

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 <- seqapply(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 of length 2

\$ctcf

GRanges with 450096 ranges and 0 elementMetadata values

	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]	+	
[6]	chr10	[3012969, 3012992]	+	
[7]	chr10	[3012978, 3013001]	+	
[8]	chr10	[3013071, 3013094]	+	
[9]	chr10	[3018464, 3018487]	+	
...
[450088]	chr12	[121220518, 121220541]	-	
[450089]	chr12	[121222581, 121222604]	-	
[450090]	chr12	[121235756, 121235779]	-	
[450091]	chr12	[121236634, 121236657]	-	
[450092]	chr12	[121239376, 121239399]	-	
[450093]	chr12	[121245849, 121245872]	-	
[450094]	chr12	[121245895, 121245918]	-	
[450095]	chr12	[121246344, 121246367]	-	
[450096]	chr12	[121253499, 121253522]	-	
...				

<1 more element>

seqlengths

chr10	chr11	chr12
NA	NA	NA

`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 with 450096 ranges and 0 elementMetadata values

	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]	+	
[6]	chr10	[3012969, 3012992]	+	
[7]	chr10	[3012978, 3013001]	+	
[8]	chr10	[3013071, 3013094]	+	

[9]	chr10	[3018464, 3018487]	+	
...
[450088]	chr12	[121220518, 121220541]	-	
[450089]	chr12	[121222581, 121222604]	-	
[450090]	chr12	[121235756, 121235779]	-	
[450091]	chr12	[121236634, 121236657]	-	
[450092]	chr12	[121239376, 121239399]	-	
[450093]	chr12	[121245849, 121245872]	-	
[450094]	chr12	[121245895, 121245918]	-	
[450095]	chr12	[121246344, 121246367]	-	
[450096]	chr12	[121253499, 121253522]	-	

```
seqlengths
chr10 chr11 chr12
NA     NA     NA
```

The mouse genome

The data we have refer to alignments to a genome, and only makes sense in that context. Bioconductor has genome packages containing the full sequences of several genomes. The one relevant for us is

```
> library(BSgenome.Mmusculus.UCSC.mm9)
> seqlevels(cstest) <- seqlevels(Mmusculus)
> seqlengths(cstest) <- seqlengths(Mmusculus)
```

We will only make use of the chromosome lengths, but the actual sequence will be needed for motif finding, etc.

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)
> fraglen[!is.na(fraglen)]

chr10 chr11 chr12
179.6794 172.4884 181.6732
```

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 with 450096 ranges and 0 elementMetadata values

	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]	+	
[6]	chr10	[3012969, 3013168]	+	
[7]	chr10	[3012978, 3013177]	+	
[8]	chr10	[3013071, 3013270]	+	
[9]	chr10	[3018464, 3018663]	+	
...
[450088]	chr12	[121220342, 121220541]	-	
[450089]	chr12	[121222405, 121222604]	-	
[450090]	chr12	[121235580, 121235779]	-	
[450091]	chr12	[121236458, 121236657]	-	
[450092]	chr12	[121239200, 121239399]	-	
[450093]	chr12	[121245673, 121245872]	-	
[450094]	chr12	[121245719, 121245918]	-	
[450095]	chr12	[121246168, 121246367]	-	
[450096]	chr12	[121253323, 121253522]	-	

seqlengths

chr1	chr2	chr3 ... chrY_random	chrUn_random
197195432	181748087	159599783 ... 58682461	5900358

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
```

SimpleRleList 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
```

```
SimpleRleViewsList 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)
```

```
SimpleIntegerList 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)
```

```
SimpleIntegerList 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 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. A function that is useful for this purpose is `seqapply`, which applies a function to a *Sequence* and returns the result as another *Sequence*, if possible. In this case, our input *Sequence* is *GRangesList*, and our expected output is a *DataFrameList*. 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.

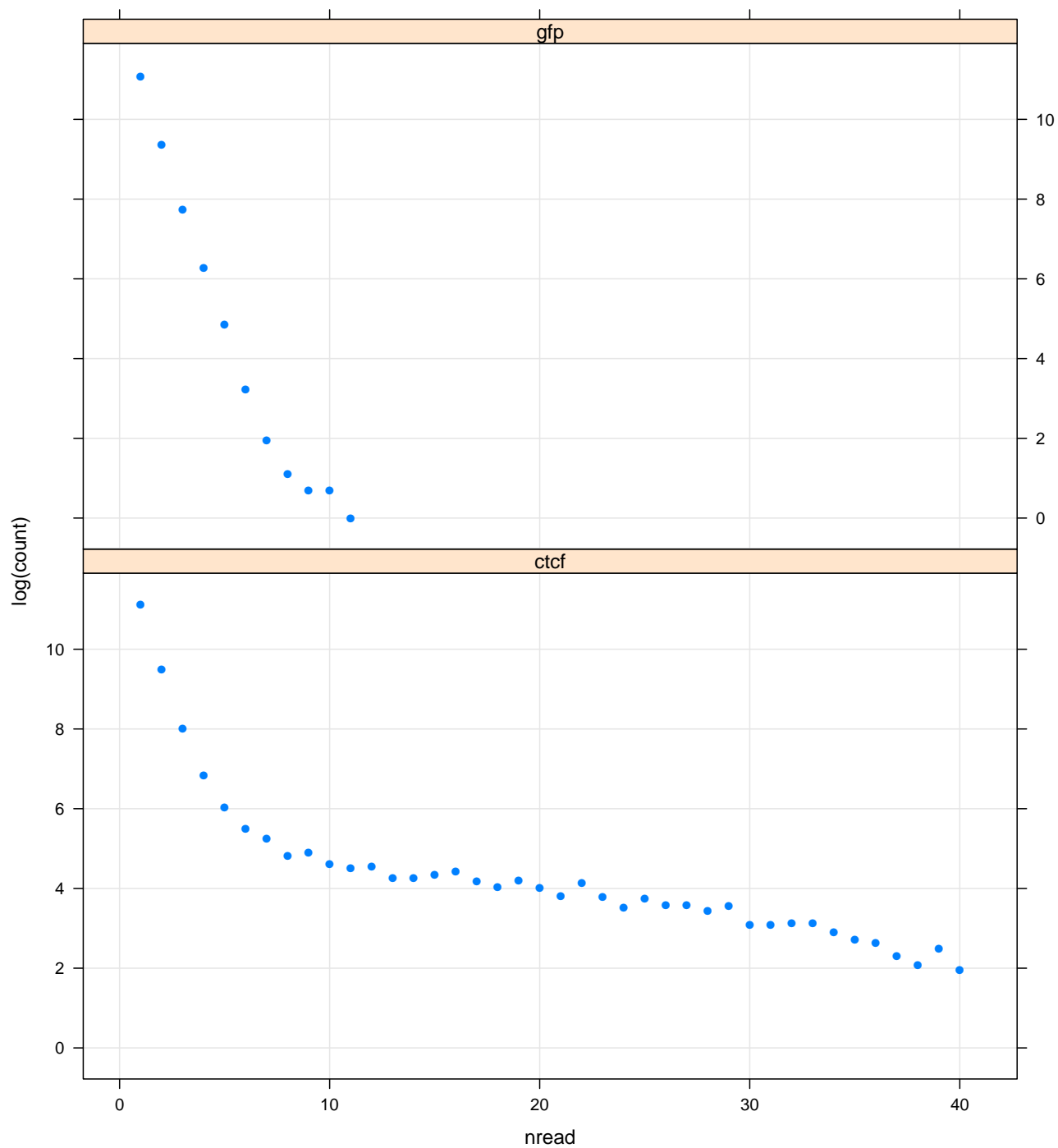
```
> nread.islands <- seqapply(cstest, islandReadSummary)
> nread.islands <- stack(nread.islands, "sample")
> nread.islands
```

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
6	ctcf	chr6	1	0
7	ctcf	chr7	1	0

8	ctcf	chr8	1	0
9	ctcf	chr9	1	0
...
4017	gfp	chr7_random	34	0
4018	gfp	chr8_random	34	0
4019	gfp	chr9_random	34	0
4020	gfp	chr13_random	34	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"))
```

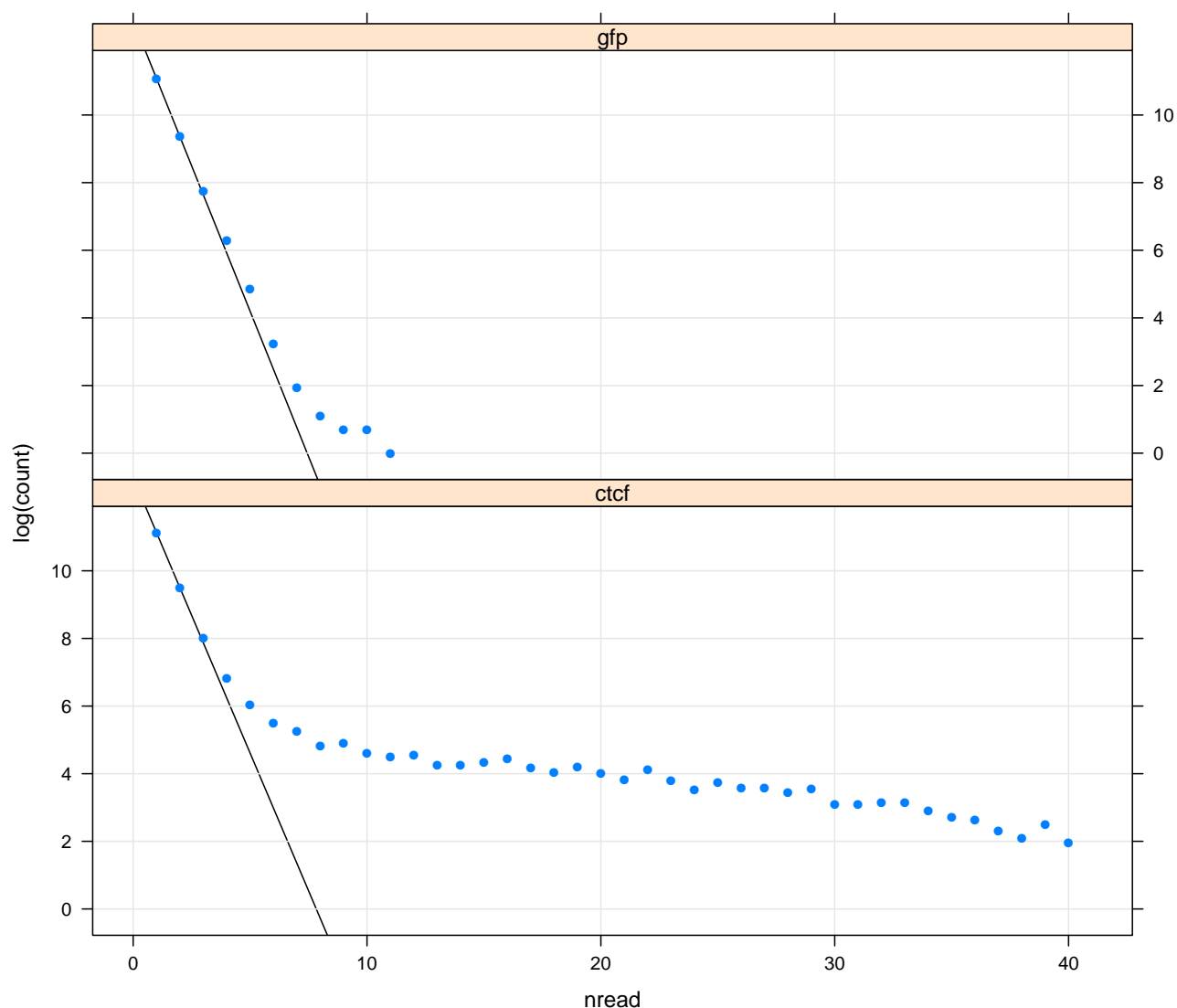


If reads were sampled randomly from the genome, then the null distribution number of reads per island would have a geometric distribution; that is,

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

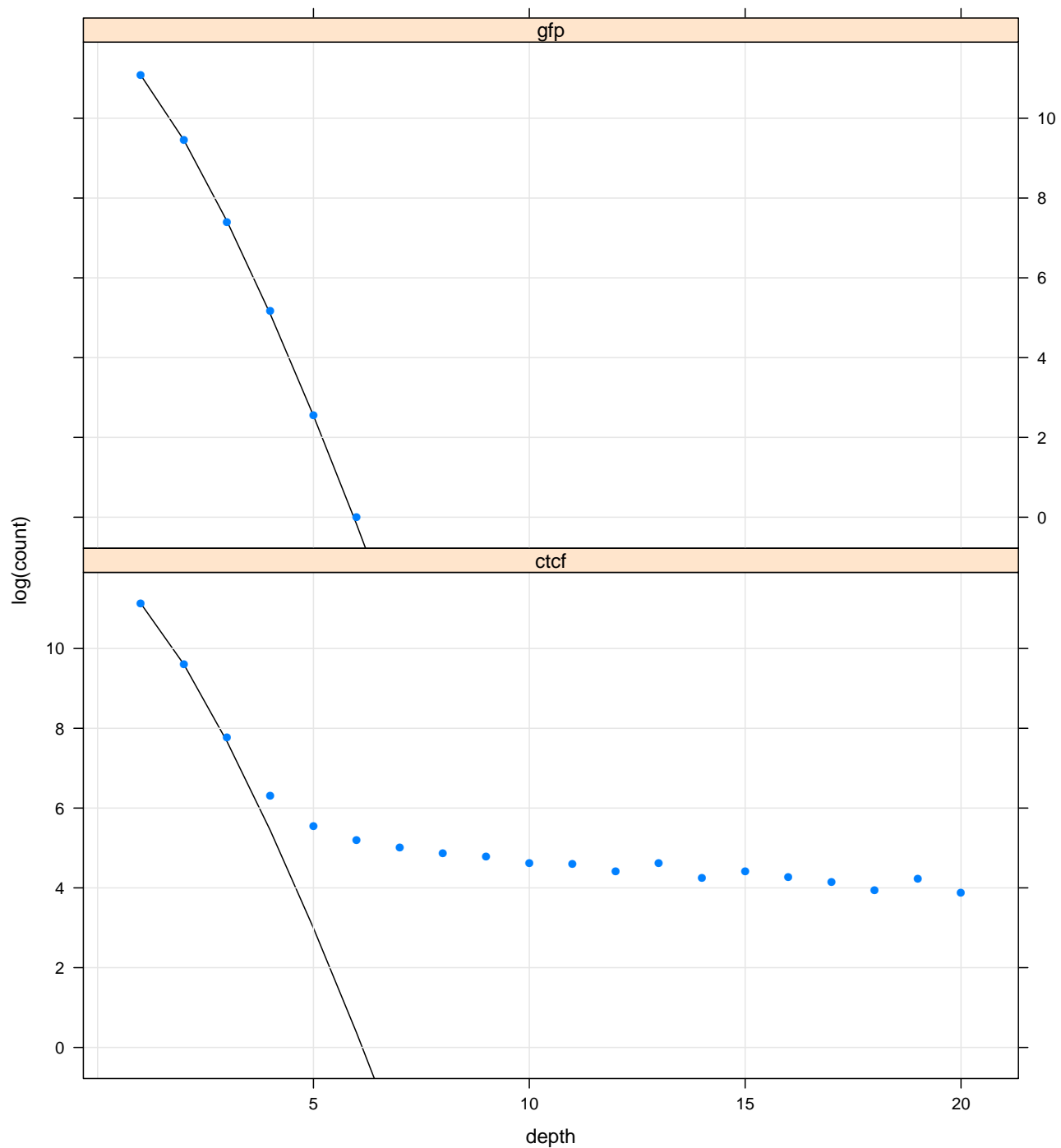
In other words, $\log P(X = k)$ is linear in k . Although our samples are not random, the islands with just one or two reads may be representative of the null distribution.

```
> 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 <- seqapply(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
```

```
SimpleRleViewsList 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, peaks.ctcf)
```

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

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

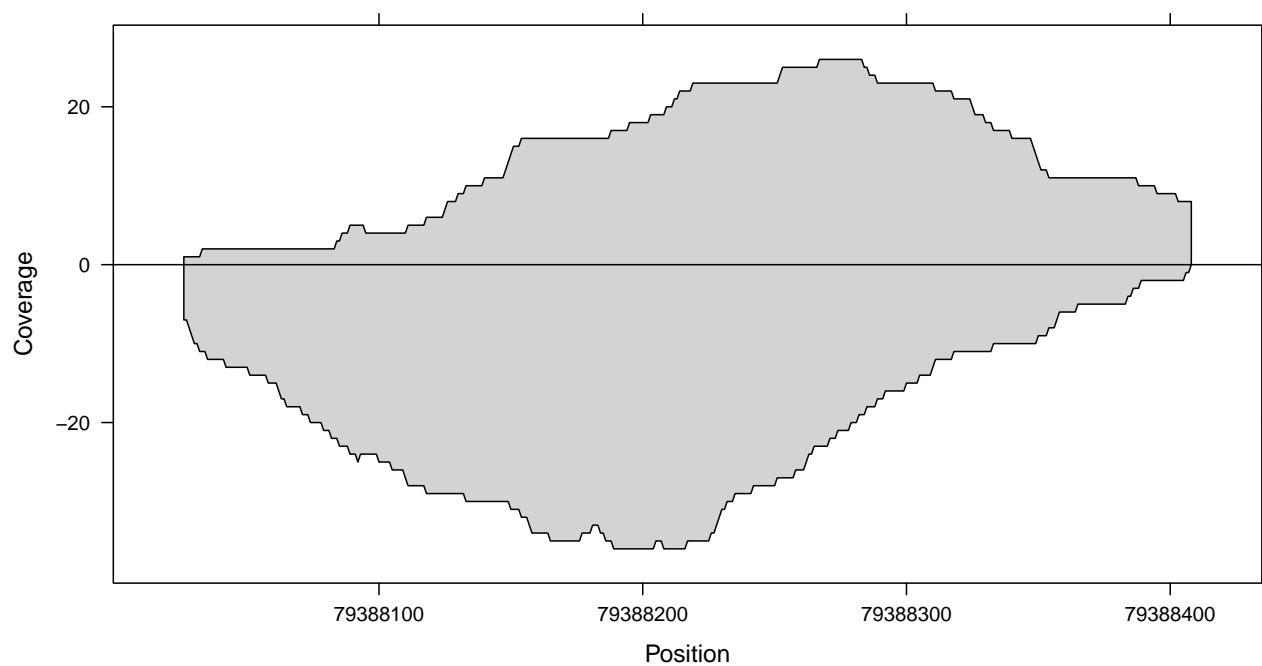
```
> wpeaks
```

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

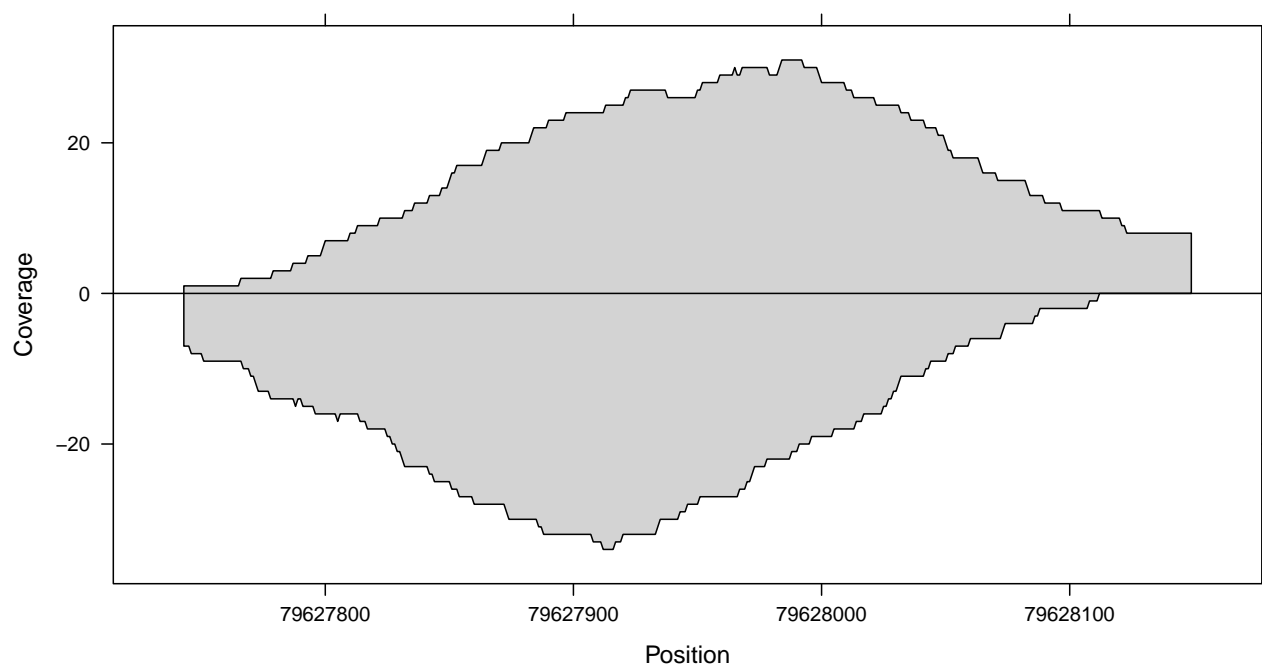
```
>
```

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

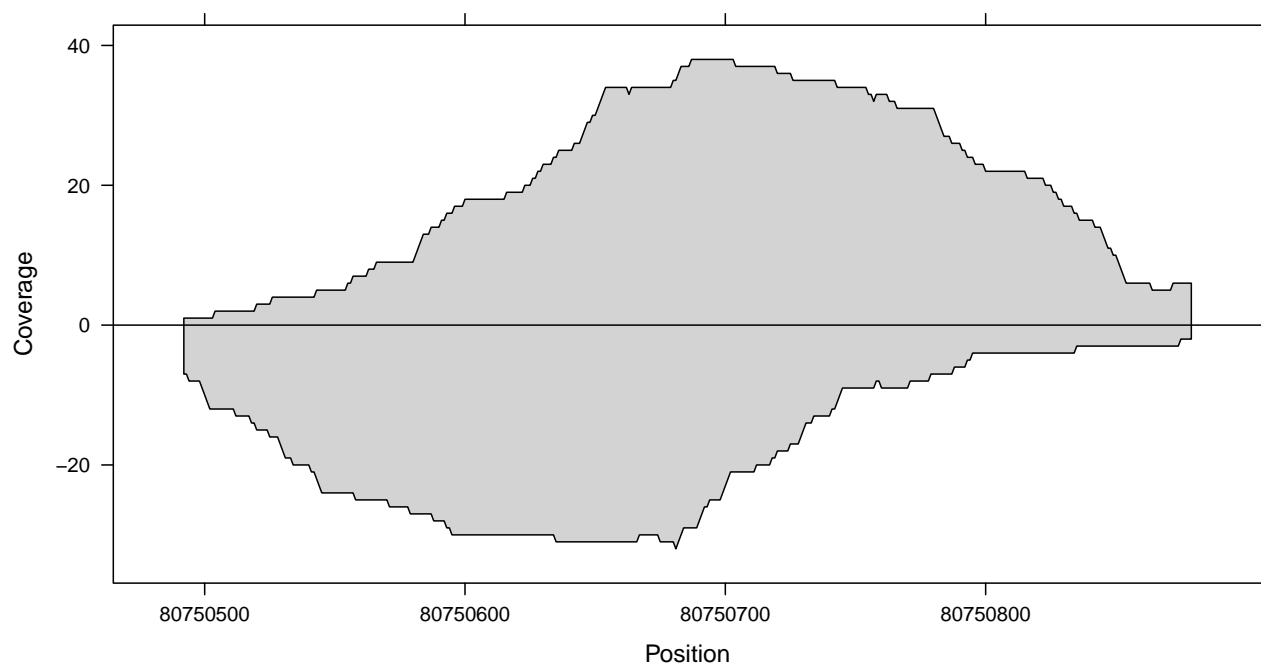

```
> coverageplot(peaks.pos$chr10[wpeaks[1]], peaks.neg$chr10[wpeaks[1]])
```



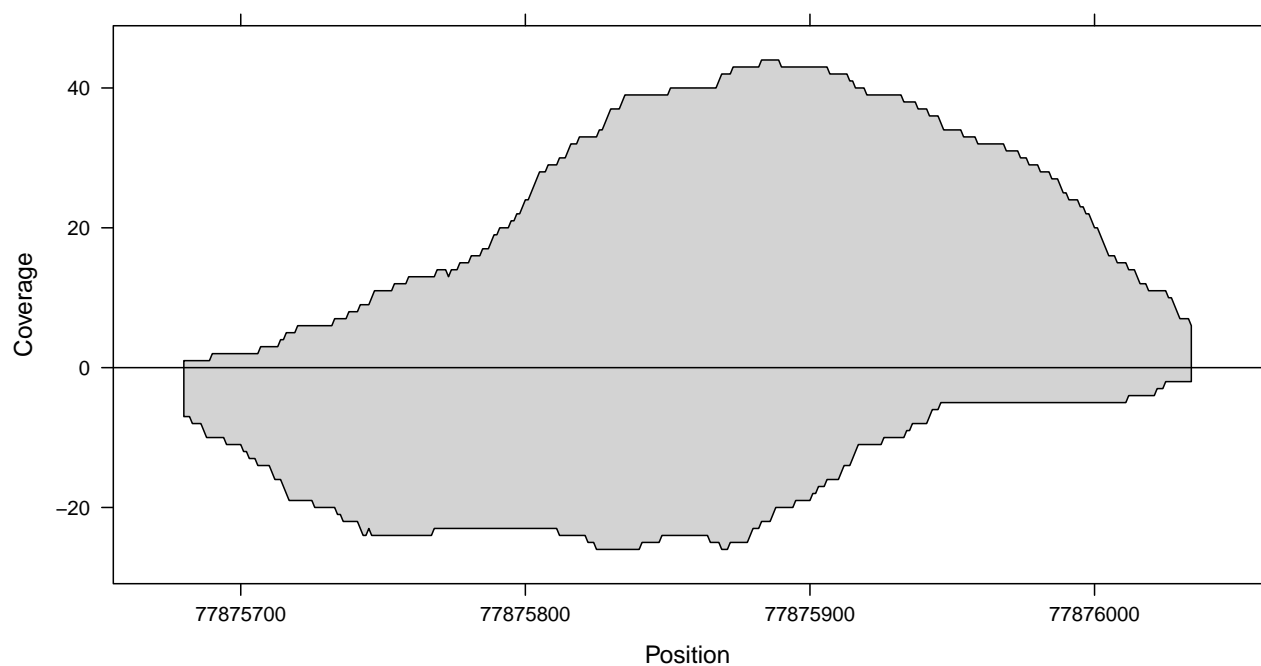
```
> coverageplot(peaks.pos$chr10[wpeaks[2]], peaks.neg$chr10[wpeaks[2]])
```



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



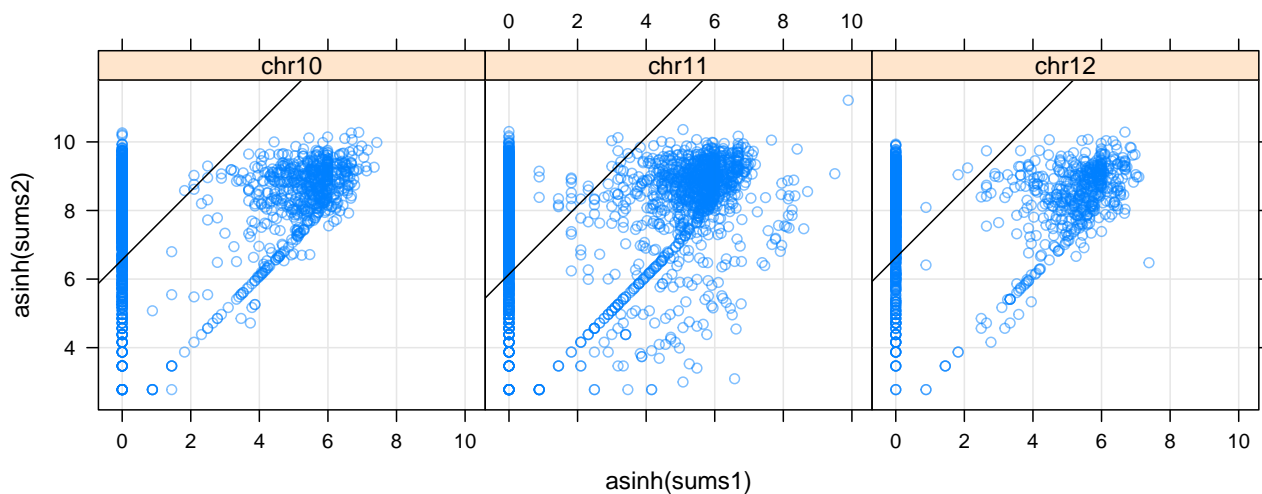
```
> coverageplot(peaks.pos$chr10[wpeaks[4]], peaks.neg$chr10[wpeaks[4]])
```



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. Below, we 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).

```
> db <- makeTranscriptDbFromUCSC("mm9")
> gregions <- transcripts(db)
> gregions
```

GRanges with 49409 ranges and 2 elementMetadata values

	seqnames	ranges	strand	tx_id	tx_name
	<Rle>	<IRanges>	<Rle>	<integer>	<character>
[1]	chr1	[4797974, 4832908]	+	14	uc007afg.1
[2]	chr1	[4797974, 4836816]	+	15	uc007afh.1
[3]	chr1	[4847895, 4887985]	+	16	uc007afi.1
[4]	chr1	[4848119, 4880877]	+	17	uc007afj.1
[5]	chr1	[5073254, 5089858]	+	20	uc007afm.1
[6]	chr1	[5073254, 5152630]	+	21	uc007afn.1
[7]	chr1	[5578574, 5592947]	+	22	uc007afo.1
[8]	chr1	[5578574, 5592947]	+	23	uc007afp.1
[9]	chr1	[5586599, 5592947]	+	24	uc007afq.1
...
[49401]	chrY_random	[42903555, 42936135]	-	49280	uc009vhr.1
[49402]	chrY_random	[43008001, 43010364]	-	49281	uc009vhs.1
[49403]	chrY_random	[44315018, 44341235]	-	49285	uc009vhw.1
[49404]	chrY_random	[46075785, 46078095]	-	49288	uc009vhz.1
[49405]	chrY_random	[48319175, 48321522]	-	49293	uc009vie.1
[49406]	chrY_random	[48388361, 48390745]	-	49294	uc009vif.1
[49407]	chrY_random	[50814754, 50817087]	-	49296	uc009vih.1
[49408]	chrY_random	[52063165, 52089373]	-	49298	uc009vij.1
[49409]	chrY_random	[52063165, 52089373]	-	49299	uc009vik.1

seqlengths

chr1	chr2	chr3	...	chrX_random	chrY_random
197195432	181748087	159599783	...	1785075	58682461

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 %in% promoters
> xtabs(~ inPromoter + change, peakSummary)
```

	change	
inPromoter	down	flat
FALSE	21	5182
TRUE	2	601

Or somewhere upstream or in a gene:

```
> peakSummary$inUpstream <- peakSummary %in% flank(gregions, 20000)
> peakSummary$inGene <- peakSummary %in% 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 2.13.0 (2011-04-13)
Platform: i386-pc-mingw32/i386 (32-bit)
```

locale:

```
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.1252
[3] LC_MONETARY=English_United States.1252
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.1252
```

attached base packages:

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

other attached packages:

```
[1] BSgenome.Mmusculus.UCSC.mm9_1.3.17 GenomicFeatures_1.4.0
[3] chipseq_1.2.0                      ShortRead_1.10.0
[5] Rsamtools_1.4.0                    lattice_0.19-23
[7] BSgenome_1.20.0                    Biostrings_2.20.0
[9] GenomicRanges_1.4.0                IRanges_1.10.0
```

loaded via a namespace (and not attached):

```
[1] Biobase_2.12.0    DBI_0.2-5          RCurl_1.5-0.1      RSQLite_0.9-4
[5] XML_3.2-0.2       biomaRt_2.8.0      grid_2.13.0        hwriter_1.3
[9] rtracklayer_1.12.0 tools_2.13.0
```