

Bioconductor's PADOG package

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1 Overview

This package implements the *Pathway Analysis with Down-weighting of Overlapping Genes (PADOG)* algorithm described in Tarca et al. (2012). The method can be applied to analyze any type of gene sets yet in here it is illustrated using KEGG pathways. The method computes a gene set score as the mean of absolute values of weighted moderated gene *t*-scores. The gene weights are chosen to favor genes appearing in few pathways versus genes that appear in many pathways. The significance of pathway scores is evaluated using sample/array labels permutation that preserve the gene-gene correlation structure. The package also contains a benchmark for gene set analysis in general and allows a new gene set analysis method to be benchmarked against PADOG or other existing methods (e.g. GSA). The benchmark uses 24 different data sets, each involving a disease (e.g. Colorectal Cancer) for which there is a KEGG pathway with the same name. The only assumption we make (proven to hold in Tarca et al. (2012)) is that the KEGG's pathway with the same name as the disease under the study should be found significant and/or ranked near the top by gene set analysis methods when analyzing a dataset that compares normal with diseased samples.

2 Pathway / gene set analysis with PADOG package

This document provides basic introduction on how to use the PADOG package. For extended description of the methods used by this package please consult Tarca et al. (2012).

We demonstrate the functionality of this package using a colorectal cancer dataset obtained using Affymetrix GeneChip technology and available through GEO (GSE9348) and incorporated in the `KEGGdzPathwaysGEO` package. This experiment contains 12 normal samples and 70 colorectal cancer samples and is described in Hong et al. (2010). The RMA preprocessed data using the `affy` package is the entry point for the `padog` function:

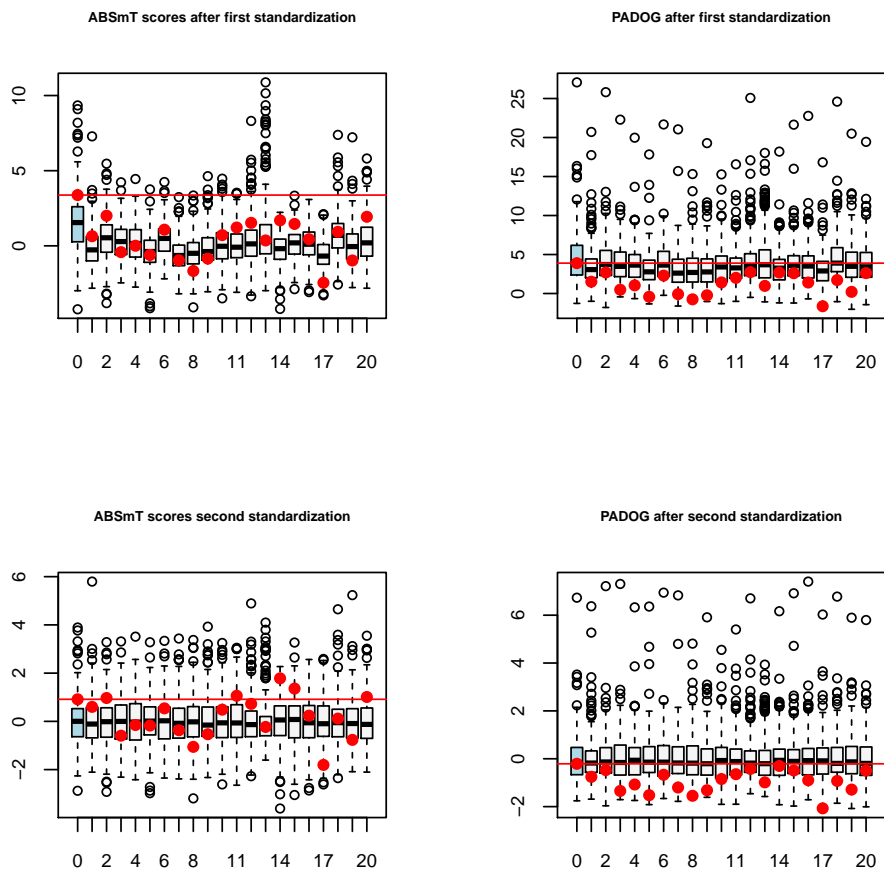
```
> library(KEGGdzPathwaysGEO)
> library(PADOG)
> set.seed(1)
```

```

> set="GSE9348"
> data(list=set,package="KEGGdzPathwaysGEO")
> x=get(set)
> #Extract from the dataset the required info
> exp=experimentData(x);
> dataset= exp@name
> dat.m=exprs(x)
> ano=pData(x)
> design= notes(exp)$design
> annotation= paste(x@annotation, ".db", sep="")
> targetGeneSets= notes(exp)$targetGeneSets
> #run padog function on KEGG pathways
> #use NI=1000 for accurate results
> myr=padog(
+ esetm=dat.m,
+ group=ano$Group,
+ paired=design=="Paired",
+ block=ano$Block,
+ targetgs=targetGeneSets,
+ annotation=annotation,
+ gslist="KEGG.db",
+ organism="hsa",
+ verbose=FALSE,
+ Nmin=3,
+ NI=50,
+ plots=TRUE)
> myr[1:15, -c(4,5)]

```

| | Name | ID | Size | PmeanAbsT | Ppadog |
|-------|---|-------|------|-----------|--------|
| 04110 | Cell cycle | 04110 | 122 | 0.0002 | 2e-04 |
| 03008 | Ribosome biogenesis in eukaryotes | 03008 | 70 | 0.0002 | 2e-04 |
| 00230 | Purine metabolism | 00230 | 153 | 0.0002 | 2e-04 |
| 04976 | Bile secretion | 04976 | 71 | 0.0002 | 2e-04 |
| 00071 | Fatty acid metabolism | 00071 | 42 | 0.0200 | 2e-04 |
| 00062 | Fatty acid elongation in mitochondria | 00062 | 7 | 0.0002 | 2e-04 |
| 00460 | Cyanoamino acid metabolism | 00460 | 7 | 0.0002 | 2e-04 |
| 04964 | Proximal tubule bicarbonate reclamation | 04964 | 23 | 0.0800 | 2e-02 |
| 00920 | Sulfur metabolism | 00920 | 11 | 0.1400 | 2e-02 |
| 05210 | Colorectal cancer | 05210 | 62 | 0.1600 | 2e-02 |
| 05223 | Non-small cell lung cancer | 05223 | 54 | 0.2600 | 2e-02 |
| 03013 | RNA transport | 03013 | 139 | 0.0400 | 4e-02 |
| 00500 | Starch and sucrose metabolism | 00500 | 37 | 0.0600 | 4e-02 |
| 00983 | Drug metabolism - other enzymes | 00983 | 38 | 0.0600 | 4e-02 |
| 05222 | Small cell lung cancer | 05222 | 85 | 0.0400 | 4e-02 |



Note that for this colorectal cancer dataset it is reasonable to expect that the KEGG's Colorectal cancer pathway will be found significant and/or ranked close to the top. P_{meanAbsT} corresponds to the p-value obtained without using gene weights and hence the result is worse (higher p-value) compared to P_{padog} obtained by using the gene weights that are inversely related to how often the genes appear across all gene sets to be analyzed. The plot created when `plots=TRUE` in the call to `padog` shows how gene weighting improves the gene set analysis for the target pathway set via the `targetgs` argument. Figure above shows the distribution of pathway/gene set scores (y axis) for PADOG and ABSmT (which is PADOG without weights) after the first standardization (row randomization) and after second standardization (between gene sets standardization). The x axis represents the number of iterations. Iteration 0 uses true class labels, all others used randomly permuted labels. The target pathway (set via the `targetgs` argument) in this dataset is the *Colorectal Cancer pathway* (KEGG ID 05210). Its score is shown with a red bullet throughout all 4 panels, and a red horizontal line marks its level when obtained with the true class labels ($ite = 0$, x -axis). The box plots of scores obtained with the true class labels are also highlighted in blue. With PADOG, after the second standardization, the target pathway scores obtained from permutations are less frequently above the red line (0/20) (more extreme) than for ABSmT (5/20). Over 1,000 iterations, p_{PADOG} was estimated to be 0.013 while p_{ABSmT} worse, i.e. 0.135.

Table 1: **The 24 datasets used in the benchmark of pathway analysis methods**

| GEOID | Pubmed | Ref. | Disease/Target pathway | KEGGID | Tissue |
|----------|----------|--------------------------------|----------------------------|----------|--------------------|
| GSE1297 | 14769913 | Blalock et al. (2004) | Alzheimer’s Disease | hsa05010 | Hippocampus |
| GSE5281 | 17077275 | Liang et al. (2007) | Alzheimer’s Disease | hsa05010 | Brain, Entorhinal |
| GSE5281 | 17077275 | Liang et al. (2007) | Alzheimer’s Disease | hsa05010 | Brain, hippocampus |
| GSE5281 | 17077275 | Liang et al. (2007) | Alzheimer’s Disease | hsa05010 | Brain, Primary |
| GSE20153 | 20926834 | Zheng et al. (2010) | Parkinson’s disease | hsa05012 | Lymphoblastoid |
| GSE20291 | 15965975 | Zhang et al. (2005) | Parkinson’s disease | hsa05012 | Postmortem |
| GSE8762 | 17724341 | Runne et al. (2007) | Huntington’s disease | hsa05016 | Lymphocytes |
| GSE4107 | 17317818 | Hong et al. (2007) | Colorectal Cancer | hsa05210 | Mucosa |
| GSE8671 | 18171984 | Sabates-Bellver et al. (2007) | Colorectal Cancer | hsa05210 | Colon |
| GSE9348 | 20143136 | Hong et al. (2010) | Colorectal Cancer | hsa05210 | Colon |
| GSE14762 | 19252501 | Wang et al. (2009) | Renal Cancer | hsa05211 | Kidney |
| GSE781 | 14641932 | Lenburg et al. (2003) | Renal Cancer | hsa05211 | Kidney |
| GSE15471 | 19260470 | Badea et al. (2008) | Pancreatic Cancer | hsa05212 | Pancreas |
| GSE16515 | 19732725 | Pei et al. (2009) | Pancreatic Cancer | hsa05212 | Pancreas |
| GSE19728 | - | - | Glioma | hsa05214 | Brain |
| GSE21354 | - | - | Glioma | hsa05214 | Brain, Spinal |
| GSE6956 | 18245496 | Wallace et al. (2008) | Prostate Cancer | hsa05215 | Prostate |
| GSE6956 | 18245496 | Wallace et al. (2008) | Prostate Cancer | hsa05215 | Prostate |
| GSE3467 | 16365291 | He et al. (2005) | Thyroid Cancer | hsa05216 | Thyroid |
| GSE3678 | - | - | Thyroid Cancer | hsa05216 | Thyroid |
| GSE9476 | 17910043 | Stirewalt et al. (2008) | Acute myeloid leukemia | hsa05221 | Blood, Bone |
| GSE18842 | 20878980 | Sanchez-Palencia et al. (2010) | Non-Small Cell Lung Cancer | hsa05223 | Lung |
| GSE19188 | 20421987 | Hou et al. (2010) | Non-Small Cell Lung Cancer | hsa05223 | Lung |
| GSE3585 | 17045896 | Barth et al. (2006) | Dilated cardiomyopathy | hsa05414 | Heart |

The 24 datasets used to compare the pathway analysis methods were obtained from GEO.

3 Benchmark of gene set analysis methods

The entire collection of 24 datasets available in KEGGdzPathwaysGEO package that can be used to benchmark PADOG against existing approaches is given in Table 1:

To illustrate how to compare PADOG against a user defined gene set analysis method we create a function called `randomF` that assigns random uniform P-values to gene sets. The user defined function has to take in 3 arguments:

1. `set`: the name of a dataset available in from the KEGGdzPathwaysGEO package;
2. `mygslist`: a list with elements being vectors of gene ids for a given geneset
3. `minsize`: minimum number of genes in a geneset to be considered for analysis

The output should be a dataframe with columns: ID, P, Rank, Dataset, Method for the geneset(s) considered to be relevant in that dataset (`targetGeneSets`).

```

> randomF=function(set,mygslist,minsize){
+ set.seed(1)
+ #this loads the dataset in an ExpressionSet object called x
+ data(list=set,package="KEGGdzPathwaysGEO")
+ x=get(set)
+
+ #Extract from the dataset the required info to be passed to padog
+ exp=experimentData(x);
+ dat.m=exprs(x)
+ ano=pData(x)
+ dataset= exp@name
+ design= notes(exp)$design
+ annotation= paste(x@annotation, ".db", sep="")
+ targetGeneSets= notes(exp)$targetGeneSets
+
+
+ #get rid of duplicates probesets per ENTREZ ID by keeping the probeset
+ #with smallest p-value (computed using limma)
+ aT1=filteranot(esetm=dat.m,group=ano$Group,paired=(design=="Paired"),
+ block=ano$Block,annotation=annotation)
+ #create an output dataframe for this toy method with random gene set p-values
+ mygslistSize=unlist(lapply(mygslist,function(x){length(intersect(aT1$ENTREZID,x))}))
+ res=data.frame(ID=names(mygslist),P=runif(length(mygslist)),
+ Size=mygslistSize,stringsAsFactors=FALSE)
+ res$FDR=p.adjust(res$P,"fdr")
+ #drop genesets with less than minsize genes in the current dataset
+ res=res[res$Size>=minsize,]
+ #compute ranks
+ res$Rank=rank(res$P)/dim(res)[1]*100
+ #needed to compare ranks between methods; must be the same as given
+ #in mymethods argument "list(myRand="
+ res$Method="myRand";
+ #needed because comparisons of ranks between methods is paired at dataset level
+ res$Dataset<-dataset;
+ #output only result for the targetGeneSets
+ #which are gene sets expected to be relevant in this dataset
+ return(res[res$ID %in% targetGeneSets,])
+ }
> #run the analysis on all 24 datasets and compare the new method "myRand" with
> #PADOG and GSA (if installed) (chosen as reference since is listed first in the existingMetho
> #if the package parallel is installed datasets are analyzed in parallel.
> #out=compPADOG(datasets=NULL,existingMethods=c("GSA","PADOG"),
> #mymethods=list(myRand=randomF),
> #gslist="KEGG.db",Nmin=3,NI=1000,plots=TRUE,verbose=FALSE)
>

```

```

> #compare myRand against PADOG on 4 datasets only
> #mysets=data(package="KEGGdzPathwaysGEO")$results[, "Item"]
> mysets=c("GSE9348", "GSE8671", "GSE1297")
> out=compPADOG(datasets=mysets, existingMethods=c("PADOG"),
+ mymethods=list(myRand=randomF),
+ gslist="KEGG.db", Nmin=3, NI=40, plots=TRUE, verbose=FALSE)
> print(out)

```

```
$summary
```

| Method | p geomean | p med | % p.value<0.05 | % q.value<0.05 | rank mean | rank med |
|----------|-------------|-----------|----------------|----------------|-----------|----------|
| 1 PADOG | 0.006786044 | 0.025 | 66.67 | 33.33 | 5.463127 | 5.752212 |
| 2 myRand | 0.1675201 | 0.5995658 | 33.33 | 0 | 39.97116 | 59.73451 |

| | p Wilcox. | p LME | coef. LME |
|---|-----------|-----------|-----------|
| 1 | 1 | 1.0000000 | 0.00000 |
| 2 | 0.875 | 0.8395572 | 34.50803 |

```
$ranks
```

```
$ranks$PADOG
```

```
[1] 5.752212 6.637168 4.000000
```

```
$ranks$myRand
```

```
[1] 59.7345133 59.7345133 0.4444444
```

```
$pvalues
```

```
$pvalues$PADOG
```

```
[1] 0.02500 0.00025 0.05000
```

```
$pvalues$myRand
```

```
[1] 0.59956583 0.59956583 0.01307758
```

```
$qvalues
```

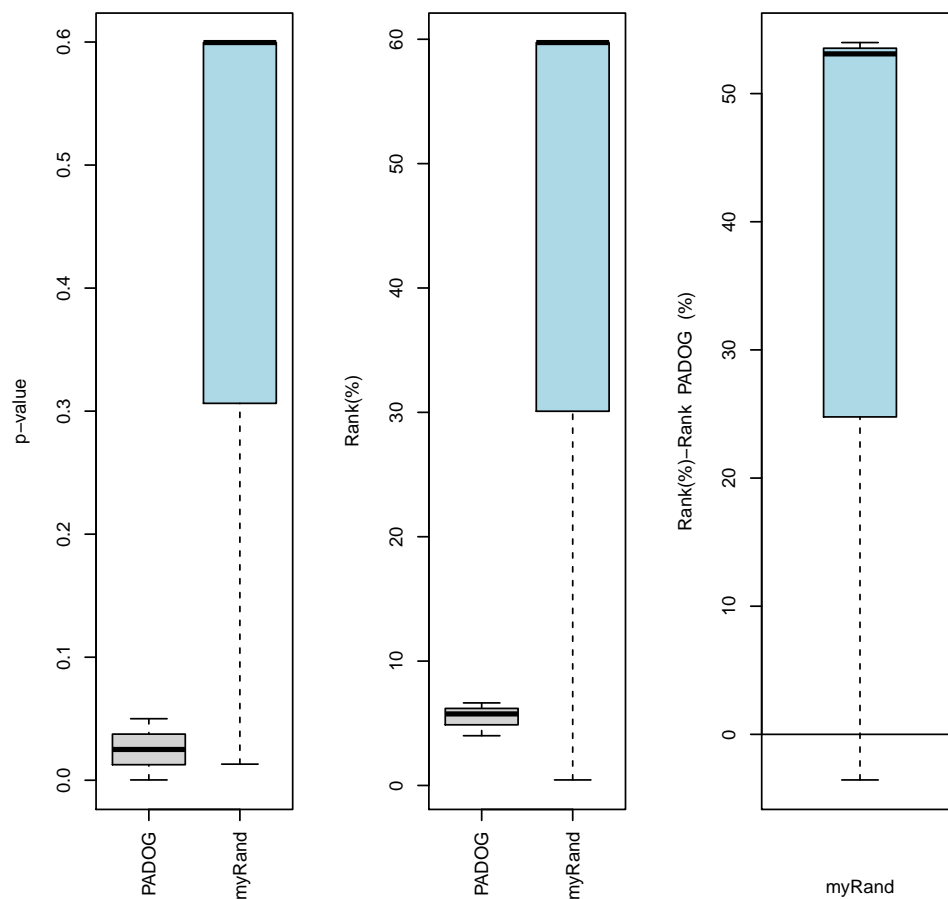
```
$qvalues$PADOG
```

```
[1] 0.40357143 0.00353125 0.70312500
```

```
$qvalues$myRand
```

```
[1] 0.9691438 0.9691438 0.9691438
```

```
>
```



Details about the meaning of the columns in the out table are given in Tarca et al. (2012). The better the method, the smaller the p-values and ranks for the target pathways, since these are supposed to be significant to their respective datasets.

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