

An Introduction to *PROMISE*

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1 Introduction

PROMISE, PROjection onto the Most Interesting Statistical Evidence, is a general procedure to identify genomic features that exhibit a specific biologically interesting pattern of association with multiple phenotypic endpoint variables. Biological knowledge of the endpoint variables is used to define a vector that represents the biologically most interesting values for a set of association statistics. PROMISE performs one hypothesis test for each genomic feature, and is flexible to accommodate various types of endpoints.

In this document, we describe how to perform PROMISE procedure using hypothetical example data sets provided with the package.

2 Requirements

The PROMISE package depends on *Biobase* and *GSEABase*. The understanding of *ExpressionSet* and *GeneSetCollection* is a prerequisite to perform the PROMISE procedure. Due to the internal handling of multiple endpoints, the consistency of *ExpressionSet* and *GeneSetCollection* is assumed. The detailed requirements are illustrated below.

Load the PROMISE package and the example data sets: `sampExprSet`, `sampGeneSet`, and `phPatt` into R.

```
> library(PROMISE)
> data(sampExprSet)
> data(sampGeneSet)
> data(phPatt)
```

The *ExpressionSet* should contain at least two components: *exprs* (array data) and *phenoData* (endpoint data). *exprs* is a data frame with column names representing the array identifiers (IDs) and row names representing the probe (genomic feature) IDs. *phenoData* is an *AnnotatedDataFrame* with column names representing the endpoint variables and row names representing array. The array IDs of *phenoData* and *exprs* should be matched.

```

> arrayData<-exprs(sampExprSet)
> ptData<- pData(phenoData(sampExprSet))
> head(arrayData[, 1:4])

```

```

      array_1 array_2 array_3 array_4
probe_1 7.594327 6.710827 8.151585 5.885169
probe_2 4.719728 5.611497 5.819049 3.896193
probe_3 8.815163 5.451243 6.670862 7.295233
probe_4 5.187320 5.142358 6.105922 5.333343
probe_5 4.102526 2.655307 4.139362 1.801595
probe_6 5.415526 4.498429 4.393805 5.219712

```

```

> head(ptData)

```

```

      drugLevel residualDisease  obsTime obsCensor strat
array_1  2.486889                3 0.6117827         1     2
array_2  2.931522                3 1.2657796         1     2
array_3  2.569262                3 1.6318570         0     2
array_4  2.157207                2 0.3879765         0     1
array_5  1.649005                3 0.5763599         1     2
array_6  2.795997                3 0.5474852         0     1

```

```

> all(colnames(arrayData)==rownames(ptData))

```

```

[1] TRUE

```

The *GeneSetCollection* should be extractable in the following way. The probe IDs should be a subset of probe IDs of *exprs*.

```

> GS.data<-NULL
> for (i in 1:length(sampGeneSet)){
+   tt<-sampGeneSet[i][[1]]
+   this.name<-unlist(geneIds(tt))
+   this.set<-setName(tt)
+   this.data<- cbind.data.frame(featureID=as.character(this.name),
+                               setID=rep(as.character(this.set), length(this.name)))
+   GS.data<-rbind.data.frame(GS.data, this.data)
+ }
> sum(!is.element(GS.data[,1], rownames(arrayData)))==0

```

```

[1] TRUE

```

The association pattern definition is critical. The prior biological knowledge is required to define the vector that represents the biologically most interesting values for statistics. In this hypothetical example, we are interested in identifying genomic features that are positively associated with active drug level, negatively associated with minimum disease, and positively associated with survival. The three endpoints are represented in three rows as shown below:

```
> phPatt
```

	stat.coef	stat.func	endpt.vars
Association 1	1	spearman.rstat	drugLevel
Association 2	-1	spearman.rstat	residualDisease
Association 3	1	jung.rstat	obsTime,obsCensor

3 PROMISE Analysis

As mentioned in section 2, the *ExpressionSet* and pattern definition are required by PROMISE procedure. *GeneSetCollection* is required if a gene set enrichment analysis (GSEA) is to be performed within the PROMISE analysis.

The code below performs a PROMISE analysis without GSEA. As mentioned above, *GeneSetCollection* is not needed. The gene set result is NULL.

```
> test1<-PROMISE(exprSet=sampExprSet,  
+               geneSet=NULL,  
+               promise.pattern=phPatt,  
+               strat.var=NULL,  
+               seed=13,  
+               nperms=100)
```

Gene level (genomic feature) result:

```
> gene.res<-test1$generes  
> head(gene.res)
```

	probeid	drugLevel.stat	residualDisease.stat	
1	probe_1	0.50745310	-0.4410378	
2	probe_2	-0.05129198	0.1083797	
3	probe_3	0.34392723	-0.3069893	
4	probe_4	-0.21510307	0.1812378	
5	probe_5	-0.43215514	0.3725875	
6	probe_6	0.06213032	-0.1796821	
	obsTime.obsCensor.stat	PROMISE.stat	perm.p.drugLevel.stat	
1	-0.328713893	0.20659234	0.00	
2	0.050025633	-0.03654867	0.68	
3	-0.277173083	0.12458114	0.02	
4	0.003140076	-0.13106692	0.10	
5	0.346205081	-0.15284585	0.01	
6	-0.201508221	0.01343473	0.67	
	perm.p.residualDisease.stat	perm.p.obsTime.obsCensor.stat		
1	0.00	0.00		
2	0.46	0.76		
3	0.03	0.01		
4	0.17	0.99		
5	0.00	0.00		

6		0.18	0.17
	perm.p.PROMISE.stat		
1		0.00	
2		0.65	
3		0.06	
4		0.07	
5		0.03	
6		0.81	

Gene set level result:

```
> set.res<-test1$setres
> head(set.res)
```

NULL

The code below performs a PROMISE analysis with GSEA. As mentioned above, *GeneSetCollection* is required. *sampGeneSet*, a *GeneSetCollection*, is passed as an argument to PROMISE.

```
> test2<-PROMISE(exprSet=sampExprSet,
+               geneSet=sampGeneSet,
+               promise.pattern=phPatt,
+               strat.var=NULL,
+               seed=13,
+               nperms=100)
```

Gene level (genomic feature) result:

```
> gene.res2<-test2$generes
> head(gene.res2)
```

	probeid	drugLevel.stat	residualDisease.stat	
1	probe_1	0.50745310	-0.4410378	
2	probe_2	-0.05129198	0.1083797	
3	probe_3	0.34392723	-0.3069893	
4	probe_4	-0.21510307	0.1812378	
5	probe_5	-0.43215514	0.3725875	
6	probe_6	0.06213032	-0.1796821	
	obsTime.obsCensor.stat	PROMISE.stat	perm.p.drugLevel.stat	
1	-0.328713893	0.20659234		0.00
2	0.050025633	-0.03654867		0.68
3	-0.277173083	0.12458114		0.02
4	0.003140076	-0.13106692		0.10
5	0.346205081	-0.15284585		0.01
6	-0.201508221	0.01343473		0.67
	perm.p.residualDisease.stat	perm.p.obsTime.obsCensor.stat		
1		0.00		0.00

2	0.46	0.76
3	0.03	0.01
4	0.17	0.99
5	0.00	0.00
6	0.18	0.17

```
perm.p.PROMISE.stat
1 0.00
2 0.65
3 0.06
4 0.07
5 0.03
6 0.81
```

Gene set level result:

```
> set.res2<-test2$setres
> head(set.res2)
```

```
      setid drugLevel.stat residualDisease.stat
1 GeneSet 1  0.30998611      0.28204640
2 GeneSet 2  0.18012248      0.15382306
3 GeneSet 3  0.19852231      0.18092662
4 GeneSet 4  0.07289261      0.13631292
5 GeneSet 5  0.11745341      0.06539079
6 GeneSet 6  0.08167737      0.08478505
      obsTime.obsCensor.stat PROMISE.stat perm.p.drugLevel.stat
1      0.20105155  0.13032699      0.00
2      0.13759326  0.09124962      0.03
3      0.20620859  0.06608593      0.05
4      0.12875576  0.04299261      0.95
5      0.09114311  0.06327372      0.42
6      0.09922607  0.03234743      0.88
      perm.p.residualDisease.stat perm.p.obsTime.obsCensor.stat
1      0.00      0.01
2      0.03      0.09
3      0.02      0.00
4      0.14      0.23
5      0.95      0.82
6      0.79      0.69
      perm.p.PROMISE.stat
1 0.00
2 0.00
3 0.23
4 0.85
5 0.33
6 0.92
```