## Class 17: Essential UNIX for Bioinformatics

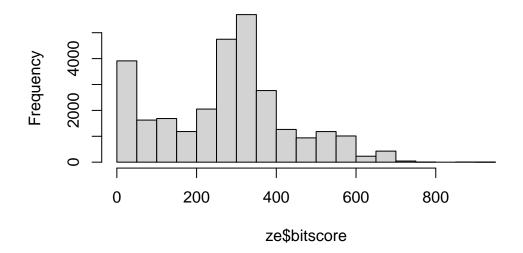
Helen Le (PID: A16300695)

```
ze <- read.delim("mm-second.x.zebrafish.tsv")</pre>
  colnames(ze) <- c("qseqid", "sseqid", "pident", "length", "mismatch", "gapopen", "qstart",</pre>
  head(ze)
                      sseqid pident length mismatch gapopen qstart qend sstart
1 NP_598866.1 NP_001313634.1 46.154
                                        273
                                                 130
                                                                  4
                                                                     267
                                                                             476
2 NP_598866.1 XP_009294513.1 46.154
                                        273
                                                 130
                                                                     267
                                                                             475
3 NP_598866.1 NP_001186666.1 33.071
                                       127
                                                  76
                                                                 4
                                                                     126
                                                                             338
                                        125
                                                  82
                                                           4
4 NP_598866.1 NP_001003517.1 30.400
                                                                  4 126
                                                                             344
5 NP_598866.1 NP_001003517.1 30.645
                                         62
                                                  41
                                                                 53
                                                                     113
                                                                             43
                 NP_956073.2 34.444
                                         90
6 NP_598866.1
                                                  56
                                                                 40
                                                                     126
                                                                             527
  send
         evalue bitscore
1 740 4.51e-63
                   214.0
2 739 4.69e-63
                   214.0
3 459 5.19e-12
                    67.8
4 465 2.67e-11
                    65.5
5 103 4.40e-01
                    33.9
6 616 1.70e-10
                    63.2
```

Let's make a histogram of \$bitscore values.

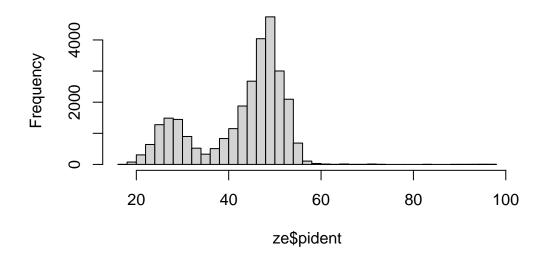
```
hist(ze$bitscore, breaks=30)
```

## Histogram of ze\$bitscore



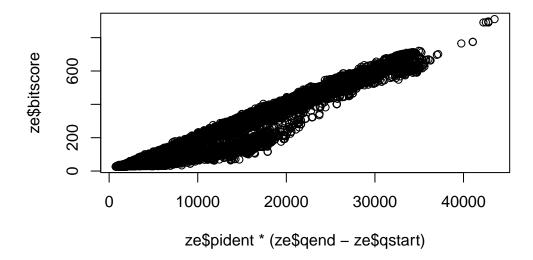
hist(ze\$pident, breaks=30)

## Histogram of ze\$pident



Bitscores are only somewhat related to pident; they take into account not only the percent identity but the length of the alignment. You can get a napkin sketch estimate of this by doing the following:

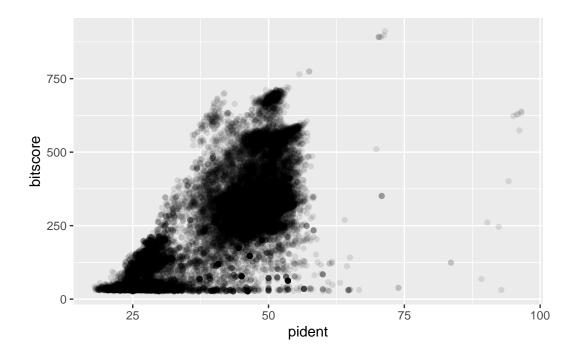
```
## Asuming your blast results are stored in an object called 'ze'
plot(ze$pident * (ze$qend - ze$qstart), ze$bitscore)
```



Let's use ggplot instead.

```
library(ggplot2)

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



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

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

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

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

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

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

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

<code>`geom\_smooth()`</code> using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'

