

# Some Basic Analysis of ChIP-Seq Data

July 23, 2010

Our goal is to describe the use of Bioconductor software to perform some basic tasks in the analysis of ChIP-Seq data. We will use several functions in the as-yet-unreleased `chipseq` package, which provides convenient interfaces to other powerful packages such as `ShortRead` and `IRanges`. We will also use the `lattice` and `rtracklayer` packages for visualization.

```
> library(chipseq)
> library(GenomicFeatures)
> library(lattice)
>
```

## Example data

The `cstest` data set is included in the `chipseq` package to help demonstrate its capabilities. The dataset contains data for three chromosomes from Solexa lanes, one from a CTCF mouse ChIP-Seq, and one from a GFP mouse ChIP-Seq. The raw reads were aligned to the reference genome (mouse in this case) using an external program (MAQ), and the results read in using the `readAligned` function in the `ShortRead`, in conjunction with a filter produced by the `chipseqFilter` function. This step filtered the reads to remove duplicates, to restrict mappings to the canonical, autosomal chromosomes and ensure that only a single read maps to a given position. A quality score cutoff was also applied. The remaining data were reduced to a set of aligned intervals (including orientation). This saves a great deal of memory, as the sequences, which are unnecessary, are discarded. Finally, we subset the data for chr10 to chr12, simply for convenience in this vignette.

We outline this process with this unevaluated code block:

```
> qa_list <- lapply(sampleFiles, qa)
> report(do.call(rbind, qa_list))
> ## spend some time evaluating the QA report, then procede
> filter <- compose(chipseqFilter(), alignQualityFilter(15))
> cstest <- GenomicRangesList(lapply(sampleFiles, function(file) {
+   as(readAligned(file, filter), "GRanges")
+ }))
> cstest <- cstest[seqnames(cstest) %in% c("chr10", "chr11", "chr12")]
```

The above step has been performed in advance, and the output has been included as a dataset in this package. We load it now:

```
> data(cstest)
> cstest
```

GRangesList object of length 2:

\$ctcf

GRanges object with 450096 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
[1]	chr10	3012936-3012959	+
[2]	chr10	3012941-3012964	+
[3]	chr10	3012944-3012967	+
[4]	chr10	3012955-3012978	+
[5]	chr10	3012963-3012986	+
...	...	...	...
[450092]	chr12	121239376-121239399	-
[450093]	chr12	121245849-121245872	-
[450094]	chr12	121245895-121245918	-
[450095]	chr12	121246344-121246367	-
[450096]	chr12	121253499-121253522	-

...

<1 more element>

-----

seqinfo: 35 sequences from an unspecified genome

cstest is an object of class *GRangesList*, and has a list-like structure, each component representing the alignments from one lane, as a *GRanges* object of stranded intervals.

> cstest\$ctcf

GRanges object with 450096 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
[1]	chr10	3012936-3012959	+
[2]	chr10	3012941-3012964	+
[3]	chr10	3012944-3012967	+
[4]	chr10	3012955-3012978	+
[5]	chr10	3012963-3012986	+
...	...	...	...
[450092]	chr12	121239376-121239399	-
[450093]	chr12	121245849-121245872	-
[450094]	chr12	121245895-121245918	-
[450095]	chr12	121246344-121246367	-
[450096]	chr12	121253499-121253522	-

-----

seqinfo: 35 sequences from an unspecified genome

## Extending reads

Solexa gives us the first few (24 in this example) bases of each fragment it sequences, but the actual fragment is longer. By design, the sites of interest (transcription factor binding sites) should be somewhere in the fragment, but not necessarily in its initial part. Although the actual lengths of

fragments vary, extending the alignment of the short read by a fixed amount in the appropriate direction, depending on whether the alignment was to the positive or negative strand, makes it more likely that we cover the actual site of interest.

It is possible to estimate the fragment length, through a variety of methods. There are several implemented by the `estimate.mean.fraglen` function. Generally, this only needs to be done for one sample from each experimental protocol. Here, we use SSISR, the default method:

```
> fraglen <- estimate.mean.fraglen(cstest$ctcf, method="correlation")
> fraglen[!is.na(fraglen)]
```

```
chr10 chr11 chr12
  340   340   340
```

Given the suggestion of 190 nucleotides, we extend all reads to be 200 bases long. This is done using the `resize` function, which considers the strand to determine the direction of extension:

```
> ctcf.ext <- resize(cstest$ctcf, width = 200)
> ctcf.ext
```

GRanges object with 450096 ranges and 0 metadata columns:

```
      seqnames      ranges strand
      <Rle>         <IRanges> <Rle>
 [1]   chr10     3012936-3013135    +
 [2]   chr10     3012941-3013140    +
 [3]   chr10     3012944-3013143    +
 [4]   chr10     3012955-3013154    +
 [5]   chr10     3012963-3013162    +
 ...      ...      ...      ...
[450092] chr12 121239200-121239399    -
[450093] chr12 121245673-121245872    -
[450094] chr12 121245719-121245918    -
[450095] chr12 121246168-121246367    -
[450096] chr12 121253323-121253522    -
```

-----

seqinfo: 35 sequences from an unspecified genome

We now have intervals for the CTCF lane that represent the original fragments that were precipitated.

## Coverage, islands, and depth

A useful summary of this information is the *coverage*, that is, how many times each base in the genome was covered by one of these intervals.

```
> cov.ctcf <- coverage(ctcf.ext)
> cov.ctcf
```

```
RleList of length 35
```

```
$chr1
```

```
integer-Rle of length 197195432 with 1 run
```

```
Lengths: 197195432
```

```
Values :          0

$chr2
integer-Rle of length 181748087 with 1 run
  Lengths: 181748087
  Values :          0

$chr3
integer-Rle of length 159599783 with 1 run
  Lengths: 159599783
  Values :          0

$chr4
integer-Rle of length 155630120 with 1 run
  Lengths: 155630120
  Values :          0

$chr5
integer-Rle of length 152537259 with 1 run
  Lengths: 152537259
  Values :          0

...
<30 more elements>
```

For efficiency, the result is stored in a run-length encoded form.

The regions of interest are contiguous segments of non-zero coverage, also known as *islands*.

```
> islands <- slice(cov.ctcf, lower = 1)
> islands
```

```
RleViewsList of length 35
$chr1
Views on a 197195432-length Rle subject
```

```
views: NONE
```

```
$chr2
Views on a 181748087-length Rle subject
```

```
views: NONE
```

```
$chr3
Views on a 159599783-length Rle subject
```

```
views: NONE
```

```
...
<32 more elements>
```

For each island, we can compute the number of reads in the island, and the maximum coverage depth within that island.

```
> viewSums(islands)
```

```
IntegerList of length 35
[["chr1"]] integer(0)
[["chr2"]] integer(0)
[["chr3"]] integer(0)
[["chr4"]] integer(0)
[["chr5"]] integer(0)
[["chr6"]] integer(0)
[["chr7"]] integer(0)
[["chr8"]] integer(0)
[["chr9"]] integer(0)
[["chr10"]] 2400 200 200 200 200 200 200 600 ... 200 200 400 200 200 200 200
```

```
...
<25 more elements>
```

```
> viewMaxs(islands)
```

```
IntegerList of length 35
[["chr1"]] integer(0)
[["chr2"]] integer(0)
[["chr3"]] integer(0)
[["chr4"]] integer(0)
```

```

[["chr5"]] integer(0)
[["chr6"]] integer(0)
[["chr7"]] integer(0)
[["chr8"]] integer(0)
[["chr9"]] integer(0)
[["chr10"]] 11 1 1 1 1 1 1 3 1 1 1 1 1 2 1 ... 1 2 1 1 1 1 3 1 1 1 2 1 1 1 1
...
<25 more elements>

```

```

> nread.tab <- table(viewSums(islands) / 200)
> depth.tab <- table(viewMaxs(islands))
> nread.tab[,1:10]

```

	1	2	3	4	5	6	7	8	9	10
chr1	0	0	0	0	0	0	0	0	0	0
chr2	0	0	0	0	0	0	0	0	0	0
chr3	0	0	0	0	0	0	0	0	0	0
chr4	0	0	0	0	0	0	0	0	0	0
chr5	0	0	0	0	0	0	0	0	0	0
chr6	0	0	0	0	0	0	0	0	0	0
chr7	0	0	0	0	0	0	0	0	0	0
chr8	0	0	0	0	0	0	0	0	0	0
chr9	0	0	0	0	0	0	0	0	0	0
chr10	68101	13352	3019	924	418	246	191	123	133	100
chr11	71603	15993	4334	1410	619	338	245	199	180	151
chr12	59141	11279	2613	816	344	175	140	119	84	71
chr13	0	0	0	0	0	0	0	0	0	0
chr14	0	0	0	0	0	0	0	0	0	0
chr15	0	0	0	0	0	0	0	0	0	0
chr16	0	0	0	0	0	0	0	0	0	0
chr17	0	0	0	0	0	0	0	0	0	0
chr18	0	0	0	0	0	0	0	0	0	0
chr19	0	0	0	0	0	0	0	0	0	0
chrX	0	0	0	0	0	0	0	0	0	0
chrY	0	0	0	0	0	0	0	0	0	0
chrM	0	0	0	0	0	0	0	0	0	0
chr1_random	0	0	0	0	0	0	0	0	0	0
chr3_random	0	0	0	0	0	0	0	0	0	0
chr4_random	0	0	0	0	0	0	0	0	0	0
chr5_random	0	0	0	0	0	0	0	0	0	0
chr7_random	0	0	0	0	0	0	0	0	0	0
chr8_random	0	0	0	0	0	0	0	0	0	0
chr9_random	0	0	0	0	0	0	0	0	0	0
chr13_random	0	0	0	0	0	0	0	0	0	0
chr16_random	0	0	0	0	0	0	0	0	0	0
chr17_random	0	0	0	0	0	0	0	0	0	0
chrX_random	0	0	0	0	0	0	0	0	0	0
chrY_random	0	0	0	0	0	0	0	0	0	0
chrUn_random	0	0	0	0	0	0	0	0	0	0

```
> depth.tab[,1:10]
```

	1	2	3	4	5	6	7	8	9	10
chr1	0	0	0	0	0	0	0	0	0	0
chr2	0	0	0	0	0	0	0	0	0	0
chr3	0	0	0	0	0	0	0	0	0	0
chr4	0	0	0	0	0	0	0	0	0	0
chr5	0	0	0	0	0	0	0	0	0	0
chr6	0	0	0	0	0	0	0	0	0	0
chr7	0	0	0	0	0	0	0	0	0	0
chr8	0	0	0	0	0	0	0	0	0	0
chr9	0	0	0	0	0	0	0	0	0	0
chr10	68149	14748	2386	547	256	180	150	129	120	101
chr11	71677	17945	3527	862	362	268	205	179	181	130
chr12	59181	12441	2078	482	191	131	131	108	95	77
chr13	0	0	0	0	0	0	0	0	0	0
chr14	0	0	0	0	0	0	0	0	0	0
chr15	0	0	0	0	0	0	0	0	0	0
chr16	0	0	0	0	0	0	0	0	0	0
chr17	0	0	0	0	0	0	0	0	0	0
chr18	0	0	0	0	0	0	0	0	0	0
chr19	0	0	0	0	0	0	0	0	0	0
chrX	0	0	0	0	0	0	0	0	0	0
chrY	0	0	0	0	0	0	0	0	0	0
chrM	0	0	0	0	0	0	0	0	0	0
chr1_random	0	0	0	0	0	0	0	0	0	0
chr3_random	0	0	0	0	0	0	0	0	0	0
chr4_random	0	0	0	0	0	0	0	0	0	0
chr5_random	0	0	0	0	0	0	0	0	0	0
chr7_random	0	0	0	0	0	0	0	0	0	0
chr8_random	0	0	0	0	0	0	0	0	0	0
chr9_random	0	0	0	0	0	0	0	0	0	0
chr13_random	0	0	0	0	0	0	0	0	0	0
chr16_random	0	0	0	0	0	0	0	0	0	0
chr17_random	0	0	0	0	0	0	0	0	0	0
chrX_random	0	0	0	0	0	0	0	0	0	0
chrY_random	0	0	0	0	0	0	0	0	0	0
chrUn_random	0	0	0	0	0	0	0	0	0	0

## Processing multiple lanes

Although data from one lane is often a natural analytical unit, we typically want to apply any procedure to all lanes. Here is a simple summary function that computes the frequency distribution of the number of reads.

```
> islandReadSummary <- function(x)
+ {
+   g <- resize(x, 200)
+   s <- slice(coverage(g), lower = 1)
+   tab <- table(viewSums(s) / 200)
+   df <- DataFrame(tab)
+   colnames(df) <- c("chromosome", "nread", "count")
+   df$nread <- as.integer(df$nread)
+   df
+ }
```

Applying it to our test-case, we get

```
> head(islandReadSummary(cstest$ctcf))
```

DataFrame with 6 rows and 3 columns

	chromosome	nread	count
	<factor>	<integer>	<integer>
1	chr1	1	0
2	chr2	1	0
3	chr3	1	0
4	chr4	1	0
5	chr5	1	0
6	chr6	1	0

We can now use it to summarize the full dataset, flattening the returned *DataFrameList* with the `stack` function.

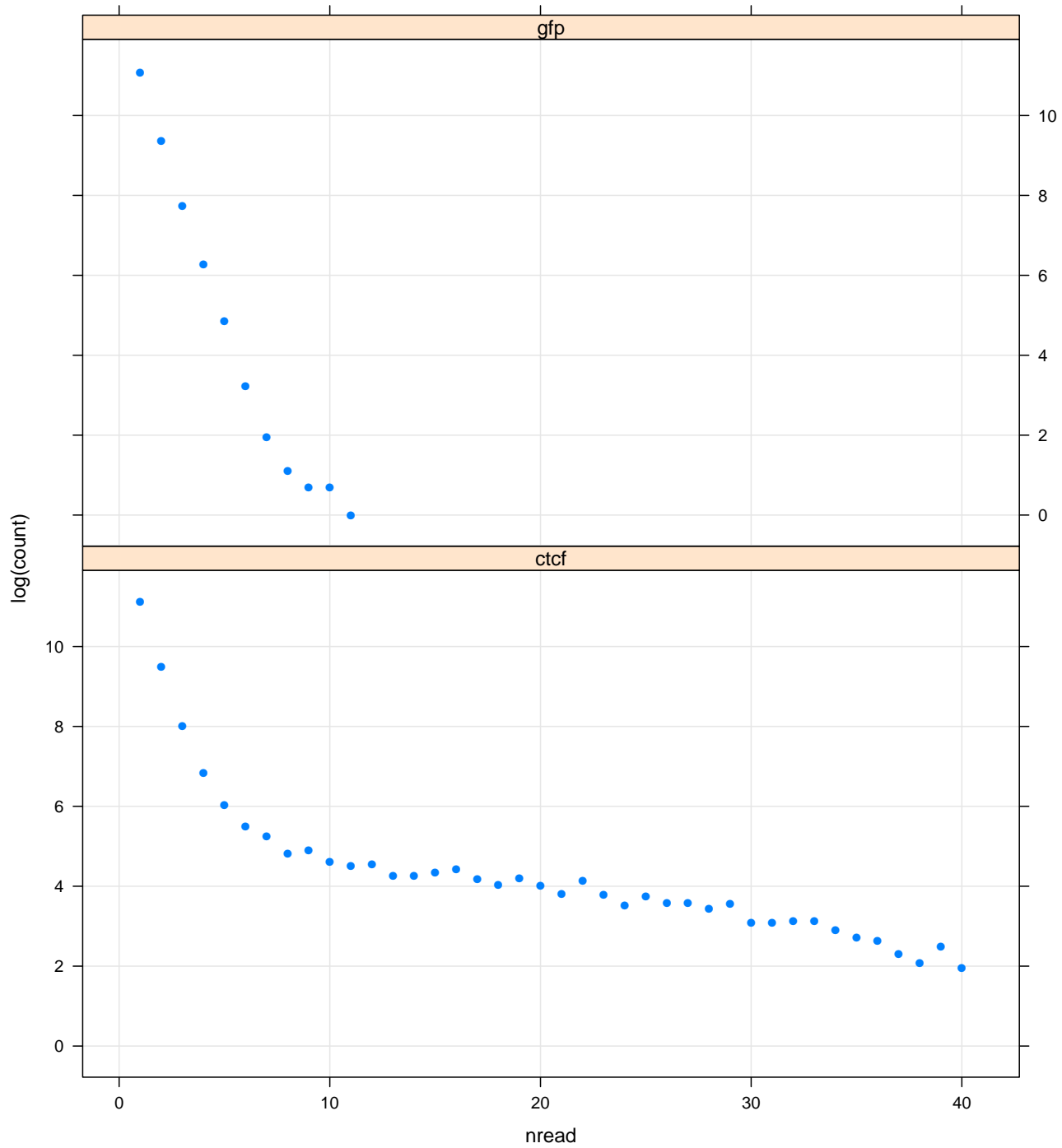
```
> nread.islands <- DataFrameList(lapply(cstest, islandReadSummary))
> nread.islands <- stack(nread.islands, "sample")
> nread.islands
```

DataFrame with 4025 rows and 4 columns

	sample	chromosome	nread	count
	<Rle>	<factor>	<integer>	<integer>
1	ctcf	chr1	1	0
2	ctcf	chr2	1	0
3	ctcf	chr3	1	0
4	ctcf	chr4	1	0
5	ctcf	chr5	1	0
...	...	...	...	...
4021	gfp	chr16_random	34	0
4022	gfp	chr17_random	34	0
4023	gfp	chrX_random	34	0
4024	gfp	chrY_random	34	0
4025	gfp	chrUn_random	34	0



```
> xyplot(log(count) ~ nread | sample, as.data.frame(nread.islands),  
+       subset = (chromosome == "chr10" & nread <= 40),  
+       layout = c(1, 2), pch = 16, type = c("p", "g"))
```

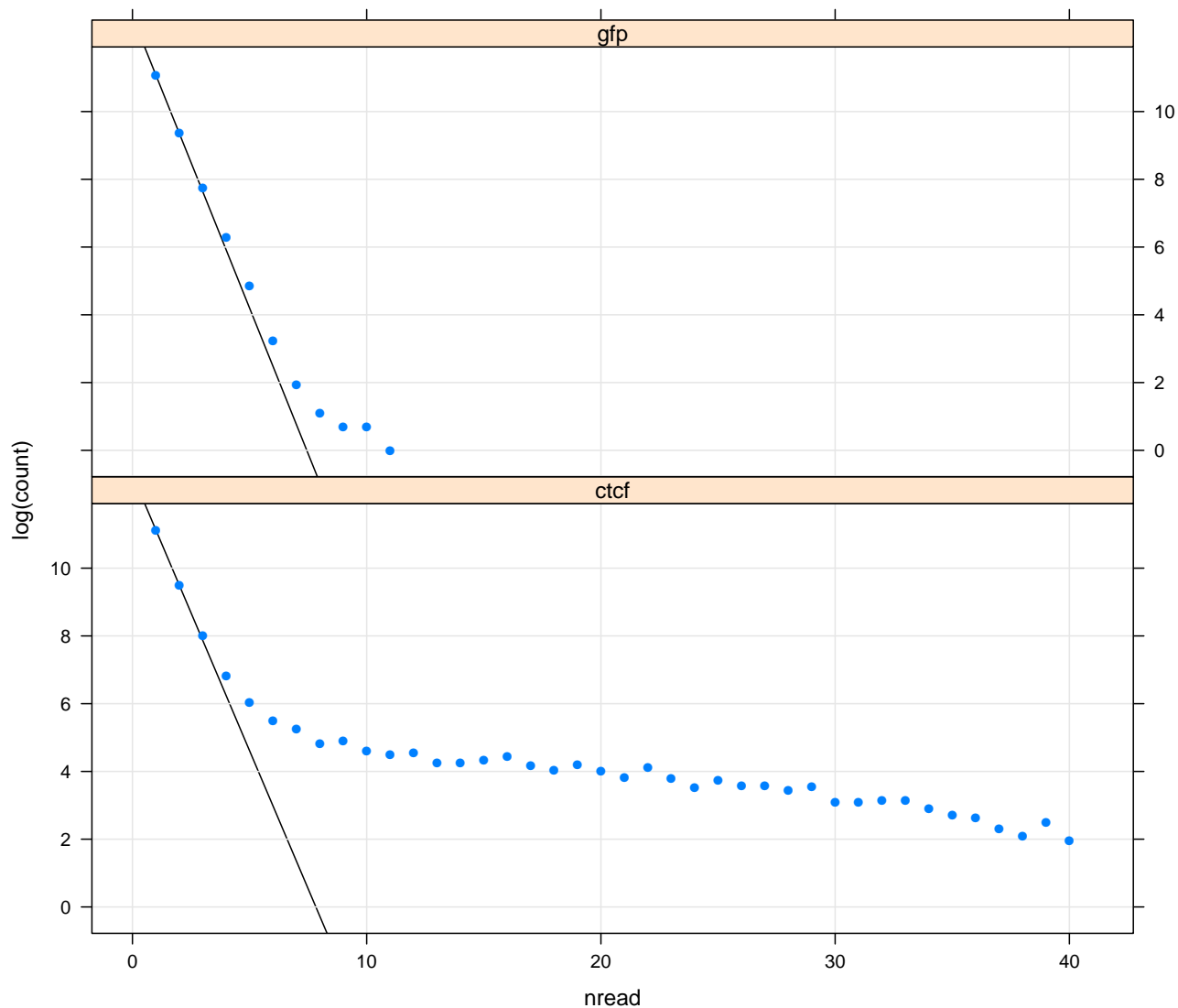


If reads were sampled randomly from the genome, then the null distribution number of reads per island would have a geometric distribution; that is,

$$P(X = k) = p^{k-1}(1 - p)$$

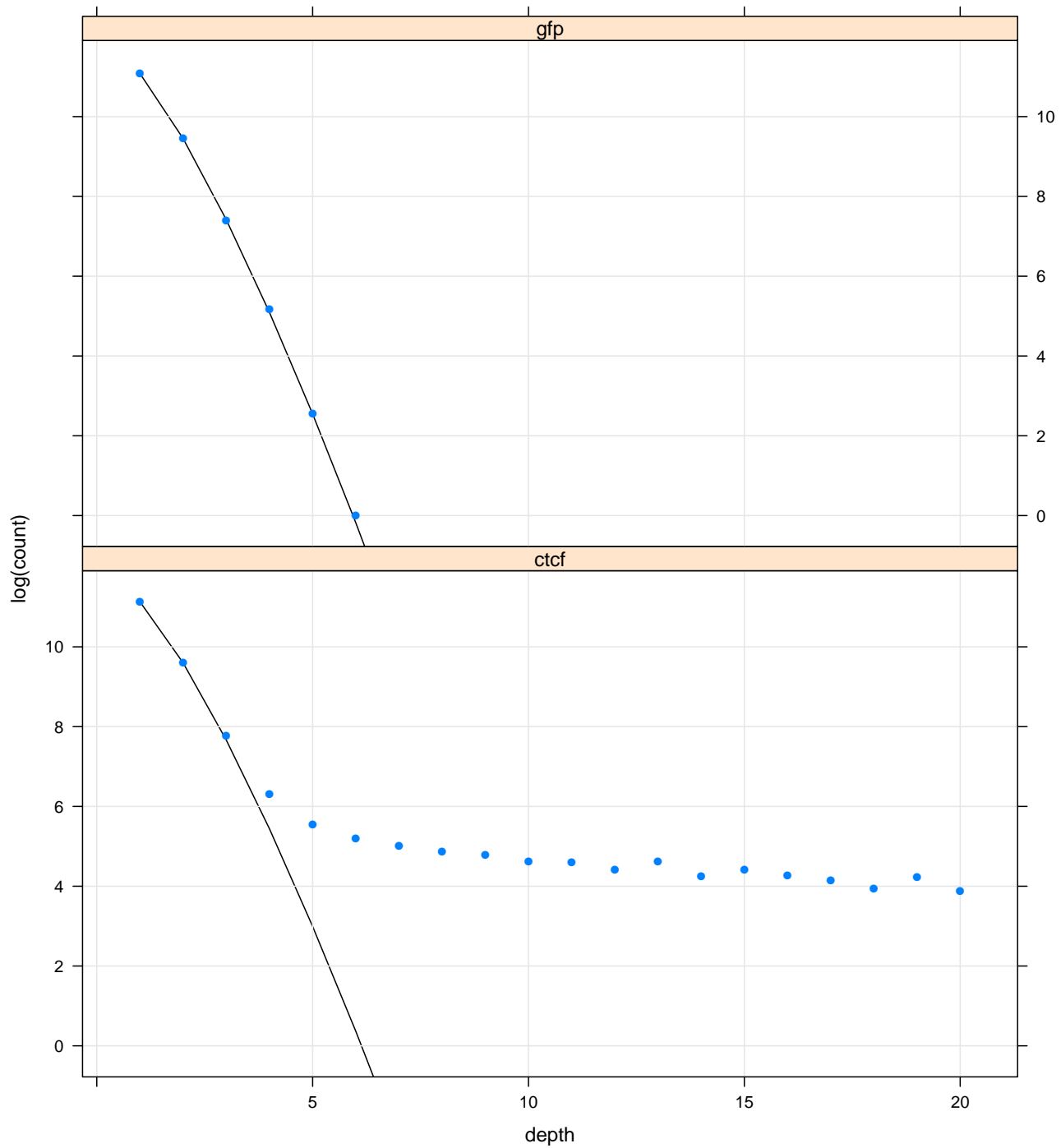
In other words,  $\log P(X = k)$  is linear in  $k$ . Although our samples are not random, the islands with just one or two reads may be representative of the null distribution.

```
> xyplot(log(count) ~ nread | sample, as.data.frame(nread.islands),  
+       subset = (chromosome == "chr10" & nread <= 40),  
+       layout = c(1, 2), pch = 16, type = c("p", "g"),  
+       panel = function(x, y, ...) {  
+         panel.lmline(x[1:2], y[1:2], col = "black")  
+         panel.xyplot(x, y, ...)  
+       })
```



We can create a similar plot of the distribution of depths.

```
> islandDepthSummary <- function(x)
+ {
+   g <- resize(x, 200)
+   s <- slice(coverage(g), lower = 1)
+   tab <- table(viewMaxs(s) / 200)
+   df <- DataFrame(tab)
+   colnames(df) <- c("chromosome", "depth", "count")
+   df$depth <- as.integer(df$depth)
+   df
+ }
> depth.islands <- DataFrameList(lapply(cstest, islandDepthSummary))
> depth.islands <- stack(depth.islands, "sample")
> xyplot(log(count) ~ depth | sample, as.data.frame(depth.islands),
+   subset = (chromosome == "chr10" & depth <= 20),
+   layout = c(1, 2), pch = 16, type = c("p", "g"),
+   panel = function(x, y, ...) {
+     lambda <- 2 * exp(y[2]) / exp(y[1])
+     null.est <- function(xx) {
+       xx * log(lambda) - lambda - lgamma(xx + 1)
+     }
+     log.N.hat <- null.est(1) - y[1]
+     panel.lines(1:10, -log.N.hat + null.est(1:10), col = "black")
+     panel.xyplot(x, y, ...)
+   })
>
> ## depth.islands <- summarizeReads(cstest, summary.fun = islandDepthSummary)
>
```



The above plot is very useful for detecting peaks, discussed in the next section. As a convenience, it can be created for the coverage over all chromosomes for a single sample by calling the `islandDepthPlot` function:

```
> islandDepthPlot(cov.ctcf)
```

## Peaks

To obtain a set of putative binding sites, i.e., peaks, we need to find those regions that are significantly above the noise level. Using the same Poisson-based approach for estimating the noise distribution as in the plot above, the `peakCutoff` function returns a cutoff value for a specific FDR:

```
> peakCutoff(cov.ctcf, fdr = 0.0001)
```

```
[1] 6.959837
```

Considering the above calculation of 7 at an FDR of 0.0001, and looking at the above plot, we might choose 8 as a conservative peak cutoff:

```
> peaks.ctcf <- slice(cov.ctcf, lower = 8)
```

```
> peaks.ctcf
```

```
RleViewsList of length 35
```

```
$chr1
```

```
Views on a 197195432-length Rle subject
```

```
views: NONE
```

```
$chr2
```

```
Views on a 181748087-length Rle subject
```

```
views: NONE
```

```
$chr3
```

```
Views on a 159599783-length Rle subject
```

```
views: NONE
```

```
...
```

```
<32 more elements>
```

To summarize the peaks for exploratory analysis, we call the `peakSummary` function:

```
> peaks <- peakSummary(peaks.ctcf)
```

The result is a *RangedData* object with two columns: the view maxs and the view sums. Beyond that, this object is often useful as a scaffold for adding additional statistics.

It is meaningful to ask about the contribution of each strand to each peak, as the sequenced region of pull-down fragments would be on opposite sides of a binding site depending on which strand it matched. We can compute strand-specific coverage, and look at the individual coverages under the combined peaks as follows:

```
> peak.depths <- viewMaxs(peaks.ctcf)
```

```
> cov.pos <- coverage(ctcf.ext[strand(ctcf.ext) == "+"])
```

```
> cov.neg <- coverage(ctcf.ext[strand(ctcf.ext) == "-"])
```

```
> peaks.pos <- Views(cov.pos, ranges(peaks.ctcf))
```

```
> peaks.neg <- Views(cov.neg, ranges(peaks.ctcf))
```

```
> wpeaks <- tail(order(peak.depths$chr10), 4)
```

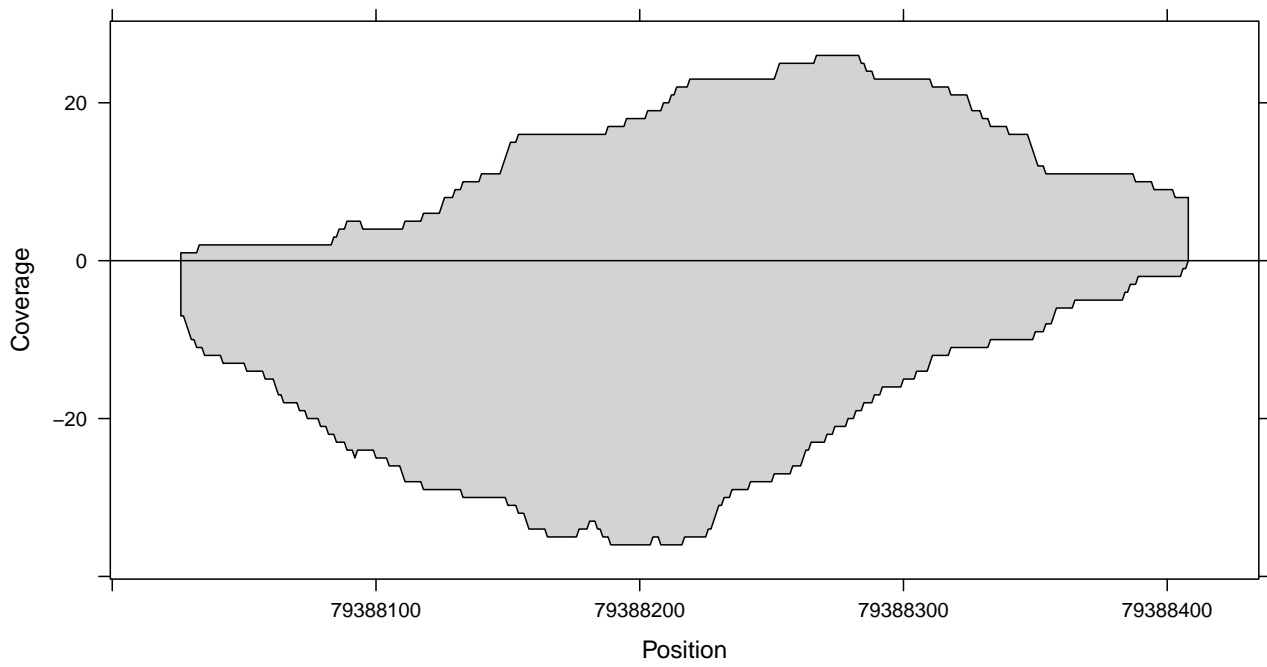
```
> wpeaks
```

```
[1] 971 989 1079 922
```

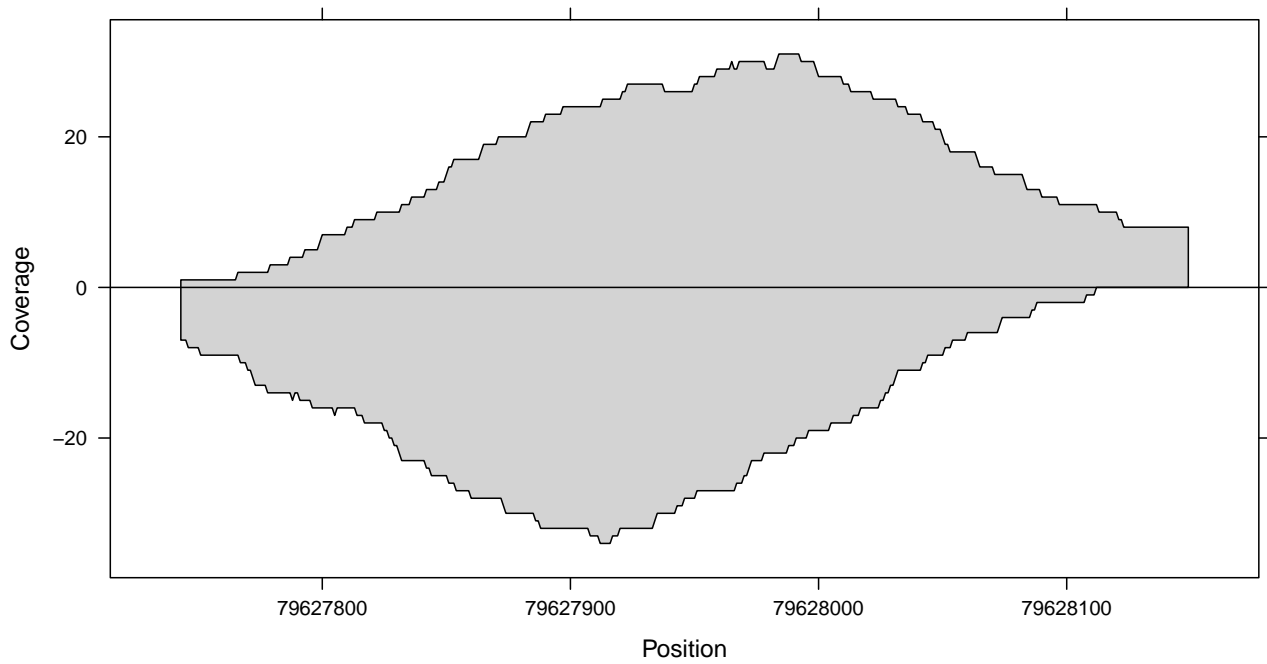
```
>
```

Below, we plot the four highest peaks on chromosome 10.

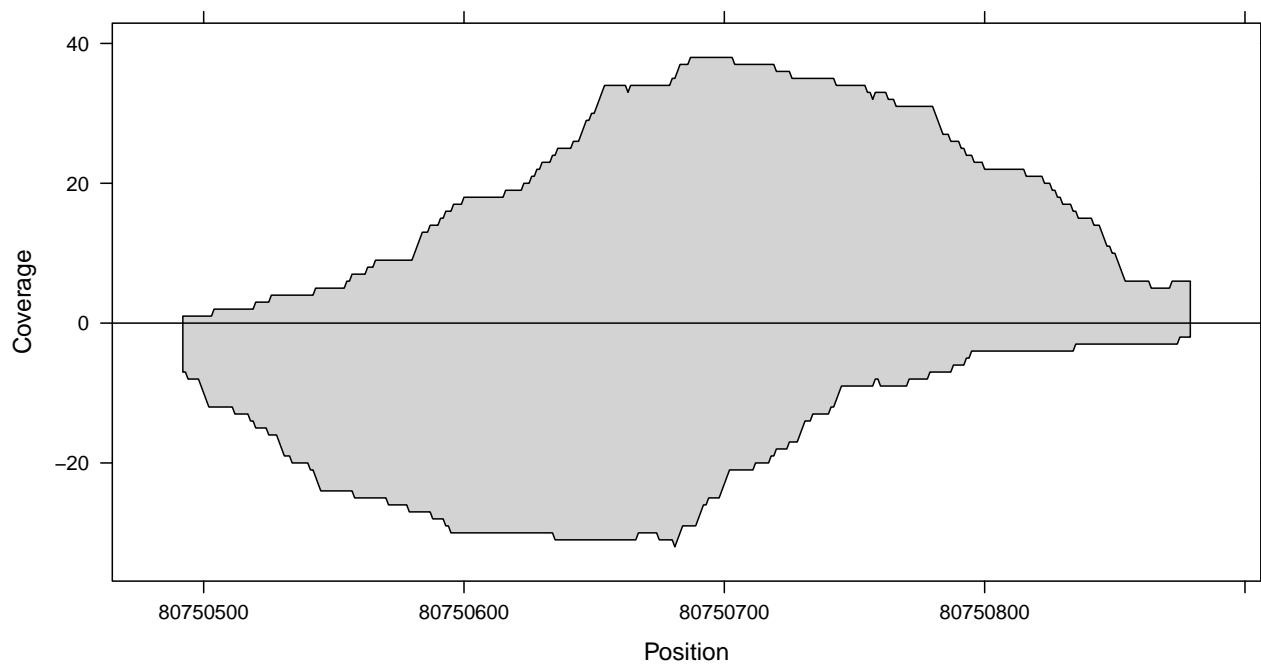
```
> coverageplot(peaks.pos$chr10[wpeaks[1]], peaks.neg$chr10[wpeaks[1]])
```



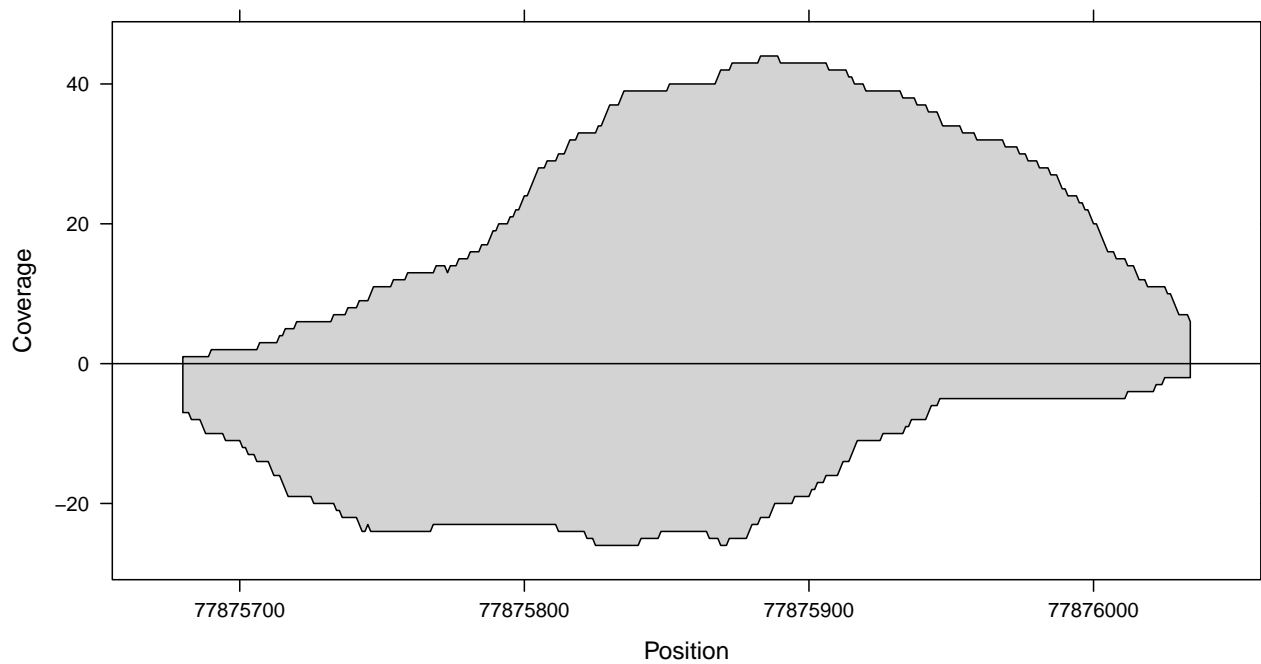
```
> coverageplot(peaks.pos$chr10[wpeaks[2]], peaks.neg$chr10[wpeaks[2]])
```



```
> coverageplot(peaks.pos$chr10[wpeaks[3]], peaks.neg$chr10[wpeaks[3]])
```



```
> coverageplot(peaks.pos$chr10[wpeaks[4]], peaks.neg$chr10[wpeaks[4]])
```

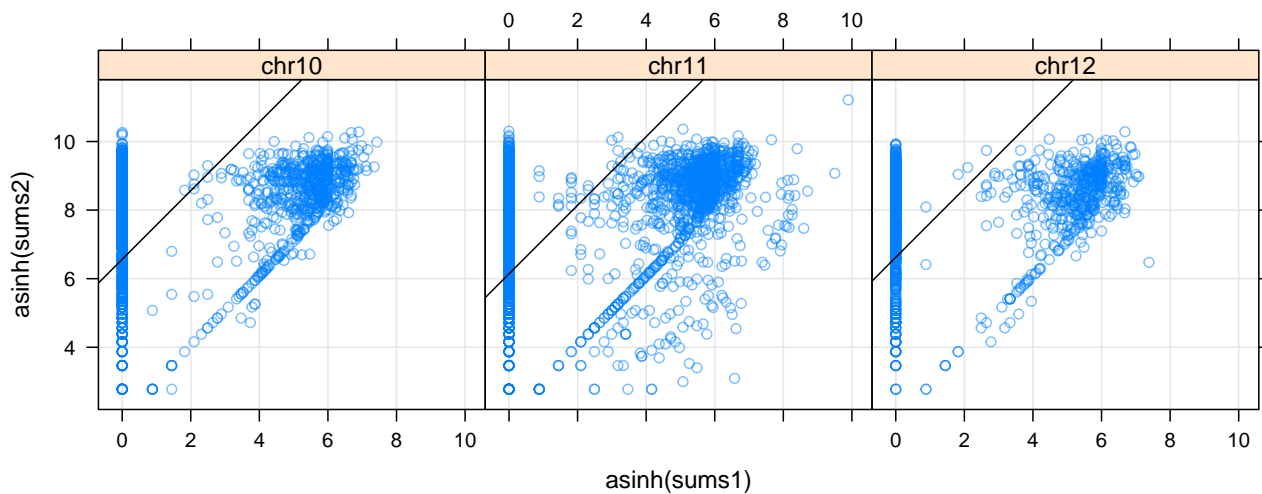




## Differential peaks

One common question is: which peaks are different in two samples? One simple strategy is the following: combine the two peak sets, and compare the two samples by calculating summary statistics for the combined peaks on top of each coverage vector.

```
> ## find peaks for GFP control
> cov.gfp <- coverage(resize(cstest$gfp, 200))
> peaks.gfp <- slice(cov.gfp, lower = 8)
> peakSummary <- diffPeakSummary(peaks.gfp, peaks.ctcf)
> xyplot(asinh(sums2) ~ asinh(sums1) | space,
+       data = as.data.frame(peakSummary),
+       panel = function(x, y, ...) {
+         panel.xyplot(x, y, ...)
+         panel.abline(median(y - x), 1)
+       },
+       type = c("p", "g"), alpha = 0.5, aspect = "iso")
>
```



We use a simple cutoff to flag peaks that are different.

```
> peakSummary <-
+   within(peakSummary,
+     {
+       diffs <- asinh(sums2) - asinh(sums1)
+       resids <- (diffs - median(diffs)) / mad(diffs)
+       up <- resids > 2
+       down <- resids < -2
+       change <- ifelse(up, "up", ifelse(down, "down", "flat"))
+     })
```

## Placing peaks in genomic context

Locations of individual peaks may be of interest. Alternatively, a global summary might look at classifying the peaks of interest in the context of genomic features such as promoters, upstream regions, etc. The `GenomicFeatures` package facilitates obtaining gene annotations from different data sources. We could download the UCSC gene predictions for the mouse genome and generate a `GRanges` object with the transcript regions (from the first to last exon, contiguous) using `makeTxDbFromUCSC`; here we use a library containing a recent snapshot.

```
> library(TxDb.Mmusculus.UCSC.mm9.knownGene)
> gregions <- transcripts(TxDb.Mmusculus.UCSC.mm9.knownGene)
> gregions
```

GRanges object with 55419 ranges and 2 metadata columns:

	seqnames	ranges	strand	tx_id	tx_name
	<Rle>	<IRanges>	<Rle>	<integer>	<character>
[1]	chr1	4797974-4832908	+	1	uc007afg.1
[2]	chr1	4797974-4836816	+	2	uc007afh.1
[3]	chr1	4847775-4887990	+	3	uc007afi.2
[4]	chr1	4847775-4887990	+	4	uc011wht.1
[5]	chr1	4848409-4887990	+	5	uc011whu.1
...	...	...	...	...	...
[55415]	chrUn_random	2204169-2216886	-	55415	uc009sjw.2
[55416]	chrUn_random	2674945-2678407	-	55416	uc009skb.2
[55417]	chrUn_random	2889607-2891056	-	55417	uc009ske.1
[55418]	chrUn_random	3830796-3837247	-	55418	uc009skg.1
[55419]	chrUn_random	4677114-4677187	-	55419	uc009skh.1

-----  
seqinfo: 35 sequences (1 circular) from mm9 genome

We can now estimate the promoter for each transcript:

```
> promoters <- flank(gregions, 1000, both = TRUE)
```

And count the peaks that fall into a promoter:

```
> peakSummary$inPromoter <- peakSummary %over% promoters
> xtabs(~ inPromoter + change, peakSummary)
```

	change	
inPromoter	down	flat
FALSE	21	5158
TRUE	2	625

Or somewhere upstream or in a gene:

```
> peakSummary$inUpstream <- peakSummary %over% flank(gregions, 20000)
> peakSummary$inGene <- peakSummary %over% gregions
```

```
> sumtab <-
+   as.data.frame(rbind(total = xtabs(~ change, peakSummary),
```

```

+         promoter = xtabs(~ change,
+           subset(peakSummary, inPromoter)),
+         upstream = xtabs(~ change,
+           subset(peakSummary, inUpstream)),
+         gene = xtabs(~ change, subset(peakSummary, inGene)))
> ##cbind(sumtab, ratio = round(sumtab[, "down"] / sumtab[, "up"], 3))

```

## Visualizing peaks in genomic context

While it is generally informative to calculate statistics incorporating the genomic context, eventually one wants a picture. The traditional genome browser view is an effective method of visually integrating multiple annotations with experimental data along the genome.

Using the `rtracklayer` package, we can upload our coverage and peaks for both samples to the UCSC Genome Browser:

```

> library(rtracklayer)
> session <- browserSession()
> genome(session) <- "mm9"
> session$gfpCov <- cov.gfp
> session$gfpPeaks <- peaks.gfp
> session$ctcfCov <- cov.ctcf
> session$ctcfPeaks <- peaks.ctcf

```

Once the tracks are uploaded, we can choose a region to view, such as the tallest peak on chr10 in the CTCF data:

```

> peak.ord <- order(unlist(peak.depths), decreasing=TRUE)
> peak.sort <- as(peaks.ctcf, "GRanges")[peak.ord]
> view <- browserView(session, peak.sort[1], full = c("gfpCov", "ctcfCov"))

```

We coerce to `GRanges` so that we can sort the ranges across chromosomes. By passing the `full` parameter to `browserView` we instruct UCSC to display the coverage tracks as a bar chart. Next, we might programmatically display a view for the top 5 tallest peaks:

```

> views <- browserView(session, head(peak.sort, 5), full = c("gfpCov", "ctcfCov"))

```

## Version information

```

> sessionInfo()

```

```

R version 3.5.0 (2018-04-23)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.4 LTS

```

```

Matrix products: default
BLAS: /home/biocbuild/bbs-3.7-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.7-bioc/R/lib/libRlapack.so

```

```

locale:

```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8       LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8   LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C              LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

```
[1] stats4    parallel  stats      graphics  grDevices  utils      datasets
[8] methods   base
```

other attached packages:

```
[1] TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2
[2] lattice_0.20-35
[3] GenomicFeatures_1.32.0
[4] AnnotationDbi_1.42.0
[5] chipseq_1.30.0
[6] ShortRead_1.38.0
[7] GenomicAlignments_1.16.0
[8] SummarizedExperiment_1.10.0
[9] DelayedArray_0.6.0
[10] matrixStats_0.53.1
[11] Biobase_2.40.0
[12] Rsamtools_1.32.0
[13] Biostrings_2.48.0
[14] XVector_0.20.0
[15] BiocParallel_1.14.0
[16] GenomicRanges_1.32.0
[17] GenomeInfoDb_1.16.0
[18] IRanges_2.14.0
[19] S4Vectors_0.18.0
[20] BiocGenerics_0.26.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.16      compiler_3.5.0      RColorBrewer_1.1-2
[4] prettyunits_1.0.2 bitops_1.0-6        tools_3.5.0
[7] zlibbioc_1.26.0   progress_1.1.2      biomaRt_2.36.0
[10] digest_0.6.15     bit_1.1-12          RSQLite_2.1.0
[13] memoise_1.1.0     pkgconfig_2.0.1     Matrix_1.2-14
[16] DBI_0.8            GenomeInfoDbData_1.1.0 rtracklayer_1.40.0
[19] httr_1.3.1        stringr_1.3.0       hwriter_1.3.2
[22] bit64_0.9-7       grid_3.5.0          R6_2.2.2
[25] XML_3.98-1.11     latticeExtra_0.6-28 magrittr_1.5
[28] blob_1.1.1        assertthat_0.2.0    stringi_1.1.7
[31] RCurl_1.95-4.10
```