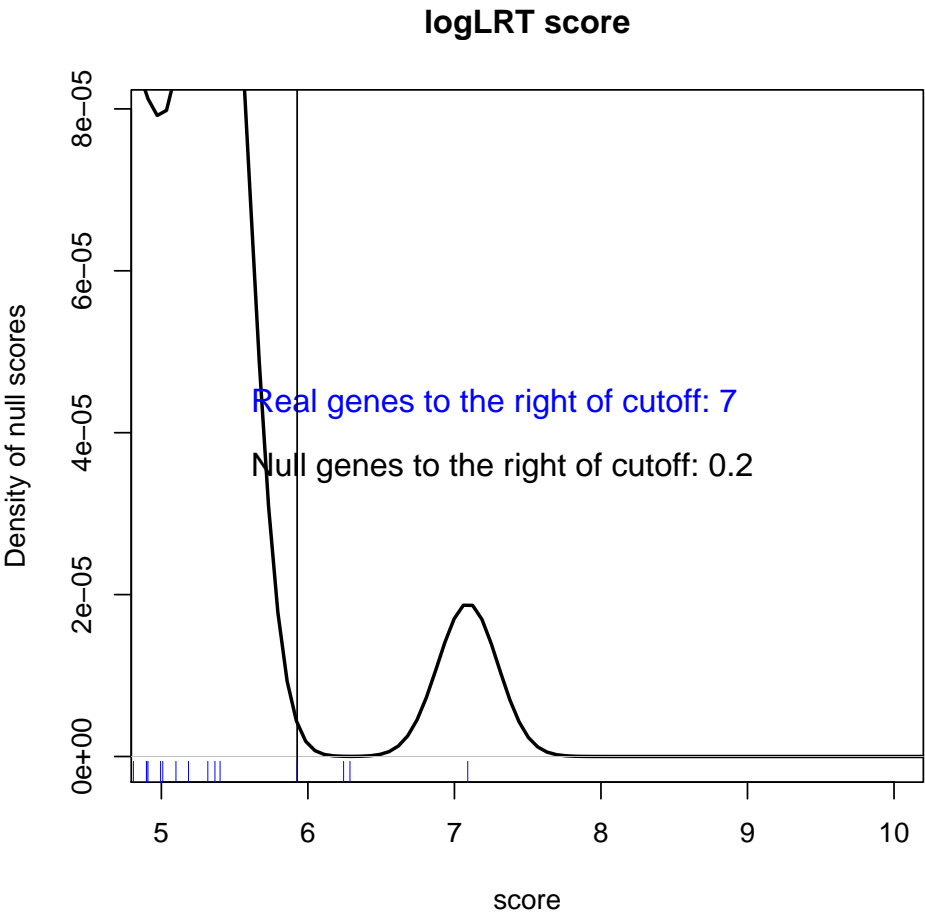
PATHID2EXTID map for KEGG (object of class "AnnDbBimap")

Since the genes in the GBM datasets are annotated by gene names, while `KEGGPATHID2EXTID` uses EntrezGene identifiers, we also need to load the vector mapping the identifiers to the names, which we obtained by using the `biomaRt` package [2].

Figure 1: Example of figure obtained by setting `showFigure=TRUE` in the `cma.fdr` function.

Score: logLRT.

	Score	F	F0	Fdr	fdr	p0
PCOTH@@18196	5.837195e-05	20671	20671	1	1	1
PMS2L3@@9470	9.693291e-05	20670	20670	1	1	1
ENST00000360216@@16327	1.011182e-04	20669	20669	1	1	1
CCL4L2@@14948	1.029200e-04	20668	20668	1	1	1
Q6PDB4_HUMAN@@17521	1.036599e-04	20667	20667	1	1	1
LOC149643@@15875	1.085358e-04	20666	20666	1	1	1



```
> data(EntrezID2Name)
```

We now use the function `cma.set.stat` to perform the gene-set analyses on three KEGG sets:

```
> 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"
```

```
> SetResultsGBM <-
+   cma.set.stat(cma.alter = GeneAlterGBM,
+               cma.cov = GeneCovGBM,
+               cma.samp = GeneSampGBM,
+               GeneSets = KEGGPATHID2EXTID[c("hsa05213",
+               "hsa05223", "hsa00250")]),
+               ID2name = EntrezID2Name,
+               gene.method = FALSE,
+               perm.null.method = TRUE,
+               perm.null.het.method = FALSE,
+               pass.null.method = TRUE,
+               pass.null.het.method = FALSE)
```

The resulting object is a data-frame containing p-values and q-values for the methods which were implemented:

```
> SetResultsGBM
```

	p.values.perm.null	q.values.perm.null	p.values.pass.null
hsa05213	9.198666e-16	2.759600e-15	2.108377e-10
hsa05223	1.678783e-15	2.518175e-15	3.403831e-11
hsa00250	3.109024e-01	3.109024e-01	6.340137e-01
	q.values.pass.null		
hsa05213	3.162565e-10		
hsa05223	1.021149e-10		
hsa00250	6.340137e-01		

6 Simulating data for gene-sets

We now demonstrate the use of the `cma.set.sim` function, which simulates datasets under either the permutation or passenger null (see [1]), 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 [1]). 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 `cma.set.sim` is of the class `SetMethodsSims`. Note that this code takes several minutes to run:

```
> set.seed(831984)
> resultsSim <-
+   cma.set.sim(cma.alter = GeneAlterGBM,
+               cma.cov = GeneCovGBM,
+               cma.samp = GeneSampGBM,
+               GeneSets = KEGGPATHID2EXTID[c("hsa05213",
+               "hsa05223", "hsa00250")],
+               ID2name = EntrezID2Name,
+               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)
> 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" "GeneSets"
[5] "cma.alter"      "cma.cov"        "cma.samp"         "Scores"
[9] "results"
```

```
> resultsSim@null.dist
```

```
[1] "Passenger null"
```

6.1 Manipulating the SetMethodsSims objects

We provide 2 functions to help manipulate the `SetMethodsSims` objects which result from the `cma.set.sim` 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      1.790842e-02 3.326939e-01
hsa05223      2.142885e-02 6.030915e-01
hsa00250      5.652371e-01 2.824730e-01
gene.set.50.75 8.521175e-10 4.210103e-14
gene.set.50.95 1.048898e-17 8.187030e-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

- [1] S.M. Boca, K.W. Kinzler, V.E. Velculescu, B. Vogelstein, and G. Parmigiani. Patient-oriented gene set analysis for cancer mutation data. *Genome Biology*, 11(11):R112, 2010.
- [2] Steffen Durinck and Wolfgang Huber. *biomaRt: Interface to BioMart databases (e.g. Ensembl, COSMIC, Wormbase and Gramene)*. R package version 2.8.1.
- [3] G. Getz, H. Höfling, J. P. Mesirov, T. R. Golub, M. Meyerson, R. Tibshirani, and E. S. Lander. Comment on "the consensus coding sequences of human breast and colorectal cancers". *Science*, 317(5844):1500, 2007.
- [4] S. Jones, X. Zhang, D.W. Parsons, J.C.H. Lin, R.J. Leary, P. Angenendt, P. Mankoo, H. Carter, H. Kamiyama, A. Jimeno, et al. Core signaling pathways in human pancreatic cancers revealed by global genomic analyses. *Science*, 321(5897):1801, 2008.
- [5] M. Kanehisa and S. Goto. KEGG: Kyoto encyclopedia of genes and genomes. *Nucleic Acids Research*, 28(1):27, 2000.

- [6] J. Lin, C.M. Gan, X. Zhang, S. Jones, T. Sjöblom, L.D. Wood, W. Parsons, N. Papadopoulos, K.W. Kinzler, B. Vogelstein, G. Parmigiani, and V.V. Velculescu. A multidimensional analysis of genes mutated in breast and colorectal and colorectal cancers. *Genome Research*, 17(9):1304–1318, 2007.
- [7] J. Michaud, K.M. Simpson, R. Escher, K. Buchet-Poyau, T. Beissbarth, C. Carmichael, M.E. Ritchie, F. Schütz, P. Cannon, M. Liu, et al. Integrative analysis of RUNX 1 downstream pathways and target genes. *BMC Genomics*, 9(1):363, 2008.
- [8] G. Parmigiani, J. Lin, S. Boca, T. Sjöblom, KW Kinzler, VE Velculescu, and B. Vogelstein. Statistical methods for the analysis of cancer genome sequencing data. *Johns Hopkins University, Dept. of Biostatistics Working Paper 126*, 2007.
- [9] D.W. Parsons, S. Jones, X. Zhang, J.C.H. Lin, R.J. Leary, P. Angenendt, P. Mankoo, H. Carter, I. Siu, et al. An integrated genomic analysis of human glioblastoma multiforme. *Science*, 321(5897):1807, 2008.
- [10] D.W. Parsons, M. Li, X. Zhang, S. Jones, R.J. Leary, J.C.H. Lin, S.M. Boca, H. Carter, J. Samayoa, C. Bettegowda, et al. The genetic landscape of the childhood cancer medulloblastoma. *Science*, 331(6016):435, 2011.
- [11] EM Schaeffer, L. Marchionni, Z. Huang, B. Simons, A. Blackman, W. Yu, G. Parmigiani, and DM Berman. Androgen-induced programs for prostate epithelial growth and invasion arise in embryogenesis and are reactivated in cancer. *Oncogene*, 27(57):7180–7191, 2008.
- [12] T. Sjöblom, S. Jones, L.D. Wood, D.W. Parsons, J. Lin, T.D. Barber, D. Mandelker, R.J. Leary, J. Ptak, N. Silliman, et al. The consensus coding sequences of human breast and colorectal cancers. *Science*, 314(5797):268–274, 2006.
- [13] L.D. Wood, D.W. Parsons, S. Jones, J. Lin, T. Sjöblom, R.J. Leary, D. Shen, S.M. Boca, T. Barber, J. Ptak, et al. The genomic landscapes of human breast and colorectal cancers. *Science*, 318(5853):1108, 2007.

7 Acknowledgments

We would like to thank Michael A. Newton and Luigi Marchionni for generously sharing their code and Benjamin Langmead, Fernando Pineda, and Michael Ochs for some very helpful discussions.