Final_Project

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```
smoke <- read.csv(file = 'frmgham2.csv') %>%
  clean_names()
```

```
#checking missing values (5% rule)
pMiss <- function(x){sum(is.na(x))/length(x)*100}
apply(smoke,2,pMiss) #2 indicates columns
```

```
##      randid         sex     totchol         age       sysbp       diabp
##  0.00000000  0.00000000  3.51767438  0.00000000  0.00000000  0.00000000
##    cursmoke     cigpday         bmi    diabetes      bpmeds    heartrte
##  0.00000000  0.67945300  0.44723488  0.00000000  5.10019782  0.05160403
##     glucose        educ     prevchd      prevap      prevmi    prevstrk
## 12.38496603  2.53719790  0.00000000  0.00000000  0.00000000  0.00000000
##     prevhyp        time      period        hdlc        ldlc       death
##  0.00000000  0.00000000  0.00000000 73.96576933 73.97437000  0.00000000
##      angina      hospmi     mi_fchd      anychd      stroke         cvd
##  0.00000000  0.00000000  0.00000000  0.00000000  0.00000000  0.00000000
##    hyperten      timeap      timemi    timemifc     timechd    timestrk
##  0.00000000  0.00000000  0.00000000  0.00000000  0.00000000  0.00000000
##     timecvd      timedth     timehyp
##  0.00000000  0.00000000  0.00000000
```

```
#Remove hdlc, ldlc, glucose, and bpmeds for having more than 5% of missing values.
```

It is okay as hdlc, ldlc are highly correlated with totchol, glucose is highy correlated with diabetes, bpmeds is highly correlated with sysbp and diabp. Therefore it won't lose much information to just drop these features.

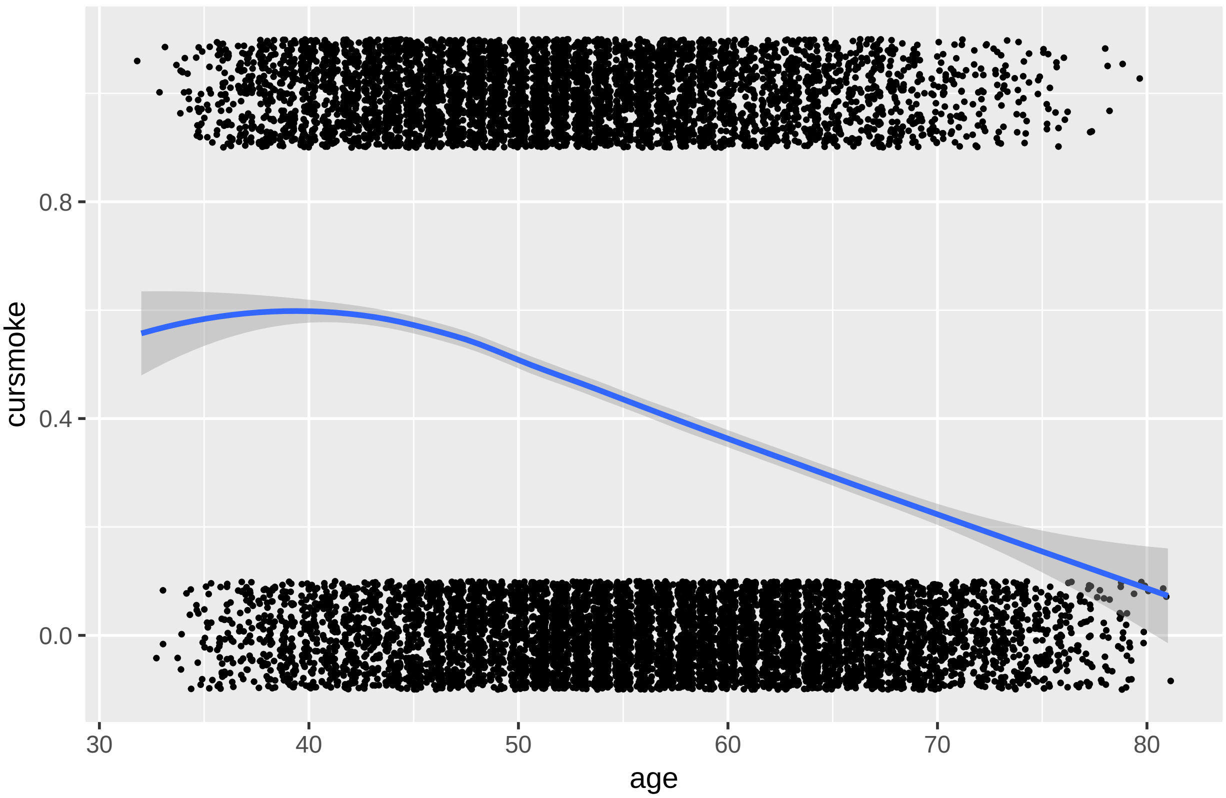
Part1

Question 1

Figure 1 shows that as individuals age, the likelihood that they are smoking decreases. We can see that when we breaking individuals down by sex, it appears that the overall trend is the same between sexes with males having an overall higher likelihood of being smokers as age increases.

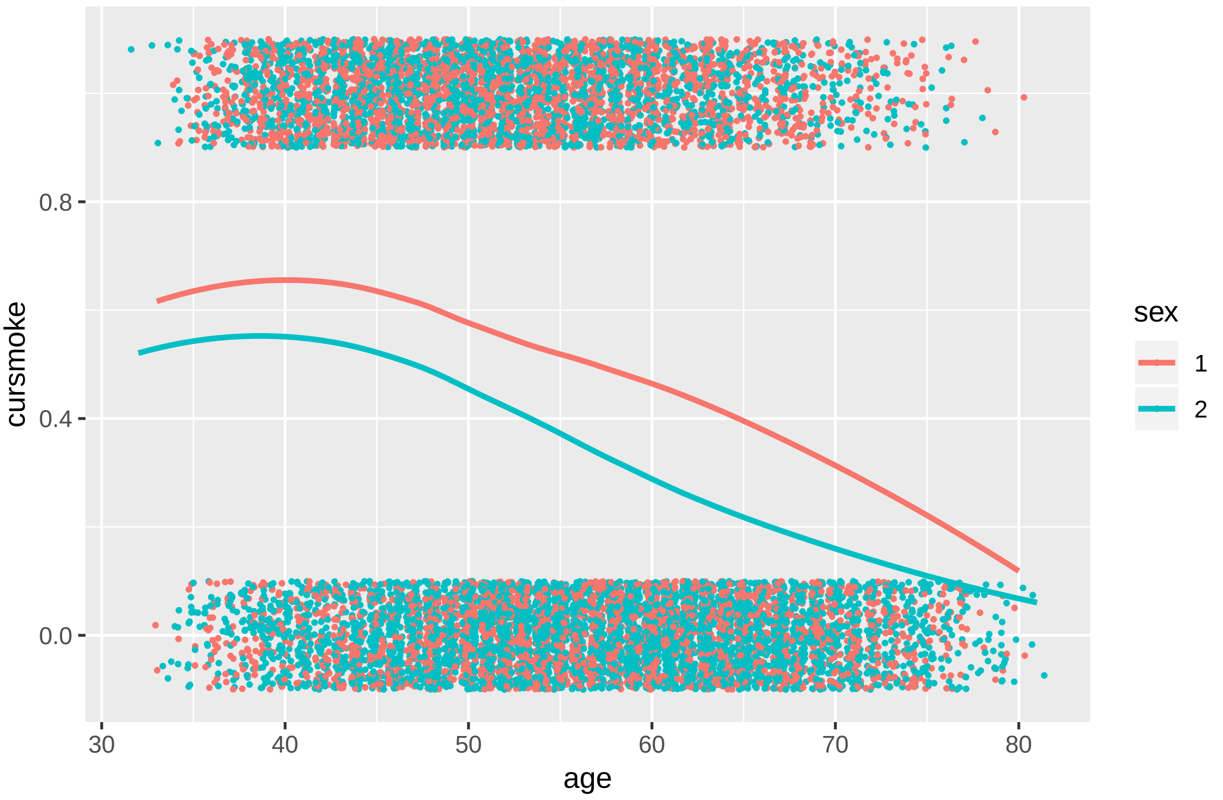
```
smoke %>%
  ggplot(aes(age, cursmoke)) +
  geom_jitter(height = 0.1, size = 0.5) +
  geom_smooth(method = "loess") +
  ggtitle("Figure 1: Current Smoking Status across Age")
```

Figure 1: Current Smoking Status across Age



```
#BY SEX
smoke %>%
  mutate(sex = as.factor(sex)) %>%
  ggplot(aes(age, cursmoke, group = sex, color = sex)) +
  geom_jitter(height = 0.1, size = 0.5) +
  geom_smooth(method = "loess", se = F) +
  ggtitle("Figure 2: Current Smoking Status across Age")
```

Figure 2: Current Smoking Status across Age



```r
smoke_vs1 = smoke %>%
  filter(period==1) %>%
  dplyr::select(c(randid,sex,age,cursmoke,totchol,bmi,heartrte,educ,diabp,sysbp,diabetes,prevap,prevchd
  mutate(cursmoke = as.factor(cursmoke), sex=as.factor(sex), diabetes=as.factor(diabetes)) %>%
  na.omit()
```

```r
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+prevhyp, data=smoke_vs1,family = 'binomial')
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```r
exp(b)
```

```
## [1] 0.9563489
```

```r
exp(c)
```

```
## [1] 0.9529738
```

```r
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```r
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
```

```r
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```r
exp(e)
```

```
## [1] 0.4819127
```

```r
exp(f)
```

```
## [1] 0.4226504
```

```r
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

prevhyp is not confounder for sex and age with cursmoke

```r
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+prevstrk, data=smoke_vs1,family = 'binomial')
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```r
exp(b)
```

```
## [1] 0.9563489
```

```r
exp(c)
```

```
## [1] 0.9493691
```

```r
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```r
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```r
exp(e)
```

```
## [1] 0.4819127
```

```r
exp(f)
```

```
## [1] 0.4244159
```

```r
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

prevstrk is not confounder for sex and age with cursmoke

```r
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+prevmi, data=smoke_vs1,family = 'binomial')
```

```
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```
exp(b)
```

```
## [1] 0.9563489
```

```
exp(c)
```

```
## [1] 0.948613
```

```
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```
exp(e)
```

```
## [1] 0.4819127
```

```
exp(f)
```

```
## [1] 0.4290085
```

```
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

prevmi is not confounder for sex and age with cursmoke

```
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+prevchd, data=smoke_vs1,family = 'binomial')
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```
exp(b)
```

```
## [1] 0.9563489
```

```
exp(c)
```

```
## [1] 0.9489226
```

```
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
```

```r
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```r
exp(e)
```

```
## [1] 0.4819127
```

```r
exp(f)
```

```
## [1] 0.4256095
```

```r
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

prevchd is not confounder for sex and age with cursmoke

```r
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+prevap, data=smoke_vs1,family = 'binomial')
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```r
exp(b)
```

```
## [1] 0.9563489
```

```r
exp(c)
```

```
## [1] 0.94959
```

```r
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```r
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```r
exp(e)
```

```
## [1] 0.4819127
```

```r
exp(f)
```

```
## [1] 0.4233239
```

```r
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

prevap is not confounder for sex and age with cursmoke

```r
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+totchol, data=smoke_vs1,family = 'binomial')
```

```
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```
exp(b)
```

```
## [1] 0.9563489
```

```
exp(c)
```

```
## [1] 0.9480594
```

```
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```
exp(e)
```

```
## [1] 0.4819127
```

```
exp(f)
```

```
## [1] 0.4218472
```

```
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

totchol is not confounder for sex and age with cursmoke

```
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+sysbp, data=smoke_vs1,family = 'binomial')
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```
exp(b)
```

```
## [1] 0.9563489
```

```
exp(c)
```

```
## [1] 0.9541667
```

```
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
```

```
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```
exp(e)
```

```
## [1] 0.4819127
```

```
exp(f)
```

```
## [1] 0.4275944
```

```
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

sysbp is not confounder for sex and age with cursmoke

```
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+diabp, data=smoke_vs1,family = 'binomial')
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```
exp(b)
```

```
## [1] 0.9563489
```

```
exp(c)
```

```
## [1] 0.9528767
```

```
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```
exp(e)
```

```
## [1] 0.4819127
```

```
exp(f)
```

```
## [1] 0.4149985
```

```
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

diabp is is not confounder for sex and age with cursmoke

```
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+bmi, data=smoke_vs1,family = 'binomial')
```

```
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```
exp(b)
```

```
## [1] 0.9563489
```

```
exp(c)
```

```
## [1] 0.9530611
```

```
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```
exp(e)
```

```
## [1] 0.4819127
```

```
exp(f)
```

```
## [1] 0.3907743
```

```
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

bmi is is not confounder for sex and age with cursmoke

```
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+heartrte, data=smoke_vs1,family = 'binomial')
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```
exp(b)
```

```
## [1] 0.9563489
```

```
exp(c)
```

```
## [1] 0.9491648
```

```
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
```

```
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```
exp(e)
```

```
## [1] 0.4819127
```

```
exp(f)
```

```
## [1] 0.4069115
```

```
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

heartrte is is not confounder for sex and age with cursmoke

```
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+educ, data=smoke_vs1,family = 'binomial')
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```
exp(b)
```

```
## [1] 0.9563489
```

```
exp(c)
```

```
## [1] 0.9483645
```

```
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```
exp(e)
```

```
## [1] 0.4819127
```

```
exp(f)
```

```
## [1] 0.4237448
```

```
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

educ is not confounder for sex and age with cursmoke

```
glm1 <- glm(cursmoke ~ age+sex, data=smoke_vs1,family = 'binomial')
glm2 <- glm(cursmoke ~ age+sex+diabetes, data=smoke_vs1,family = 'binomial')
```

```r
a=(summary(glm1)$coefficients[2])-(1.96 * (summary(glm1)$coefficients[5]))
b= (summary(glm1)$coefficients[2])+(1.96 * (summary(glm1)$coefficients[5]))
c=summary(glm2)$coefficients[2]
exp(a)
```

```
## [1] 0.9422074
```

```r
exp(b)
```

```
## [1] 0.9563489
```

```r
exp(c)
```

```
## [1] 0.949986
```

```r
!(exp(c)>=exp(a) & exp(c)<=exp(b))
```

```
## [1] FALSE
```

```r
d=(summary(glm1)$coefficients[3])-(1.96 * (summary(glm1)$coefficients[6]))
e=(summary(glm1)$coefficients[3])+(1.96 * (summary(glm1)$coefficients[6]))
f=summary(glm2)$coefficients[3]
exp(d)
```

```
## [1] 0.3737987
```

```r
exp(e)
```

```
## [1] 0.4819127
```

```r
exp(f)
```

```
## [1] 0.4229651
```

```r
!(exp(f)>=exp(d) & exp(f)<=exp(e))
```

```
## [1] FALSE
```

diabetes is not confounder for sex and age with cursmoke

None of these are confounders. It makes sense as nothing could affect age. Same for question 2. So we only put age and sex into the model.

```r
smoke_vs3 = smoke %>%
  dplyr::select(c(randid,sex,age,cursmoke)) %>%
  mutate(cursmoke = as.factor(cursmoke), sex=as.factor(sex)) %>%
  na.omit()
glmer_1 <- glmer(cursmoke ~ age *sex + (1 | randid),
                 data = smoke_vs3,
                 family = binomial)
summary(glmer_1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cursmoke ~ age * sex + (1 | randid)
##    Data: smoke_vs3
##
##      AIC      BIC   logLik deviance df.resid
##  10840.6  10877.4  -5415.3  10830.6    11622
##
```

```
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5920 -0.1412 -0.0524  0.1965  3.5958
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  randid (Intercept) 34.34    5.86
## Number of obs: 11627, groups:  randid, 4434
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 13.71738    0.84790  16.178  < 2e-16 ***
## age         -0.23847    0.01456 -16.383  < 2e-16 ***
## sex2        -6.93043    1.09252  -6.344 2.25e-10 ***
## age:sex2     0.05611    0.01671   3.358 0.000785 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) age    sex2
## age      -0.974
## sex2     -0.833  0.810
## age:sex2  0.761 -0.788 -0.950
```

significant.

```
#CI age
-0.23847-1.96*0.01456
```

```
## [1] -0.2670076
```

```
-0.23847+1.96*0.01456
```

```
## [1] -0.2099324
```

```
#CI sex
-6.93043-1.96*1.09252
```

```
## [1] -9.071769
```

```
-6.93043+1.96*1.09252
```

```
## [1] -4.789091
```

```
#CIage:sex2
0.05611-1.96*0.01671
```

```
## [1] 0.0233584
```

```
0.05611+1.96*0.01671
```

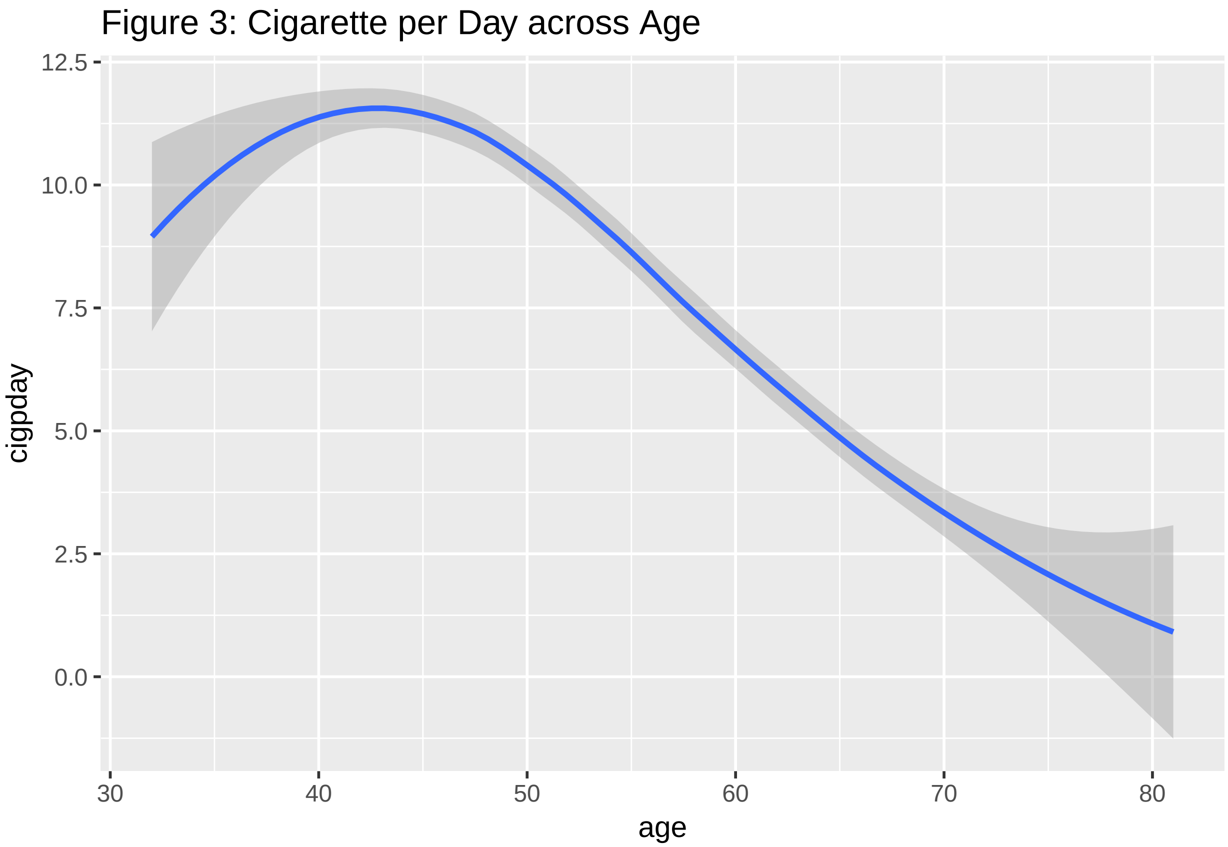
```
## [1] 0.0888616
```

Question 2

When looking at cigarette packs smoked per day, it appears that the number steadily decreases as individuals get older. The trend once again is the same in each sex however females are smoking less packs a day overall.

```r
smoke %>%
  ggplot(aes(age, cigpday)) +
  geom_smooth(method = "loess") +
  ggtitle("Figure 3: Cigarette per Day across Age")
```

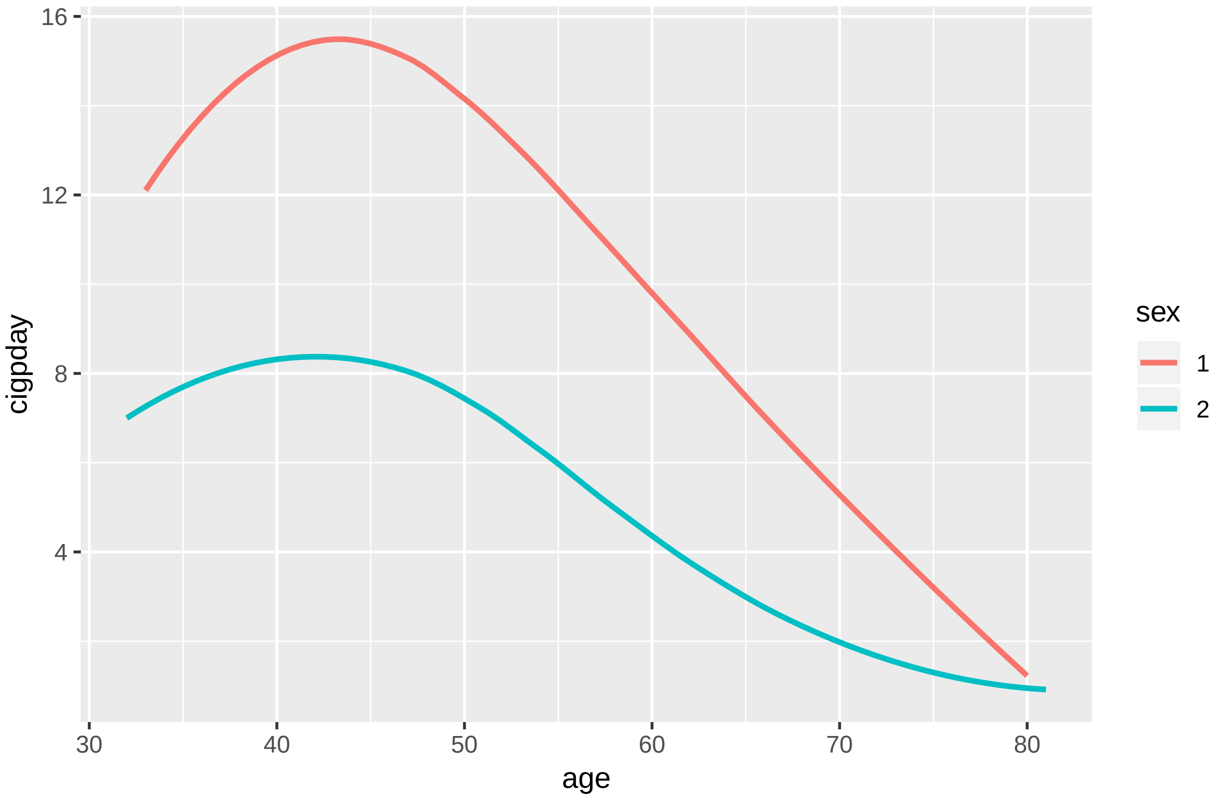
```
## Warning: Removed 79 rows containing non-finite values (stat_smooth).
```



```r
smoke %>%
  mutate(sex = as.factor(sex)) %>%
  ggplot(aes(age, cigpday, group = sex, color = sex)) +
  geom_smooth(method = "loess", se = F) +
  ggtitle("Figure 4: Cigarettes per Day across Age")
```

```
## Warning: Removed 79 rows containing non-finite values (stat_smooth).
```

Figure 4: Cigarettes per Day across Age



Variable Selection and confounder identidication:

```
smoke_vs2 = smoke %>%
  filter(period==1) %>%
  dplyr::select(c(randid,sex,age,cigpday,totchol,bmi,heartrte,educ,diabp,sysbp,diabetes)) %>%
  mutate(sex=as.factor(sex), diabetes=as.factor(diabetes)) %>%
  na.omit()
```

```
lm1 <- lm(cigpday ~ age+sex, data=smoke_vs2)
lm2 <- lm(cigpday ~ age+sex+totchol, data=smoke_vs2)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[5]))
b= (summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[5]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -0.2971391
```

```
b
```

```
## [1] -0.2200154
```

```
c
```

```
## [1] -0.2750505
```

```
!(c=a & c<=b)
```

```
## [1] FALSE
```

```
d=(summary(lm1)$coefficients[3])-(1.96 * (summary(lm1)$coefficients[6]))
e=(summary(lm1)$coefficients[3])+(1.96 * (summary(lm1)$coefficients[6]))
```

```
f=summary(lm2)$coefficients[3]
d
```

```
## [1] -8.361345
```

```
e
```

```
## [1] -7.01624
```

```
f
```

```
## [1] -7.762696
```

```
!(f>=d & f<=e)
```

```
## [1] FALSE
```

totchol is not confounder for age and sex with cigpday

```
lm1 <- lm(cigpday ~ age+sex, data=smoke_vs2)
lm2 <- lm(cigpday ~ age+sex+bmi, data=smoke_vs2)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[5]))
b= (summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[5]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -0.2971391
```

```
b
```

```
## [1] -0.2200154
```

```
c
```

```
## [1] -0.2414477
```

```
!(c=a & c<=b)
```

```
## [1] FALSE
```

```
d=(summary(lm1)$coefficients[3])-(1.96 * (summary(lm1)$coefficients[6]))
e=(summary(lm1)$coefficients[3])+(1.96 * (summary(lm1)$coefficients[6]))
f=summary(lm2)$coefficients[3]
d
```

```
## [1] -8.361345
```

```
e
```

```
## [1] -7.01624
```

```
f
```

```
## [1] -7.853529
```

```
!(f>=d & f<=e)
```

```
## [1] FALSE
```

bmi is not confounder for age and sex with cigpday

```
lm1 <- lm(cigpday ~ age+sex, data=smoke_vs2)
lm2 <- lm(cigpday ~ age+sex+heartrte, data=smoke_vs2)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[5]))
b= (summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[5]))
```

```
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -0.2971391
```

```
b
```

```
## [1] -0.2200154
```

```
c
```

```
## [1] -0.256792
```

```
!(c=a & c<=b)
```

```
## [1] FALSE
```

```
d=(summary(lm1)$coefficients[3])-(1.96 * (summary(lm1)$coefficients[6]))
e=(summary(lm1)$coefficients[3])+(1.96 * (summary(lm1)$coefficients[6]))
f=summary(lm2)$coefficients[3]
d
```

```
## [1] -8.361345
```

```
e
```

```
## [1] -7.01624
```

```
f
```

```
## [1] -7.960397
```

```
!(f>=d & f<=e)
```

```
## [1] FALSE
```

heartrte is not confounder for age and sex with cigpday

```
lm1 <- lm(cigpday ~ age+sex, data=smoke_vs2)
lm2 <- lm(cigpday ~ age+sex+educ, data=smoke_vs2)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[5]))
b= (summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[5]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -0.2971391
```

```
b
```

```
## [1] -0.2200154
```

```
c
```

```
## [1] -0.2659276
```

```
!(c=a & c<=b)
```

```
## [1] FALSE
```

```
d=(summary(lm1)$coefficients[3])-(1.96 * (summary(lm1)$coefficients[6]))
e=(summary(lm1)$coefficients[3])+(1.96 * (summary(lm1)$coefficients[6]))
f=summary(lm2)$coefficients[3]
d
```

```
## [1] -8.361345
```

```
e
```

```
## [1] -7.01624
```

```
f
```

```
## [1] -7.697665
```

```
!(f>=d & f<=e)
```

```
## [1] FALSE
```

educ is not confounder for age and sex with cigpday

```
lm1 <- lm(cigpday ~ age+sex, data=smoke_vs2)
lm2 <- lm(cigpday ~ age+sex+diabp, data=smoke_vs2)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[5]))
b= (summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[5]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -0.2971391
```

```
b
```

```
## [1] -0.2200154
```

```
c
```

```
## [1] -0.2479103
```

```
!(c=a & c<=b)
```

```
## [1] FALSE
```

```
d=(summary(lm1)$coefficients[3])-(1.96 * (summary(lm1)$coefficients[6]))
e=(summary(lm1)$coefficients[3])+(1.96 * (summary(lm1)$coefficients[6]))
f=summary(lm2)$coefficients[3]
d
```

```
## [1] -8.361345
```

```
e
```

```
## [1] -7.01624
```

```
f
```

```
## [1] -7.734606
```

```
!(f>=d & f<=e)
```

```
## [1] FALSE
```

diabp is not confounder for age and sex with cigpday

```
lm1 <- lm(cigpday ~ age+sex, data=smoke_vs2)
lm2 <- lm(cigpday ~ age+sex+sysbp, data=smoke_vs2)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[5]))
b= (summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[5]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -0.2971391
```

```
b
```

```
## [1] -0.2200154
```

```
c
```

```
## [1] -0.2525008
```

```
!(c=a & c<=b)
```

```
## [1] FALSE
```

```
d=(summary(lm1)$coefficients[3])-(1.96 * (summary(lm1)$coefficients[6]))
e=(summary(lm1)$coefficients[3])+(1.96 * (summary(lm1)$coefficients[6]))
f=summary(lm2)$coefficients[3]
d
```

```
## [1] -8.361345
```

```
e
```

```
## [1] -7.01624
```

```
f
```

```
## [1] -7.678295
```

```
!(f>=d & f<=e)
```

```
## [1] FALSE
```

sysbp is not confounder for age and sex with cigpday

```
lm1 <- lm(cigpday ~ age+sex, data=smoke_vs2)
lm2 <- lm(cigpday ~ age+sex+diabetes, data=smoke_vs2)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[5]))
b= (summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[5]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -0.2971391
```

```
b
```

```
## [1] -0.2200154
```

```
c
```

```
## [1] -0.2546299
```

```
!(c=a & c<=b)
```

```
## [1] FALSE
```

```
d=(summary(lm1)$coefficients[3])-(1.96 * (summary(lm1)$coefficients[6]))
e=(summary(lm1)$coefficients[3])+(1.96 * (summary(lm1)$coefficients[6]))
f=summary(lm2)$coefficients[3]
d
```

```
## [1] -8.361345
```

```
e
```

```
## [1] -7.01624
```

```
f
```

```
## [1] -7.701157
```

```
!(f>=d & f<=e)
```

```
## [1] FALSE
```

diabetes is not confounder for age and sex with cigpday

```
smoke_vs4 = smoke %>%
  dplyr::select(c(randid,cigpday,sex,age)) %>%
  mutate(sex=as.factor(sex)) %>%
  na.omit()

smoke_vs4_nonsmoker = smoke_vs4 %>% filter(cigpday == 0) %>% group_by(randid) %>%
summarize(cig_count = sum(cigpday)) %>% filter(cig_count == 0)
nonsmoker_id = unique(smoke_vs4_nonsmoker$randid)
smoke_vs4_smoker = smoke_vs4 %>% filter(!randid %in% nonsmoker_id)
```

```
lmer_2 <- lmer(cigpday ~ age * sex + (1 | randid),
                   data = smoke_vs4_smoker)
summary(lmer_2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: cigpday ~ age * sex + (1 | randid)
##    Data: smoke_vs4_smoker
##
## REML criterion at convergence: 28186.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5916 -0.4739 -0.0653  0.3832  5.9827
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  randid   (Intercept) 75.99    8.717
##  Residual             41.15    6.415
## Number of obs: 3895, groups:  randid, 1584
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  26.99220    1.42418  18.953
## age          -0.06629    0.02622  -2.528
## sex2        -15.59130    2.00555  -7.774
## age:sex2      0.17357    0.03739   4.642
##
## Correlation of Fixed Effects:
##          (Intr) age    sex2
## age      -0.971
## sex2     -0.710  0.689
## age:sex2  0.681 -0.701 -0.970
```

Ignore those who did not smoke through the whole study.

pvalue

```
coefs2 <- data.frame(coef(summary(lmer_2)))
# use normal distribution to approximate p-value
coefs2$p_value <- 2 * (1 - pnorm(abs(coefs2$t.value)))
```

```
coefs2
```

```
##                 Estimate Std..Error   t.value      p_value
## (Intercept)  26.99220050 1.42417703 18.952841 0.000000e+00
## age          -0.06628581 0.02622214 -2.527856 1.147613e-02
## sex2        -15.59130302 2.00555088 -7.774075 7.549517e-15
## age:sex2      0.17356605 0.03739421  4.641522 3.458523e-06
```

```
#CI age
-0.06629-1.96*0.02622
```

```
## [1] -0.1176812
```

```
-0.06629+1.96*0.02622
```

```
## [1] -0.0148988
```

```
#CI sex
-15.59130-1.96*2.00555
```

```
## [1] -19.52218
```

```
-15.59130+1.96*2.00555
```

```
## [1] -11.66042
```

```
#CI age:sex2
0.17357-1.96*0.03739
```

```
## [1] 0.1002856
```

```
0.17357+1.96*0.03739
```

```
## [1] 0.2468544
```

Part 2

In Figure 5, we see that as systolic blood pressure increases the likelihood of smoking decreases. The trend is not as profound in Figure 6 with diastolic BP or with serum total cholesterol in Figure 7.

```
smoke %>%
  mutate(cursmoke = as.factor(cursmoke)) %>%
  ggplot(aes(age ,sysbp, group = cursmoke, color = cursmoke)) +
  geom_smooth(method = "loess", se = F) +
  ggtitle("Figure 5: Systolic Blood Pressure across Age")
```

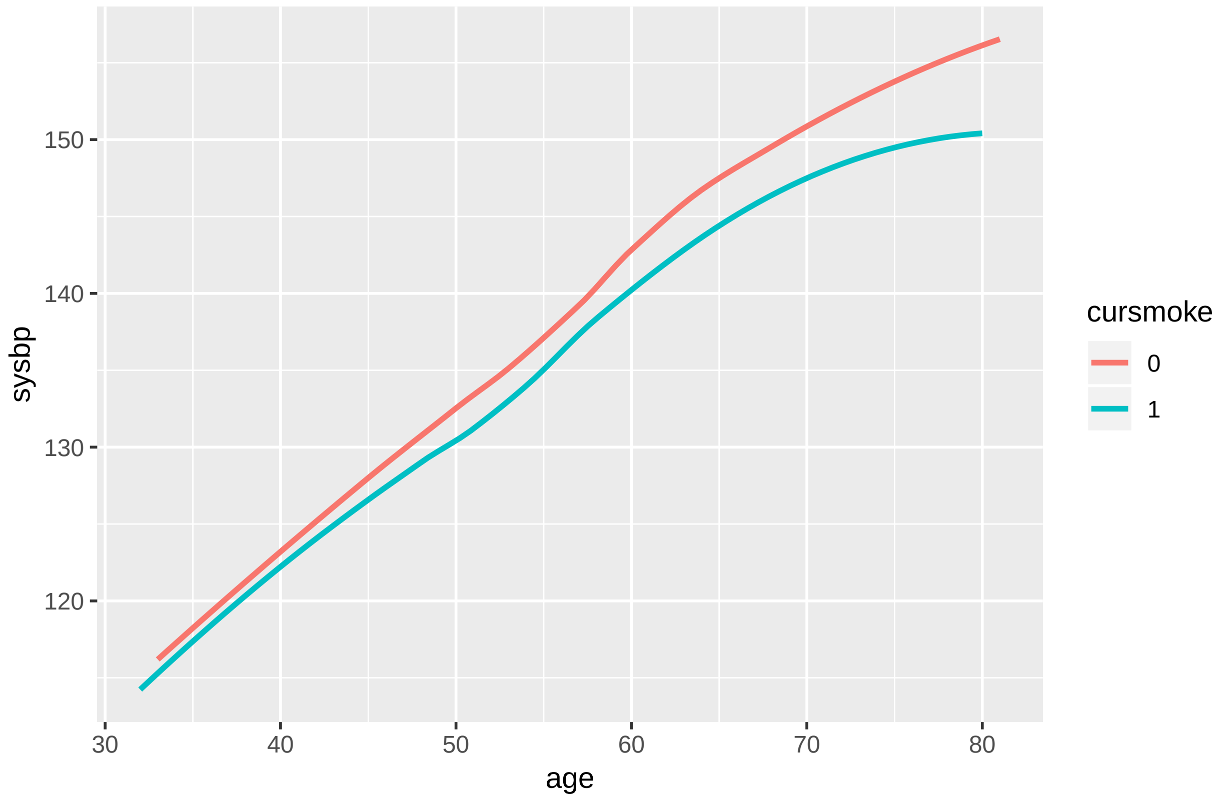
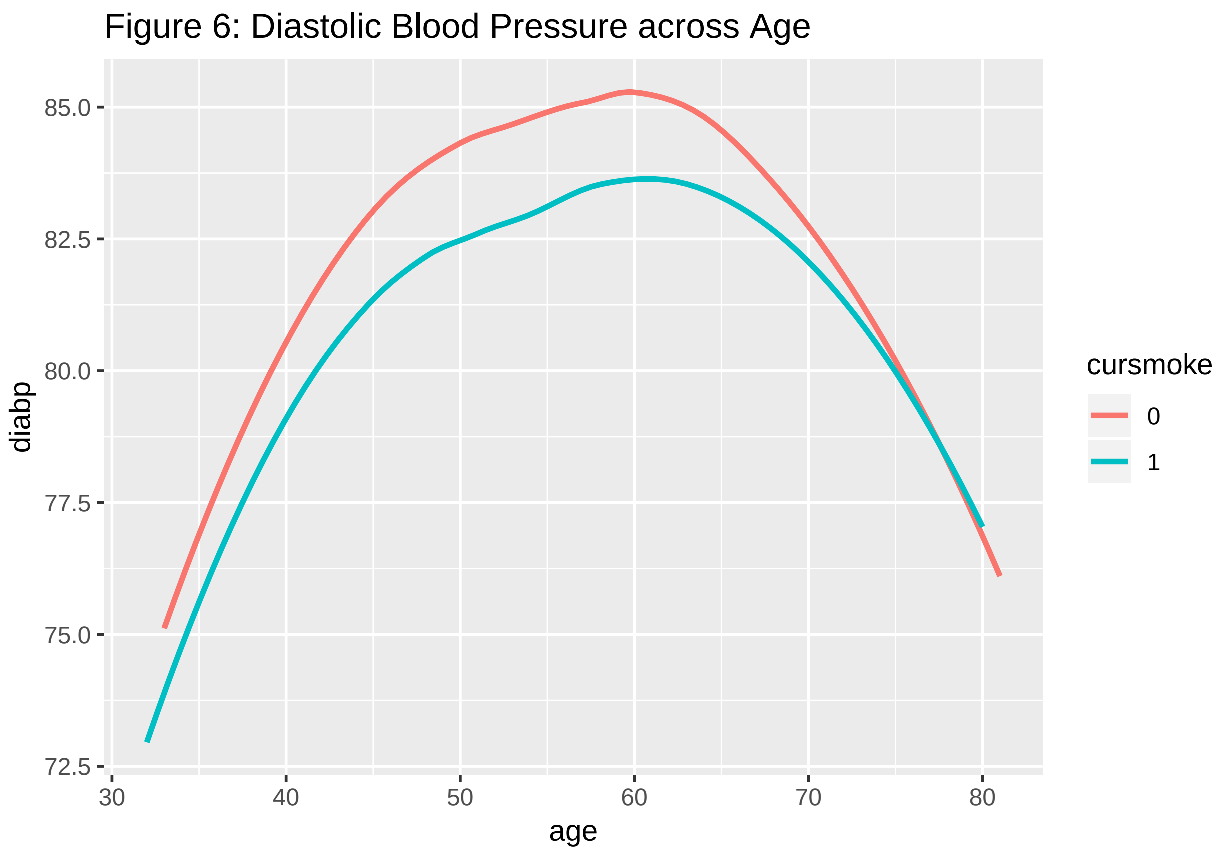


Figure 5: Systolic Blood Pressure across Age

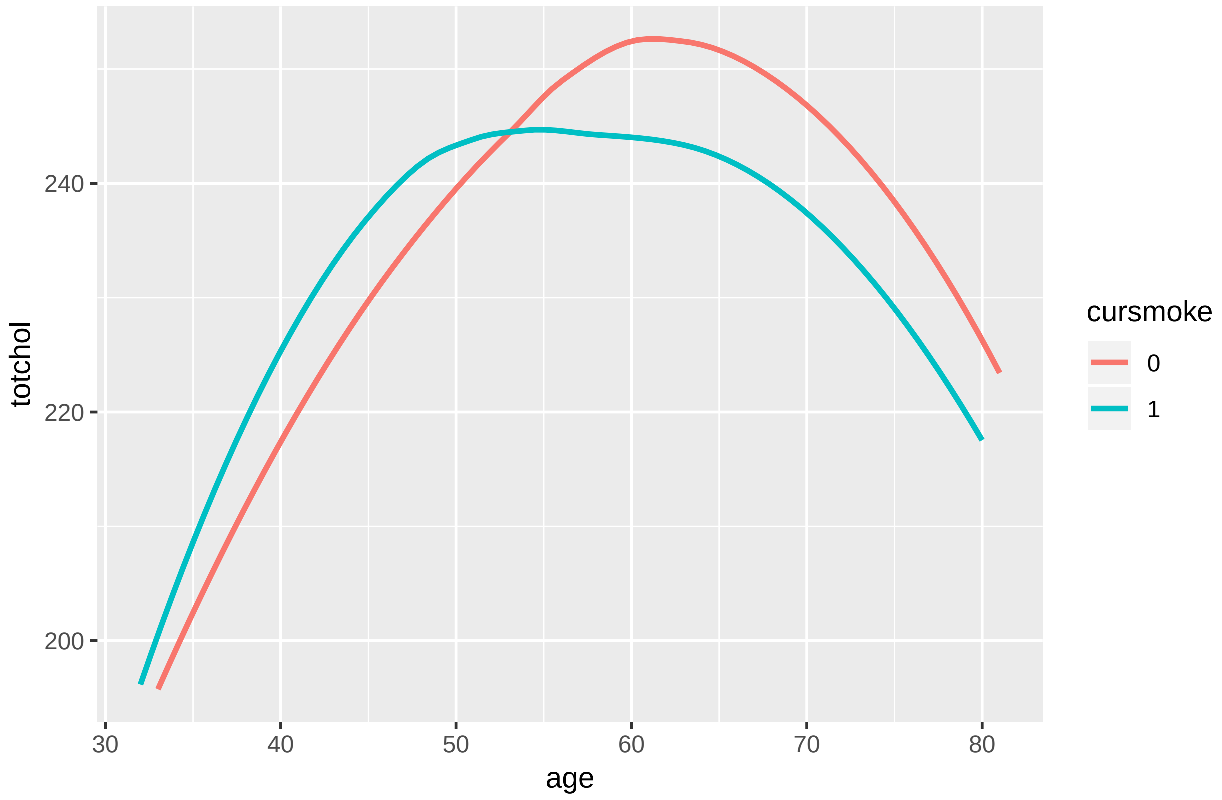
```
smoke %>%
  mutate(cursmoke = as.factor(cursmoke)) %>%
  ggplot(aes(age, diabp, group = cursmoke, color = cursmoke)) +
  geom_smooth(method = "loess", se = F) +
  ggtitle("Figure 6: Diastolic Blood Pressure across Age")
```



```
smoke %>%
  mutate(cursmoke = as.factor(cursmoke)) %>%
  ggplot(aes(age, totchol, cursmoke, group = cursmoke, color = cursmoke)) +
  geom_smooth(method = "loess", se = F) +
  ggtitle("Figure 7: Total Cholesterol across Age")
```

```
## Warning: Removed 409 rows containing non-finite values (stat_smooth).
```

Figure 7: Total Cholesterol across Age



Question 3

```
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + sex, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```
b
```

```
## [1] -4.761322
```

```
c
```

```
## [1] -5.909267
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

sex is not confounder

```
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + age, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
```

```r
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```r
b
```

```
## [1] -4.761322
```

```r
c
```

```
## [1] -2.440408
```

```r
!(c>=a & c<=b)
```

```
## [1] TRUE
```

age is confounder

```r
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + totchol, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```r
b
```

```
## [1] -4.761322
```

```r
c
```

```
## [1] -5.642857
```

```r
!(c>=a & c<=b)
```

```
## [1] FALSE
```

totchol is not confounder

```r
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + bmi, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```r
b
```

```
## [1] -4.761322
```

```r
c
```

```
## [1] -3.774433
```

```r
!(c>=a & c<=b)
```

```
## [1] TRUE
```

bmi is confounder

```r
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + heartrte, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```r
b
```

```
## [1] -4.761322
```

```r
c
```

```
## [1] -6.583046
```

```r
!(c>=a & c<=b)
```

```
## [1] FALSE
```

heartrte is not confounder

```r
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + educ, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```r
b
```

```
## [1] -4.761322
```

```r
c
```

```
## [1] -6.009864
```

```r
!(c>=a & c<=b)
```

```
## [1] FALSE
```

educ is not confounder

```r
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + diabetes, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```r
b
```

```
## [1] -4.761322
```

```r
c
```

```
## [1] -5.876455
```

```r
!(c>=a & c<=b)
```

```
## [1] FALSE
```

diabetes is not confounder

```
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + prevap, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```
b
```

```
## [1] -4.761322
```

```
c
```

```
## [1] -5.941756
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

prevap is not confounder

```
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + prevchd, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```
b
```

```
## [1] -4.761322
```

```
c
```

```
## [1] -6.016597
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

```
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + prevmi, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```
b
```

```
## [1] -4.761322
```

```
c
```

```
## [1] -6.139762
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

```
lm1 <- lm(sysbp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(sysbp ~ cursmoke + prevstrk, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.429258
```

```
b
```

```
## [1] -4.761322
```

```
c
```

```
## [1] -6.023463
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

By rule of thumb, age and bmi are confounders. Based on the literature view, sex can be potential confounders as they can affect smoke status and sysbp at the same time. So we still put it into model.

```
smoke_vs5 = smoke %>%
  dplyr::select(c(randid,cursmoke,sex,age,bmi,sysbp)) %>%
  mutate(sex=as.factor(sex),cursmoke=as.factor(cursmoke)) %>%
  na.omit()
```

```
lmer_3 <- lmer(sysbp ~ cursmoke + bmi + sex + age + (1|randid), data = smoke_vs5)
summary(lmer_3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: sysbp ~ cursmoke + bmi + sex + age + (1 | randid)
##    Data: smoke_vs5
##
## REML criterion at convergence: 98637.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2514 -0.5336 -0.0511  0.4610  6.0665
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  randid   (Intercept) 261.1    16.16
##  Residual             156.3    12.50
## Number of obs: 11575, groups:  randid, 4420
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) 51.118109   1.973388  25.904
## cursmoke1   -0.008418   0.432847  -0.019
## bmi          1.443149   0.057512  25.093
## sex2         2.609485   0.552576   4.722
## age          0.855104   0.020583  41.544
##
## Correlation of Fixed Effects:
##           (Intr) crsmk1 bmi    sex2
## cursmoke1 -0.355
## bmi       -0.767  0.132
## sex2      -0.227  0.124  0.068
## age       -0.582  0.244 -0.020  0.010
```

Calculating p value using normal approximation:

```
coefs3 <- data.frame(coef(summary(lmer_3)))
# use normal distribution to approximate p-value
coefs3$p_value <- 2 * (1 - pnorm(abs(coefs3$t.value)))
coefs3
```

```
##                 Estimate Std..Error     t.value      p_value
## (Intercept) 51.118109258 1.97338760 25.90373493 0.000000e+00
## cursmoke1   -0.008418291 0.43284706 -0.01944865 9.844832e-01
## bmi          1.443149377 0.05751195 25.09303303 0.000000e+00
## sex2         2.609485119 0.55257636  4.72239734 2.330807e-06
## age          0.855103777 0.02058297 41.54423412 0.000000e+00
```

No interaction term because not significant

Cursmoke not significant,but include because this is our interest

```
#cursmoke 95% CI
-0.008418-1.96*0.432847
```

```
## [1] -0.8567981
```

```
-0.008418+1.96*0.432847
```

```
## [1] 0.8399621
```

```
#CI bmi
1.443149-1.96*0.057512
```

```
## [1] 1.330425
```

```
1.443149+1.96*0.057512
```

```
## [1] 1.555873
```

```
#95%CI sex
2.609485-1.96*0.552576
```

```
## [1] 1.526436
```

```
2.609485+1.96*0.552576
```

```
## [1] 3.692534
```

```
#age
0.855104-1.96*0.020583
```

```
## [1] 0.8147613
```

```
0.855104+1.96*0.020583
```

```
## [1] 0.8954467
```

Question 4

```
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + sex, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```
b
```

```
## [1] -1.922971
```

```
c
```

```
## [1] -2.982803
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

sex is not confounder

```
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + age, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```
b
```

```
## [1] -1.922971
```

```
c
```

```
## [1] -1.662623
```

```
!(c>=a & c<=b)
```

```
## [1] TRUE
```

age is confounder

```
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + totchol, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```
b
```

```
## [1] -1.922971
```

```
c
```

```
## [1] -2.441814
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

totchol is not confounder

```
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + bmi, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```
b
```

```
## [1] -1.922971
```

```
c
```

```
## [1] -1.168078
```

```
!(c>=a & c<=b)
```

```
## [1] TRUE
```

bmi is confounder

```
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + heartrte, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```
b
```

```
## [1] -1.922971
```

```
c
```

```
## [1] -2.910674
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

heartrte is not confounder

```
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + educ, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```
b
```

```
## [1] -1.922971
```

```
c
```

```
## [1] -2.623741
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

educ is not confounder

```
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + diabetes, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```
b
```

```
## [1] -1.922971
```

```
c
```

```
## [1] -2.593779
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

diabetes is not confounder

```
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + prevap, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```
b
```

```
## [1] -1.922971
```

```
c
```

```
## [1] -2.586016
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

```
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + prevchd, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```r
b
```

```
## [1] -1.922971
```

```r
c
```

```
## [1] -2.619172
```

```r
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

```r
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + prevmi, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```r
b
```

```
## [1] -1.922971
```

```r
c
```

```
## [1] -2.65378
```

```r
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

```r
lm1 <- lm(diabp ~ cursmoke, data=smoke_vs1)
lm2 <- lm(diabp ~ cursmoke + prevstrk, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -3.365883
```

```r
b
```

```
## [1] -1.922971
```

```r
c
```

```
## [1] -2.618415
```

```r
!(c>=a & c<=b)
```

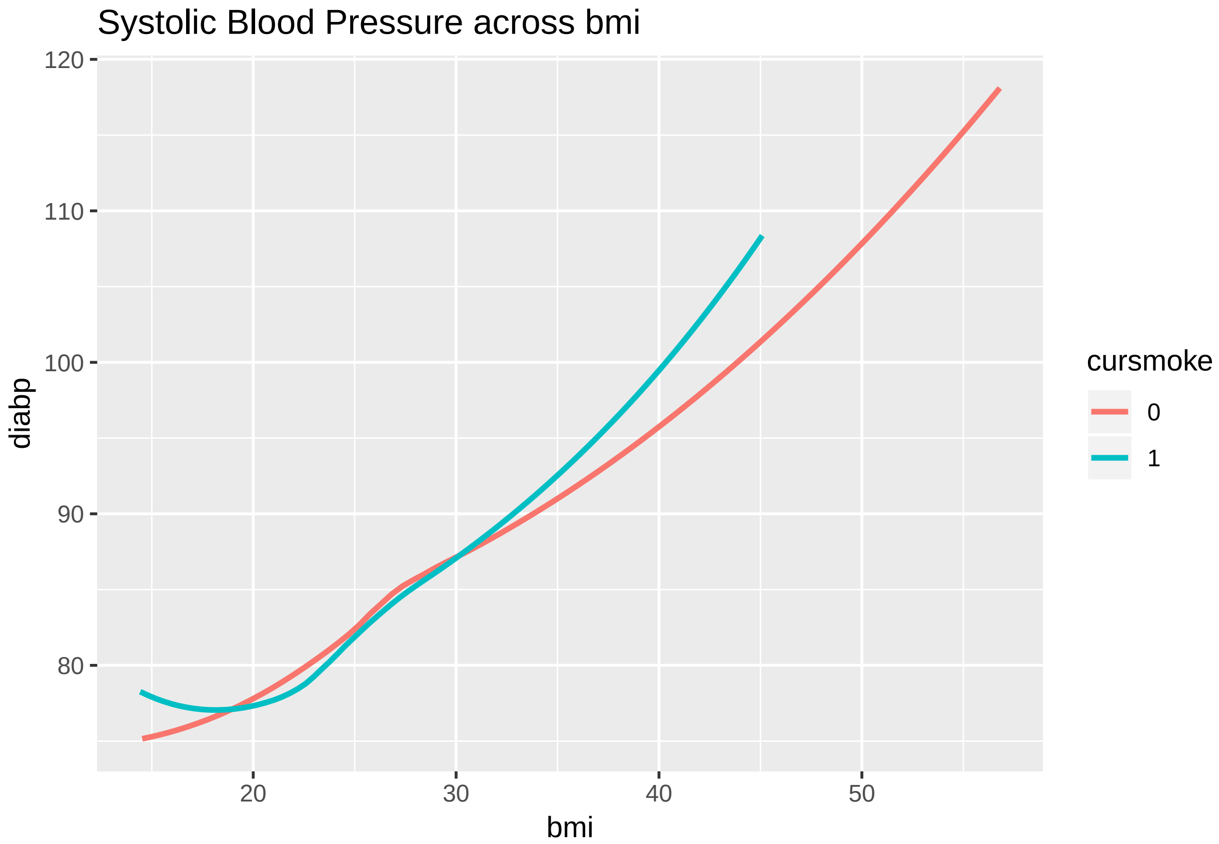
```
## [1] FALSE
```

not confounder

By rule of thumb, age, bmi is confounder. Based on the literature view, sex can be potential confounders as it can affect smoke status and diabp at the same time. So we still put them into model.

checking interactions

```
smoke_vs6 = smoke %>%
  dplyr::select(c(randid,cursmoke,sex,age,bmi,diabp)) %>%
  mutate(sex=as.factor(sex),cursmoke=as.factor(cursmoke)) %>%
  na.omit()
smoke_vs6 %>%
  mutate(cursmoke = as.factor(cursmoke)) %>%
  ggplot(aes(bmi ,diabp, group = cursmoke, color = cursmoke)) +
  geom_smooth(method = "loess", se = F) +
  ggtitle("Systolic Blood Pressure across bmi")
```



This plot argues for some interaction of the two predictors, as the lines are not parallel.

```
lmer_4 <- lmer(diabp ~  cursmoke*bmi + sex  +cursmoke*age + (1|randid), data = smoke_vs6)
summary(lmer_4)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: diabp ~ cursmoke * bmi + sex + cursmoke * age + (1 | randid)
##    Data: smoke_vs6
##
## REML criterion at convergence: 85394.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -5.6356 -0.5401 -0.0204  0.5116  4.5821
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  randid   (Intercept) 69.18    8.318
##  Residual             53.74    7.331
## Number of obs: 11575, groups:  randid, 4420
##
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)    61.12030    1.32853  46.006
## cursmoke1     -11.20762    1.83644  -6.103
## bmi             0.98322    0.03816  25.763
## sex2           -0.51623    0.29304  -1.762
## age            -0.05122    0.01442  -3.553
## cursmoke1:bmi   0.09296    0.05477   1.697
## cursmoke1:age   0.16113    0.02129   7.570
##
## Correlation of Fixed Effects:
##             (Intr) crsmk1 bmi    sex2   age    crsmk1:b
## cursmoke1   -0.607
## bmi         -0.763  0.460
## sex2        -0.160 -0.023  0.040
## age         -0.616  0.403 -0.003 -0.005
## cursmok1:bm  0.434 -0.768 -0.569  0.033 -0.005
## cursmoke1:g  0.375 -0.626 -0.013  0.023 -0.596 -0.001
```

pvalue

```
coefs4 <- data.frame(coef(summary(lmer_4)))
# use normal distribution to approximate p-value
coefs4$p_value <- 2 * (1 - pnorm(abs(coefs4$t.value)))
coefs4
```

```
##                   Estimate Std..Error   t.value      p_value
## (Intercept)    61.12030268 1.32853361 46.005838 0.000000e+00
## cursmoke1     -11.20761771 1.83643655 -6.102916 1.041507e-09
## bmi             0.98321831 0.03816339 25.763391 0.000000e+00
## sex2           -0.51623272 0.29303940 -1.761650 7.812853e-02
## age            -0.05121702 0.01441670 -3.552618 3.814175e-04
## cursmoke1:bmi   0.09296139 0.05476822  1.697360 8.962862e-02
## cursmoke1:age   0.16113017 0.02128536  7.569999 3.730349e-14
```

cursmoke1:bmi not siginificant, remove this iteraction

```
lmer_41 <- lmer(diabp ~  bmi + sex  +cursmoke*age + (1|randid), data = smoke_vs6)
summary(lmer_41)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: diabp ~ bmi + sex + cursmoke * age + (1 | randid)
##    Data: smoke_vs6
##
## REML criterion at convergence: 85393.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -5.6246 -0.5402 -0.0196  0.5121  4.5793
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  randid   (Intercept) 69.18    8.318
##  Residual             53.76    7.332   
## Number of obs: 11575, groups:  randid, 4420
## 
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)   60.14237    1.19720  50.236
## bmi            1.02005    0.03139  32.496
## sex2          -0.53287    0.29288  -1.819
## cursmoke1     -8.81416    1.17670  -7.491
## age           -0.05110    0.01442  -3.544
## cursmoke1:age  0.16118    0.02129   7.572
## 
## Correlation of Fixed Effects:
##             (Intr) bmi    sex2   crsmk1 age   
## bmi         -0.697                            
## sex2        -0.194  0.072                     
## cursmoke1   -0.475  0.044  0.004              
## age         -0.682 -0.006 -0.005  0.623       
## cursmoke1:g  0.417 -0.016  0.023 -0.979 -0.596
```

```
coefs41 <- data.frame(coef(summary(lmer_41)))
# use normal distribution to approximate p-value
coefs41$p_value <- 2 * (1 - pnorm(abs(coefs41$t.value)))
coefs41
```

```
##                  Estimate Std..Error   t.value      p_value
## (Intercept)   60.14236703 1.19720071 50.235827 0.000000e+00
## bmi            1.02005040 0.03139016 32.495866 0.000000e+00
## sex2          -0.53287471 0.29288259 -1.819414 6.884828e-02
## cursmoke1     -8.81416214 1.17669748 -7.490593 6.861178e-14
## age           -0.05109733 0.01441770 -3.544068 3.940029e-04
## cursmoke1:age  0.16118028 0.02128724  7.571684 3.685940e-14
```

```
#CI cursmoke
-8.81416-1.96*1.17670
```

```
## [1] -11.12049
```

```
-8.81416+1.96*1.17670
```

```
## [1] -6.507828
```

```
#CIbmi
1.02005-1.96*0.03139
```

```
## [1] 0.9585256
```

```
1.02005+1.96*0.03139
```

```
## [1] 1.081574
```

sex although not significant, it is confounder, so we still put in into the model

```
#CI sex
-0.53287-1.96*0.29288
```

```
## [1] -1.106915
```

```
-0.53287+1.96*0.29288
```

```
## [1] 0.0411748
```

```
#CI age
-0.05110-1.96*0.01442
```

```
## [1] -0.0793632
```

```
-0.05110+1.96*0.01442
```

```
## [1] -0.0228368
```

```
#cursmoke1:age
0.16118-1.96*0.02129
```

```
## [1] 0.1194516
```

```
0.16118+1.96*0.02129
```

```
## [1] 0.2029084
```

QUestion 5

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + sex, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -3.398869
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

sex is not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + age, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] 0.3207259
```

```
!(c>=a & c<=b)
```

```
## [1] TRUE
```

age is confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + diabp, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -2.923499
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

diabp is not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + bmi, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -2.802548
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

bmi is confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + heartrte, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -5.013823
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

heartrte is not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + educ, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -4.505649
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

educ is not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + sysbp, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -2.111556
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

sysbp is not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + diabetes, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -4.361909
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

diabetes is not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + prevap, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -4.450606
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + prevchd, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -4.492534
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + prevmi, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -4.56068
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + prevstrk, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -4.526573
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

not confounder

```
lm1 <- lm(totchol ~ cursmoke, data=smoke_vs1)
lm2 <- lm(totchol ~ cursmoke + prevhyp, data=smoke_vs1)
a=(summary(lm1)$coefficients[2])-(1.96 * (summary(lm1)$coefficients[4]))
b=(summary(lm1)$coefficients[2])+(1.96 * (summary(lm1)$coefficients[4]))
c=summary(lm2)$coefficients[2]
a
```

```
## [1] -7.188361
```

```
b
```

```
## [1] -1.871145
```

```
c
```

```
## [1] -2.94428
```

```
!(c>=a & c<=b)
```

```
## [1] FALSE
```

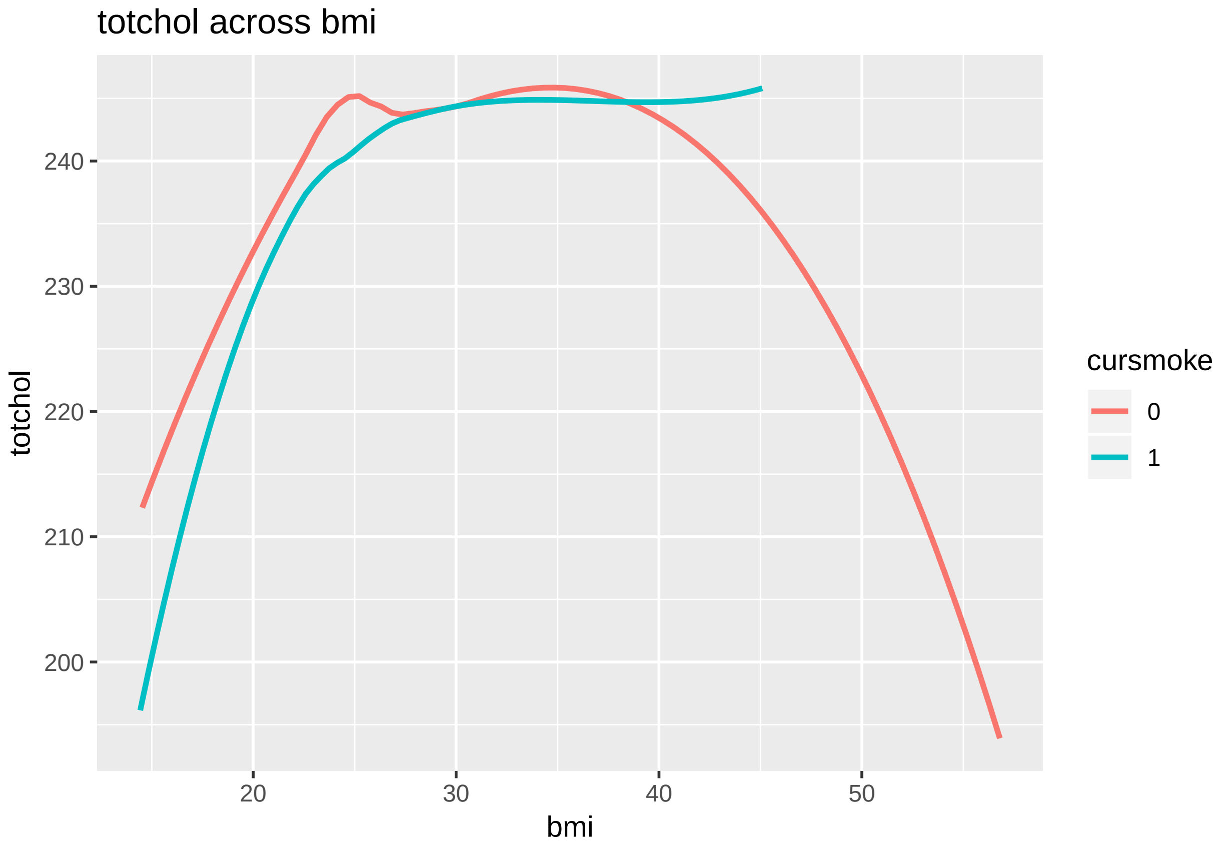
not confounder

By rule of thumb, age, bmi is confounder. Based on the literature view, sex can be potential confounders as it can affect smoke status and totchol at the same time. So we still put them into model.

```
smoke_vs7 = smoke %>%
  dplyr::select(c(randid,cursmoke,sex,age,bmi,totchol)) %>%
  mutate(sex=as.factor(sex),cursmoke=as.factor(cursmoke)) %>%
  na.omit()
```

checking interactions

```
smoke_vs7 %>%
  mutate(cursmoke = as.factor(cursmoke)) %>%
  ggplot(aes(bmi ,totchol, group = cursmoke, color = cursmoke)) +
  geom_smooth(method = "loess", se = F) +
  ggtitle("totchol across bmi")
```



This plot argues for some interaction of the two predictors, as the lines are not parallel.

```
lmer_5 <- lmer(totchol ~ cursmoke*bmi + sex +cursmoke*age + (1|randid), data = smoke_vs7)
summary(lmer_5)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: totchol ~ cursmoke * bmi + sex + cursmoke * age + (1 | randid)
##    Data: smoke_vs7
##
## REML criterion at convergence: 112160.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -8.8193 -0.5216 -0.0140  0.4864  9.1134
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  randid   (Intercept) 1305.5   36.13
##  Residual              674.1   25.96
## Number of obs: 11173, groups:  randid, 4405
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)   176.51441    5.22462  33.785
## cursmoke1     -29.38692    7.05633  -4.165
## bmi             1.45643    0.15257   9.546
## sex2           13.94202    1.22545  11.377
## age             0.32861    0.05514   5.960
## cursmoke1:bmi   0.74739    0.21240   3.519
## cursmoke1:age   0.26381    0.08053   3.276
##
## Correlation of Fixed Effects:
##             (Intr) crsmk1 bmi    sex2   age    crsmk1:b
## cursmoke1   -0.599
## bmi         -0.775  0.458
## sex2        -0.169 -0.019  0.040
## age         -0.599  0.393 -0.002 -0.003
## cursmok1:bm  0.434 -0.776 -0.559  0.029 -0.005
## cursmoke1:g  0.363 -0.617 -0.016  0.022 -0.589  0.001
```

```
coefs5 <- data.frame(coef(summary(lmer_5)))
# use normal distribution to approximate p-value
coefs5$p_value <- 2 * (1 - pnorm(abs(coefs5$t.value)))
coefs5
```

```
##                   Estimate Std..Error   t.value      p_value
## (Intercept)   176.5144115  5.2246199 33.785120 0.000000e+00
## cursmoke1     -29.3869178  7.0563288 -4.164619 3.118735e-05
## bmi             1.4564332  0.1525716  9.545900 0.000000e+00
## sex2           13.9420172  1.2254514 11.377046 0.000000e+00
## age             0.3286111  0.0551388  5.959708 2.526892e-09
## cursmoke1:bmi   0.7473888  0.2123986  3.518803 4.334990e-04
## cursmoke1:age   0.2638118  0.0805312  3.275896 1.053273e-03
```

```
#CI cursmoke
-29.38692-1.96*7.05633
```

```
## [1] -43.21733
```

```
-29.38692+1.96*7.05633
```

```
## [1] -15.55651
```

```
#CI bmi
1.45643-1.96*0.15257
```

```
## [1] 1.157393
```

```
1.45643+1.96*0.15257
```

```
## [1] 1.755467
```

```
#CI sex
13.94202-1.96*1.22545
```

```
## [1] 11.54014
```

```
13.94202+1.96*1.22545
```

```
## [1] 16.3439
```

```
#CI age
0.32861-1.96*0.05514
```

```
## [1] 0.2205356
```

```
0.32861+1.96*0.05514
```

```
## [1] 0.4366844
```

```
#CI cursmoke1:bmi
0.74739-1.96*0.21240
```

```
## [1] 0.331086
```

```
0.74739+1.96*0.21240
```

```
## [1] 1.163694
```

```
#CI  cursmoke1:age
0.26381-1.96*0.08053
```

```
## [1] 0.1059712
```

```
0.26381+1.96*0.08053
```

```
## [1] 0.4216488
```

Please include a table which shows point estimate, 95 CI and p value for each term in the model(calculated above)