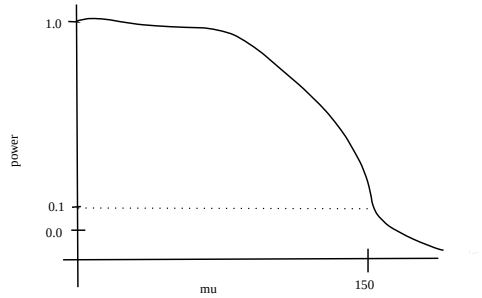
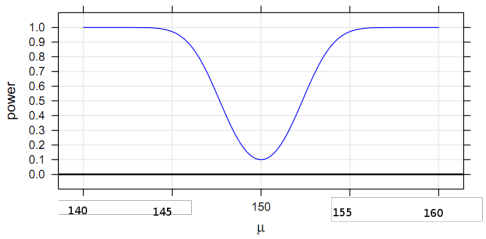
Stat 571 - HW10 - Nathanael Fillmore

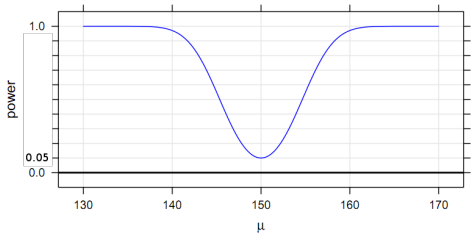
1. (a) Minimum is at 150.
   (b) Value at minimum is 0.10.
   (c) The minimum is in the middle of the graph, as opposed to being at one extreme.
   (d) 146, 154.
   (e) The minimum occurs as $\mu \to \infty$ and is 0.1 at $\mu = 150$:



   (f) The curve is tighter around the minimum, i.e., there is more power because the sample size is bigger:

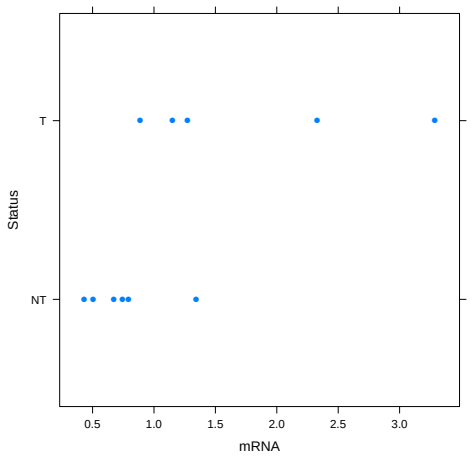


   (g) The value at minimum 0.05 instead of 0.10:

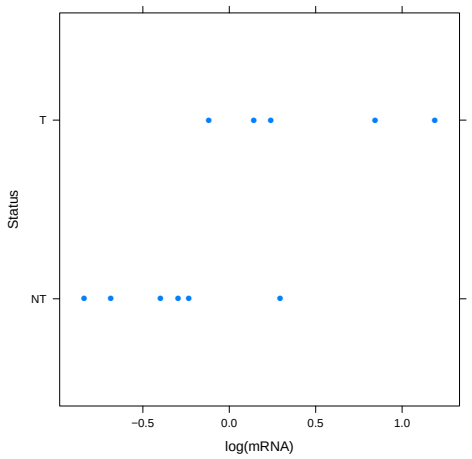


2. Please see attached sheets.
3. (a)

```
> c = read.csv("cichlids.csv")
> str(c)
'data.frame':        11 obs. of  2 variables:
 $ Status: Factor w/ 2 levels "NT","T": 1 1 1 1 1 1 2 2 2 2 ...
 $ mRNA  : num  0.504 0.432 0.744 0.792 0.672 ...
> plot(xyplot(Status~mRNA, data=c, pch=16))
```



(b)
```
> plot(xyplot(Status~log(mRNA), data=c, pch=16))
```



(c) The second one shows less skewness.

(d)
```
> a = c[c$Status == "NT", "mRNA"]
> b = c[c$Status == "T", "mRNA"]
> o = t.test(a, b, paired=FALSE)
> o$conf.int

[1] -2.2631808  0.1879808
attr(,"conf.level")
[1] 0.95
```

(e)
```
> a = log(c[c$Status == "NT", "mRNA"])
> b = log(c[c$Status == "T", "mRNA"])
> o = t.test(a, b, paired=FALSE)
> exp(o$conf.int)

[1] 0.2227028 0.8728930
attr(,"conf.level")
[1] 0.95
```

(f) The intervals are substantially different. The second one looks more reasonable, since based on the plots it seems that T "definitely" has a bigger mean than NT.