

ChIPseeker: an R package for ChIP peak Annotation, Comparison and Visualization

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Contents

1	Introduction	2
2	ChIP profiling	2
2.1	ChIP peaks over Chromosomes	3
2.2	Profile of ChIP peaks binding to TSS regions	4
2.2.1	Heatmap of ChIP binding to TSS regions	5
2.2.2	Average Profile of ChIP peaks binding to TSS region	5
3	Peak Annotation	6
3.1	Visualize Genomic Annotation	8
3.2	Visualize distribution of TF-binding loci relative to TSS	10
4	Functional enrichment analysis	10
5	ChIP peak data set comparison	11
5.1	Profile of several ChIP peak data binding to TSS region	11
5.1.1	Average profiles	12
5.1.2	Peak heatmaps	12
5.2	ChIP peak annotation comparison	13
5.3	Functional profiles comparison	14
5.4	Overlap of peaks and annotated genes	15
6	Statistical testing of ChIP seq overlap	16
6.1	Shuffle genome coordination	16
6.2	Peak overlap enrichment analysis	17
7	Data Mining with ChIP seq data deposited in GEO	17
7.1	GEO data collection	18
7.2	Download GEO ChIP data sets	21
7.3	Overlap significant testing	21
8	Session Information	21

1 Introduction

Chromatin immunoprecipitation followed by high-throughput sequencing (ChIP-seq) has become standard technologies for genome wide identification of DNA-binding protein target sites. After read mappings and peak callings, the peak should be annotated to answer the biological questions. Annotation also create the possibility of integrate expression profile data to predict gene expression regulation. *ChIPseeker* was developed for annotating nearest genes and genomic features to peaks.

ChIP peak data set comparison is also very important. We can use it as an index to estimate how well biological replications are. Even more important is applying to infer cooperative regulation. If two ChIP seq data, obtained by two different binding proteins, overlap significantly, these two proteins may form a complex or have interaction in regulation chromosome remodelling or gene expression. *ChIPseeker* support statistical testing of significant overlap among ChIP seq data sets, and incorporate open access database GEO for users to compare their own dataset to those deposited in database. Protein interaction hypothesis can be generated by mining data deposited in database. Converting genome coordinations from one genome version to another is also supported, making this comparison available for different genome version and different species.

Several visualization functions are implemented to visualize the coverage of the ChIP seq data, peak annotation, average profile and heatmap of peaks binding to TSS region.

Functional enrichment analysis of the peaks can be performed by my Bioconductor packages *DOSE* , *ReactomePA*, *clusterProfiler* [1] .

```
## loading packages
require(ChIPseeker)
require(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
require(clusterProfiler)
```

2 ChIP profiling

The datasets CBX6 and CBX7 in this vignettes were downloaded from GEO (GSE40740) [2] while ARmo_0M, ARmo_1nM and ARmo_100nM were downloaded from GEO (GSE48308) [3] . *ChIPseeker* provides `readPeakFile` to load the peak and store in `GRanges` object. Most of the functions in *ChIPseeker* can accept input in peak file (bed format) or `GRanges` object.

```

files <- getSampleFiles()
print(files)

## $ARmo_OM
## [1] "/Volumes/DATA/opt/R-devel/R.framework/Versions/3.2/Resources/library/ChIPSe
##
## $ARmo_1nM
## [1] "/Volumes/DATA/opt/R-devel/R.framework/Versions/3.2/Resources/library/ChIPSe
##
## $ARmo_100nM
## [1] "/Volumes/DATA/opt/R-devel/R.framework/Versions/3.2/Resources/library/ChIPSe
##
## $CBX6_BF
## [1] "/Volumes/DATA/opt/R-devel/R.framework/Versions/3.2/Resources/library/ChIPSe
##
## $CBX7_BF
## [1] "/Volumes/DATA/opt/R-devel/R.framework/Versions/3.2/Resources/library/ChIPSe

peak <- readPeakFile(files[[4]])
peak

## GRanges with 1331 ranges and 2 metadata columns:
##           seqnames           ranges strand |           V4           V5
##           <Rle>           <IRanges> <Rle> |           <factor> <numeric>
##      [1]      chr1      [ 815092,   817883]   * |      MACS_peak_1      295.8
##      [2]      chr1      [1243287, 1244338]   * |      MACS_peak_2       63.2
##      [3]      chr1      [2979976, 2981228]   * |      MACS_peak_3     100.2
##      [4]      chr1      [3566181, 3567876]   * |      MACS_peak_4     558.9
##      [5]      chr1      [3816545, 3818111]   * |      MACS_peak_5       57.6
##      ...      ...      ...      ...      ...      ...
##    [1327]     chrX [135244782, 135245821]   * |      MACS_peak_1327     55.5
##    [1328]     chrX [139171963, 139173506]   * |      MACS_peak_1328    270.2
##    [1329]     chrX [139583953, 139586126]   * |      MACS_peak_1329    918.7
##    [1330]     chrX [139592001, 139593238]   * |      MACS_peak_1330    210.9
##    [1331]     chrY [ 13845133,  13845777]   * |      MACS_peak_1331     58.4
##      ---
##      seqlengths:
##      chr1 chr10 chr11 chr12 chr13 chr14 ... chr6 chr7 chr8 chr9 chrX chrY
##      NA   NA   NA   NA   NA   NA   ...  NA   NA   NA   NA   NA   NA

```

2.1 ChIP peaks over Chromosomes

After peak calling, we would like to know the peak locations over the whole genome, `plotChrCov` function calculates the coverage of peak regions over chromosomes and generate a figure to visualize.

```
plotChrCov(peak, weightCol = "V5")
```

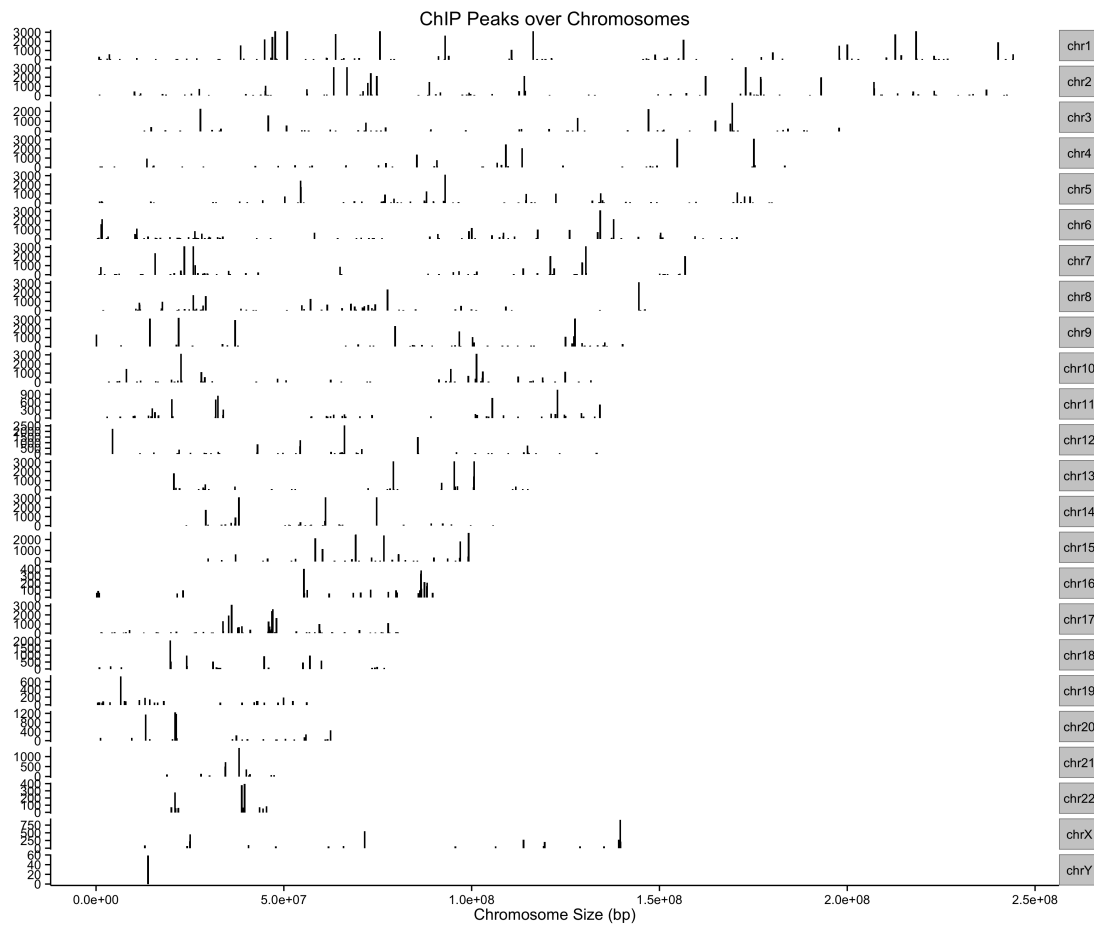


Figure 1: ChIP peaks over Chromosomes

2.2 Profile of ChIP peaks binding to TSS regions

First of all, for calculate the profile of ChIP peaks binding to TSS regions, we should prepare the TSS regions, which are defined as the flanking sequence of the TSS sites. Then align the peaks that are mapping to these regions, and generate the tagMatrix.

```
## promoter <- getPromoters(TranscriptDb=txdb,
## upstream=3000, downstream=3000) tagMatrix <-
## getTagMatrix(peak, windows=promoter) to speed up
## the compilation of this vignettes, we use a
## precalculated tagMatrix
data("tagMatrixList")
tagMatrix <- tagMatrixList[[4]]
```

In the above code, you should notice that `tagMatrix` is not restricted to TSS regions. The regions can be other types that defined by the user.

2.2.1 Heatmap of ChIP binding to TSS regions

```
tagHeatmap(tagMatrix, xlim = c(-3000, 3000), color = "red")
```

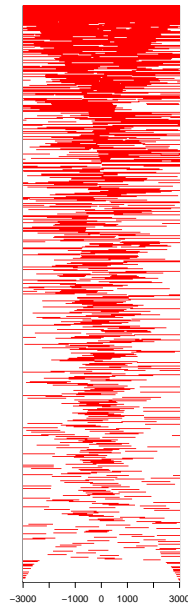


Figure 2: Heatmap of ChIP peaks binding to TSS regions

ChIPseeker provide a one step function to generate this figure from bed file. The following function will generate the same figure as above.

```
peakHeatmap(files[[4]], TranscriptDb = txdb, upstream = 3000,  
            downstream = 3000, color = "red")
```

2.2.2 Average Profile of ChIP peaks binding to TSS region

```
plotAvgProf(tagMatrix, xlim = c(-3000, 3000), xlab = "Genomic Region (5'→3')",  
            ylab = "Read Count Frequency")
```

The function `plotAvgProf2` provide a one step from bed file to average profile plot. The following command will generate the same figure as shown above.

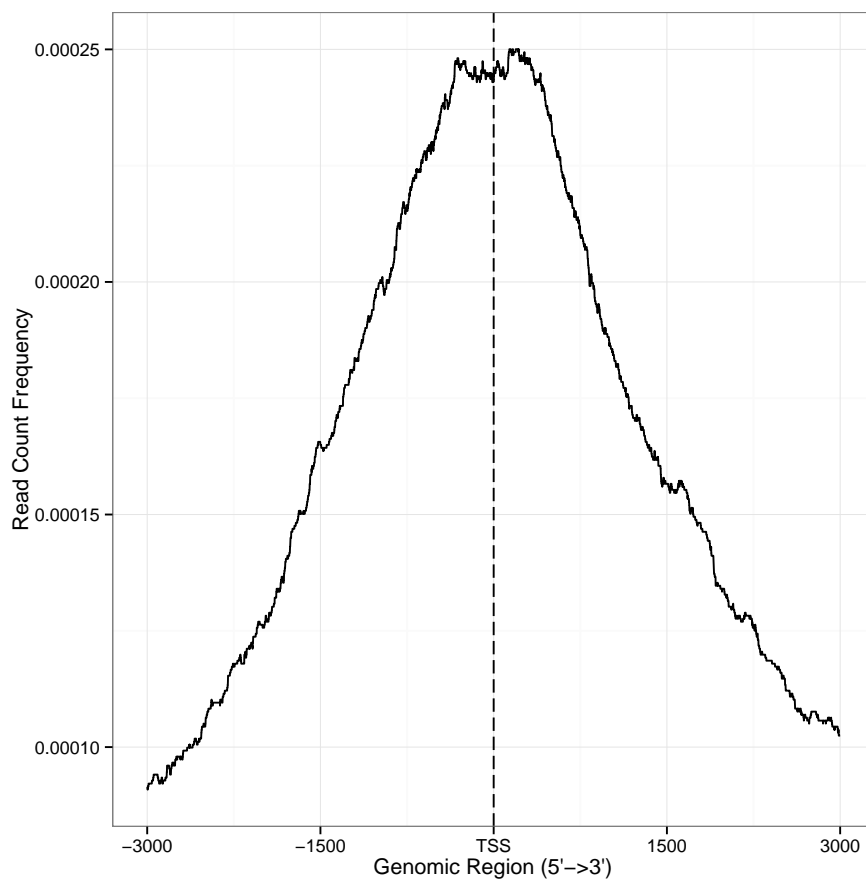


Figure 3: Average Profile of ChIP peaks binding to TSS region

```
plotAvgProf2(files[[4]], TranscriptDb = txdb, upstream = 3000,
  downstream = 3000, xlab = "Genomic Region (5' to 3')",
  ylab = "Read Count Frequency")
```

3 Peak Annotation

```
peakAnno <- annotatePeak(files[[4]], tssRegion = c(-3000,
  3000), as = "GRanges", TranscriptDb = txdb, annoDb = "org.Hs.eg.db")

## >> loading peak file... 2014-06-12 01:11:13
## >> preparing features information... 2014-06-12 01:11:13
## >> identifying nearest features... 2014-06-12 01:11:19
## >> calculating distance from peak to TSS... 2014-06-12 01:11:21
## >> assigning genomic annotation... 2014-06-12 01:11:21
## >> adding gene annotation... 2014-06-12 01:11:53
## >> assigning chromosome lengths 2014-06-12 01:11:54
## >> done... 2014-06-12 01:11:54
```

```
head(peakAnno)
```

```
## GRanges with 6 ranges and 13 metadata columns:
```

```
##      seqnames      ranges strand |      V4      V5
##      <Rle>        <IRanges> <Rle> |  <factor> <numeric>
## [1]    chr1 [ 815092,  817883]    * | MACS_peak_1    295.8
## [2]    chr1 [1243287, 1244338]    * | MACS_peak_2     63.2
## [3]    chr1 [2979976, 2981228]    * | MACS_peak_3    100.2
## [4]    chr1 [3566181, 3567876]    * | MACS_peak_4    558.9
## [5]    chr1 [3816545, 3818111]    * | MACS_peak_5     57.6
## [6]    chr1 [6304864, 6305704]    * | MACS_peak_6     54.6
```

```
##      annotation geneChr geneStart  geneEnd geneLength geneStrand
##      <character> <factor> <integer> <integer> <integer> <factor>
## [1] Distal Intergenic    chr1    803451    812182      8732      -
## [2] Promoter (<=1kb)    chr1   1227764   1244989   17226      -
## [3] Promoter (<=1kb)    chr1   2976181   2984289    8109      -
## [4] Promoter (<=1kb)    chr1   3547331   3566671   19341      -
## [5] Promoter (<=1kb)    chr1   3816968   3833879   16912      +
## [6] Promoter (<=1kb)    chr1   6304252   6305638   1387       +
```

```
##      geneId distanceToTSS      ENSEMBL      SYMBOL
##      <character> <numeric> <character> <character>
## [1]    284593      -5701 ENSG00000230368    FAM41C
## [2]    116983         0 ENSG00000131584    ACAP3
## [3]    440556         0 ENSG00000177133    LINC00982
## [4]     49856         0 ENSG00000116213    WRAP73
## [5]   100133612         0 ENSG00000236423    LINC01134
## [6]    390992         0 ENSG00000173673    HES3
```

```
##      GENENAME
##      <character>
## [1] family with sequence similarity 41, member C
## [2] ArfGAP with coiled-coil, ankyrin repeat and PH domains 3
## [3] long intergenic non-protein coding RNA 982
## [4] WD repeat containing, antisense to TP73
## [5] long intergenic non-protein coding RNA 1134
## [6] hes family bHLH transcription factor 3
```

```
## ---
```

```
## seqlengths:
```

```
##      chr1      chr10      chr11      chr12 ...      chr9      chrX      chrY
## 249250621 135534747 135006516 133851895 ... 141213431 155270560 59373566
```

Peak Annotation is performed by `annotatePeak`. User can define TSS (transcription start site) region, by default TSS is defined from -3kb to +3kb. The argument `as` can be one of "GRanges", "data.frame" and "txt" to specify the output format return by `annotatePeak`. If `as` is set to "txt", the output will save to a TXT file with name suffix by `anno.txt`.

`TranscriptDb` object contained transcript-related features of a particular genome. Bioconductor provides several package that containing `TranscriptDb` object of

model organisms with multiple commonly used genome version, for instance *TxDb.Hsapiens.UCSC.hg19.knownGene* and *TxDb.Hsapiens.UCSC.hg18.knownGene* for human genome hg19 and hg18, *TxDb.Mmusculus.UCSC.mm10.knownGene* and *TxDb.Mmusculus.UCSC.mm9.knownGene* for mouse genome mm10 and mm9, etc. User can also prepare their own `TranscriptDb` object by retrieving information from UCSC Genome Bioinformatics and BioMart data resources by R function `makeTranscriptDbFromBiomart` and `makeTranscriptDbFromUCSC`. `TranscriptDb` object should be passed for peak annotation.

All the peak information contained in peakfile will be retained in the output of `annotatePeak`. The position and strand information of nearest genes are reported. The distance from peak to the TSS of its nearest gene is also reported. The genomic region of the peak is reported in annotation column. Since some annotation may overlap, *ChIPseeker* adopted the following priority in genomic annotation.

- Promoter
- 5' UTR
- 3' UTR
- Exon
- Intron
- Downstream
- Intergenic

Downstream is defined as the downstream of gene end.

`annotatePeak` report detail information when the annotation is Exon or Intron, for instance "Exon (uc002sbe.3/9736, exon 69 of 80)", means that the peak is overlap with an Exon of transcript uc002sbe.3, and the corresponding Entrez gene ID is 9736 (Transcripts that belong to the same gene ID may differ in splice events), and this overlapped exon is the 69th exon of the 80 exons that this transcript uc002sbe.3 possess.

Parameter `annoDb` is optional, if provided, extra columns including SYMBOL, GENENAME, ENSEMBL/ENTREZID will be added. The `geneID` column in annotation output will be consistent with the `geneID` in `TranscriptDb`. If it is ENTREZID, ENSEMBL will be added if `annoDb` is provided, while if it is ENSEMBL ID, ENTREZID will be added.

3.1 Visualize Genomic Annotation

To annotate the location of a given peak in terms of genomic features, `annotatePeak` assigns peaks to genomic annotation in "annotation" column of the output, which

includes whether a peak is in the TSS, Exon, 5' UTR, 3' UTR, Intronic or Inter-genic. Many researchers are very interesting in these annotations. TSS region can be defined by user and `annotatePeak` output in details of which exon/intron of which genes as illustrated in previous section.

Pie and Bar plot are supported to visualize the genomic annotation.

```
plotAnnoPie(peakAnno)
```

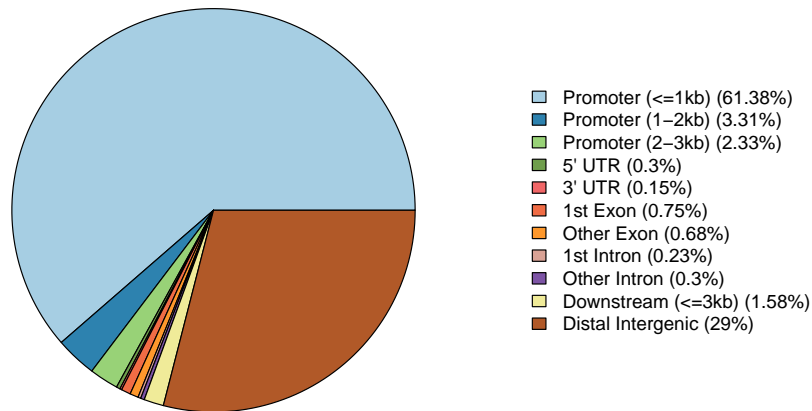


Figure 4: Genomic Annotation by pieplot

```
plotAnnoBar(peakAnno)
```

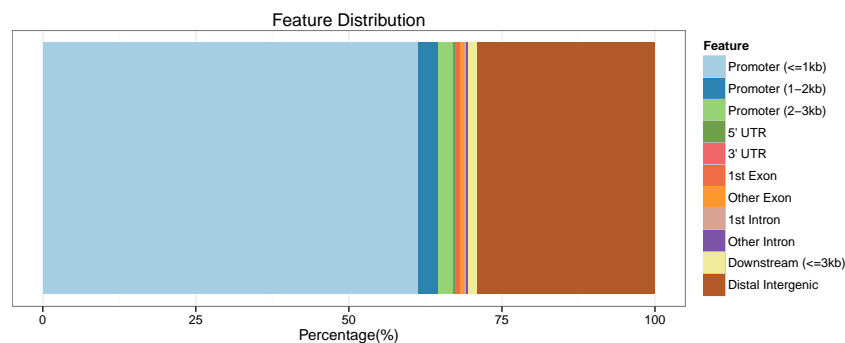


Figure 5: Genomic Annotation by barplot

3.2 Visualize distribution of TF-binding loci relative to TSS

The distance from the peak (binding site) to the TSS of the nearest gene is calculated by `annotatePeak` and reported in the output. We provide `plotDistToTSS` to calculate the percentage of binding sites upstream and downstream from the TSS of the nearest genes, and visualize the distribution.

```
plotDistToTSS(peakAnno, title = "Distribution of transcription factor-binding loci  
## Warning: Stacking not well defined when ymin != 0
```

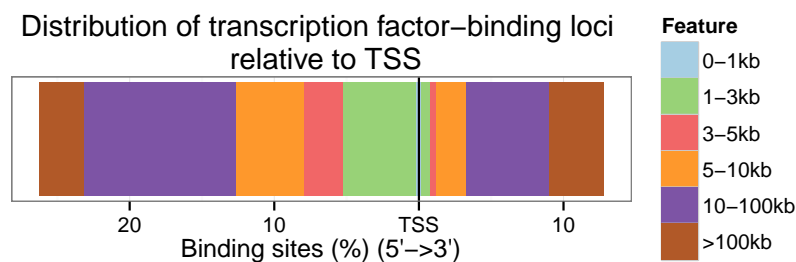


Figure 6: Distribution of Binding Sites

4 Functional enrichment analysis

Once we have obtained the annotated nearest genes, we can perform functional enrichment analysis to identify predominant biological themes among these genes by incorporating biological knowledge provided by biological ontologies. For instance, Gene Ontology (GO) [4] annotates genes to biological processes, molecular functions, and cellular components in a directed acyclic graph structure, Kyoto Encyclopedia of Genes and Genomes (KEGG) [5] annotates genes to pathways, Disease Ontology (DO) [6] annotates genes with human disease association, and Reactome [7] annotates gene to pathways and reactions.

Enrichment analysis is a widely used approach to identify biological themes. I have developed several Bioconductor packages for investigating whether the number of selected genes associated with a particular biological term is larger than expected, including *DOSE* for Disease Ontology, *ReactomePA* for reactome pathway, *clusterProfiler* [1] for Gene Ontology and KEGG enrichment analysis.

```
require(clusterProfiler)  
bp <- enrichGO(unlist(peakAnno$geneId), ont = "BP",  
  readable = TRUE)  
  
## Loading required package: GO.db
```

```
head(summary(bp))
```

```
##                                ID                                Description GeneRatio
## GO:0007275 GO:0007275 multicellular organismal development 389/735
## GO:0032502 GO:0032502 developmental process 419/735
## GO:0044767 GO:0044767 single-organism developmental process 416/735
## GO:0048731 GO:0048731 system development 344/735
## GO:0008150 GO:0008150 biological_process 735/735
## GO:0048856 GO:0048856 anatomical structure development 371/735
##                                BgRatio    pvalue p.adjust    qvalue
## GO:0007275 4274/18207 1.00e-69 1.67e-66 6.80e-67
## GO:0032502 4899/18207 5.08e-69 4.25e-66 1.73e-66
## GO:0044767 4848/18207 1.02e-68 5.70e-66 2.32e-66
## GO:0048731 3530/18207 1.80e-66 7.52e-64 3.06e-64
## GO:0008150 15034/18207 2.98e-63 8.70e-61 3.53e-61
## GO:0048856 4141/18207 3.12e-63 8.70e-61 3.53e-61
##
## GO:0007275
## GO:0032502
## GO:0044767
## GO:0048731
## GO:0008150 TCF24/SP9/ZNF717/CDH6/OCLN/CASP12/DNM1L/CDH8/ABCC9/EDIL3/FAM13A/PRMT3
## GO:0048856
##                                Count
## GO:0007275 389
## GO:0032502 419
## GO:0044767 416
## GO:0048731 344
## GO:0008150 735
## GO:0048856 371
```

More information can be found in the vignettes of Bioconductor packages *DOSE* , *ReactomePA*, *clusterProfiler* [1], which also provide several methods to visualize enrichment results. The *clusterProfiler* package is designed for comparing and visualizing functional profiles among gene clusters, and can directly applied to compare biological themes at GO, DO, KEGG, Reactome perspective.

5 ChIP peak data set comparison

5.1 Profile of several ChIP peak data binding to TSS region

Function `plotAvgProf` and `tagHeatmap` can accept a list of `tagMatrix` and visualize profile or heatmap among several ChIP experiments, while `plotAvgProf2` and

peakHeatmap can accept a list of bed files and perform the same task in one step.

5.1.1 Average profiles

```
## promoter <- getPromoters(TranscriptDb=txdb,  
## upstream=3000, downstream=3000) tagMatrixList <-  
## lapply(files, getTagMatrix, windows=promoter) to  
## speed up the compilation of this vignettes, we  
## load a precalculated tagMatrixList  
data("tagMatrixList")  
plotAvgProf(tagMatrixList, xlim = c(-3000, 3000))
```

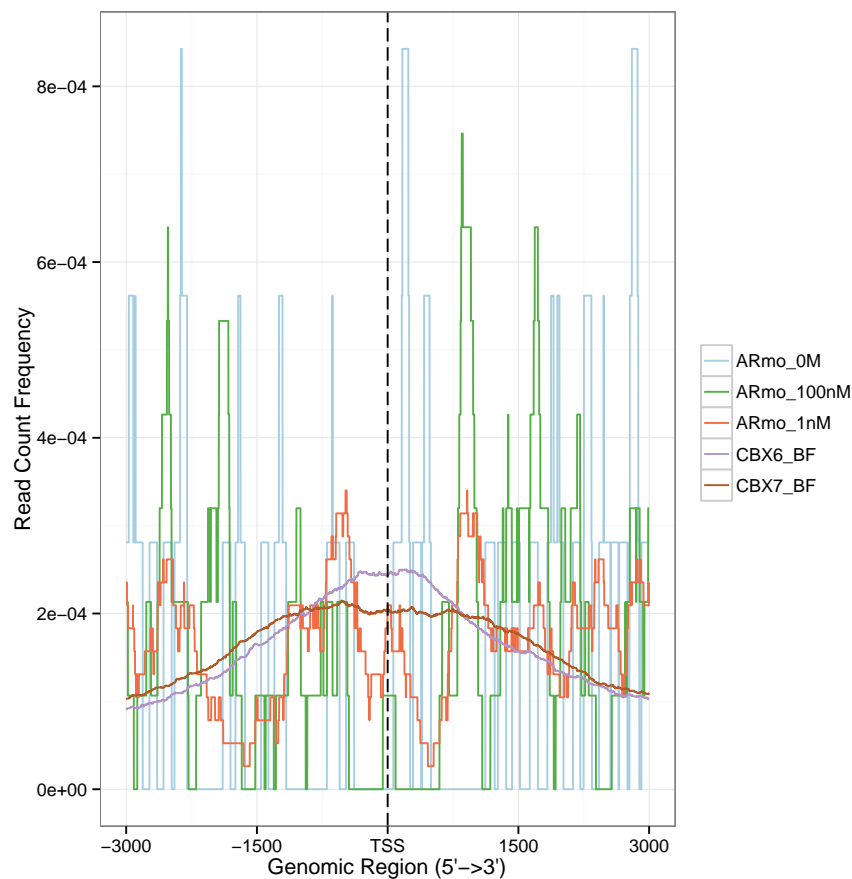


Figure 7: Average Profiles of ChIP peaks among different experiments

5.1.2 Peak heatmaps

```
tagHeatmap(tagMatrixList, xlim = c(-3000, 3000), color = NULL)
```

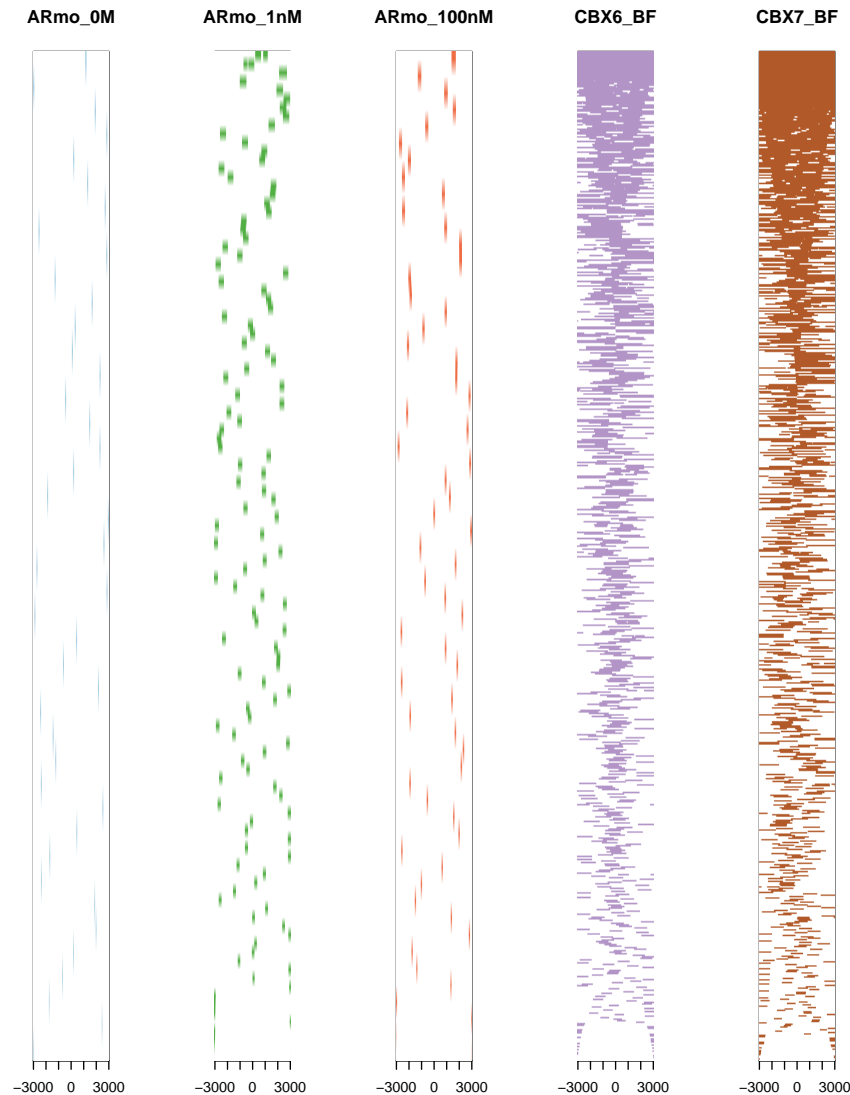


Figure 8: Heatmap of ChIP peaks among different experiments

5.2 ChIP peak annotation comparison

The `plotAnnoBar` and `plotDistToTSS` can also accept input of a named list of annotated peaks (output of `annotatePeak`).

```
peakAnnoList <- lapply(files, annotatePeak, TranscriptDb = txdb,
  tssRegion = c(-3000, 3000), verbose = FALSE)
```

We can use `plotAnnoBar` to comparing their genomic annotation.

```
plotAnnoBar(peakAnnoList)
```

R function `plotDistToTSS` can use to comparing distance to TSS profiles among ChIPseq data.

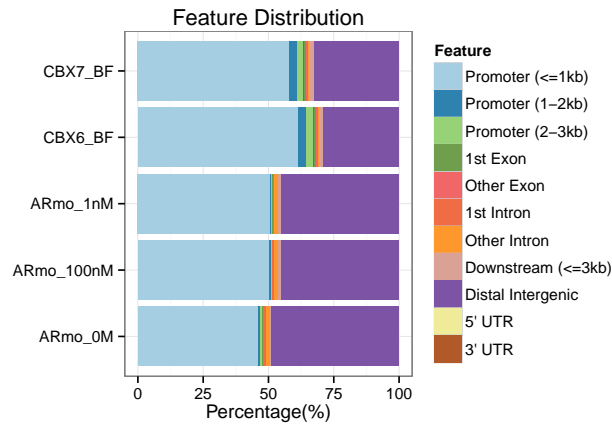


Figure 9: Genomic Annotation among different ChIPseq data

```
plotDistToTSS(peakAnnoList)
```

```
## Warning: Stacking not well defined when ymin != 0
```

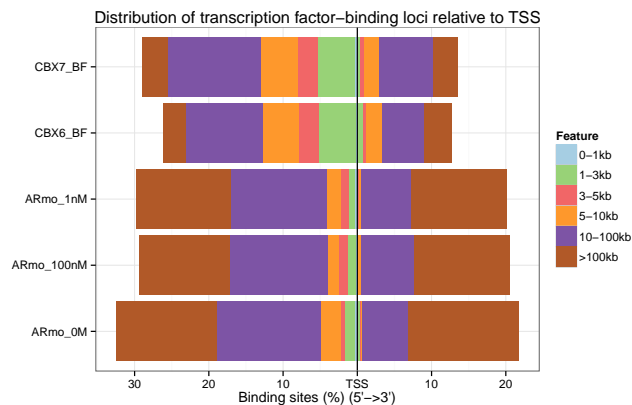


Figure 10: Distribution of Binding Sites among different ChIPseq data

5.3 Functional profiles comparison

As shown in section 4, the annotated genes can be analyzed by *clusterProfiler*, *DOSE* and *ReactomePA* for Gene Ontology, KEGG, Disease Ontology and Reactome Pathway enrichment analysis.

The *clusterProfiler* package provides the `compareCluster` function for comparing biological themes among gene clusters, and can be easily adopted to compare different ChIP peak experiments.

```
genes = lapply(peakAnnoList, function(i) i$geneId)
names(genes) = sub("_", "\\n", names(genes))
```

```
compGO <- compareCluster(geneCluster = genes, fun = "enrichGO",
  ont = "MF", organism = "human", pvalueCutoff = 0.05,
  pAdjustMethod = "BH")
plot(compGO, showCategory = 20, title = "Molecular Function Enrichment")
```

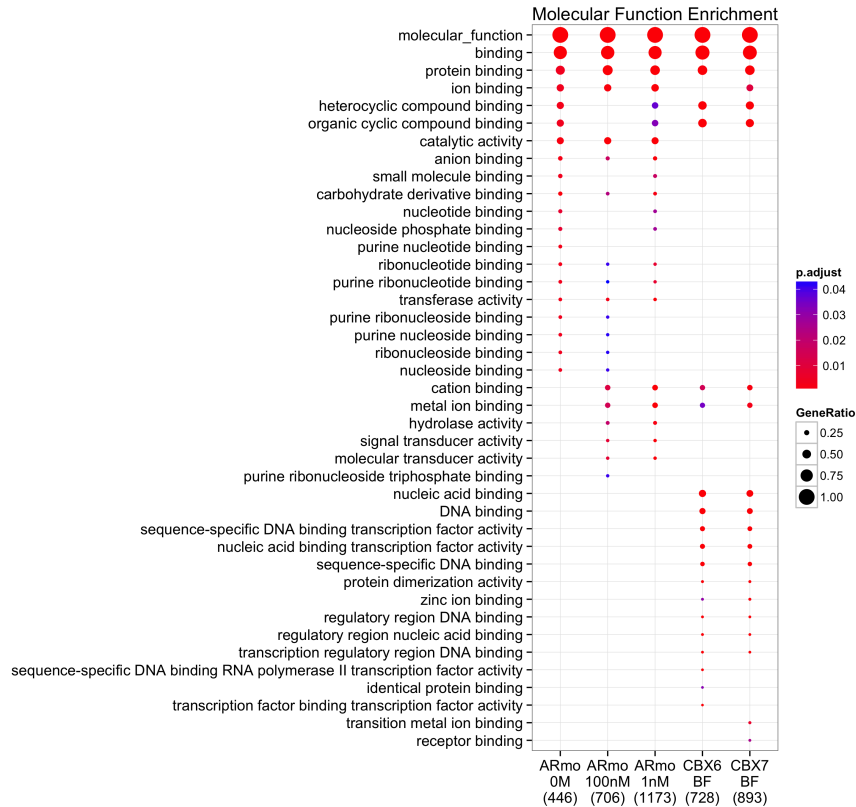


Figure 11: Compare Biological themes among different experiments

5.4 Overlap of peaks and annotated genes

User may want to compare the overlap peaks of replicate experiments or from different experiments. *ChIPseeker* provides `peak2GRanges` that can read peak file and stored in `GRanges` object. Several files can be read simultaneously using `lapply`, and then passed to `vennplot` to calculate their overlap and draw venn plot.

`vennplot` accept a list of object, can be a list of `GRanges` or a list of vector. Here, I will demonstrate using `vennplot` to visualize the overlap of the nearest genes stored in `peakAnnoList`.

```
genes = lapply(peakAnnoList, function(i) unlist(i$geneId))
vennplot(genes)
```

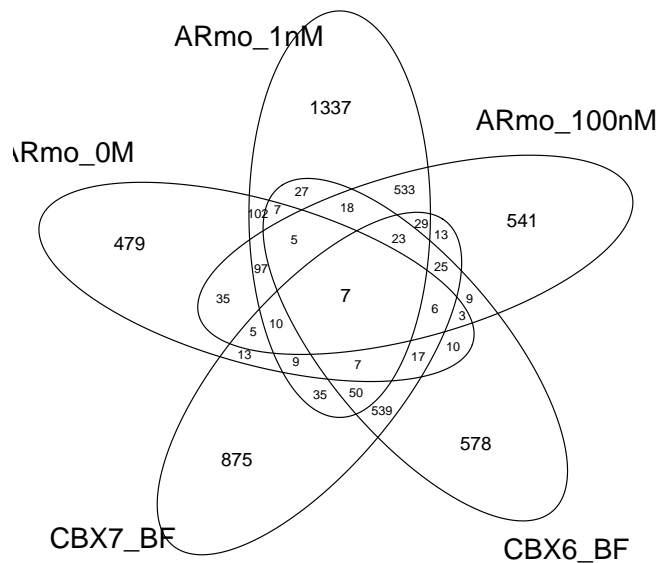


Figure 12: Overlap of annotated genes

6 Statistical testing of ChIP seq overlap

Overlap is very important, if two ChIP experiment by two different proteins overlap in a large fraction of their peaks, they may cooperative in regulation. Calculating the overlap is only touch the surface. *ChIPseeker* implemented statistical methods to measure the significance of the overlap.

6.1 Shuffle genome coordination

```
p <- GRanges(seqnames = c("chr1", "chr3"), ranges = IRanges(start = c(1,
  100), end = c(50, 130)))
shuffle(p, TranscriptDb = txdb)

## GRanges with 2 ranges and 0 metadata columns:
##      seqnames      ranges strand
##      <Rle>         <IRanges> <Rle>
## [1]   chr1 [93444494, 93444544]   *
## [2]   chr3 [30016281, 30016312]   *
## ---
## seqlengths:
##   chr1 chr3
##    NA  NA
```


We implement the `shuffle` function to randomly permute the genomic locations of ChIP peaks defined in a genome which stored in `TranscriptDb` object.

6.2 Peak overlap enrichment analysis

With the ease of this `shuffle` method, we can generate thousands of random ChIP data and calculate the background null distribution of the overlap among ChIP data sets.

```
enrichPeakOverlap(queryPeak = files[[5]], targetPeak = unlist(files[1:4]),
  TranscriptDb = txdb, pAdjustMethod = "BH", nShuffle = 50,
  chainFile = NULL)
```

##		qSample			
##	ARmo_OM	GSM1295077_CBX7_BF_ChipSeq_mergedReps_peaks.bed.gz			
##	ARmo_1nM	GSM1295077_CBX7_BF_ChipSeq_mergedReps_peaks.bed.gz			
##	ARmo_100nM	GSM1295077_CBX7_BF_ChipSeq_mergedReps_peaks.bed.gz			
##	CBX6_BF	GSM1295077_CBX7_BF_ChipSeq_mergedReps_peaks.bed.gz			
##		tSample	qLen	tLen	N_OL
##	ARmo_OM	GSM1174480_ARmo_OM_peaks.bed.gz	1663	812	0
##	ARmo_1nM	GSM1174481_ARmo_1nM_peaks.bed.gz	1663	2296	8
##	ARmo_100nM	GSM1174482_ARmo_100nM_peaks.bed.gz	1663	1359	3
##	CBX6_BF	GSM1295076_CBX6_BF_ChipSeq_mergedReps_peaks.bed.gz	1663	1331	968
##		pvalue	p.adjust		
##	ARmo_OM	0.90	0.90		
##	ARmo_1nM	0.20	0.40		
##	ARmo_100nM	0.42	0.56		
##	CBX6_BF	0.00	0.00		

Parameter `queryPeak` is the query ChIP data, while `targetPeak` is bed file name or a vector of bed file names from comparison; `nShuffle` is the number to shuffle the peaks in `targetPeak`. To speed up the compilation of this vignettes, we only set `nShuffle` to 50 as an example for only demonstration. User should set the number to 1000 or above for more robust result. Parameter `chainFile` are chain file name for mapping the `targetPeak` to the genome version consistent with `queryPeak` when their genome version are different. This creat the possibility of comparison among different genome version and cross species.

In the output, `qSample` is the name of `queryPeak` and `qLen` is the the number of peaks in `queryPeak`. `N_OL` is the number of overlap between `queryPeak` and `targetPeak`.

7 Data Mining with ChIP seq data deposited in GEO

There are many ChIP seq data sets that have been published and deposited in GEO database. We can compare our own dataset to those deposited in GEO to

search for significant overlap data. Significant overlap of ChIP seq data by different binding proteins may be used to infer cooperative regulation and thus can be used to generate hypotheses.

We collect about 15,000 bed files deposited in GEO, user can use `getGEOspecies` to get a summary based on species.

7.1 GEO data collection

```
getGEOspecies()
```

```
##               species Freq
## 1             Aedes aegypti  11
## 2             Anabaena      6
## 3           Anolis carolinensis  2
## 4             Apis mellifera  5
## 5   Apis mellifera scutellata  1
## 6           Arabidopsis lyrata  4
## 7           Arabidopsis thaliana 65
## 8           Atelerix albiventris  2
## 9             Brassica rapa   8
## 10          Caenorhabditis elegans 164
## 11           Candida albicans  25
## 12           Candida dubliniensis 20
## 13           Canis lupus familiaris  7
## 14          Chlorocebus aethiops  2
## 15           Cleome hassleriana  1
## 16           Columba livia    6
## 17           Crassostrea gigas  1
## 18          Cryptococcus neoformans 39
## 19             Danio rerio  122
## 20          Drosophila melanogaster 551
## 21          Drosophila pseudoobscura  7
## 22          Drosophila simulans  9
## 23          Drosophila virilis  2
## 24          Drosophila yakuba  8
## 25            Equus caballus  1
## 26          Escherichia coli  1
## 27          Escherichia coli BW25113  4
## 28          Escherichia coli K-12  2
## 29 Escherichia coli str. K-12 substr. MG1655  8
## 30            Gallus gallus  43
## 31          Geobacter sulfurreducens PCA  3
## 32            Gorilla gorilla  2
## 33          Histophilus somni  1
## 34            Homo sapiens 7347
```

## 35	Human herpesvirus 6B	2
## 36	Human herpesvirus 8	6
## 37	Legionella pneumophila	5
## 38	Leishmania amazonensis	4
## 39	Leishmania major	2
## 40	Leishmania tarentolae	15
## 41	Macaca mulatta	28
## 42	Monodelphis domestica	4
## 43	Moraxella catarrhalis 035E	6
## 44	Mus musculus	5558
## 45	Mus musculus x Mus spretus	1
## 46	Mycobacterium tuberculosis	2
## 47	Myotis brandtii	15
## 48	Nematostella vectensis	23
## 49	Ornithorhynchus anatinus	5
## 50	Oryza sativa	23
## 51	Oryzias latipes	2
## 52	Pan troglodytes	3
## 53	Plasmodium falciparum 3D7	29
## 54	Pseudomonas putida KT2440	2
## 55	Pyrococcus furiosus	4
## 56	Rattus norvegicus	38
## 57	Rhodopseudomonas palustris	6
## 58	Rhodopseudomonas palustris CGA009	3
## 59	Saccharomyces cerevisiae	360
## 60	Saccharomyces paradoxus	8
## 61	Schizosaccharomyces japonicus	2
## 62	Schizosaccharomyces pombe	88
## 63	Schmidtea mediterranea	7
## 64	Streptomyces coelicolor A3(2)	6
## 65	Sus scrofa	17
## 66	Tupaia chinensis	7
## 67	Xenopus (Silurana) tropicalis	62
## 68	Zea mays	54

The summary can also be based on genome version as illustrated below:

```
getGEOgenomeVersion()
```

##	organism	genomeVersion	Freq
## 1	Anolis carolinensis	anoCar2	2
## 2	Caenorhabditis elegans	ce10	4
## 3	Caenorhabditis elegans	ce6	64
## 4	Danio rerio	danRer6	6
## 5	Danio rerio	danRer7	40
## 6	Drosophila melanogaster	dm3	340
## 7	Gallus gallus	galGal3	20

## 8	Gallus gallus	galGal4	15
## 9	Homo sapiens	hg18	1936
## 10	Homo sapiens	hg19	4948
## 11	Mus musculus	mm10	21
## 12	Mus musculus	mm8	465
## 13	Mus musculus	mm9	4543
## 14	Monodelphis domestica	monDom5	4
## 15	Macaca mulatta	rheMac2	24
## 16	Saccharomyces cerevisiae	sacCer2	141
## 17	Saccharomyces cerevisiae	sacCer3	100
## 18	Sus scrofa	susScr2	17
## 19	Xenopus (Silurana) tropicalis	xenTro3	3

User can access the detail information by `getGEOInfo`, for each genome version.

```
hg19 <- getGEOInfo(genome = "hg19", simplify = TRUE)
head(hg19)
```

##	series_id	gsm	organism
## 111	GSE16256	GSM521889	Homo sapiens
## 112	GSE16256	GSM521887	Homo sapiens
## 113	GSE16256	GSM521883	Homo sapiens
## 114	GSE16256	GSM1010966	Homo sapiens
## 115	GSE16256	GSM896166	Homo sapiens
## 116	GSE16256	GSM910577	Homo sapiens
##			
## 111		Reference Epigenome: ChIP-Seq Analysis of H3K27me3 in IMR90 Cells;	
## 112		Reference Epigenome: ChIP-Seq Analysis of H3K27ac in IMR90 Cells;	
## 113		Reference Epigenome: ChIP-Seq Analysis of H3K14ac in IMR90 Cells;	
## 114		polyA RNA sequencing of STL003 Pancreas Cultured Cells;	
## 115		Reference Epigenome: ChIP-Seq Analysis of H4K8ac in hESC H1 Cells;	
## 116		Reference Epigenome: ChIP-Seq Analysis of H3K4me1 in Human Spleen Tissue; re	
##			
## 111		ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM521nnn/GSM521889/suppl/GSM	
## 112		ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM521nnn/GSM521887/suppl/GS	
## 113		ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM521nnn/GSM521883/suppl/GS	
## 114		ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM1010nnn/GSM1010966/suppl/GSM101096	
## 115		ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM896nnn/GSM896166/suppl	
## 116		ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM910nnn/GSM910577/suppl/GSM91	
##	genomeVersion	pubmed_id	
## 111	hg19	19829295	
## 112	hg19	19829295	
## 113	hg19	19829295	
## 114	hg19	19829295	
## 115	hg19	19829295	
## 116	hg19	19829295	

If `simplify` is set to `FALSE`, extra information including `source_name`, `extract_protocol`, `description`, `data_processing`, and `submission_date` will be incorporated.

7.2 Download GEO ChIP data sets

ChIPseeker provide function `downloadGEObedFiles` to download all the bed files of a particular genome.

```
downloadGEObedFiles(genome = "hg19", destDir = "hg19")
```

Or a vector of GSM accession number by `downloadGSMbedFiles`.

```
gsm <- hg19$gsm[sample(nrow(hg19), 10)]  
downloadGSMbedFiles(gsm, destDir = "hg19")
```

7.3 Overlap significant testing

After download the bed files from GEO, we can pass them to `enrichPeakOverlap` for testing the significant of overlap. Parameter `targetPeak` can be the folder, e.g. `hg19`, that containing bed files. `enrichPeakOverlap` will parse the folder and compare all the bed files. It is possible to test the overlap with bed files that are mapping to different genome or different genome versions, `enrichPeakOverlap` provide a parameter `chainFile` that can pass a chain file and `liftOver` the `targetPeak` to the genome version consistent with `queryPeak`. Significant overlap can be use to generate hypothesis of cooperative regulation. By mining the data deposited in GEO, we can identify some putative complex or interacted regulators in gene expression regulation or chromosome remodelling for further validation.

8 Session Information

The version number of R and packages loaded for generating the vignette were:

- R Under development (unstable) (2014-05-13 r65592),
x86_64-apple-darwin13.1.0
- Locale: C/UTF-8/C/C/C/C
- Base packages: base, datasets, grDevices, graphics, methods, parallel,
stats, utils
- Other packages: AnnotationDbi 1.27.7, Biobase 2.25.0,
BiocGenerics 0.11.2, ChIPseeker 1.1.8, DBI 0.2-7, GO.db 2.14.0,
GenomeInfoDb 1.1.6, GenomicFeatures 1.17.9, GenomicRanges 1.17.17,

IRanges 1.99.15, RSQLite 0.11.4, S4Vectors 0.0.8,
TxDb.Hsapiens.UCSC.hg19.knownGene 2.14.0, XVector 0.5.6,
clusterProfiler 1.13.1, ggplot2 1.0.0, knitr 1.6, org.Hs.eg.db 2.14.0

- Loaded via a namespace (and not attached): BBmisc 1.6, BatchJobs 1.2, BiocParallel 0.7.2, Biostrings 2.33.10, DO.db 2.8.0, DOSE 2.3.2, GOSemSim 1.23.0, GenomicAlignments 1.1.13, KEGG.db 2.14.0, KernSmooth 2.23-12, MASS 7.3-33, Matrix 1.1-3, RColorBrewer 1.0-5, RCurl 1.95-4.1, Rcpp 0.11.2, Rsamtools 1.17.23, XML 3.98-1.1, biomaRt 2.21.0, bitops 1.0-6, brew 1.0-6, caTools 1.17, codetools 0.2-8, colorspace 1.2-4, digest 0.6.4, evaluate 0.5.5, fail 1.2, foreach 1.4.2, formatR 0.10, gdata 2.13.3, gplots 2.13.0, grid 3.2.0, gtable 0.1.2, gtools 3.4.1, highr 0.3, igraph 0.7.1, iterators 1.0.7, labeling 0.2, lattice 0.20-29, munsell 0.4.2, plyr 1.8.1, proto 0.3-10, qvalue 1.39.1, reshape2 1.4, rtracklayer 1.25.11, scales 0.2.4, sendmailR 1.1-2, stats4 3.2.0, stringr 0.6.2, tools 3.2.0, zlibbioc 1.11.1

References

- [1] Guangchuang Yu, Li-Gen Wang, Yanyan Han, and Qing-Yu He. clusterProfiler: an r package for comparing biological themes among gene clusters. *OMICS: A Journal of Integrative Biology*, 16(5):284–287, May 2012.
- [2] Helen Pemberton, Emma Anderton, Harshil Patel, Sharon Brookes, Hollie Chandler, Richard Palermo, Julie Stock, Marc Rodriguez-Niedenfhr, Tomas Racek, Lucas de Breed, Aengus Stewart, Nik Matthews, and Gordon Peters. Genome-wide co-localization of polycomb orthologs and their effects on gene expression in human fibroblasts. 15(2):R23. PMID: 24485159.
- [3] A Urbanucci, B Sahu, J Seppl, A Larjo, L M Latonen, K K Waltering, T L J Tammela, R L Vessella, H Lhdesmki, O A Jnne, and T Visakorpi. Overexpression of androgen receptor enhances the binding of the receptor to the chromatin in prostate cancer. 31(17):2153–2163. PMID: 21909140.
- [4] Michael Ashburner, Catherine A. Ball, Judith A. Blake, David Botstein, Heather Butler, J. Michael Cherry, Allan P. Davis, Kara Dolinski, Selina S. Dwight, Janan T. Eppig, Midori A. Harris, David P. Hill, Laurie Issel-Tarver, Andrew Kasarskis, Suzanna Lewis, John C. Matese, Joel E. Richardson, Martin Ringwald, Gerald M. Rubin, and Gavin Sherlock. Gene ontology: tool for the unification of biology. 25:25–29.
- [5] Minoru Kanehisa, Susumu Goto, Shuichi Kawashima, Yasushi Okuno, and Masahiro Hattori. The KEGG resource for deciphering the genome. 32:D277–D280. PMID: 14681412.
- [6] L. M. Schriml, C. Arze, S. Nadendla, Y.-W. W. Chang, M. Mazaitis, V. Felix, G. Feng, and W. A. Kibbe. Disease ontology: a backbone for disease semantic integration. 40:D940–D946.

- [7] D. Croft, A. F. Mundo, R. Haw, M. Milacic, J. Weiser, G. Wu, M. Caudy, P. Garapati, M. Gillespie, M. R. Kamdar, B. Jassal, S. Jupe, L. Matthews, B. May, S. Palatnik, K. Rothfels, V. Shamovsky, H. Song, M. Williams, E. Birney, H. Hermjakob, L. Stein, and P. D'Eustachio. The reactome pathway knowledgebase. 42:D472–D477.