

# The ChIPpeakAnno user's guide

Lihua Julie Zhu\*, Jianhong Ou†

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\*julie.zhu@umassmed.edu

†jianhong.ou@umassmed.edu

# 1 Introduction

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Chromatin immunoprecipitation (ChIP) followed by high-throughput tag sequencing (ChIP-seq) and ChIP followed by genome tiling array analysis (ChIP-chip) become more and more prevalent high throughput technologies for identifying the binding sites of DNA-binding proteins in a genome-wide bases. A number of algorithms have been published to facilitate the identification of the binding sites of the DNA-binding proteins of interest. The identified binding sites in the list of peaks are usually converted to BED or WIG file format to be loaded to UCSC genome browser as custom tracks for investigators to view the proximity to various genomic features such as genes, exons and conserved elements. However, clicking through the genome browser could be a daunting task for the biologist if the number of peaks gets large or the peaks spread widely across the genome.

Here we have developed a Bioconductor package called ChIPpeakAnno to facilitate the batch annotation of the peaks identified from either ChIP-seq or ChIP-chip experiments. We have implemented functionality to find the nearest gene, exon, miRNA, gene end or custom features supplied by users such as most conserved elements and other transcription factor binding sites leveraging IRanges. Since the genome annotation gets updated from time to time, we have leveraged the [biomaRt](#) package from Bioconductor to retrieve the annotation data on the fly if the annotation of interest is available via the [biomaRt](#) package. The users also have the flexibility to pass their own annotation data as GRanges (or RangedData) or pass in annotation data from [GenomicFeatures](#). We have also leveraged [BSgenome](#) and [biomaRt](#) package on implementing functions to retrieve the sequences around the peak identified for peak validation. To understand whether the identified peaks are enriched around genes with certain GO terms, we have implemented GO enrichment test in [ChIPpeakAnno](#) package leveraging the hypergeometric test phyper in [stats](#) package and integrated with Gene Ontology (GO) annotation from [GO.db](#) package and multiplicity adjustment functions from [multtest](#) package.

## 2 Quick start

---

```
> library(ChIPpeakAnno)
> ## import the MACS output
> macs <- system.file("extdata", "MACS_peaks.xls", package="ChIPpeakAnno")
> macsOutput <- toGRanges(macs, format="MACS")
> ## annotate the peaks with ensembl annotation
> data(TSS.human.GRCh38)
> macs.anno <- annotatePeakInBatch(macsOutput, AnnotationData=TSS.human.GRCh38,
+                               output="overlapping", maxgap=5000L)
> ## add gene symbols
> library(org.Hs.eg.db)
> macs.anno <- addGeneIDs(annotatedPeak=macs.anno,
+                        orgAnn="org.Hs.eg.db",
+                        IDs2Add="symbol")
> head(macs.anno)
```

GRanges object with 6 ranges and 16 metadata columns:

	seqnames	ranges	strand	length	summit	tags
	<Rle>	<IRanges>	<Rle>	<factor>	<factor>	<factor>
X01.ENSEG00000117616	chr1	[ 25323511, 25324015]	*	505	252	45
X01.ENSEG00000187010	chr1	[ 25323511, 25324015]	*	505	252	45
X02.ENSEG00000183726	chr1	[ 25362685, 25362997]	*	313	211	33
X02.ENSEG00000188672	chr1	[ 25362685, 25362997]	*	313	211	33
X03.NA	chr1	[145558152, 145558537]	*	386	59	39
X04.NA	chr10	[ 47088702, 47089329]	*	628	484	68

	qvalue	fold_enrichment	FDR	peak	feature
	<factor>	<factor>	<factor>	<character>	<character>
X01.ENSEG00000117616	59.17	17.01	5.8	X01	ENSEG00000117616
X01.ENSEG00000187010	59.17	17.01	5.8	X01	ENSEG00000187010
X02.ENSEG00000183726	60.63	22.41	4.2	X02	ENSEG00000183726
X02.ENSEG00000188672	60.63	22.41	4.2	X02	ENSEG00000188672
X03.NA	53.10	20.68	2.3	X03	<NA>
X04.NA	56.09	16.37	0.75	X04	<NA>

	start_position	end_position	feature_strand	insideFeature
	<integer>	<integer>	<character>	<factor>
X01.ENSEG00000117616	25242237	25338213	-	inside
X01.ENSEG00000187010	25272393	25330445	+	inside
X02.ENSEG00000183726	25337917	25362361	+	downstream
X02.ENSEG00000188672	25362249	25430192	-	inside
X03.NA	<NA>	<NA>	<NA>	<NA>
X04.NA	<NA>	<NA>	<NA>	<NA>

	distancetoFeature	shortestDistance	fromOverlappingOrNearest
	<numeric>	<integer>	<character>
X01.ENSEG00000117616	14702	14198	Overlapping
X01.ENSEG00000187010	51118	6430	Overlapping
X02.ENSEG00000183726	24768	324	Overlapping
X02.ENSEG00000188672	67507	436	Overlapping
X03.NA	<NA>	<NA>	<NA>
X04.NA	<NA>	<NA>	<NA>

	symbol
	<factor>
X01.ENSEG00000117616	LOC101928189;RSRP1
X01.ENSEG00000187010	RHCE;RHD
X02.ENSEG00000183726	TMEM50A
X02.ENSEG00000188672	RHCE
X03.NA	<NA>
X04.NA	<NA>

-----

seqinfo: 12 sequences from an unspecified genome; no seqlengths

```

> if(interactive()){## annotate the peaks with UCSC annotation
+   library(GenomicFeatures)
+   library(TxDb.Hsapiens.UCSC.hg38.knownGene)
+   ucsc.hg38.knownGene <- genes(TxDb.Hsapiens.UCSC.hg38.knownGene)
+   macs.anno <- annotatePeakInBatch(macsOutput,
+                                   AnnotationData=ucsc.hg38.knownGene,
+                                   output="overlapping", maxgap=5000L)
+   macs.anno <- addGeneIDs(annotatedPeak=macs.anno,
+                           orgAnn="org.Hs.eg.db",
+                           feature_id_type="entrez_id",
+                           IDs2Add="symbol")
+   head(macs.anno)
+ }

```

### 3 Examples of using ChIPpeakAnno

### 3.1 Task 1: Find the nearest feature such as gene and the distance to the feature such as the transcription start site (TSS) of the nearest gene

We have a list of peaks identified from ChIP-seq or ChIP-chip experiments and we would like to retrieve the nearest gene and distance to the corresponding gene transcription start site. We have retrieved all the genomic locations of the genes for human genome as TSS.human.NCBI36 data package for repeated use with function `getAnnotation`, now we just pass the annotation to the `annotatePeakInBatch` function.

```
> library(ChIPpeakAnno)
> data(myPeakList)
> data(TSS.human.NCBI36)
> annotatedPeak <- annotatePeakInBatch(myPeakList[1:6,],
+                                     AnnotationData=TSS.human.NCBI36)
> annotatedPeak
```

GRanges object with 6 ranges and 9 metadata columns:

seqnames	ranges	strand	peak
<Rle>	<IRanges>	<Rle>	<character>
X1_93_556427.ENSEG000000212875	chr1 [ 556660, 556760]	*	X1_93_556427
X1_41_559455.ENSEG000000212678	chr1 [ 559774, 559874]	*	X1_41_559455
X1_12_703729.ENSEG000000197049	chr1 [ 703885, 703985]	*	X1_12_703729
X1_20_925025.ENSEG000000188290	chr1 [ 926058, 926158]	*	X1_20_925025
X1_11_1041174.ENSEG000000131591	chr1 [1041646, 1041746]	*	X1_11_1041174
X1_14_1269014.ENSEG000000107404	chr1 [1270239, 1270339]	*	X1_14_1269014

feature	start_position	end_position
<character>	<integer>	<integer>
X1_93_556427.ENSEG000000212875	ENSEG000000212875	556318
X1_41_559455.ENSEG000000212678	ENSEG000000212678	559620
X1_12_703729.ENSEG000000197049	ENSEG000000197049	711184
X1_20_925025.ENSEG000000188290	ENSEG000000188290	924209
X1_11_1041174.ENSEG000000131591	ENSEG000000131591	1007062
X1_14_1269014.ENSEG000000107404	ENSEG000000107404	1260523

feature_strand	insideFeature	distanceToFeature
<character>	<factor>	<numeric>
X1_93_556427.ENSEG000000212875	+	inside
X1_41_559455.ENSEG000000212678	+	inside
X1_12_703729.ENSEG000000197049	+	upstream
X1_20_925025.ENSEG000000188290	-	upstream
X1_11_1041174.ENSEG000000131591	-	upstream
X1_14_1269014.ENSEG000000107404	-	inside

shortestDistance	fromOverlappingOrNearest
<integer>	<character>
X1_93_556427.ENSEG000000212875	342
X1_41_559455.ENSEG000000212678	154
X1_12_703729.ENSEG000000197049	7199
X1_20_925025.ENSEG000000188290	725
X1_11_1041174.ENSEG000000131591	305
X1_14_1269014.ENSEG000000107404	4284

-----

seqinfo: 24 sequences from an unspecified genome; no seqlengths

To annotate the peaks with other genomic feature, you will need to call function `getAnnotation` with `featureType`, e.g., "Exon" for finding the nearest exon, and "miRNA" for finding the nearest miRNA, "5utr" or "3utr" for finding the overlapping 5 prime UTR or 3 prime UTR. Please refer to `getAnnotation` function for more details.

We have presented the examples using human genome as annotation source. To annotate your data with other species, you will need to pass to the function `getAnnotation` the appropriate dataset for example, `drerio_gene_ensembl` for zebrafish genome, `mmusculus_gene_ensembl` for mouse genome and `rnorvegicus_gene_ensembl` for rat genome.

For a list of available biomaRt and dataset, please refer to the [biomaRt](#) package documentation (Durinck S. et al., 2005). For fast access, in addition to `TSS.human.NCBI36`, `TSS.human.GRCh37`, `TSS.human.GRCh38`, `TSS.mouse.NCBIM37`, `TSS.mouse.GRCm38`, `TSS.rat.RGSC3.4`, `TSS.rat.Rnor_5.0`, `TSS.zebrafish.Zv8`, and `TSS.zebrafish.Zv9` are included as annotation data packages.

You could also pass your own annotation data into the function `annotatePeakInBatch`. For example, if you have a list of transcription factor binding sites from literature and are interested in obtaining the nearest binding site of the transcription factor and distance to it for the list of peaks.

```
> myPeak1 <- GRanges(seqnames=c("1", "2", "3", "4", "5", "6",
+                               "2", "6", "6", "6", "6", "5"),
+                     ranges=IRanges(start=c(967654, 2010897, 2496704, 3075869,
+                                           3123260, 3857501, 201089, 1543200,
+                                           1557200, 1563000, 1569800, 167889600),
+                                     end= c(967754, 2010997, 2496804, 3075969,
+                                           3123360, 3857601, 201089, 1555199,
+                                           1560599, 1565199, 1573799, 167893599),
+                                     names=paste("Site", 1:12, sep="")))
> TFbindingSites <- GRanges(seqnames=c("1", "2", "3", "4", "5", "6", "1", "2", "3",
+                                       "4", "5", "6", "6", "6", "6", "6", "5"),
+                            ranges=IRanges(start=c(967659, 2010898, 2496700,
+                                                    3075866, 3123260, 3857500,
+                                                    96765, 201089, 249670, 307586,
+                                                    312326, 385750, 1549800,
+                                                    1554400, 1565000, 1569400,
+                                                    167888600),
+                                            end=c(967869, 2011108, 2496920,
+                                                  3076166, 3123470, 3857780,
+                                                  96985, 201299, 249890, 307796,
+                                                  312586, 385960, 1550599, 1560799,
+                                                  1565399, 1571199, 167888999),
+                                            names=paste("t", 1:17, sep="")),
+                            strand=c("+", "+", "+", "+", "+", "+", "-", "-", "-", "-",
+                                     "-", "-", "-", "+", "+", "+", "+", "+"))
> annotatedPeak2 <- annotatePeakInBatch(myPeak1, AnnotationData=TFbindingSites)
> annotatedPeak2
```

GRanges object with 12 ranges and 9 metadata columns:

	seqnames	ranges	strand	peak	feature
	<Rle>	<IRanges>	<Rle>	<character>	<character>
Site1.t1	chr1	[ 967654, 967754]	*	Site1	t1
Site2.t2	chr2	[2010897, 2010997]	*	Site2	t2
Site3.t3	chr3	[2496704, 2496804]	*	Site3	t3
Site4.t4	chr4	[3075869, 3075969]	*	Site4	t4
Site5.t5	chr5	[3123260, 3123360]	*	Site5	t5
...	...	...	...	...	...
Site8.t14	chr6	[ 1543200, 1555199]	*	Site8	t14
Site9.t14	chr6	[ 1557200, 1560599]	*	Site9	t14
Site10.t15	chr6	[ 1563000, 1565199]	*	Site10	t15
Site11.t16	chr6	[ 1569800, 1573799]	*	Site11	t16
Site12.t17	chr5	[167889600, 167893599]	*	Site12	t17

	start_position	end_position	feature_strand	insideFeature	distanceToFeature
	<integer>	<integer>	<character>	<factor>	<numeric>
Site1.t1	967659	967869	+	overlapStart	-5

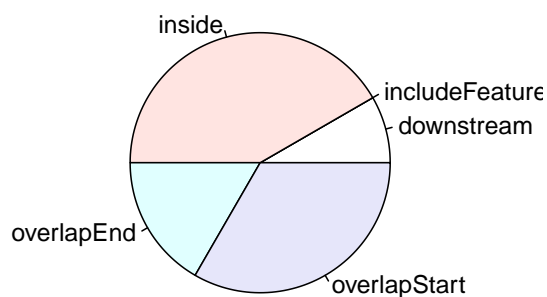


Figure 1: Pie chart of peak distribution among features.

```

Site2.t2      2010898      2011108      + overlapStart      -1
Site3.t3      2496700      2496920      +      inside        4
Site4.t4      3075866      3076166      +      inside        3
Site5.t5      3123260      3123470      +      inside        0
...          ...          ...          ...          ...
Site8.t14     1554400      1560799      + overlapStart     -11200
Site9.t14     1554400      1560799      +      inside       2800
Site10.t15    1565000      1565399      + overlapStart     -2000
Site11.t16    1569400      1571199      +      overlapEnd     400
Site12.t17    167888600    167888999    +      downstream    1000

shortestDistance fromOverlappingOrNearest
<integer>          <character>
Site1.t1           5      NearestLocation
Site2.t2           1      NearestLocation
Site3.t3           4      NearestLocation
Site4.t4           3      NearestLocation
Site5.t5           0      NearestLocation
...               ...          ...
Site8.t14          799      NearestLocation
Site9.t14          200      NearestLocation
Site10.t15         199      NearestLocation
Site11.t16         400      NearestLocation
Site12.t17         601      NearestLocation
-----
seqinfo: 6 sequences from an unspecified genome; no seqlengths
> pie(table(as.data.frame(annotatedPeak2)$insideFeature))

```

Both BED format and GFF format are common file format that provides a flexible way to define the peaks and annotations as the data lines. Therefore, conversion functions toGRanges were implemented for converting these data format to GRanges before calling `annotatePeakInBatch`

Once you annotated the peak list, you can plot the distance to nearest feature such as TSS.

## 3.2 Task 2: Obtain overlapping peaks for potential transcription factor complex and determine the significance of the overlapping and generate Venn Diagram

Here is an example of obtaining overlapping peaks with maximum gap 1kb for two peak ranges.

```
> peaks1 <- GRanges(seqnames=c("1", "2", "3", "4", "5", "6",
+                               "2", "6", "6", "6", "6", "5"),
+                   ranges=IRanges(start=c(967654, 2010897, 2496704, 3075869,
+                                           3123260, 3857501, 201089, 1543200,
+                                           1557200, 1563000, 1569800, 167889600),
+                                   end= c(967754, 2010997, 2496804, 3075969,
+                                           3123360, 3857601, 201089, 1555199,
+                                           1560599, 1565199, 1573799, 167893599),
+                                   names=paste("Site", 1:12, sep="")),
+                   strand="+")
> peaks2 <- GRanges(seqnames=c("1", "2", "3", "4", "5", "6", "1", "2", "3",
+                               "4", "5", "6", "6", "6", "6", "6", "5"),
+                   ranges=IRanges(start=c(967659, 2010898, 2496700,
+                                           3075866, 3123260, 3857500,
+                                           96765, 201089, 249670, 307586,
+                                           312326, 385750, 1549800,
+                                           1554400, 1565000, 1569400,
+                                           167888600),
+                                   end=c(967869, 2011108, 2496920,
+                                           3076166, 3123470, 3857780,
+                                           96985, 201299, 249890, 307796,
+                                           312586, 385960, 1550599, 1560799,
+                                           1565399, 1571199, 167888999),
+                                   names=paste("t", 1:17, sep="")),
+                   strand=c("+", "+", "+", "+", "+", "+", "-", "-", "-",
+                               "-", "-", "-", "+", "+", "+", "+", "+"))
> ol <- findOverlapsOfPeaks(peaks1, peaks2, maxgap=1000)
> peaklist <- ol$peaklist
```

Here is a list of overlapping peaks with maximum gap 1kb and a pie graph describing the distribution of relative position of peaks1 to peaks2 for overlapping peaks.

```
> overlappingPeaks <- ol$overlappingPeaks
> overlappingPeaks
```

```
$`peaks1//peaks2`
      peaks1 seqnames      start      end width strand
peaks1__Site1_peaks2__t1 peaks1__Site1      1  967654  967754   101    +
peaks1__Site7_peaks2__t8 peaks1__Site7      2  201089  201089     1    +
peaks1__Site2_peaks2__t2 peaks1__Site2      2 2010897 2010997   101    +
peaks1__Site3_peaks2__t3 peaks1__Site3      3 2496704 2496804   101    +
peaks1__Site4_peaks2__t4 peaks1__Site4      4 3075869 3075969   101    +
peaks1__Site5_peaks2__t5 peaks1__Site5      5 3123260 3123360   101    +
peaks1__Site12_peaks2__t17 peaks1__Site12      5 167889600 167893599 4000    +
peaks1__Site8_peaks2__t13 peaks1__Site8      6 1543200 1555199 12000    +
peaks1__Site8_peaks2__t14 peaks1__Site8      6 1543200 1555199 12000    +
peaks1__Site9_peaks2__t14 peaks1__Site9      6 1557200 1560599 3400    +
peaks1__Site10_peaks2__t15 peaks1__Site10      6 1563000 1565199 2200    +
peaks1__Site11_peaks2__t16 peaks1__Site11      6 1569800 1573799 4000    +
peaks1__Site6_peaks2__t6 peaks1__Site6      6 3857501 3857601   101    +
      peaks2 seqnames      start      end width strand
peaks1__Site1_peaks2__t1 peaks2__t1      1  967659  967869   211    +
peaks1__Site7_peaks2__t8 peaks2__t8      2  201089  201299   211    -
peaks1__Site2_peaks2__t2 peaks2__t2      2 2010898 2011108   211    +
peaks1__Site3_peaks2__t3 peaks2__t3      3 2496700 2496920   221    +
peaks1__Site4_peaks2__t4 peaks2__t4      4 3075866 3076166   301    +
```

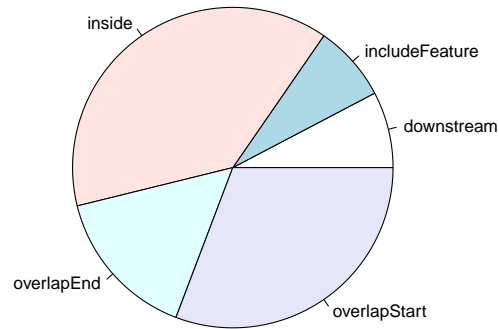


Figure 2: Pie chart of common peaks among features.

peaks1__Site5_peaks2__t5	peaks2__t5	5	3123260	3123470	211	+
peaks1__Site12_peaks2__t17	peaks2__t17	5	167888600	167888999	400	+
peaks1__Site8_peaks2__t13	peaks2__t13	6	1549800	1550599	800	+
peaks1__Site8_peaks2__t14	peaks2__t14	6	1554400	1560799	6400	+
peaks1__Site9_peaks2__t14	peaks2__t14	6	1554400	1560799	6400	+
peaks1__Site10_peaks2__t15	peaks2__t15	6	1565000	1565399	400	+
peaks1__Site11_peaks2__t16	peaks2__t16	6	1569400	1571199	1800	+
peaks1__Site6_peaks2__t6	peaks2__t6	6	3857500	3857780	281	+

	overlapFeature	shortestDistance
peaks1__Site1_peaks2__t1	overlapStart	5
peaks1__Site7_peaks2__t8	overlapEnd	0
peaks1__Site2_peaks2__t2	overlapStart	1
peaks1__Site3_peaks2__t3	inside	4
peaks1__Site4_peaks2__t4	inside	3
peaks1__Site5_peaks2__t5	inside	0
peaks1__Site12_peaks2__t17	downstream	601
peaks1__Site8_peaks2__t13	includeFeature	4600
peaks1__Site8_peaks2__t14	overlapStart	799
peaks1__Site9_peaks2__t14	inside	200
peaks1__Site10_peaks2__t15	overlapStart	199
peaks1__Site11_peaks2__t16	overlapEnd	400
peaks1__Site6_peaks2__t6	inside	1

```
> pie(table(overlappingPeaks[["peaks1///peaks2"]])$overlapFeature))
```

Here is the merged overlapping peaks, which can be used to obtain overlapping peaks with another TF binding sites from a protein complex.

```
> peaklist[["peaks1///peaks2"]]
```

GRanges object with 11 ranges and 1 metadata column:

seqnames	ranges	strand
[1] 1	[ 967654, 967869]	+
[2] 2	[ 201089, 201299]	*

```

[3]      2      [2010897, 2011108]      +      |
[4]      3      [2496700, 2496920]      +      |
[5]      4      [3075866, 3076166]      +      |
...      ...      ...      ...      ...
[7]      5 [167888600, 167893599]      +      |
[8]      6 [ 1543200, 1560799]      +      |
[9]      6 [ 1563000, 1565399]      +      |
[10]     6 [ 1569400, 1573799]      +      |
[11]     6 [ 3857500, 3857780]      +      |
                                peakNames
                                <CharacterList>
[1]      peaks1__Site1,peaks2__t1
[2]      peaks1__Site7,peaks2__t8
[3]      peaks1__Site2,peaks2__t2
[4]      peaks2__t3,peaks1__Site3
[5]      peaks2__t4,peaks1__Site4
...      ...
[7]      peaks2__t17,peaks1__Site12
[8] peaks1__Site8,peaks2__t13,peaks2__t14,...
[9]      peaks1__Site10,peaks2__t15
[10]     peaks2__t16,peaks1__Site11
[11]     peaks2__t6,peaks1__Site6
-----
seqinfo: 6 sequences from an unspecified genome; no seqlengths

```

Here is the peaks in peaks1 that not overlaps with peaks in peaks2

```

> peaklist[["peaks1"]]
NULL

```

Here is the peaks in peaks2 that not overlap with peaks in peaks1

```

> peaklist[["peaks2"]]

GRanges object with 5 ranges and 1 metadata column:
      seqnames      ranges strand |      peakNames
      <Rle>      <IRanges> <Rle> | <CharacterList>
[1]      1 [ 96765, 96985]      - |      peaks2__t7
[2]      3 [249670, 249890]      - |      peaks2__t9
[3]      4 [307586, 307796]      - |      peaks2__t10
[4]      5 [312326, 312586]      - |      peaks2__t11
[5]      6 [385750, 385960]      - |      peaks2__t12
-----
seqinfo: 6 sequences from an unspecified genome; no seqlengths

```

Venn Diagram can be generated by the following function call using the results of `findOverlapsOfPeaks` as an input (Figure 3). P-values indicate whether the extent of overlapping is significant.

```

> makeVennDiagram(ol, totalTest=1e+2)

$p.value
      peaks1 peaks2      pval
[1,]      1      1 5.890971e-12

$vennCounts
      peaks1 peaks2 Counts
[1,]      0      0      83
[2,]      0      1       5
[3,]      1      0       0
[4,]      1      1      12
attr(,"class")
[1] "VennCounts"

```

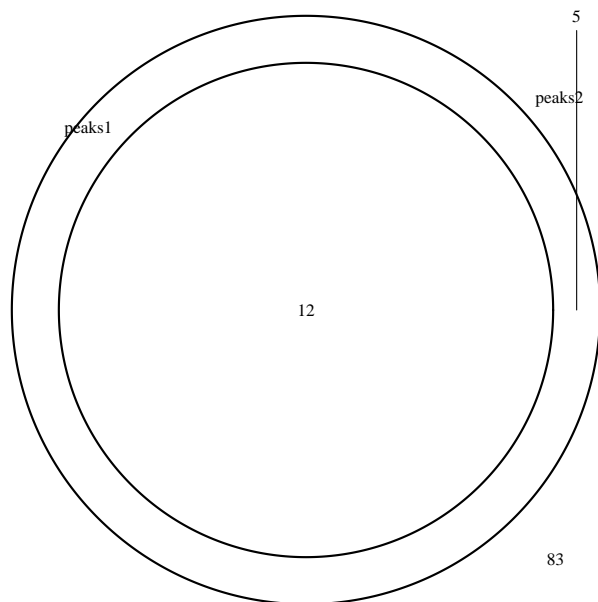


Figure 3: venn diagram of overlaps

Users can also try other tools to draw vennDiagrams such as *Vennerable*.

```
> # install.packages("Vennerable", repos="http://R-Forge.R-project.org", type="source")
> # library(Vennerable)
> # venn_cnt2venn <- function(venn_cnt){
> #     n <- which(colnames(venn_cnt)=="Counts") - 1
> #     SetNames=colnames(venn_cnt)[1:n]
> #     Weight=venn_cnt[, "Counts"]
> #     names(Weight) <- apply(venn_cnt[, 1:n], 1, paste, collapse="")
> #     Venn(SetNames=SetNames, Weight=Weight)
> # }
> #
> # v <- venn_cnt2venn(ol$venn_cnt)
> # plot(v)
```

The `findOverlapsOfPeaks` function can be called to obtain overlaps upto 5 peak lists for example, the overlap peaks in peaks1, peaks2 and peaks3 (Figure 4).

```
> peaks3 <- GRanges(seqnames=c("1", "2", "3", "4", "5",
+                               "6", "1", "2", "3", "4"),
+                   ranges=IRanges(start=c(967859, 2010868, 2496500, 3075966,
+                                           3123460, 3851500, 96865, 201189,
+                                           249600, 307386),
+                                   end= c(967969, 2011908, 2496720, 3076166,
+                                           3123470, 3857680, 96985, 201299,
+                                           249890, 307796),
+                                   names=paste("p", 1:10, sep="")),
+                   strand=c("+", "+", "+", "+", "+",
+                             "+", "-", "-", "-", "-"))
> ol <- findOverlapsOfPeaks(peaks1, peaks2, peaks3, maxgap=1000, connectedPeaks="min")
> makeVennDiagram(ol, totalTest=1e+2)
```

\$p.value

	peaks1	peaks2	peaks3	pval
[1,]	0	1	1	1.123492e-09

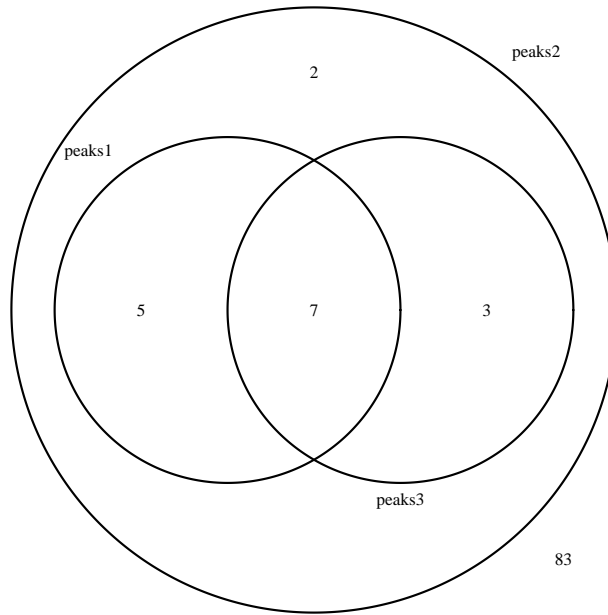


Figure 4: venn diagram of overlaps for three input peak lists

```
[2,]      1      0      1 5.131347e-06
[3,]      1      1      0 5.890971e-12
```

```
$vennCounts
  peaks1 peaks2 peaks3 Counts
[1,]     0     0     0     83
[2,]     0     0     1      0
[3,]     0     1     0      2
[4,]     0     1     1      3
[5,]     1     0     0      0
[6,]     1     0     1      0
[7,]     1     1     0      5
[8,]     1     1     1      7
attr(,"class")
[1] "VennCounts"
```

Venn Diagram can also be generated by the following function call with p-value that indicates whether the extent of overlapping is significant (Figure 5,6). Note, the maxgap is changed to 0.

```
> makeVennDiagram(list(peaks1, peaks2), NameOfPeaks=c("TF1", "TF2"),
+                 maxgap=0, minoverlap =1, totalTest=100)
```

```
$p.value
  TF1 TF2      pval
[1,]  1  1 9.837922e-10
```

```
$vennCounts
  TF1 TF2 Counts
[1,]  0  0     82
[2,]  0  1      6
[3,]  1  0      1
[4,]  1  1     11
attr(,"class")
[1] "VennCounts"
```

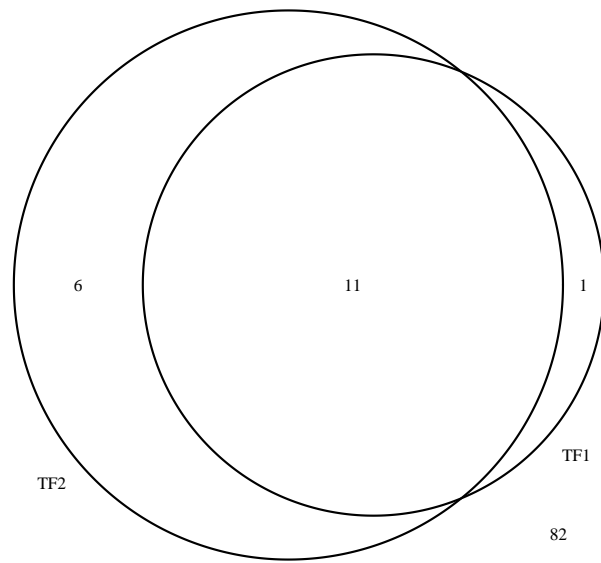


Figure 5: Venn diagram to depict the overlaps between two peak lists

```
> makeVennDiagram(list(peaks1, peaks2, peaks3),
+                  NameOfPeaks=c("TF1", "TF2", "TF3"),
+                  maxgap=0, minoverlap =1, totalTest=100)

$p.value
      TF1 TF2 TF3      pval
[1,]   0   1   1 1.123492e-09
[2,]   1   0   1 5.131347e-06
[3,]   1   1   0 9.837922e-10

$vennCounts
      TF1 TF2 TF3 Counts
[1,]   0   0   0      82
[2,]   0   0   1       0
[3,]   0   1   0       3
[4,]   0   1   1       3
[5,]   1   0   0       1
[6,]   1   0   1       0
[7,]   1   1   0       4
[8,]   1   1   1       7
attr(,"class")
[1] "VennCounts"
```

### 3.3 Task 3: Obtain sequences surrounding the peaks for PCR validation or motif discovery

Here is an example of obtaining sequences surrounding the peak intervals including 20 bp upstream and downstream sequence.

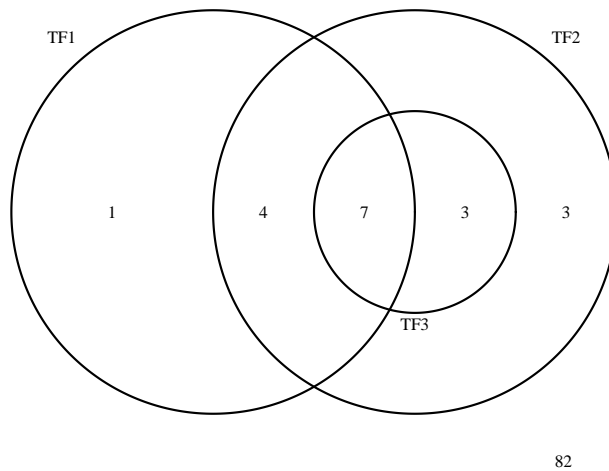


Figure 6: venn diagram of overlaps for three input peaklists directly

```
> peaks <- GRanges(seqnames=c("NC_008253", "NC_010468"),
+                   ranges=IRanges(start=c(100, 500),
+                                   end=c(300, 600),
+                                   names=c("peak1", "peak2")))
> library(BSgenome.Ecoli.NCBI.20080805)
> peaksWithSequences <- getAllPeakSequence(peaks, upstream=20,
+                                           downstream=20, genome=Ecoli)
```

You can easily convert the obtained sequences into fasta format for motif discovery by calling the function `write2FASTA`.

```
> write2FASTA(peaksWithSequences, "test.fa")
```

### 3.4 Task 4: Obtain enriched gene ontology (GO) terms or KEGG terms near the peaks

Once you have obtained the annotated peak data from the example above, you can also use the function `getEnriched` to obtain a list of enriched gene ontology (GO) terms via [GOstats](#). The ontology could also be set as KEGG or reactome.

Once you have obtained the annotated peak data from the example above, you can also use the function `getEnrichedGO` to obtain a list of enriched gene ontology (GO) terms using hypergeometric test.

```
library(org.Hs.eg.db)
```

*enrichedGO* = *getEnrichedGO* (annotatedPeak, orgAnn = "org.Hs.eg.db", maxP = 0.01, multiAdj = TRUE, minGOTerm = 10, multiAdjMethod = "BH" )

```
> library(org.Hs.eg.db)
> over <- getEnrichedGO(annotatedPeak, orgAnn="org.Hs.eg.db",
+ maxP=0.01, multiAdj=FALSE, minGOTerm=10, multiAdjMethod="")
> head(over[["bp"]])
```

	go.id	go.term
1	G0:0001736	establishment of planar polarity
2	G0:0001840	neural plate development
3	G0:0001941	postsynaptic membrane organization
4	G0:0001964	startle response
5	G0:0007164	establishment of tissue polarity
6	G0:0031122	cytoplasmic microtubule organization

```
1
2 The process whose specific outcome is the progression of the neural plate over time, from its formation to the mature structure
3
4
5
6
```

	Ontology	count.InDataset	count.InGenome	pvalue	totaltermInDataset
1	BP	1	28	0.008619994	405
2	BP	1	11	0.003395307	405
3	BP	1	22	0.006779114	405
4	BP	1	23	0.007086164	405
5	BP	1	28	0.008619994	405
6	BP	1	32	0.009845356	405

	totaltermInGenome	EntrezID
1	1310084	1855
2	1310084	1855
3	1310084	1855
4	1310084	1855
5	1310084	1855
6	1310084	1855

```
> head(over[["cc"]])
```

	go.id	go.term
1	G0:0016328	lateral plasma membrane

```
1 The portion of the plasma membrane at the lateral side of the cell. In epithelial cells, lateral plasma membranes are on the surface
Ontology count.InDataset count.InGenome pvalue totaltermInDataset
1 CC 1 48 0.008016845 61
totaltermInGenome EntrezID
1 363819 1855
```

```
> head(over[["mf"]])
```

	go.id	go.term
1	G0:0005109	frizzled binding
2	G0:0017048	Rho GTPase binding
3	G0:0048365	Rac GTPase binding

```
1
2 Interacting selectively and non-covalently with Rho protein, any member of the Rho subfamily of the Ras superfamily of monomeric GTPases
3
```

	Ontology	count.InDataset	count.InGenome	pvalue	totaltermInDataset
1	MF	1	37	0.003861301	24
2	MF	1	71	0.007396923	24
3	MF	1	32	0.003340340	24

	totaltermInGenome	EntrezID
1	229560	1855
2	229560	1855

Please note that org.Hs.eg.db is the GO gene mapping for Human, for other organisms, please refer to <http://www.bioconductor.org/packages/release/data/annotation/> for additional org.xx.eg.db packages. Or you can try egOrgMap to get the annotation database.

```
> egOrgMap("Mus musculus")

[1] "org.Mm.eg.db"

> egOrgMap("Homo sapiens")

[1] "org.Hs.eg.db"
```

### 3.5 Task 5: Find peaks with bi-directional promoters

Here is an example to find peaks with bi-directional promoters and output percent of peaks near bi-directional promoters.

```
> data(myPeakList)
> data(TSS.human.NCBI36)
> annotatedBDP <- peaksNearBDP(myPeakList[1:10,],
+                               AnnotationData=TSS.human.NCBI36,
+                               MaxDistance=5000,
+                               PeakLocForDistance="middle",
+                               FeatureLocForDistance="TSS")
> annotatedBDP$peaksWithBDP
```

GRanges object with 6 ranges and 9 metadata columns:

	seqnames	ranges	strand	peak
	<Rle>	<IRanges>	<Rle>	<character>
X1_14_1300250.ENSEG000000218550	chr1	[1300503, 1300603]	*	X1_14_1300250
X1_14_1300250.ENSEG000000175756	chr1	[1300503, 1300603]	*	X1_14_1300250
X1_41_559455.ENSEG000000212678	chr1	[ 559774, 559874]	*	X1_41_559455
X1_41_559455.ENSEG000000209350	chr1	[ 559774, 559874]	*	X1_41_559455
X1_93_556427.ENSEG000000212875	chr1	[ 556660, 556760]	*	X1_93_556427
X1_93_556427.ENSEG000000209349	chr1	[ 556660, 556760]	*	X1_93_556427

	feature	start_position	end_position
	<character>	<integer>	<integer>
X1_14_1300250.ENSEG000000218550	ENSEG000000218550	1303908	1304275
X1_14_1300250.ENSEG000000175756	ENSEG000000175756	1298974	1300443
X1_41_559455.ENSEG000000212678	ENSEG000000212678	559620	560165
X1_41_559455.ENSEG000000209350	ENSEG000000209350	557860	557930
X1_93_556427.ENSEG000000212875	ENSEG000000212875	556318	557859
X1_93_556427.ENSEG000000209349	ENSEG000000209349	556240	556304

	feature_strand	insideFeature	distancetoFeature
	<character>	<factor>	<numeric>
X1_14_1300250.ENSEG000000218550	+	upstream	-3355
X1_14_1300250.ENSEG000000175756	-	upstream	-110
X1_41_559455.ENSEG000000212678	+	inside	204
X1_41_559455.ENSEG000000209350	-	upstream	-1894
X1_93_556427.ENSEG000000212875	+	inside	392
X1_93_556427.ENSEG000000209349	-	upstream	-406

	shortestDistance	fromOverlappingOrNearest
	<integer>	<character>
X1_14_1300250.ENSEG000000218550	3305	NearestLocation
X1_14_1300250.ENSEG000000175756	60	NearestLocation
X1_41_559455.ENSEG000000212678	154	NearestLocation
X1_41_559455.ENSEG000000209350	1844	NearestLocation
X1_93_556427.ENSEG000000212875	342	NearestLocation
X1_93_556427.ENSEG000000209349	356	NearestLocation

```

-----
seqinfo: 24 sequences from an unspecified genome; no seqlengths
> c(annotatedBDP$percentPeaksWithBDP,
+   annotatedBDP$n.peaks,
+   annotatedBDP$n.peaksWithBDP)
[1] 0.3 10.0 3.0

```

### 3.6 Task 6: Output a summary of motif occurrence in the peaks.

Here is an example to search the peaks for the motifs in examplepattern.fa file.

```

> peaks <- GRanges(seqnames=c("NC_008253", "NC_010468"),
+                 ranges=IRanges(start=c(100, 500),
+                               end=c(300, 600),
+                               names=c("peak1", "peak2")))
> filepath <- system.file("extdata", "examplePattern.fa", package="ChIPpeakAnno")
> library(BSgenome.Ecoli.NCBI.20080805)
> summarizePatternInPeaks(patternFilePath=filepath, format="fasta", skip=0L,
+                         BSgenomeName=Ecoli, peaks=peaks)

      n.peaksWithPattern n.totalPeaks Pattern
[1,] "0"                "2"            "GGNCCK"
[2,] "1"                "2"            "AACCNM"

```

### 3.7 Task 7: Add other IDs to annotated peaks or enrichedGO

Here is an example to add gene symbol to annotated peaks .

```

> data(annotatedPeak)
> library(org.Hs.eg.db)
> addGeneIDs(annotatedPeak[1:6,], orgAnn="org.Hs.eg.db", IDs2Add=c("symbol"))

```

GRanges object with 6 ranges and 9 metadata columns:

seqnames	ranges	strand	peak
<Rle>	<IRanges>	<Rle>	<character>
X1_11_100272487.ENSEG00000202254	1 [100272801, 100272900]	+	1_11_100272487
X1_11_108905539.ENSEG00000186086	1 [108906026, 108906125]	+	1_11_108905539
X1_11_110106925.ENSEG00000065135	1 [110107267, 110107366]	+	1_11_110106925
X1_11_110679983.ENSEG00000197106	1 [110680469, 110680568]	+	1_11_110679983
X1_11_110681677.ENSEG00000197106	1 [110682125, 110682224]	+	1_11_110681677
X1_11_110756560.ENSEG00000116396	1 [110756823, 110756922]	+	1_11_110756560

feature	start_position	end_position
<character>	<numeric>	<numeric>
X1_11_100272487.ENSEG00000202254	100257218	100257309
X1_11_108905539.ENSEG00000186086	108918435	109013624
X1_11_110106925.ENSEG00000065135	110091233	110136975
X1_11_110679983.ENSEG00000197106	110693108	110744824
X1_11_110681677.ENSEG00000197106	110693108	110744824
X1_11_110756560.ENSEG00000116396	110753965	110776666

insideFeature	distancetoFeature	shortestDistance
<character>	<numeric>	<numeric>
X1_11_100272487.ENSEG00000202254	downstream	15582
X1_11_108905539.ENSEG00000186086	upstream	-12410
X1_11_110106925.ENSEG00000065135	inside	16033
X1_11_110679983.ENSEG00000197106	upstream	-12640
X1_11_110681677.ENSEG00000197106	upstream	-10984
X1_11_110756560.ENSEG00000116396	inside	2857

```

                                fromOverlappingOrNearest  symbol
                                <character> <factor>
X1_11_100272487.ENSEG00000202254      NearestStart      <NA>
X1_11_108905539.ENSEG00000186086      NearestStart      NBPF6
X1_11_110106925.ENSEG00000065135      NearestStart      GNAI3
X1_11_110679983.ENSEG00000197106      NearestStart      SLC6A17
X1_11_110681677.ENSEG00000197106      NearestStart      SLC6A17
X1_11_110756560.ENSEG00000116396      NearestStart      KCNC4
-----
seqinfo: 24 sequences from an unspecified genome; no seqlengths

> addGeneIDs(annotatedPeak$feature[1:6], orgAnn="org.Hs.eg.db", IDs2Add=c("symbol"))

ensembl_gene_id  symbol
1 ENSG00000065135  GNAI3
2 ENSG00000116396  KCNC4
3 ENSG00000197106  SLC6A17
4 ENSG00000186086  NBPF6
5 ENSG00000202254  <NA>

```

## 3.8 Task 8: annotate ChIP results from BED or GFF files or MACS output xls file

Here is an example to annotate peaks in BED file format and GFF file format.

```

> bed <- system.file("extdata", "MACS_output.bed", package="ChIPpeakAnno")
> gr1 <- toGRanges(bed, format="BED", header=FALSE)
> ## one can also try import from rtracklayer
> library(rtracklayer)
> gr1.import <- import(bed, format="BED")
> identical(start(gr1), start(gr1.import))

[1] TRUE

> gr1[1:2]

GRanges object with 2 ranges and 1 metadata column:
      seqnames      ranges strand |      score
      <Rle>        <IRanges> <Rle> | <numeric>
MACS_peak_1    chr1 [28341, 29610]   * |    160.81
MACS_peak_2    chr1 [90821, 91234]   * |    133.12
-----
seqinfo: 1 sequence from an unspecified genome; no seqlengths

> gr1.import[1:2] #note the name slot is different from gr1

GRanges object with 2 ranges and 2 metadata columns:
      seqnames      ranges strand |      name      score
      <Rle>        <IRanges> <Rle> | <character> <numeric>
[1]    chr1 [28341, 29610]   * | MACS_peak_1    160.81
[2]    chr1 [90821, 91234]   * | MACS_peak_2    133.12
-----
seqinfo: 1 sequence from an unspecified genome; no seqlengths

> gff <- system.file("extdata", "GFF_peaks.gff", package="ChIPpeakAnno")
> gr2 <- toGRanges(gff, format="GFF", header=FALSE, skip=3)
> ol <- findOverlapsOfPeaks(gr1, gr2)
> makeVennDiagram(ol)

$p.value
      gr1 gr2 pval
[1,]   1   1   0

```

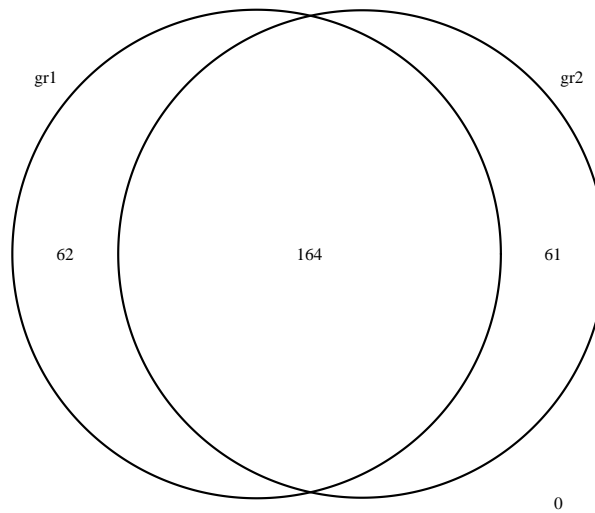


Figure 7: venn diagram of overlaps for duplicated experiments

```
$vennCounts
      gr1 gr2 Counts
[1,]    0  0      0
[2,]    0  1      61
[3,]    1  0      62
[4,]    1  1     164
attr(,"class")
[1] "VennCounts"
```

```
> pie(table(ol$overlappingPeaks[["gr1//gr2"]]$overlapFeature))
```

Find all features within 5kb away from the overlapping peaks using `annotatePeakInBatch`.

```
> data(TSS.human.GRCh37)
> overlaps <- ol$peaklist[["gr1//gr2"]]
> overlaps.anno <- annotatePeakInBatch(overlaps, AnnotationData=TSS.human.GRCh37,
+                                     output="overlapping", maxgap=5000L)
> overlaps.anno <- addGeneIDs(overlaps.anno, "org.Hs.eg.db", "symbol")
> head(overlaps.anno)
```

GRanges object with 6 ranges and 11 metadata columns:

	seqnames	ranges	strand	
	<Rle>	<IRanges>	<Rle>	
X001.ENSEG00000228327	chr1	[713791, 715578]	*	
X001.ENSEG00000237491	chr1	[713791, 715578]	*	
X001.ENSEG00000242937	chr1	[713791, 715578]	*	
X002.ENSEG00000237491	chr1	[724851, 727191]	*	
X002.ENSEG00000242937	chr1	[724851, 727191]	*	
X002.ENSEG00000197049	chr1	[724851, 727191]	*	

	peakNames	peak
	<CharacterList>	<character>
X001.ENSEG00000228327	gr1__MACS_peak_13,gr2__region_0,gr2__region_1	001
X001.ENSEG00000237491	gr1__MACS_peak_13,gr2__region_0,gr2__region_1	001
X001.ENSEG00000242937	gr1__MACS_peak_13,gr2__region_0,gr2__region_1	001

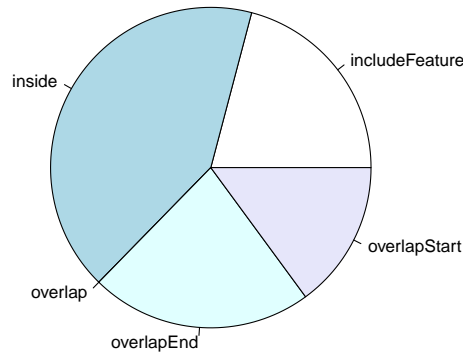


Figure 8: Pie chart of common peaks among features

```

X002.ENSEG00000237491      gr2__region_2,gr1__MACS_peak_14      002
X002.ENSEG00000242937      gr2__region_2,gr1__MACS_peak_14      002
X002.ENSEG00000197049      gr2__region_2,gr1__MACS_peak_14      002
      feature start_position end_position feature_strand
      <character>      <integer>      <integer>      <character>
X001.ENSEG00000228327  ENSG00000228327      700238      714006      -
X001.ENSEG00000237491  ENSG00000237491      714163      740255      +
X001.ENSEG00000242937  ENSG00000242937      717326      720070      +
X002.ENSEG00000237491  ENSG00000237491      714163      740255      +
X002.ENSEG00000242937  ENSG00000242937      717326      720070      +
X002.ENSEG00000197049  ENSG00000197049      721321      722513      +
      insideFeature distanceToFeature shortestDistance
      <factor>      <numeric>      <integer>
X001.ENSEG00000228327  overlapStart      215      215
X001.ENSEG00000237491  overlapStart      -372      372
X001.ENSEG00000242937  upstream      -3535      1748
X002.ENSEG00000237491  inside      10688      10688
X002.ENSEG00000242937  downstream      7525      4781
X002.ENSEG00000197049  downstream      3530      2338
      fromOverlappingOrNearest      symbol
      <character>      <factor>
X001.ENSEG00000228327  Overlapping  LOC100288069;LOC101929540
X001.ENSEG00000237491  Overlapping      LOC100287934
X001.ENSEG00000242937  Overlapping      <NA>
X002.ENSEG00000237491  Overlapping      LOC100287934
X002.ENSEG00000242937  Overlapping      <NA>
X002.ENSEG00000197049  Overlapping      <NA>

```

-----  
seqinfo: 1 sequence from an unspecified genome; no seqlengths

Plot the distribution of aggregated peak scores or peak numbers around transcript start sites (Figure 9).

```

> gr1.copy <- gr1
> gr1.copy$score <- 1

```

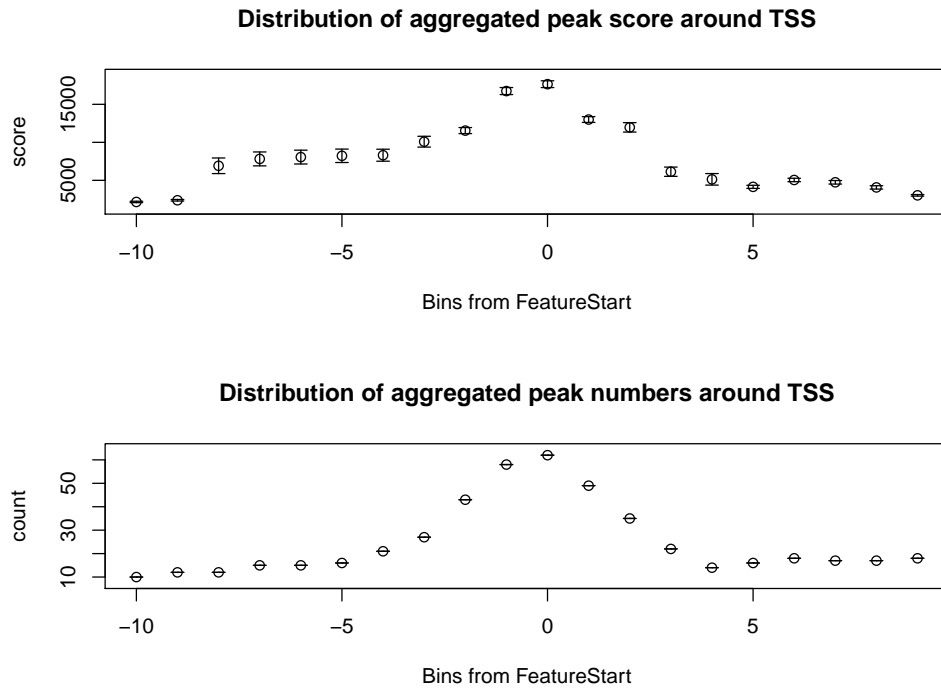


Figure 9: Distribution of aggregated peak scores or peak numbers around transcript start sites.

```
> binOverFeature(gr1, gr1.copy, annotationData=TSS.human.GRCh37,
+               radius=5000, nbins=10, FUN=c(sum, length),
+               ylab=c("score", "count"),
+               main=c("Distribution of aggregated peak score around TSS",
+                     "Distribution of aggregated peak numbers around TSS"))
```

Summarize peak distribution over exon, intron, enhancer, proximal promoter, 5 prime UTR and 3 prime UTR in peak centric and nucleotide centric view using function `assignChromosomeRegion`(Figure 10). Setting `nucleotideLevel = TRUE` will give a nucleotide level distribution over different features.

```
> if(require(TxDb.Hsapiens.UCSC.hg19.knownGene)){
+   aCR<-assignChromosomeRegion(gr1, nucleotideLevel=FALSE,
+                             precedence=c("Promoters", "immediateDownstream",
+                                           "fiveUTRs", "threeUTRs",
+                                           "Exons", "Introns"),
+                             TxDb=TxDb.Hsapiens.UCSC.hg19.knownGene)
+   barplot(aCR$percentage)
+ }
```

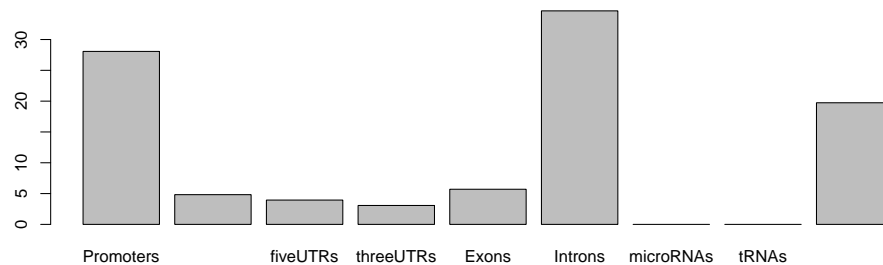


Figure 10: Peak distribution over different genomic features.

## 4 References

1. Y. Benjamini and Y. Hochberg (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *J. R. Statist. Soc. B*. Vol. 57: 289-300.
2. Y. Benjamini and D. Yekutieli (2001). The control of the false discovery rate in multiple hypothesis testing under dependency. *Annals of Statistics*. Accepted.
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## 5 Session Info

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```
> toLatex(sessionInfo())
```

- R version 3.2.0 Patched (2015-04-23 r68254), x86\_64-apple-darwin13.4.0
- Locale: C/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8
- Base packages: base, datasets, grDevices, graphics, grid, methods, parallel, stats, stats4, utils
- Other packages: AnnotationDbi 1.30.1, BSgenome 1.36.0, BSgenome.Ecoli.NCBI.20080805 1.3.1000, Biobase 2.28.0, BiocGenerics 0.14.0, Biostrings 2.36.1, ChIPpeakAnno 3.2.2, DBI 0.3.1, FDb.UCSC.tRNAs 1.0.1, GenomeInfoDb 1.4.0, GenomicFeatures 1.20.1, GenomicRanges 1.20.3, IRanges 2.2.1, RSQLite 1.0.0, S4Vectors 0.6.0, TxDb.Hsapiens.UCSC.hg19.knownGene 3.1.2, VennDiagram 1.6.9, XVector 0.8.0, biomaRt 2.24.0, mirbase.db 1.2.0, org.Hs.eg.db 3.1.2, rtracklayer 1.28.2
- Loaded via a namespace (and not attached): BiocInstaller 1.18.2, BiocParallel 1.2.1, BiocStyle 1.6.0, GO.db 3.1.2, GenomicAlignments 1.4.1, MASS 7.3-40, RBGL 1.44.0, RCurl 1.95-4.6, Rsamtools 1.20.2, XML 3.98-1.1, bitops 1.0-6, futile.logger 1.4.1, futile.options 1.0.0, graph 1.46.0, lambda.r 1.1.7, limma 3.24.4, multtest 2.24.0, splines 3.2.0, survival 2.38-1, tools 3.2.0, zlibbioc 1.14.0