Introduction to iBBiG

Aedin Culhane, Daniel Gusenleitner

May 11, 2023

1 iBBiG

Iterative Binary Bi-clustering of Gene sets (iBBiG) is a bi-clustering algorithm optimized for discovery of overlapping biclusters in spare binary matrices of data (Gusenleitner *et al.* in review).

We have optimized this method for the discovery of modules in matrices of discretized *p*-values from gene set enrichment analysis (GSA) of hundreds of datasets. However, it could be applied to any binary (1,0) matrix, such as discretized *p*-values from any sources of binary data. We apply iBBiG to meta-GSA to enable integrated analysis over hundreds of gene expression datasets. By integrating data at the levels of GSA results, we avoid the need to match probes/genes across multiple datasets, making large scale data integration a tractable problem.

iBBiG scales well with the dimensions of meta-datasets and is tolerant to noise characteristic of genomic data. It outperformed other traditional clustering approaches (Hierarchical clustering, k-means) or biclustering methods (bimax, fabia, coalesce) when applied to simulated data.

2 Application to simulated dataset

To demonstrate iBBiG, we will use a simulated binary dataset of 400 rows x 400 columns (as described by Gusenleitner *et al.*), in which a 1 indicates a positive association (or $p < 0.05$) between a gene set (row) and the results of a pairwise test between clinical covariates (column), and a 0 represents a lack of association.

To simulate random noise characteristically observed in genomic data, 10% random background noise (value of 1) was introduced into the matrix.

The matrix was seeded with seven artificial modules or bi-clusters (M1-M7; Figure 1) by assigning associations (value of 1) to its column and row pairs. To replicate the expected properties of real data, seeded modules partially overlapped in columns, in rows and in both rows and columns simultaneously. M1 gene sets overlap with most other modules with the exception of M3. M2 has overlapping pairwise tests with modules M4-7.

Artificial modules also have highly varying sizes and aspect ratios, including "wide" modules driven by a large number of pairwise tests and only a few gene sets and "tall" modules like M1 which consist of 25 pairwise tests and a large number of gene sets ($n = 250$). This latter type of module might represent a complex, well-characterized biological process such as proliferation.

In a real data set the signal strength will vary both between and within modules. Variance between modules was simulated by imposing random noise (1 -> 0 replacement) with different signal strengths on the modules (Figure 1). Within a module, we expect to see a few strong signals (gene sets associated with all pairwise tests) and many weaker signals. Therefore within each module, a noise gradient was also applied so that the first gene sets had the greatest number of associations (Figure 1). This overlaid noise gradient ranged from 10 to 60% and varied between modules (Table 1).

To create this simulated data as described in Gusenleitner, *et al.* use the function `makeArtifical` which creates an object of class *iBBiG*, an extension of *biclust*.

```
> library(iBBiG)
> binMat<-makeArtificial()
```

```
[1] "***** Summary of Design Matrix ******"
   Rows Cols DensityLow DenistyHigh
M1  250   25        0.4         0.9
M2   75  175        0.4         0.8
M3   50   50        0.5         0.8
M4   40   40        0.4         0.9
M5   30   30        0.4         0.8
M6   20   20        0.6         0.9
M7   40   40        0.5         0.6

Cluster sizes in new iBBiG (Biclust) data object
Number of Modules: 7
Rows        250        75        50        40        30        20        40
Columns        25        175        50        40        30        20        40
```

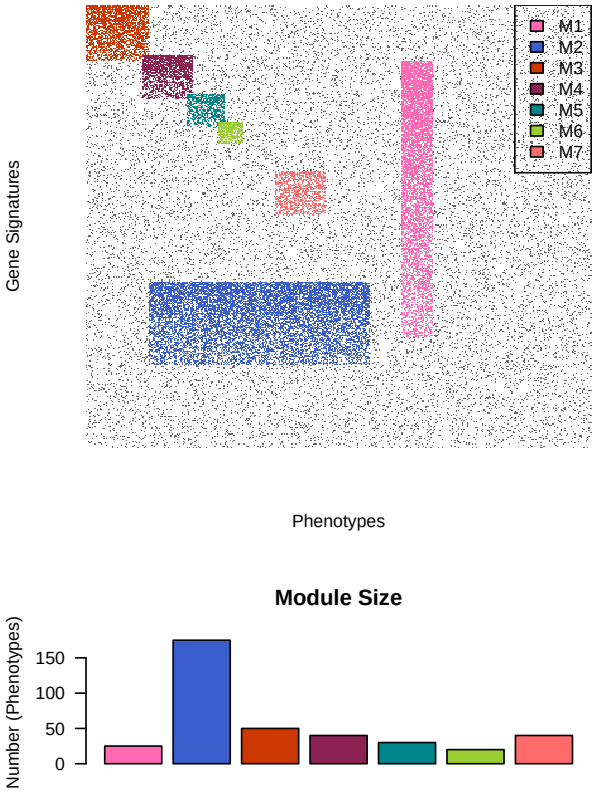
> binMat

```
An object of class iBBiG

Number of Clusters found:  7

First  5  Cluster scores and sizes:
                  [,1] [,2] [,3] [,4] [,5]
Cluster Score       NA   NA   NA   NA   NA
Number of Rows:    250   75   50   40   30
Number of Columns:  25  175   50   40   30
```

> plot(binMat)



The class *BiClust* contains the number of clusters and two logical matrices which indicate whether a row or column are present in the cluster.

```
> str(binMat)

Formal class 'iBBiG' [package "iBBiG"] with 8 slots
  ..@ Seeddata       : num [1:400, 1:400] 1 1 1 1 1 1 0 0 1 1 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:400] "sig_1" "sig_2" "sig_3" "sig_4" ...
  .. .. ..$ : chr [1:400] "cov_1" "cov_2" "cov_3" "cov_4" ...
  ..@ RowScorexNumber: num[0 , 0 ]
  ..@ Clusterscores  : num(0)
  ..@ Parameters     :List of 3
  .. ..$ designMatrix: num [1:7, 1:6] 251 51 1 46 81 106 151 51 251 1 ...
  .. .. ..- attr(*, "dimnames")=List of 2
  .. .. .. ..$ : chr [1:7] "M1" "M2" "M3" "M4" ...
  .. .. .. ..$ : chr [1:6] "startC" "startR" "endC" "endR" ...
  .. ..$ nRow        : num 400
  .. ..$ nCol        : num 400
  ..@ RowxNumber     : logi [1:400, 1:7] FALSE FALSE FALSE FALSE FALSE FALSE ...
  ..@ NumberxCol     : logi [1:7, 1:400] FALSE FALSE TRUE FALSE FALSE FALSE ...
```

```
  ..@ Number          : int 7
  ..@ info            : list()
```

```
> Number(binMat)
```

```
[1] 7
```

```
> RowxNumber(binMat)[1:2,]
```

```
      [,1]  [,2] [,3]  [,4]  [,5]  [,6]  [,7]
[1,] FALSE FALSE TRUE FALSE FALSE FALSE FALSE
[2,] FALSE FALSE TRUE FALSE FALSE FALSE FALSE
```

```
> NumberxCol(binMat)[,1:2]
```

```
      [,1]  [,2]
[1,] FALSE FALSE
[2,] FALSE FALSE
[3,]  TRUE  TRUE
[4,] FALSE FALSE
[5,] FALSE FALSE
[6,] FALSE FALSE
[7,] FALSE FALSE
```

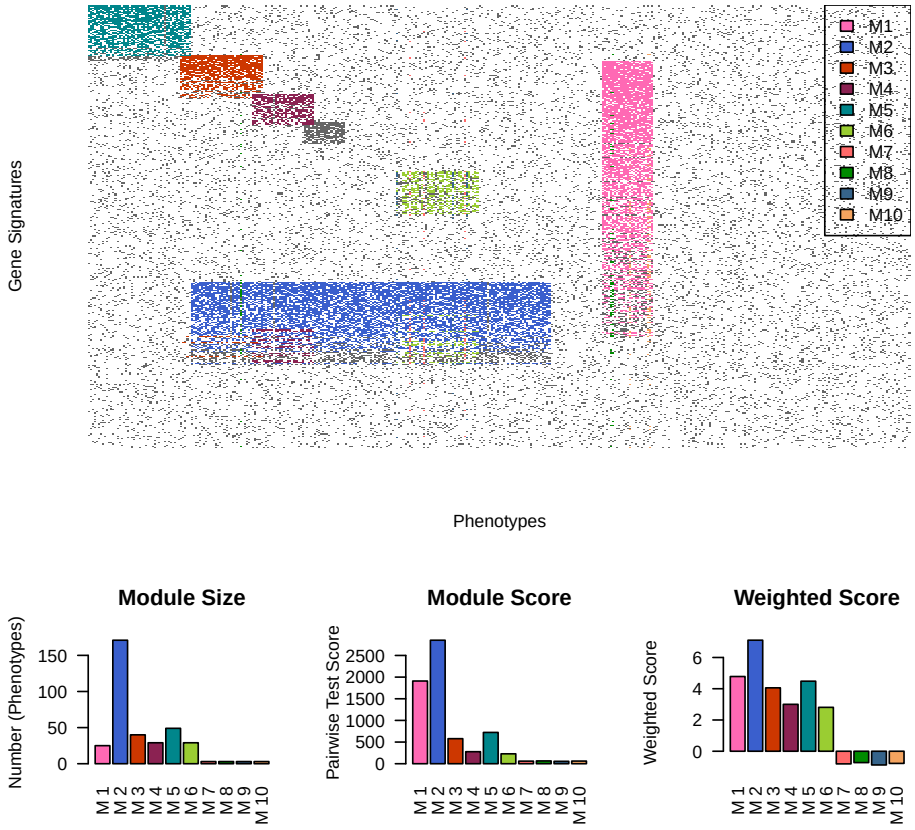
The matrix *RowxNumber* is a logical matrix having a number of rows equal to that of *binMat* and a number of columns equal to the number of detected clusters. *NumberxCol* is reversed; this class has a row count equal to the number of clusters and a column count of the number of columns of *binMat*.

To run iBBiG on this artificial binary matrix, simply call the function `iBBiG`. The function `plot` and `statClust` will provide a visual representation and statistical summary of the results of the cluster analysis.

```
> res<- iBBiG(binMat@Seeddata, nModules=10)
```

```
Module:  1 ... done
Module:  2 ... done
Module:  3 ... done
Module:  4 ... done
Module:  5 ... done
Module:  6 ... done
Module:  7 ... done
Module:  8 ... done
Module:  9 ... done
Module:  10 ... done
```

```
> plot(res)
```



If you wish to compare two `iBBiG` or `Biclust` results, for example a prediction and a gold standard (GS), the function `JIdist` will calculate the Jaccard Index distance between two *Biclust* or *iBBiG* result objects. By default, it calculates the distances between each column. Setting $margin = row$ or $margin = both$ will cause the function to calculate instead the JI distance between the rows, or an average of rows/columns.

By default, RfunctionJIdist returns a *data.frame* with 2 columns, the column n indicating which cluster was the best match (maximum JI) to each cluster of the second iBBiG object (GS). The column JI contains the Jaccard Index distance between the columns of these two clusters. If $best = FALSE$, the function will return the distance matrix instead of the best match.

```
> JIdist(res,binMat)
```

```
      n    JI
GS_1 1 1.000
GS_2 2 0.977
GS_3 5 0.980
GS_4 3 1.000
GS_5 4 0.967
GS_6 2 0.117
GS_7 6 0.725
```

```
> JIdist(res,binMat, margin="col", best=FALSE)
```

```
           GS_1        GS_2       GS_3       GS_4
M 1  1.00000000 0.000000000 0.00000000 0.00000000
M 2  0.00000000 0.977142857 0.00000000 0.18539326
M 3  0.00000000 0.194444444 0.05882353 1.00000000
M 4  0.00000000 0.165714286 0.00000000 0.07812500
M 5  0.00000000 0.000000000 0.98000000 0.05952381
M 6  0.00000000 0.165714286 0.00000000 0.00000000
M 7  0.00000000 0.017142857 0.00000000 0.00000000
M 8  0.07692308 0.005649718 0.00000000 0.02380952
M 9  0.00000000 0.017142857 0.00000000 0.00000000
M 10 0.12000000 0.000000000 0.00000000 0.00000000
           GS_5      GS_6      GS_7
M 1  0.00000000 0.0000000 0.0000000
M 2  0.16860465 0.1169591 0.2339181
M 3  0.07692308 0.0000000 0.0000000
M 4  0.96666667 0.1136364 0.0000000
M 5  0.00000000 0.0000000 0.0000000
M 6  0.00000000 0.0000000 0.7250000
M 7  0.00000000 0.0000000 0.0750000
M 8  0.00000000 0.0000000 0.0000000
M 9  0.00000000 0.0000000 0.0750000
M 10 0.00000000 0.0000000 0.0000000

> JIdist(res,binMat, margin="col")

     n    JI
GS_1 1 1.000
GS_2 2 0.977
GS_3 5 0.980
GS_4 3 1.000
GS_5 4 0.967
GS_6 2 0.117
GS_7 6 0.725

> JIdist(res,binMat, margin="row")

     n    JI
GS_1 1 0.764
GS_2 2 0.800
GS_3 5 0.880
GS_4 3 0.767
GS_5 4 0.610
GS_6 1 0.099
GS_7 6 0.620

> JIdist(res,binMat, margin="both")

     n    JI
GS_1 1 1.764
GS_2 2 1.777
GS_3 5 1.860
GS_4 3 1.767
```

```
GS_5 4 1.576
GS_6 4 0.170
GS_7 6 1.345
```

To view the code of the function JIdist

```
> showMethods(JIdist)
> getMethod(iBBiG:::JIdist, signature(clustObj = "iBBiG", GS = "iBBiG"))
> getMethod("JIdist",  signature(clustObj="iBBiG", GS="iBBiG"))
```

To extract performance statistics between two `iBBiG` results, use `analyzeClust`, which will take a single *iBBiG* result object or a list of objects and compare these to a gold standard (another *iBBiG* or *biclust* object). Again results can be based on matches to the best row, column or both.

```
> analyzeClust(res,binMat)
```

```
[1] "list"
     Run n    JI nRow nCol col-accuracy col-sensitivity
GS_1   1 1 1.000  191   25        1.000           1.000
GS_2   1 2 0.977   60  171        0.990           0.977
GS_3   1 5 0.980   44   49        0.998           0.980
GS_4   1 3 1.000   36   40        1.000           1.000
GS_5   1 4 0.967   36   29        0.998           0.967
GS_6   1 2 0.117   60  171        0.623           1.000
GS_7   1 6 0.725   41   29        0.973           0.725
     col-specificity col-PPV col-NPV row-accuracy
GS_1           1.000   1.000   1.000        0.853
GS_2           1.000   1.000   0.983        0.963
GS_3           1.000   1.000   0.997        0.985
GS_4           1.000   1.000   1.000        0.975
GS_5           1.000   1.000   0.997        0.960
GS_6           0.603   0.117   1.000        0.800
GS_7           1.000   1.000   0.970        0.953
     row-sensitivity row-specificity row-PPV row-NPV
GS_1           0.764           1.000   1.000   0.718
GS_2           0.800           1.000   1.000   0.956
GS_3           0.880           1.000   1.000   0.983
GS_4           0.825           0.992   0.917   0.981
GS_5           0.833           0.970   0.694   0.986
GS_6           0.000           0.842   0.000   0.941
GS_7           0.775           0.972   0.756   0.975
```

```
> analyzeClust(res,binMat, margin="col")
```

```
[1] "list"
     Run n    JI nRow nCol col-accuracy col-sensitivity
GS_1   1 1 1.000  191   25        1.000           1.000
GS_2   1 2 0.977   60  171        0.990           0.977
GS_3   1 5 0.980   44   49        0.998           0.980
GS_4   1 3 1.000   36   40        1.000           1.000
GS_5   1 4 0.967   36   29        0.998           0.967
GS_6   1 2 0.117   60  171        0.623           1.000
GS_7   1 6 0.725   41   29        0.973           0.725
```

```
     col-specificity col-PPV col-NPV row-accuracy
GS_1           1.000   1.000   1.000        0.853
GS_2           1.000   1.000   0.983        0.963
GS_3           1.000   1.000   0.997        0.985
GS_4           1.000   1.000   1.000        0.975
GS_5           1.000   1.000   0.997        0.960
GS_6           0.603   0.117   1.000        0.800
GS_7           1.000   1.000   0.970        0.953
     row-sensitivity row-specificity row-PPV row-NPV
GS_1           0.764           1.000   1.000   0.718
GS_2           0.800           1.000   1.000   0.956
GS_3           0.880           1.000   1.000   0.983
GS_4           0.825           0.992   0.917   0.981
GS_5           0.833           0.970   0.694   0.986
GS_6           0.000           0.842   0.000   0.941
GS_7           0.775           0.972   0.756   0.975
```

Again to view the code of the function, you could:

```
> showMethods(analyzeClust)
> getMethod("analyzeClust",  signature(clustObj="iBBiG", GS="iBBiG"))
```

The structure of *iBBiG* differs from *BiClust* in that it contains ClusterScores. ClusterScores are the scores for each module. RowScoreNumber are the scores for each row in the cluster. *Seeddata* is a copy of *binMat*.

```
> str(binMat)
```

```
Formal class 'iBBiG' [package "iBBiG"] with 8 slots
  ..@ Seeddata       : num [1:400, 1:400] 1 1 1 1 1 1 0 0 1 1 ...
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:400] "sig_1" "sig_2" "sig_3" "sig_4" ...
  .. .. ..$ : chr [1:400] "cov_1" "cov_2" "cov_3" "cov_4" ...
  ..@ RowScorexNumber: num[0 , 0 ]
  ..@ Clusterscores  : num(0)
  ..@ Parameters     :List of 3
  .. ..$ designMatrix: num [1:7, 1:6] 251 51 1 46 81 106 151 51 251 1 ...
  .. .. ..- attr(*, "dimnames")=List of 2
  .. .. .. ..$ : chr [1:7] "M1" "M2" "M3" "M4" ...
  .. .. .. ..$ : chr [1:6] "startC" "startR" "endC" "endR" ...
  .. ..$ nRow        : num 400
  .. ..$ nCol        : num 400
  ..@ RowxNumber     : logi [1:400, 1:7] FALSE FALSE FALSE FALSE FALSE FALSE ...
  ..@ NumberxCol     : logi [1:7, 1:400] FALSE FALSE TRUE FALSE FALSE FALSE ...
  ..@ Number         : int 7
  ..@ info           : list()
```

```
> RowScorexNumber(res)[1:2,]
```

```
      M 1 M 2 M 3 M 4      M 5 M 6 M 7 M 8 M 9 M 10
sig_1   0   0   0   0 28.20243   0   0   0   0    0
sig_2   0   0   0   0 32.10346   0   0   0   0    0
```

```
> Clusterscores(res)
```

```
       M 1        M 2        M 3        M 4        M 5
1909.84107 2852.13652  578.31967  277.69906  722.63187
       M 6        M 7        M 8        M 9       M 10
 228.82878   59.35658   64.47562   55.44468   61.18355
```

```
> Seeddata(res)[1:2,1:2]
```

```
      cov_1 cov_2
sig_1     1     1
sig_2     1     0
```

There are also the slots for info and Parameters which can contain additional user-entered information about the analysis. We can subset or reorder the results like so:

```
> res[1:3]
```

```
An object of class iBBiG

Number of Clusters found:  3

First  3  Cluster scores and sizes:
                        M 1      M 2      M 3
Cluster Score      1909.841 2852.137 578.3197
Number of Rows:     191.000   60.000  36.0000
Number of Columns:   25.000  171.000  40.0000
```

```
> res[c(4,2,1)]
```

```
An object of class iBBiG

Number of Clusters found:  3

First  3  Cluster scores and sizes:
                        M 4      M 2      M 1
Cluster Score      277.6991 2852.137 1909.841
Number of Rows:     36.0000   60.000  191.000
Number of Columns:  29.0000  171.000   25.000
```

```
> res[1, drop=FALSE]
```

```
An object of class iBBiG

There was one cluster found with Score 1909.841 and
  191 Rows and  25 columns
```

3 Using biclust functions

An object from *iBBiG* extends the class *biclust* and can therefore use methods available to a *biclust* object. For example, there are several plot functions in *BiClust*

```
> class(res)
> par(mfrow=c(2,1))
> drawHeatmap2(res@Seeddata, res, number=4)
```

```
> biclustmember(res,res@Seeddata)
> biclustbarchart(res@Seeddata, Bicres=res)
> plotclust(res, res@Seeddata)
```

Statistical measures of biclustering performance including the Chia and Karuturi Function, Coherence measures and F Statistics are available within the *biclust* R packages.

There are function to process data, binarize or discretize data. For example, given gene expression data we can binarize or discretize the data matrix as follows and this can be input into iBBiG

```
> data(BicatYeast)
> BicatYeast[1:5,1:5]
> binarize(BicatYeast[1:5,1:5], threshold=0.2)
> discretize(BicatYeast[1:5,1:5])
```

The sub-matrices of each cluster can be extracted from the original matrix, using the function `bicluster`

```
> Modules<-bicluster(res@Seeddata, res, 1:3)
> str(Modules)
```

```
List of 3
 $ Bicluster1: num [1:191, 1:25] 1 1 1 1 1 1 1 1 1 1 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:191] "sig_51" "sig_52" "sig_53" "sig_54" ...
  .. ..$ : chr [1:25] "cov_251" "cov_252" "cov_253" "cov_254" ...
 $ Bicluster2: num [1:60, 1:171] 0 1 1 1 1 1 0 0 1 1 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:60] "sig_251" "sig_252" "sig_253" "sig_254" ...
  .. ..$ : chr [1:171] "cov_51" "cov_52" "cov_53" "cov_54" ...
 $ Bicluster3: num [1:36, 1:40] 1 1 0 1 1 1 1 1 1 1 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:36] "sig_46" "sig_47" "sig_48" "sig_49" ...
  .. ..$ : chr [1:40] "cov_46" "cov_47" "cov_48" "cov_49" ...
```

```
> Modules[[1]][1:3,1:4]
```

```
       cov_251 cov_252 cov_253 cov_254
sig_51       1       1       1       1
sig_52       1       1       1       1
sig_53       1       1       1       1
```

To write results to a file use the following:

```
> writeBiclusterResults("Modules.txt", res, bicName="Output from iBBiG with default pa
>
```

4 Session Info

- R version 4.3.0 RC (2023-04-13 r84257), `x86_64-apple-darwin20`
- Locale: `C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8`
- Time zone: `America/New_York`
- TZcode source: `internal`

- Running under: `macOS Monterey 12.6.4`
- Matrix products: default
- BLAS:
  `/Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRblas.0.dylib`
- LAPACK:
  `/Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRlapack.dylib`
  ; LAPACK version3.11.0
- Base packages: base, datasets, grDevices, graphics, grid, methods, stats, utils
- Other packages: MASS 7.3-60, biclust 2.0.3, colorspace 2.1-0, iBBiG 1.44.0, lattice 0.21-8
- Loaded via a namespace (and not attached): R6 2.5.1, Rcpp 1.0.10, additivityTests 1.1-4.1, ade4 1.7-22, class 7.3-22, cli 3.6.1, compiler 4.3.0, dplyr 1.1.2, fansi 1.0.4, flexclust 1.4-1, generics 0.1.3, ggplot2 3.4.2, glue 1.6.2, gtable 0.3.3, lifecycle 1.0.3, magrittr 2.0.3, modeltools 0.2-23, munsell 0.5.0, parallel 4.3.0, pillar 1.9.0, pkgconfig 2.0.3, purrr 1.0.1, rlang 1.1.1, scales 1.2.1, stats4 4.3.0, tibble 3.2.1, tidyr 1.3.0, tidyselect 1.2.0, tools 4.3.0, utf8 1.2.3, vctrs 0.6.2, xtable 1.8-4

References