## Class 16 Zebrafish TSV

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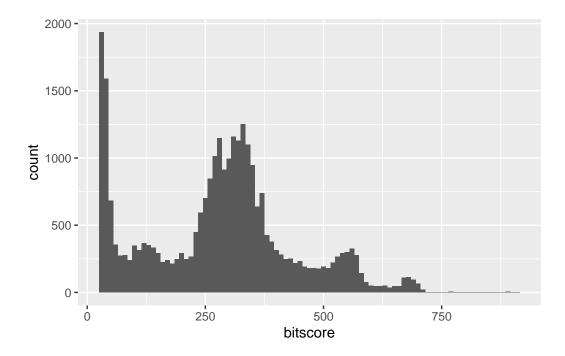
## TSV file

class16/mm-second.x.zebrafish.tsv

```
library(ggplot2)
  library(bio3d)
  df <- read.table(file = 'mm-second.x.zebrafish.tsv', sep = '\t', header = F)</pre>
  colnames(df) <- c("qseqid", "sseqid", "pident", "length", "mismatch", "gapopen", "qstart",
  head(df)
       qseqid
                      sseqid pident length mismatch gapopen qstart qend sstart
1 NP_598866.1 XP_009294521.1 46.154
                                        273
                                                 130
                                                                      267
                                                                             420
2 NP_598866.1 NP_001313634.1 46.154
                                        273
                                                 130
                                                                      267
                                                                             476
3 NP_598866.1 XP_009294513.1 46.154
                                        273
                                                                   4
                                                 130
                                                                      267
                                                                             475
4 NP_598866.1 NP_001186666.1 33.071
                                        127
                                                  76
                                                           5
                                                                      126
                                                                             338
5 NP_598866.1 NP_001003517.1 30.400
                                                                   4
                                        125
                                                  82
                                                           4
                                                                      126
                                                                             344
6 NP_598866.1 NP_001003517.1 30.645
                                         62
                                                  41
                                                           2
                                                                  53 113
                                                                              43
  send
         evalue bitscore
1 684 1.70e-63
                   214.0
2 740 4.51e-63
                   214.0
3 739 4.69e-63
                   214.0
4 459 5.19e-12
                    67.8
5 465 2.67e-11
                    65.5
6 103 4.40e-01
                    33.9
```

## Histogram

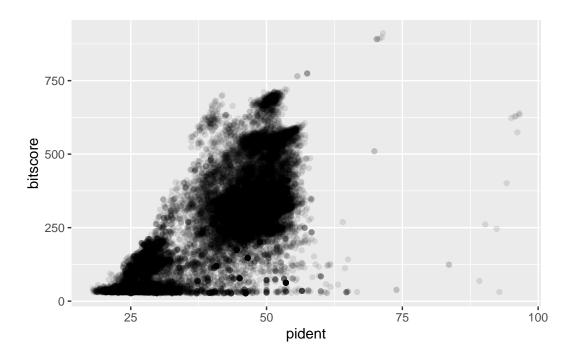
```
ggplot(df, aes(x=bitscore), breaks = 30) +
  geom_histogram(binwidth=10)
```



What do you notice here? Note that larger bitscores are better.

I notice that the distribution looks more or less bimodal, with peaks near 30 and then around 275. There is also a skewness with a few very high bitscores above 750.

```
ggplot(df, aes(pident, bitscore)) + geom_point(alpha=0.1)
```



Is there a straightforward relationship between percent identity (pident)andbitscore (bitscore) for the alignments we generated?

There appears to be a positively correlated relationship between pident and bitscore. We notice, in general, that larger pidents tend to be associated with larger bitscores.

```
ggplot(df, aes((df$pident * (df$qend - df$qstart)), bitscore)) + geom_point(alpha=0.1) + g
```

Warning: Use of `df\$pident` is discouraged. i Use `pident` instead.

Warning: Use of `df\$qend` is discouraged. i Use `qend` instead.

Warning: Use of `df\$qstart` is discouraged. i Use `qstart` instead.

Warning: Use of `df\$pident` is discouraged. i Use `pident` instead.

Warning: Use of `df\$qend` is discouraged. i Use `qend` instead.

Warning: Use of `df\$qstart` is discouraged. i Use `qstart` instead.

 $\ensuremath{\text{`geom\_smooth()`}}\ using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'$ 

