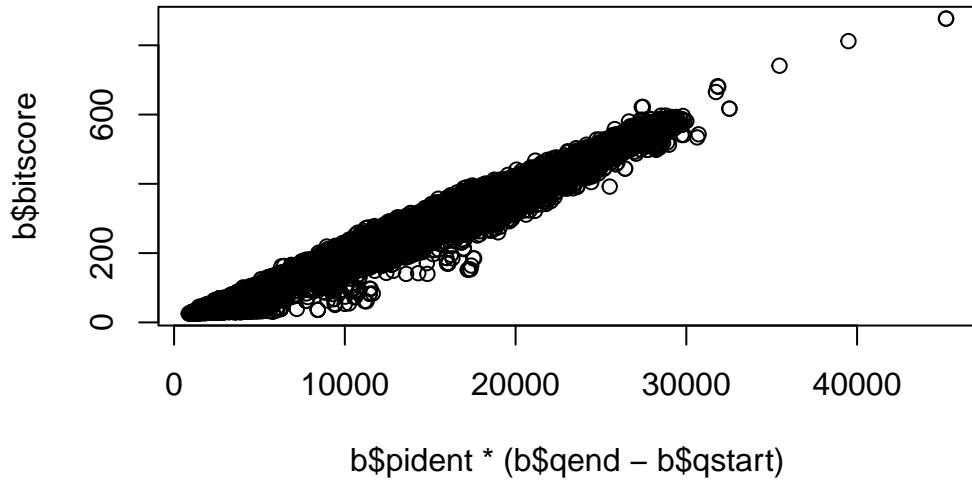


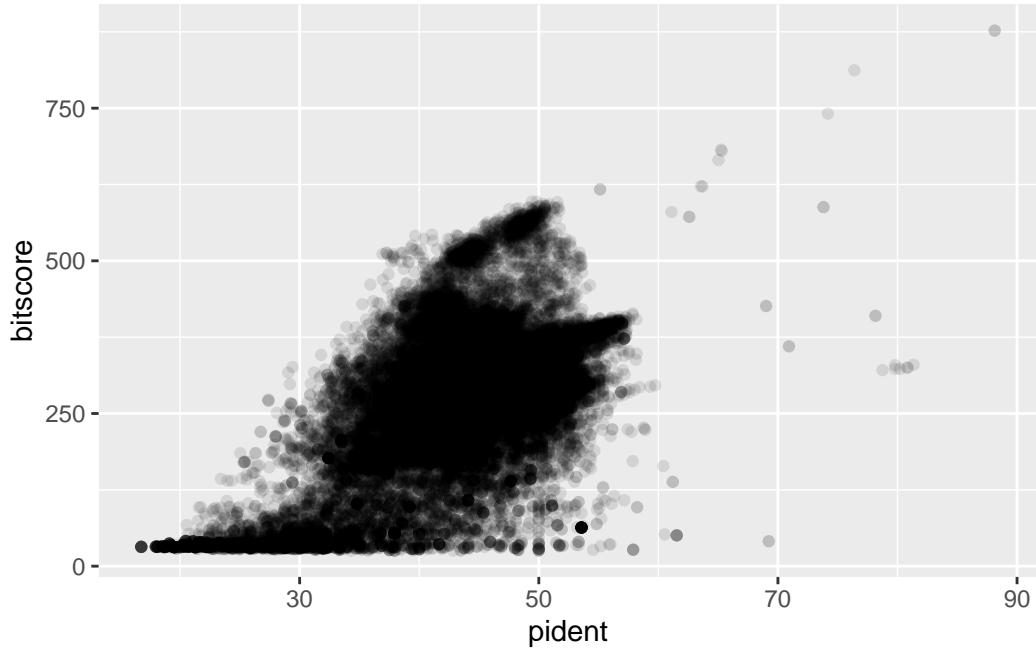
Class 15 : Essential UNIX for Bioinformatics

```
b <- read.table("mm-second.x.zebrafish.tsv", col.names = c("qseqid", "sseqid", "pident", "length", "mismatch", "gapopen", "qstart", "qend", "bitscore"))

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



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



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

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

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

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

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

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

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

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

