

Class 15: Unix Basics

Kaitlyn Powell

```
library(readr)  
  
directory <- ("./class13")
```

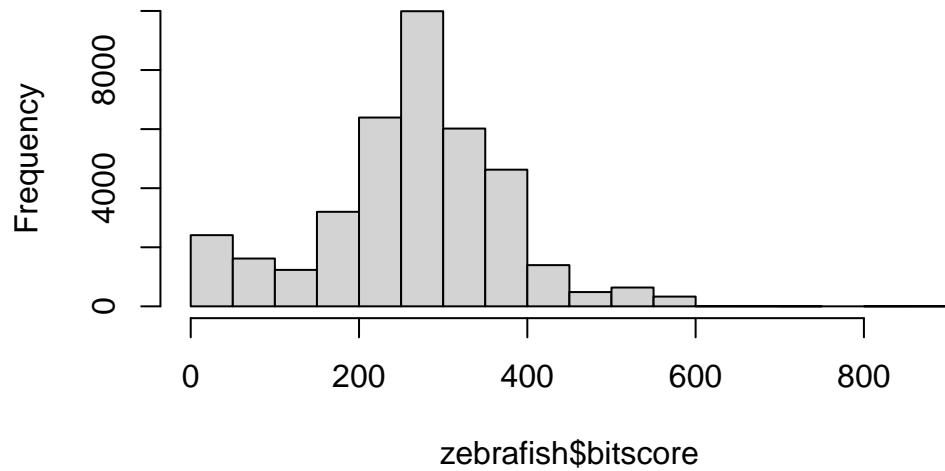
Note: The `zebrafish` file contained too much data to show the whole table.

```
zebrafish <- read.table("mm-second.x.zebrafish.tsv", col.names = c("qseqid", "sseqid", "pi  
#zebrafish
```

Another way to read the file:

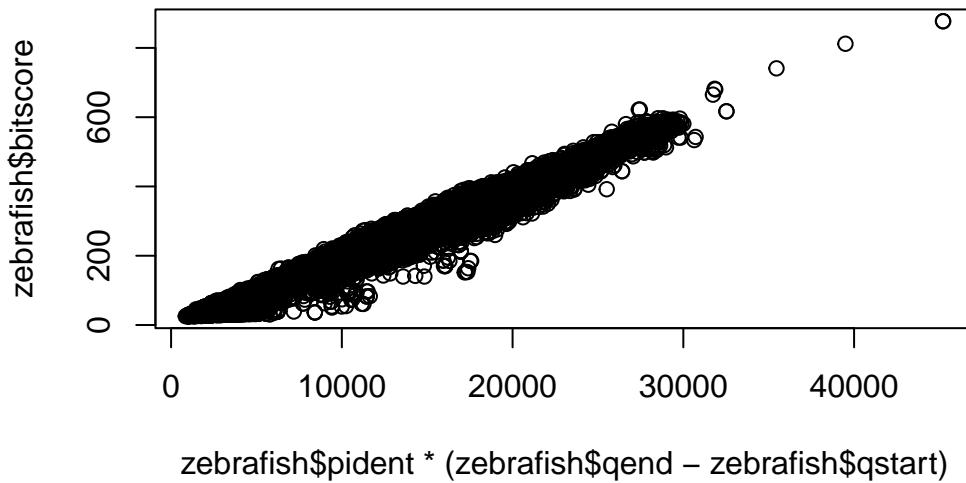
```
#read_tsv("mm-second.x.zebrafish.tsv")  
  
hist(zebrafish$bitscore, breaks = 30)
```

Histogram of zebrafish\$bitscore

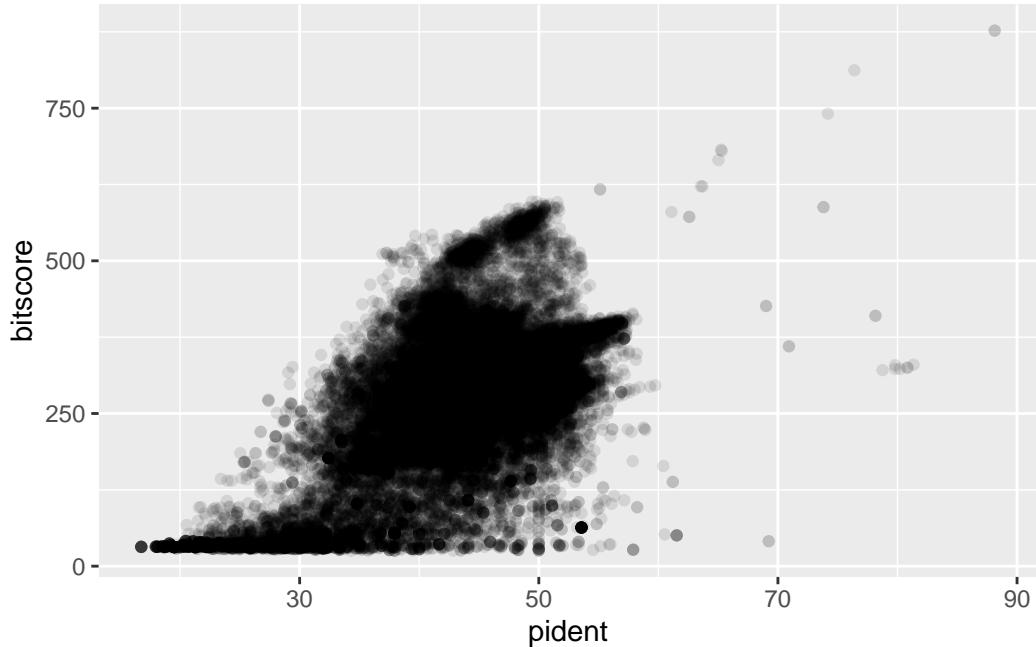


Asuming your blast results are stored in an object called 'zebrafish'

```
plot(zebrafish$pident * (zebrafish$qend - zebrafish$qstart), zebrafish$bitscore)
```



```
library(ggplot2)  
  
ggplot(zebrafish, aes(pident, bitscore)) + geom_point(alpha=0.1)
```



```
ggplot(zebrafish, aes((zebrafish$pident * (zebrafish$qend - zebrafish$qstart)), bitscore))
```

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

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

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

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

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

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

`geom_smooth()` using method = 'gam' and formula 'y ~ s(x, bs = "cs")'

