STA610 Lab03

Hun Kang

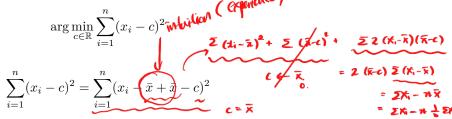
2024-09-13

- Write down your answers in any blank sheet and submit your work in paper during the lab.
- Your work will not be graded. As long as you submit, you will get a full credit.
- For those who missed the lab today, you can submit it via email to me for half credit.

Least Squares Review

How can we find c such that

One way is to start from



Another approach is use calculus



$$\frac{d}{dc}\sum_{i=1}^{n}(x_{i}-c)^{2}=0$$

$$=\sum_{i=1}^{n}\left(\frac{1}{dc}(x_{i}-c)^{2}\right)=\sum_{i=1}^{n}\left(2c-2x_{i}\right)=0 \quad \text{at } c=\bar{x}$$
oroaches.

Q1-1: Compute c using both approaches.

$$\frac{1}{4}(f_{\alpha})+g_{\alpha})=\frac{1}{4}f_{\alpha}+\frac{1}{4}g_{\alpha}$$

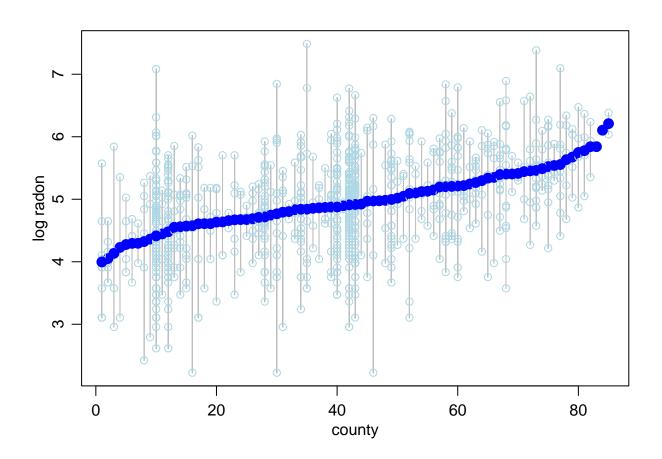
Confidence Interval for Group Effects

radon<-readRDS(url("https://www2.stat.duke.edu/~pdh10/Teaching/610/Code/radonMN.rds"))
head(radon)</pre>

```
##
        county
                   lon
                          lat
                                  Uppm
                                            radon
## 5081 AITKIN -93.415 46.608 0.502054
                                        82.43790
  5082 AITKIN -93.415 46.608 0.502054
                                        82.43790
## 5083 AITKIN -93.415 46.608 0.502054 108.09157
## 5084 AITKIN -93.415 46.608 0.502054
                                        39.18363
## 5085
         ANOKA -93.246 45.273 0.428565 115.44118
## 5086
         ANOKA -93.246 45.273 0.428565
```

The following is the code to produce the first plot of the lecture slide s5GroupEstNP. We will modify this code to plot various confidence intervals of the group means.

```
gdotplot<-function(y,g,xlab="group",ylab="response",mcol="blue",</pre>
                    ocol="lightblue",sortgroups=TRUE,...)
{
  m<-length(unique(g))</pre>
  rg<-rank( tapply(y,g,mean),ties.method="first")</pre>
  if(sortgroups==FALSE){ rg<-1:m ; names(rg)<-unique(g)}</pre>
  plot(c(1,m),range(y),type="n",xlab=xlab,ylab=ylab)
  for(j in unique(g))
    yj \leftarrow y[g==j]
    rj<-rg[ match(as.character(j),names(rg)) ]</pre>
    nj<-length(yj)
    segments( rep(rj,nj) ,max(yj),rep(rj,nj),min(yj),col="gray")
    points( rep(rj,nj), yj,col=ocol,...)
    points(rj,mean(yj),pch=16,cex=1.5,col=mcol)
  }
}
par(mar=c(3,3,1,1), mgp=c(1.75,.75,0))
gdotplot(log(radon$radon),
         radon$county,
         xlab="county", ylab="log radon")
```



Q2-1: Identify the code lines that 1) compute the mean of each group, 2) order the

counties, 3) plot data points, 4) plot vertical lines.

Q2-2: Modify the plot so that counties are sorted according to the number of observations within county and draw a horizontal line marking the grand mean.

We first use ANOVA to evaluate statistical evidence of heterogeneity in across-county means.

```
## Analysis of Variance Table

## Response: log(radon)

## county 84 126.93 1.51103 2.6406 2.981e-12 ***

## Residuals 834 477.23 0.57222

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 '' 1

Sex XX XY
```

Now we fit the hierarchical normal model to the data. Descriptions about the package with many useful examples can be found in https://www.jstatsoft.org/article/view/v067i01.

```
library(lme4)
```

Q2-3: Write down the model in the following code and identify the parameters and the random variables with corresponding distribution.

```
mod <- lmer(log(radon) ~ 1 + (1 | county), data = radon, REML = FALSE)
summary(mod)

## Linear mixed model fit by maximum likelihood ['lmerMod']
## Formula: log(radon) ~ 1 + (1 | county)</pre>
```

```
##
      Data: radon
##
##
        AIC
                 BIC
                        logLik deviance df.resid
     2164.1
                      -1079.0
                                 2158.1
##
              2178.5
                                              916
##
##
  Scaled residuals:
##
       Min
                10
                    Median
                                 30
                                        Max
##
   -3.6165 -0.6141
                    0.0292
                             0.6526
                                     3.4932
##
## Random effects:
                          Variance Std.Dev.
##
    Groups
             Name
##
    county
             (Intercept) 0.08804 0.2967
##
    Residual
                          0.57154 0.7560
##
   Number of obs: 919, groups: county, 85
##
## Fixed effects:
               Estimate Std. Error t value
##
  (Intercept) 4.94656
                            0.04664
                                      106.1
```

We can extract the estimates of μ , τ and σ as below. Here, the estimate of σ is a pooled estimate.

```
fixef(mod)

## (Intercept)
## 4.946557

data.frame(VarCorr(mod))
```

```
## grp var1 var2 vcov sdcor
## 1 county (Intercept) <NA> 0.08804027 0.2967158
## 2 Residual <NA> <NA> 0.57153536 0.7559996
```

There are two different types of confidence interval we learned in class. One is the t-interval for group mean with pooled variance estimate:

$$\bar{y}_j \pm \frac{t_{1-\alpha/2}}{\sqrt{n_j/\hat{\sigma}^2}}$$

and the other is the Empirical Bayes interval

$$\left(\frac{\hat{\tau}^2}{\hat{\tau}^2+\hat{\sigma}^2/n_j}\hat{\mu}+\frac{\hat{\sigma}^2/n_j}{\hat{\tau}^2+\hat{\sigma}^2/n_j}\bar{y}_j\right)\pm\frac{t_{1-\alpha/2}}{\sqrt{n_j/\hat{\sigma}^2+1/\tau^2}}$$

Q2-4: Describe the differences between two intervals.

```
# pooled estimates
muhat = fixef(mod)
sighat = data.frame(VarCorr(mod))$sdcor[1]
tauhat = data.frame(VarCorr(mod))$sdcor[2]

# group-wise statistics
ybars = aggregate(log(radon) ~ county, data = radon, mean)[,2]
njs = aggregate(log(radon) ~ county, data = radon, length)[,2]
```

Q2-5: Plot two credible intervals for each group using the code above.