

# Some Basic Analysis of ChIP-Seq Data

January 23, 2009

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` package for visualization.

```
> library(chipseq)
> library(GenomicFeatures.Mmusculus.UCSC.mm9)
> 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 `readReads` function, which in turn uses the `readAligned` function in the `ShortRead`. This step removed all duplicate reads and applied a quality score cutoff. The remaining data were reduced to a set of alignment start positions (including orientation).

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

```
GenomeDataList of length 2
names(2): ctfp gfp
```

`cstest` is an object of class “*GenomeDataList*”, and has a list-like structure, each component representing data from one lane.

```
> cstest$ctcf
```

```
A GenomeData instance for Mmusculus
chromosomes(3): chr10 chr11 chr12
```

Each of these are themselves lists containing positive and negative strand alignments:

```
> str(cstest$ctcf$chr10)
```

```
List of 2
```

```
$ -: int [1:72371] 3012999 3013096 3013098 3013135 3032735 3040511 3040520 3041297 3044041 304504
$ +: int [1:73179] 3012936 3012941 3012944 3012955 3012963 3012969 3012978 3013071 3018464 302076
```

The aligned position of the first cycle is stored.

## 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)
> mouse.chromlens <- seqlengths(Mmusculus)
> head(mouse.chromlens)

      chr1      chr2      chr3      chr4      chr5      chr6
197195432 181748087 159599783 155630120 152537259 149517037
```

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.

We extend all reads to be 200 bases long. This is done using the `extendReads()` function, which can work on data from one chromosome in one lane.

```
> ext <- extendReads(cstest$ctcf$chr10, seqLen = 200)
> head(ext)
```

```
IRanges of length 6
      start      end width
[1] 3012936 3013135   200
[2] 3012941 3013140   200
[3] 3012944 3013143   200
[4] 3012955 3013154   200
[5] 3012963 3013162   200
[6] 3012969 3013168   200
```

The result is essentially a collection of intervals (ranges) over the reference genome.

## 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 <- coverage(ext, width = mouse.chromlens["chr10"])
> cov
```

```
'integer' Rle of length 129993255 with 288928 runs
Lengths:  3012799 97 2 37 5 3 11 8 6 9 ...
Values  :  0 1 2 3 5 6 7 8 9 10 ...
```

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, lower = 1)
> islands
```

Views on a 129993255-length Rle subject

views:

	start	end	width	
[1]	3012800	3013270	471	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[2]	3018464	3018663	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[3]	3020766	3020965	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[4]	3023019	3023218	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[5]	3023240	3023439	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[6]	3032536	3032735	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[7]	3038377	3038576	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[8]	3040312	3040554	243	[1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 ...]
[9]	3041098	3041297	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
...	...	...	...	...
[87957]	129973175	129973447	273	[1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 ...]
[87958]	129974813	129975012	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[87959]	129975575	129975774	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[87960]	129978669	129978868	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[87961]	129979209	129979571	363	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[87962]	129980253	129980452	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[87963]	129981957	129982156	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[87964]	129982330	129982529	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[87965]	129987020	129987219	200	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]

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

```
> viewSums(head(islands))
```

```
[1] 2400 200 200 200 200 200
```

```
> viewMaxs(head(islands))
```

```
[1] 11 1 1 1 1 1
```

```
> nread.tab <- table(viewSums(islands) / 200)
```

```
> depth.tab <- table(viewMaxs(islands))
```

```
> head(nread.tab, 10)
```

1	2	3	4	5	6	7	8	9	10
68111	13350	3022	925	415	247	191	122	132	100

```
> head(depth.tab, 10)
```

1	2	3	4	5	6	7	8	9	10
68159	14745	2388	547	256	180	150	129	120	102

## Processing multiple lanes

Although data from one chromosome within one lane is often the natural unit to work with, we typically want to apply any procedure to all chromosomes in all lanes. A function that is useful for this purpose is `gdapply`, which recursively applies a summary function to a full dataset. If the summary function produces a data frame, the result can be coerced into a flat data frame that is often easier to work with. Here is a simple summary function that computes the frequency distribution of the number of reads.

```
> islandReadSummary <- function(x)
+ {
+   g <- extendReads(x, seqLen = 200)
+   s <- slice(coverage(g), lower = 1)
+   tab <- table(viewSums(s) / 200)
+   ans <- data.frame(nread = as.numeric(names(tab)), count = as.numeric(tab))
+   ans
+ }
```

Applying it to our test-case, we get

```
> head(islandReadSummary(cstest$ctcf$chr10))
```

	nread	count
1	1	68111
2	2	13350
3	3	3022
4	4	925
5	5	415
6	6	247

We can now use it to summarize the full dataset.

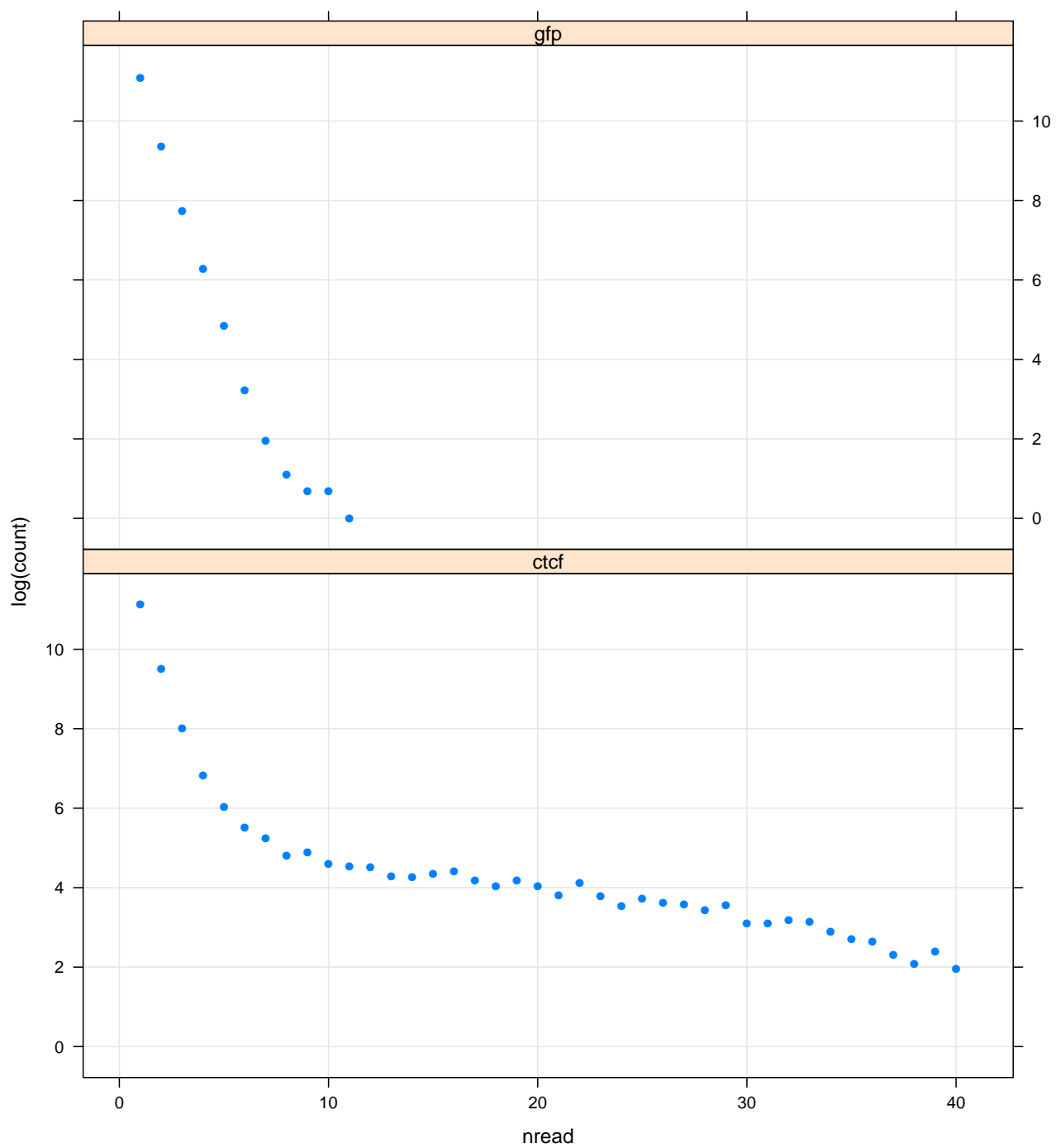
```
> nread.islands <- gdapply(cstest, islandReadSummary)
> nread.islands <- as(nread.islands, "data.frame")
> head(nread.islands)
```

	nread	count	chromosome	sample
1	1	68111	chr10	ctcf
2	2	13350	chr10	ctcf
3	3	3022	chr10	ctcf
4	4	925	chr10	ctcf
5	5	415	chr10	ctcf
6	6	247	chr10	ctcf

```

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

```

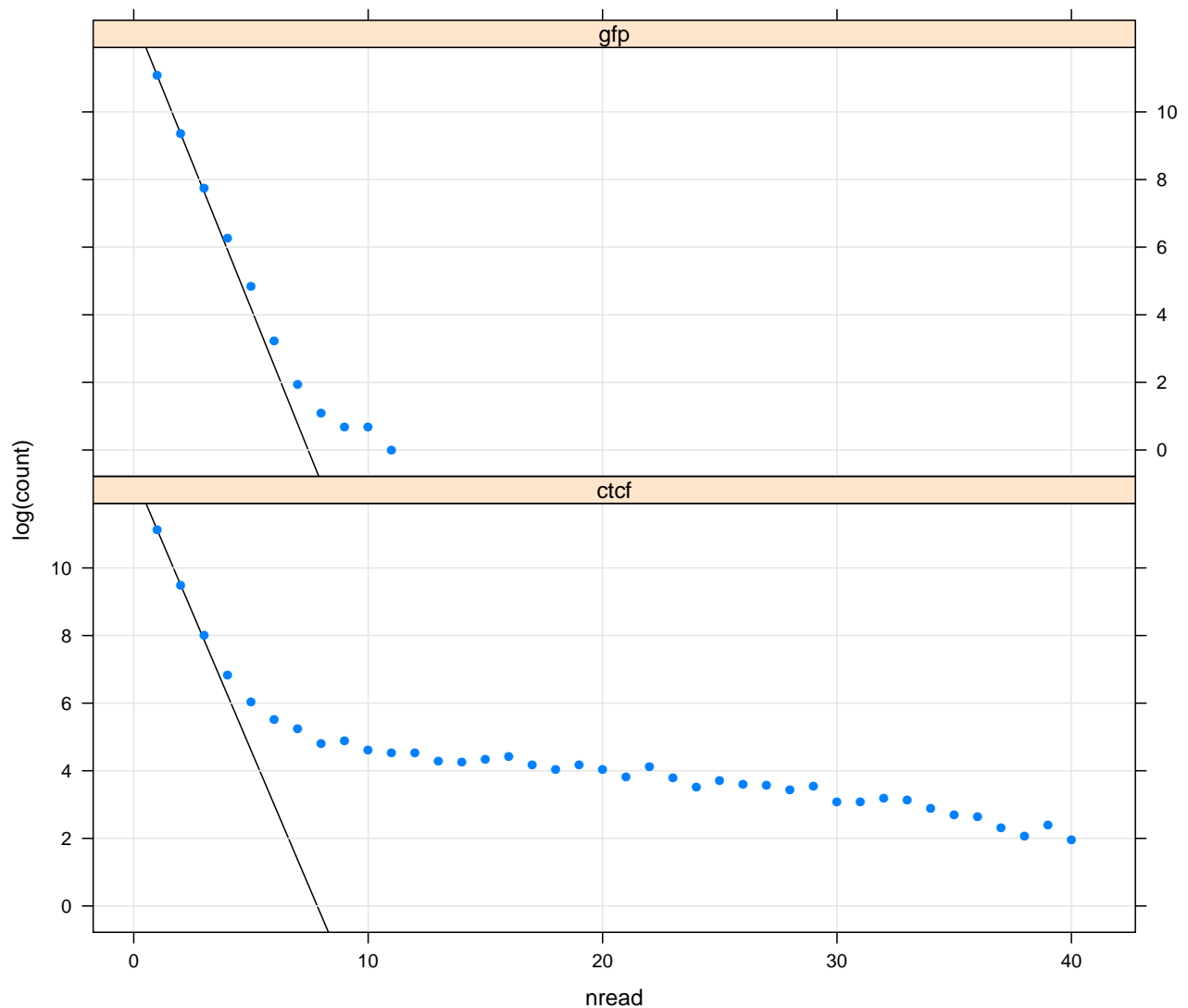


If reads were sampled randomly from the genome, then the null distribution number of reads per island would have a geometric distribution; that is,

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

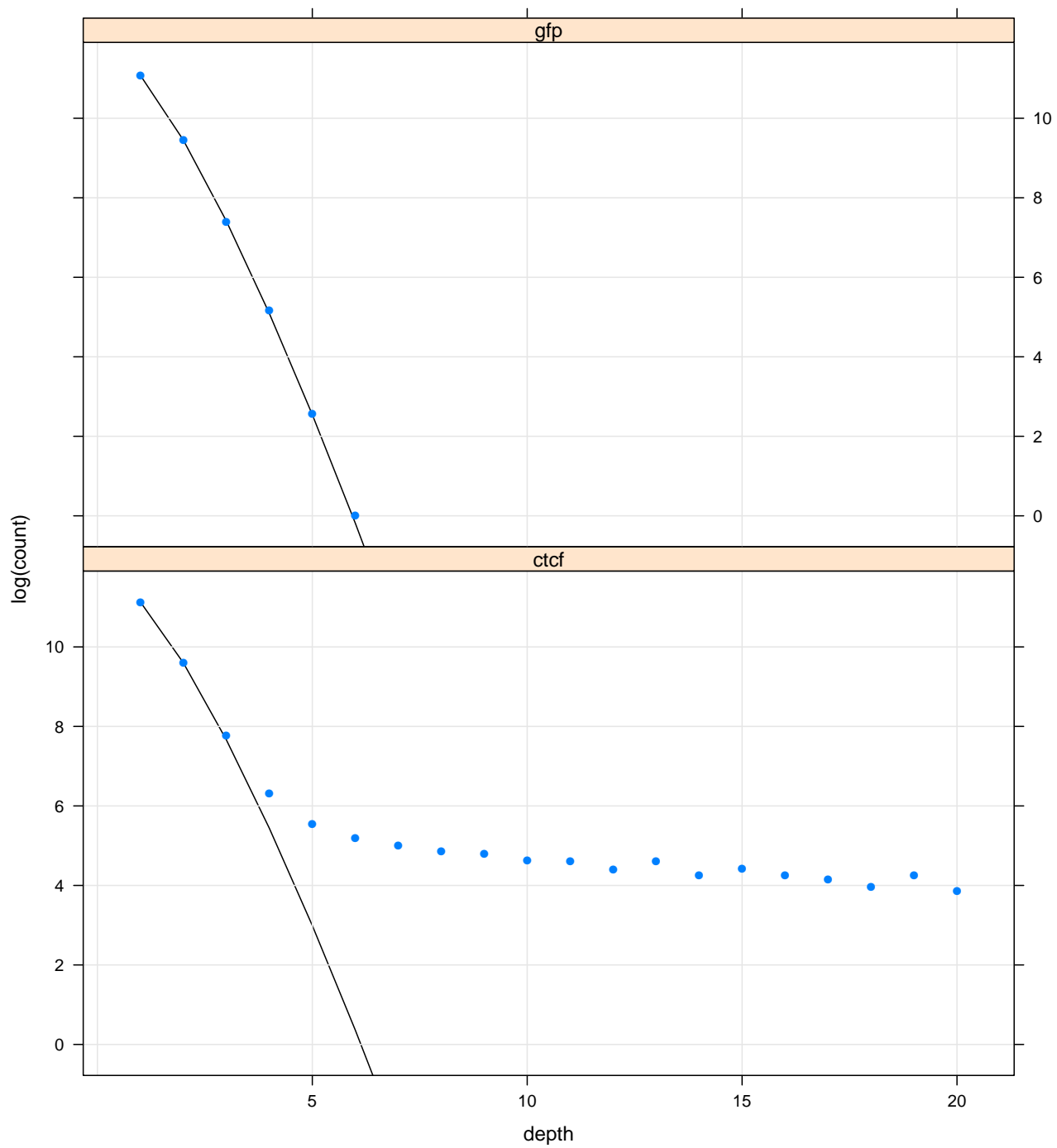
In other words,  $\log P(X = k)$  is linear in  $k$ . Although our samples are not random, the islands with just one or two reads may be representative of the null distribution.

```
> xyplot(log(count) ~ nread | sample, 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 <- extendReads(x, seqLen = 200)
+   s <- slice(coverage(g), lower = 1)
+   tab <- table(viewMaxs(s))
+   ans <- data.frame(depth = as.numeric(names(tab)), count = as.numeric(tab))
+   ans
+ }
> depth.islands <- gdapply(cstest, islandDepthSummary)
> depth.islands <- as(depth.islands, "data.frame")
> xyplot(log(count) ~ depth | sample, 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, ...)
+   })
```



## Peaks

Going back to our example of chr10 of the first sample, we can define “peaks” to be regions of the genome where coverage is 8 or more.

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

Views on a 129993255-length Rle subject

views:

	start	end	width	
[1]	3012955	3013135	181	[ 8 8 8 8 8 8 8 8 9 9 9 9 9 ...]
[2]	3234799	3234895	97	[ 8 8 8 8 8 8 8 8 8 8 8 8 8 ...]
[3]	3270012	3270297	286	[8 8 8 9 9 9 9 9 8 8 8 8 8 8 8 8 8 ...]
[4]	3277662	3277832	171	[ 8 8 8 8 8 8 8 8 8 8 8 8 8 8 ...]
[5]	3277848	3277859	12	[8 8 8 8 8 8 8 8 8 8 8 8]
[6]	3460857	3460973	117	[ 8 8 8 8 8 8 8 8 8 8 8 8 8 8 ...]
[7]	3617850	3617983	134	[ 8 8 8 8 8 8 8 9 9 9 9 10 10 ...]
[8]	3651712	3651992	281	[ 8 8 9 9 9 10 10 10 10 10 10 10 10 ...]
[9]	4310402	4310712	311	[ 8 8 8 9 9 9 9 9 9 9 9 9 10 10 ...]
...	...	...	...	...
[1747]	128986519	128986595	77	[8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 ...]
[1748]	128986604	128986610	7	[8 8 8 8 8 8 8]
[1749]	128986638	128986673	36	[8 8 8 8 8 8 9 9 9 9 8 8 8 8 9 9 9 8 8 ...]
[1750]	129058889	129058980	92	[8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 ...]
[1751]	129530031	129530201	171	[ 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 ...]
[1752]	129533303	129533381	79	[8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 ...]
[1753]	129665351	129665586	236	[ 8 9 9 9 9 9 9 9 9 10 10 10 10 ...]
[1754]	129666784	129666947	164	[8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 ...]
[1755]	129750671	129750849	179	[ 8 8 8 8 8 8 9 9 9 9 9 9 9 9 ...]

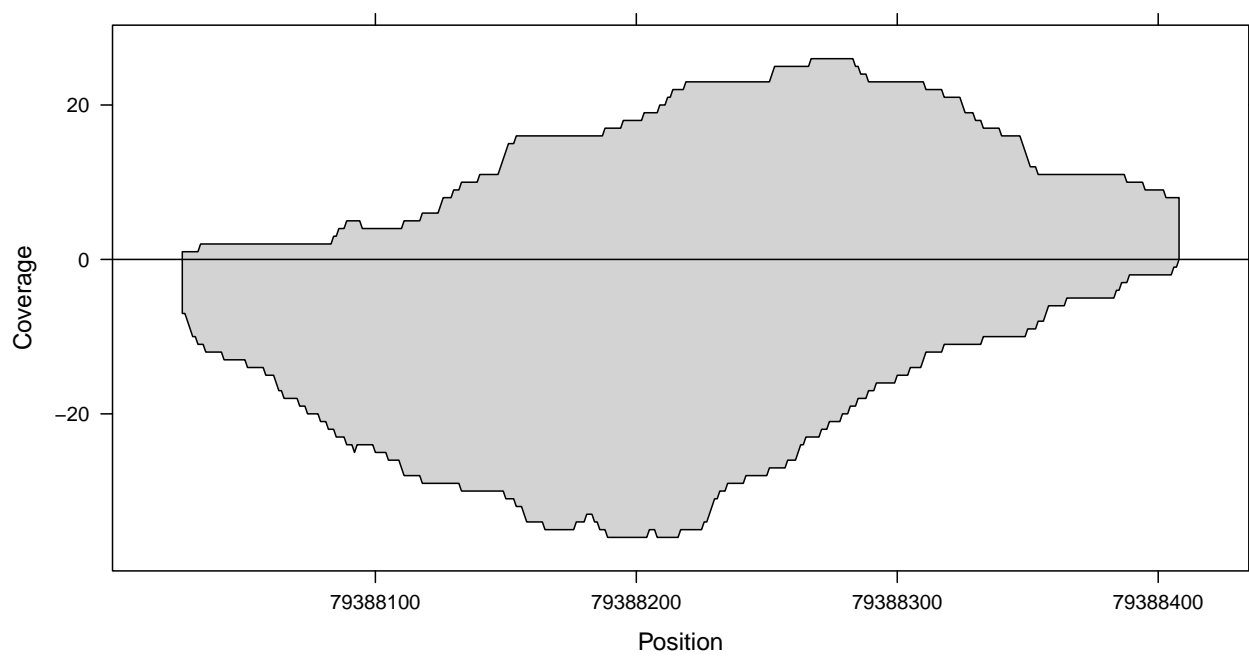
It is meaningful to ask about the contribution of each strand to each peak, as the sequenced region of pull-down fragments would be on opposite sides of a binding site depending on which strand it matched. We can compute strand-specific coverage, and look at the individual coverages under the combined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

```
> peak.depths <- viewMaxs(peaks)
> cov.pos <- coverage(extendReads(cstest$ctcf$chr10, strand = "+", seqLen = 200),
+                       width = mouse.chromlens["chr10"])
> cov.neg <- coverage(extendReads(cstest$ctcf$chr10, strand = "-", seqLen = 200),
+                       width = mouse.chromlens["chr10"])
> peaks.pos <- copyIRanges(peaks, cov.pos)
> peaks.neg <- copyIRanges(peaks, cov.neg)
> wpeaks <- tail(order(peak.depths), 4)
> wpeaks
```

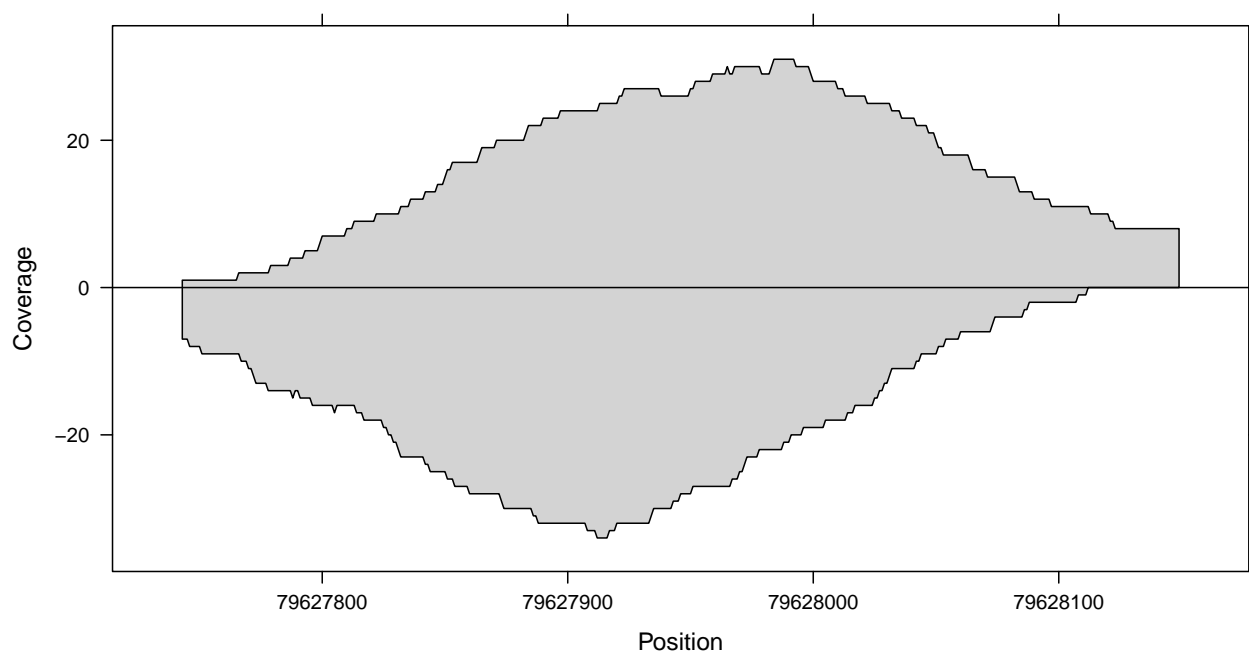
```
[1] 971 989 1079 922
```

We plot four highest peaks below.

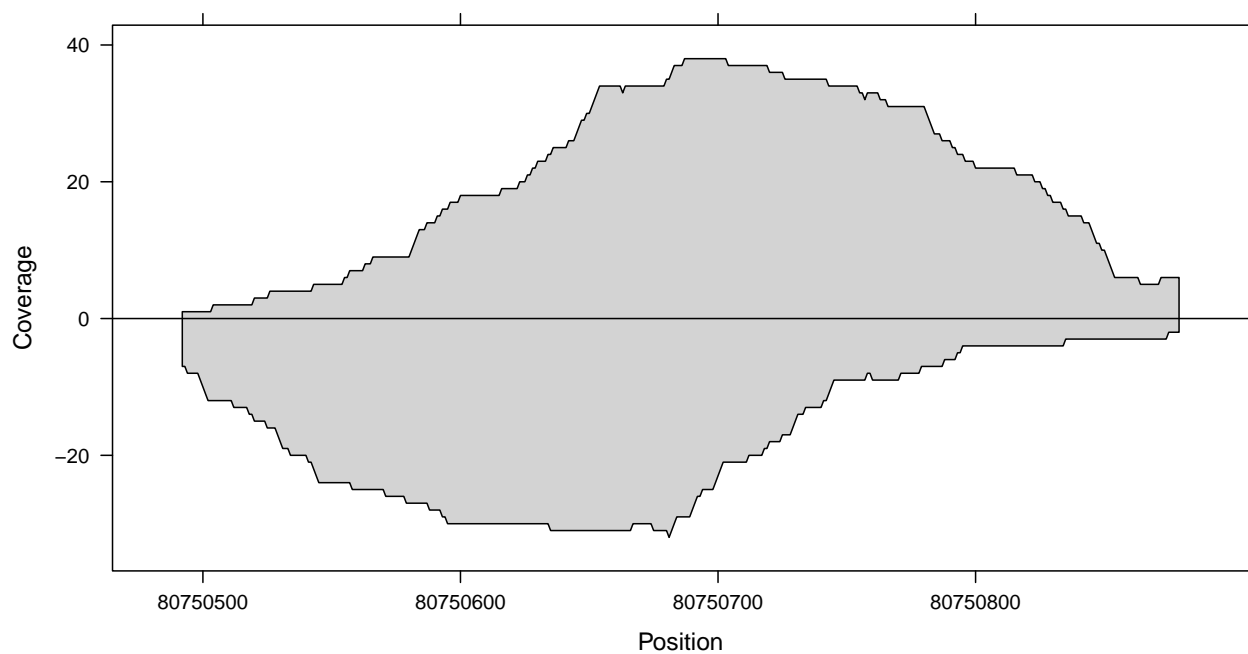
```
> coverageplot(peaks.pos[wpeaks[1]], peaks.neg[wpeaks[1]])
```



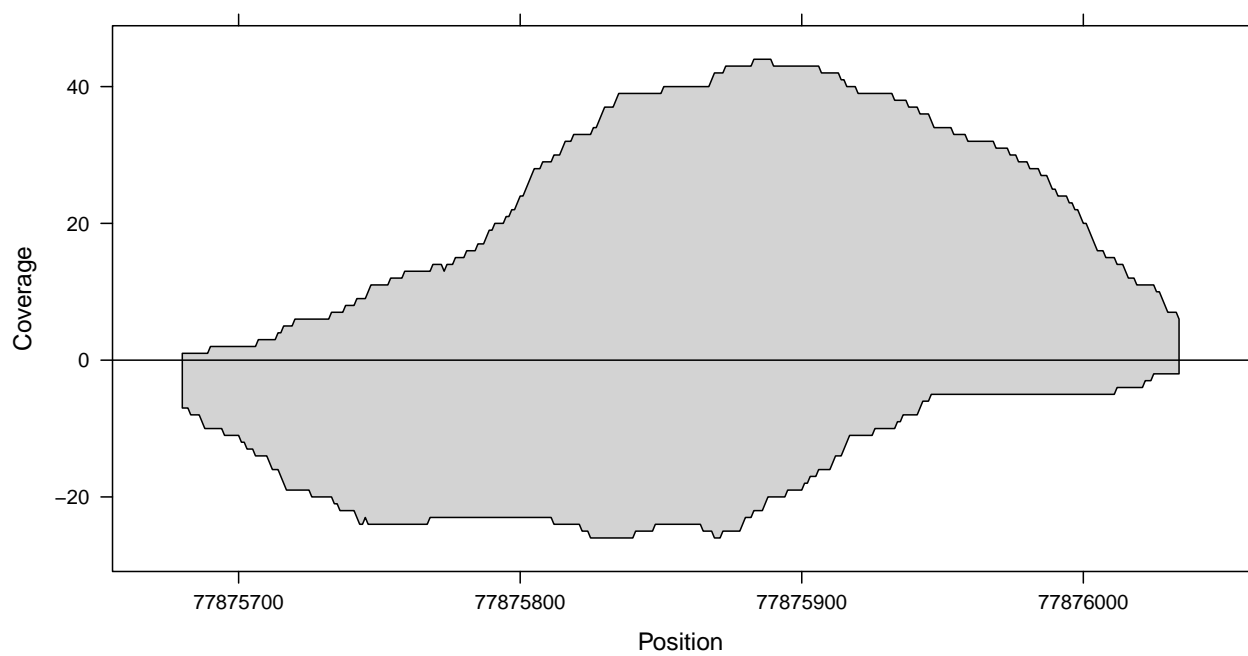
```
> coverageplot(peaks.pos[wpeaks[2]], peaks.neg[wpeaks[2]])
```



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



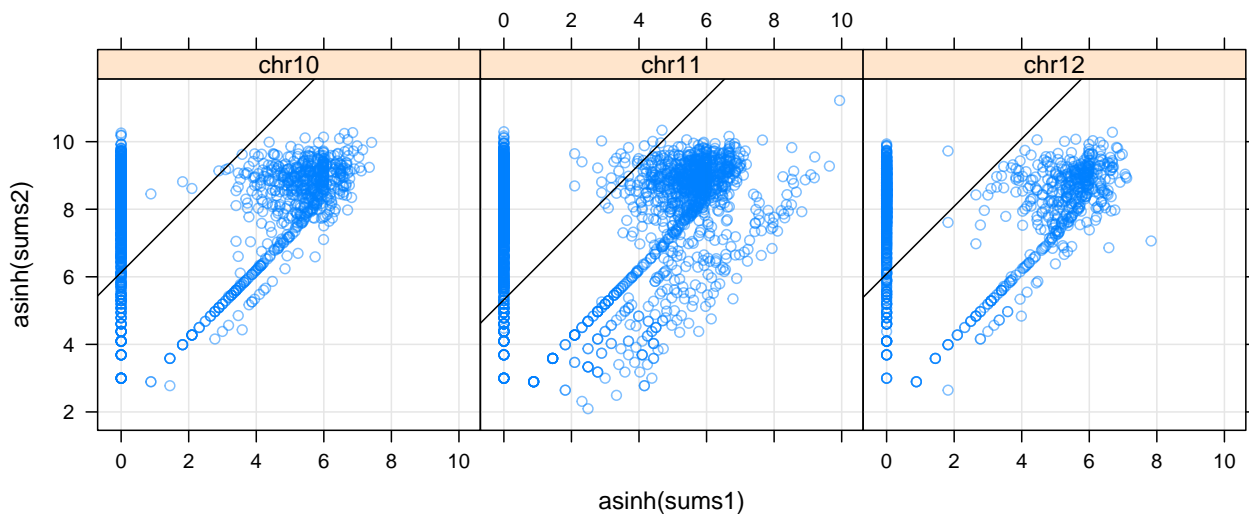
```
> coverageplot(peaks.pos[wpeaks[4]], peaks.neg[wpeaks[4]])
```



## Differential peaks

One common question is: which peaks are different in two samples? One simple strategy is the following: combine data from the two samples, find peaks in the combined data, and compare the contributions of the two samples.

```
> extRanges <- gdapply(cstest, extendReads, seqLen = 200)
> peakSummary <-
+   diffPeakSummary(extRanges$gfp, extRanges$ctcf,
+                   chrom.lens = mouse.chromlens, lower = 10)
> xyplot(asinh(sums2) ~ asinh(sums1) | chromosome,
+        data = peakSummary,
+        ## subset = (chromosome %in% c("chr1", "chr2")),
+        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
+   })
> head(peakSummary)
```

	chromosome	start	end	comb.max	overlap1	overlap2	sums1	sums2	maxs1	maxs2
1	chr10	3012969	3013098	11	0	12	0	1348	0	11
2	chr10	3234832	3234882	10	0	10	0	510	0	10
3	chr10	3270059	3270295	20	1	23	158	3614	1	19
4	chr10	3277695	3277775	13	0	13	0	924	0	13
5	chr10	3460894	3460924	10	0	10	0	310	0	10
6	chr10	3617861	3617909	10	0	10	0	490	0	10

	down	up	resids	diffs
1	FALSE	FALSE	0.5247940	7.899525
2	FALSE	FALSE	0.2834625	6.927559
3	FALSE	FALSE	-0.6594503	3.129965
4	FALSE	FALSE	0.4310227	7.521860
5	FALSE	FALSE	0.1598535	6.429722
6	FALSE	FALSE	0.2735295	6.887554

## 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 `geneMouse` function defined in the `GenomicFeatures.Mmusculus.UCSC.mm9` package returns gene location information from UCSC. The `genomic_regions` function converts this into a set of ranges defining promoters, upstream regions, etc.

```
> gregions <- transcripts(genes = geneMouse(), proximal = 2000)
> ## gregions$gene <- as.character(gregions$gene)
> gregions
```

RangedData with 43856 rows and 5 value columns across 33 spaces

	space	ranges	gene	promoter
	<character>	<IRanges>	<character>	<IRanges>
1	chr1	[3195985, 3205713]	uc007aet.1	[3203714, 3207713]
2	chr1	[3204563, 3661579]	uc007aeu.1	[3659580, 3663579]
3	chr1	[3638392, 3648985]	uc007aev.1	[3646986, 3650985]
4	chr1	[4280927, 4399322]	uc007aew.1	[4397323, 4401322]
5	chr1	[4334224, 4350473]	uc007aex.1	[4348474, 4352473]
6	chr1	[4481009, 4483816]	uc007aey.1	[4481817, 4485816]
7	chr1	[4481009, 4486494]	uc007aez.1	[4484495, 4488494]
8	chr1	[4764015, 4775768]	uc007afd.1	[4773769, 4777768]
9	chr1	[4766458, 4775768]	uc007aff.1	[4773769, 4777768]
10	chr1	[4797974, 4832908]	uc007afg.1	[4795974, 4799973]

	threeprime	upstream	downstream
	<IRanges>	<IRanges>	<IRanges>
1	[3193985, 3197984]	[3207714, 3215713]	[3185985, 3193984]
2	[3202563, 3206562]	[3663580, 3671579]	[3194563, 3202562]
3	[3636392, 3640391]	[3650986, 3658985]	[3628392, 3636391]
4	[4278927, 4282926]	[4401323, 4409322]	[4270927, 4278926]
5	[4332224, 4336223]	[4352474, 4360473]	[4324224, 4332223]
6	[4479009, 4483008]	[4485817, 4493816]	[4471009, 4479008]

```

7 [4479009, 4483008] [4488495, 4496494] [4471009, 4479008]
8 [4762015, 4766014] [4777769, 4785768] [4754015, 4762014]
9 [4764458, 4768457] [4777769, 4785768] [4756458, 4764457]
10 [4830909, 4834908] [4787974, 4795973] [4834909, 4842908]
...
<43846 more rows>

```

This can be used to obtain a tabulation of the peaks.

```

> ans <- contextDistribution(peakSummary, gregions)
> head(ans)

```

	type	total	gene	promoter	threeprime	upstream	downstream	chromosome
1	all	1544	746	233	182	294	313	chr10
2	up	0	0	0	0	0	0	chr10
3	down	0	0	0	0	0	0	chr10
4	all	2499	1367	428	387	629	740	chr11
5	up	0	0	0	0	0	0	chr11
6	down	0	0	0	0	0	0	chr11

```

> sumtab <-
+   as.data.frame(rbind(total = xtabs(total ~ type, ans),
+   promoter = xtabs(promoter ~ type, ans),
+   threeprime = xtabs(threeprime ~ type, ans),
+   upstream = xtabs(upstream ~ type, ans),
+   downstream = xtabs(downstream ~ type, ans),
+   gene = xtabs(gene ~ type, ans)))
> cbind(sumtab, ratio = round(sumtab[, "down"] / sumtab[, "up"], 3))

```

	all	up	down	ratio
total	5180	0	0	NaN
promoter	801	0	0	NaN
threeprime	655	0	0	NaN
upstream	1080	0	0	NaN
downstream	1242	0	0	NaN
gene	2652	0	0	NaN

## Version information

```
> sessionInfo()
```

```

R version 2.10.0 Patched (2009-10-27 r50222)
i386-apple-darwin9.8.0

```

```
locale:
```

```
[1] C/en_US.UTF-8/C/C/C/C
```

```
attached base packages:
```

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

[8] base

other attached packages:

- [1] BSgenome.Mmusculus.UCSC.mm9\_1.3.16
- [2] GenomicFeatures.Mmusculus.UCSC.mm9\_0.1.0
- [3] GenomicFeatures\_0.2.0
- [4] rtracklayer\_1.6.0
- [5] RCurl\_1.3-0
- [6] bitops\_1.0-4.1
- [7] chipseq\_0.2.1
- [8] ShortRead\_1.4.0
- [9] lattice\_0.17-26
- [10] BSgenome\_1.14.2
- [11] Biostrings\_2.14.7
- [12] IRanges\_1.4.7

loaded via a namespace (and not attached):

- [1] Biobase\_2.6.0 DBI\_0.2-4      RSQLite\_0.7-3 XML\_2.6-0      grid\_2.10.0
- [6] hwriter\_1.1