Ch.2-Ex.2: (a) To detect the difference between different delivery modes, we can use R program as follows:

```r
> data(ToothGrowth)
> dose=function(d){
  len=ToothGrowth$len; supp=ToothGrowth$supp; dose=ToothGrowth$dose
  len_vc=len[supp=="VC" & dose==d]; len_oj=len[supp=="OJ" & dose==d]
  diff=len_vc-len_oj
  hist(diff,freq=F,xlab="len(VC)-len(OJ)",main=paste("dose=",d))
  lines(density(diff))
  abline(v=0,col="red")
  cat(c("Pr[len(VC)<len(OJ)]=",mean(diff<0),"\n"),fill=T)
  cat("summary of len(VC)-len(OJ):",fill=T)
  summary(diff)}
> dose(d=1)
Pr[len(VC)<len(OJ)]= 0.8
summary of len(VC)-len(OJ)
  Min. 1st Qu.  Median    Mean 3rd Qu.   Max.
> dose(d=2)
Pr[len(VC)<len(OJ)]= 0.4
summary of len(VC)-len(OJ)
  Min. 1st Qu.  Median    Mean 3rd Qu.   Max.
-7.900   -4.825  0.650   0.080  1.600  11.500
```

The code creates a function in R that can be used repeatedly at different dose levels. The code executes the probability that length of tooth using delivery mode “VC” would be lower than that using “OJ” at a given dose level and also provides a summary of the differences. A histogram of the difference is also plotted overlaid with a smoothed density and a location of zero (using the vertical red line).
Notice that when dose level is 1(mg), the probability that the difference is negative is 0.8 indicating that is highly likely that at this dose, length of tooth is greater (by about 5.93 units) using the delivery mode “OJ” as compared to “VC”. On the other hand when dose level is 2(mg), the probability that the difference is negative is only about 0.4 indicating that is not likely that at this dose length of tooth is greater (by about only 0.08 units) using the delivery method “OJ” as compared to “VC”.

Hence it seems that delivery mode has different effects at different doses.

(b) Here we want to estimate the effect of doses for delivery modes “VC” and “OJ”.

```r
> delivery=function(mode){
  len=ToothGrowth$len;supp=ToothGrowth$supp;dose=ToothGrowth$dose
  len_d1=len[supp==mode & dose==1];len_d2=len[supp==mode & dose==2]
  diff=len_d1-len_d2
  hist(diff,freq=F,xlab="len(dose1)-len(dose2)",main=paste("delivery=" ,mode))
  lines(density(diff))
  abline(v=0,col="red")
  cat(c("Pr[\text{len(dose1)}<\text{len(dose2)}]="," ,mean(diff<0)),fill=T)
  cat("summary of \text{len(dose1)}-\text{len(dose2)}:",fill=T)
  summary(diff)
  > delivery(mode="VC")
  Pr[\text{len(dose1)}<\text{len(dose2)}]= 1
  summary of \text{len(dose1)}-\text{len(dose2)}:
    Min. 1st Qu. Median Mean 3rd Qu. Max.
  > delivery(mode="OJ")
  Pr[\text{len(dose1)}<\text{len(dose2)}]= 0.7
  summary of \text{len(dose1)}-\text{len(dose2)}:
    Min. 1st Qu. Median Mean 3rd Qu. Max.
```

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It appears that when the delivery mode is “VC” the probability that the difference is negative is 1 indicating that is almost certain that at this delivery mode, length of tooth is greater (by about 9.37 units) using the dose level 2(mg) as compared to dose level of 1(mg). Also a similar conclusion can be concluded when the delivery mode is “OJ” but the probability that the difference is negative is about 0.7 and mean difference is about $-3.36$.

Hence it appears that delivery mode changes the effect of dose but to a lesser extent.

(c) R codes:

```r
boxplot(len ~ dose, data = ToothGrowth, 
       boxwex = 0.25, at = 1:3 - 0.2, 
       subset = supp == "VC", col = "yellow", 
       main = "Delivery Mode=VC", 
       xlab = "Vitamin C dose mg", 
       ylab = "tooth length", 
       xlim = c(0.5, 3.5), ylim = c(0, 35), yaxs = "i")

boxplot(len ~ dose, data = ToothGrowth, 
       boxwex = 0.25, at = 1:3 - 0.2, 
       subset = supp == "OJ", col = "yellow", 
       main = "Delivery Mode=OJ", 
       xlab = "OJ dose mg", 
       ylab = "tooth length", 
       xlim = c(0.5, 3.5), ylim = c(0, 35), yaxs = "i")
```
From the boxplot, we can see that there exists difference among the three doses under either VC or OJ. However the differences due to doses under the delivery mode “VC” are little more pronounced than that under “OJ.”

Ch.2-Ex.3: (a) R codes:

```r
> data(faithful)
> help(faithful)
> plot(faithful$waiting, faithful$eruptions, main="Old Faithful geyser")
```

It appears that eruptions time (in mons) tend to increase with waiting time to next eruption (in mins) with two clusters; one near the waiting time around 55min and another around 85min. Thus, it seems that if the waiting time to
next eruption is longer (say 85min as compared to 55min) we expect to see a longer duration of eruption (e.g., 4.5min in duration as compared to only 2min in duration).

(b) After running \texttt{ts.plot(faithful eruptions[1 : 50], main = "faithful eruptions[1:50]")}
and \texttt{ts.plot(faithful eruptions[1 : 50], main = "faithful eruptions[51:100]")}, we got the following two graphs.

From the graphs, we can see that the observations is fluctuate around a vertical line randomly. And long and short duration are interwoven, as are long and short intervals. Also by executing the following R codes, we find that eruption duration time is almost doubled when the waiting time to next eruption is greater that 70 min as compared to those that are less than 70min.

\begin{verbatim}
> eru1=eruptions[waiting<=70]
> eru2=eruptions[waiting>70]
> boxplot(eru1,eru2,names=c("waiting<70","waiting>70"),ylab="eruptions")
> summary(eru1)
   Min. 1st Qu.  Median    Mean 3rd Qu.   Max.    
   1.600  1.850  2.000    2.206  2.275   4.100
> summary(eru2)
   Min. 1st Qu.  Median    Mean 3rd Qu.   Max.    
   2.383  4.083  4.366    4.319  4.600   5.100
\end{verbatim}
Ch.2-Ex.5: If \( N \) change from 145 to 1450 and \( n \) change from 8 to 80, the new likelihood function
\[
l(\theta) = \binom{1450}{80} \theta^{80} (1 - \theta)^{1370}
\]
Use R to plot the new likelihood function:

```r
theta=seq(0, .2, length=100)
lik=dbinom(80, 1450, theta)
lik=lik/max(lik)
plot(theta, lik, xlab=expression(theta),
ylab="likelihood", main="New Likelihood Function", type="l", yaxt="n")
```

To compare the new likelihood function with the previous one, I put the two graphs in a line. (New one on the left and previous one on the right).

By comparing the two graphs, we can see that after adding more people but having the same incidence rate (i.e. \( n/N \approx 0.05 \)), the likelihood function tends to be tighter around the value of 0.05, at which the likelihood function is maximized.