Parametric Gene Set Enrichement Analysis

Karl Dykema

April 30, 2018

Laboratory of Computational Biology, Van Andel Research Institute

1 PGSEA basics

PGSEA analyzes gene expression data to determine miss-regulation of defined gene signatures or "molecular concepts". To run PGSEA() all that you need is a matrix of expression data and some lists of related genes. Your expression data must either be in ratio form already or you must include reference samples from which to generate ratios. The identifiers used in your gene lists must also be in the same format as the gene names in your data matrix. All identifiers in the example data and signatures included in this package are Entrez Gene identifiers. The actual gene signatures themselves can come from a number of different sources but we have found the most informative ones to be experimentally derived lists of genes. (As opposed to canonical pathways...) There are many such lists that already exist in the literature as well as in publicly accessible repositories. To make use of these valuable resources, we have implemented a class to hold these gene lists called "smc", for "Simple Molecular Concepts." The class contains slots for holding many different types of information about the molecular concept, but all that is necessary is the "ids" slot. This is where the genes are stored. To begin we will show how to create your own basic concept:

```
>         library(PGSEA)
>         basic <- new("smc",ids=c("gene a","gene b"),reference="simple smc")
>         str(basic)
```

```
Formal class 'smc' [package "PGSEA"] with 10 slots
  ..@ reference : chr "simple smc"
  ..@ desc      : chr(0)
  ..@ source    : chr(0)
  ..@ design    : chr(0)
  ..@ identifier: chr(0)
  ..@ species   : chr(0)
  ..@ data      : chr(0)
  ..@ private   : chr(0)
  ..@ creator   : chr(0)
  ..@ ids       : chr [1:2] "gene a" "gene b"
```

2 Concepts from ".gmt" files

A previous published method of gene set analysis termed "Gene Set Enrichment Analysis" `http://www.broad.mit.edu/gsea/` also used lists of related genes and to hold their lists they use a file format called ".gmt". We have found it to be a simple and useful way to store our lists as well. To facilitate using this format in conjunction with our "smc" class, we have included the functions `readGmt` and `writeGmt`. An example of how to read in a ".gmt" file is shown below. The file provided contains some example molecular concepts. Genes induced and inhibited by Ras and Myc, as well as all genes on chromosome arms 5p and 5q have been included.

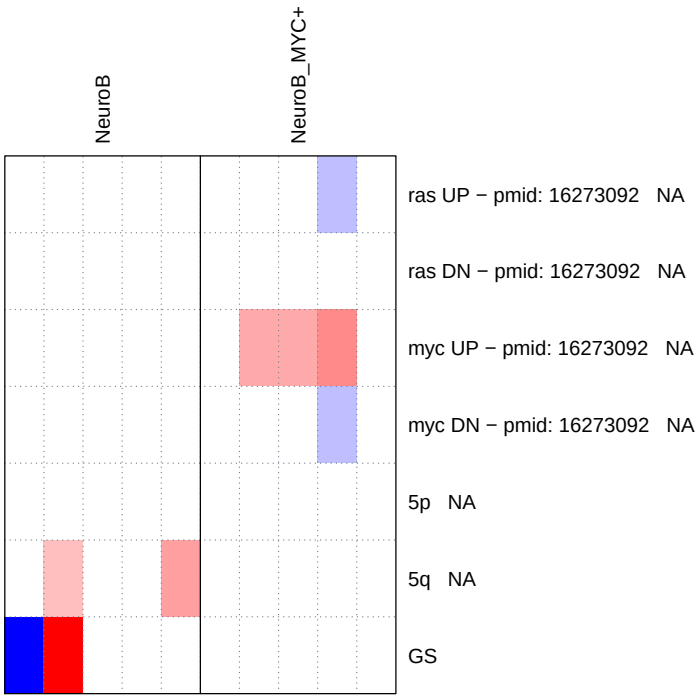
```
>         datadir <- system.file("extdata", package = "PGSEA")
>         sample <- readGmt(file.path(datadir, "sample.gmt"))
>         str(sample[1])

List of 1
 $ ras UP - pmid: 16273092   NA :Formal class 'smc' [package "PGSEA"] with 10 slots
  .. ..@ reference : chr "ras UP - pmid: 16273092  "
  .. ..@ desc      : chr "NA "
  .. ..@ source    : chr(0)
  .. ..@ design    : chr(0)
  .. ..@ identifier: chr(0)
  .. ..@ species   : chr(0)
  .. ..@ data      : chr(0)
  .. ..@ private   : chr(0)
  .. ..@ creator   : chr(0)
  .. ..@ ids       : chr [1:181] "101" "154" "384" "490" ...
```

Below some example gene expression data from primary neuroblastoma tumors is analyzed by `PGSEA` using the provided example concepts. `PGSEA` is run with an index given to the appropriate reference samples, and the data for the [non-reference] samples is displayed with `smcPlot`.

```
>         data(nbEset)
>         pg <- PGSEA(nbEset,cl=sample,ref=1:5)

>         sub <- factor(c(rep(NA,5),rep("NeuroB",5),rep("NeuroB_MYC+",5)))
>         smcPlot(pg[,],sub,scale=c(-12,12),show.grid=T,margins=c(1,1,7,13),col=.rwb)
>
```

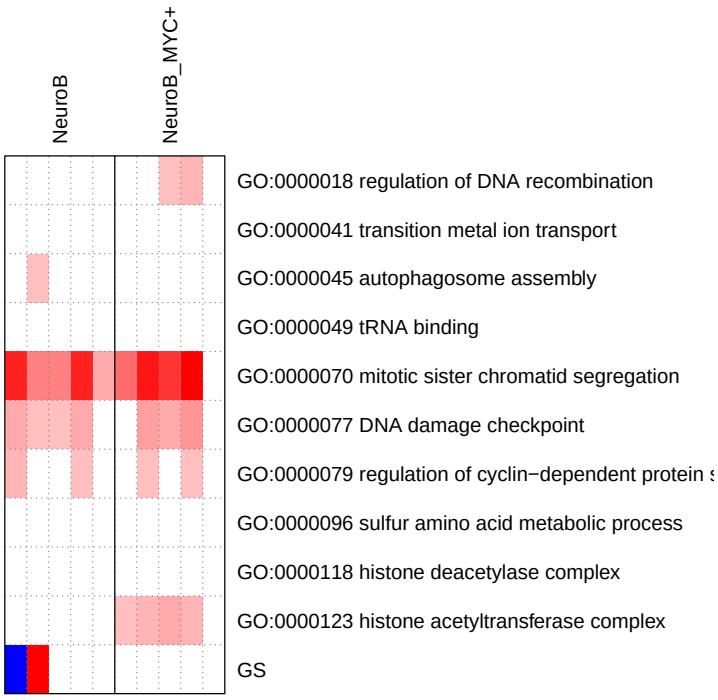


3 Using Gene Ontologies as concepts

Next, to create a list of concepts we will use the function `go2smc`. This function will convert the entire GO datbase into 'smc' objects. This is quite a large number to work with, so we will just use a few of them for illustration.

```
>         mcs <- go2smc()[1:10]
>         pg <- PGSEA(nbEset,cl=mcs,ref=1:5)
>

>         smcPlot(pg[,],sub,scale=c(-12,12),show.grid=T,margins=c(1,1,7,20),col=.rwb)
>
```

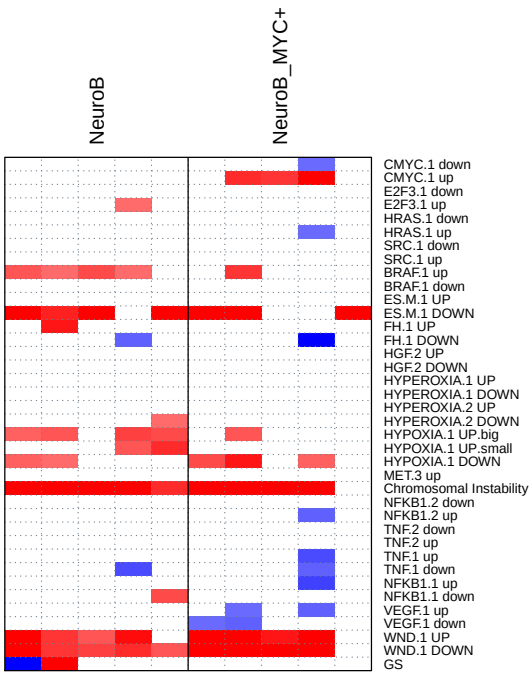


4 Concepts compiled at VAI

Lastly, we have included a list of concepts that we have manually compiled from various sources. We have found these concepts to very informative in our analysis. These concepts are included in the old "smc" style object as was used previously in PGSEA, and also in the newly created "GeneSetCollection" format. This new format allows much more flexibility and should prove useful as the format develops and matures.

```
>         #data(VAImcs)
>         data(VAIgsc)
>   pg <- PGSEA(nbEset,cl=VAIgsc,ref=1:5)
>

>         smcPlot(pg[,],sub,scale=c(-5,5),show.grid=T,margins=c(1,1,8,14),col=.rwb,r.cex=.7)
>
```



We included this particular example dataset because the tumors were tested for chromosomal aberrations which lead to amplification of important genes. The amplification we are attempting to illustrate is that of MYC. We have five samples that are confirmed to have the amplification and five samples that have standard copy numbers. Our concept of interest is "CMYC.1 up", which is the second row from the top in the above plot. It was provided by Bild et al. (PMID: 16273092). `PGSEA` reports four samples with confirmed MYC amplification have a positive score, while only one of five samples without the amplification has a positive score. These results may not be overly impressive, but in the interest of file size we could only include a portion of full the data set. Originally there were 101 samples, 81 of which had the amplification and 20 which did not. When `PGSEA` is run on the entire dataset, 18/20 (.90) of samples with confirmed amplification have show increased activity, and only 5/81 (.06) of samples confirmed to have no amplification also show increased activity.

These results are quite interesting and demonstrate the feasibility of using a technique such as PGSEA to quickly analyze a wide variety of aspects about a given data set. This type of analysis depends solely on informative concepts, so that is where we believe the efforts of the community should be directed.