

# Untitled

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```
# recode

data = read.csv("nhanes99_06_NEW.csv")

data = data %>%
  mutate(RIDRETH1 = case_when(RIDRETH1 == 4 ~ 1,
                              RIDRETH1 == 3 ~ 2,
                              RIDRETH1 %in% c(1,2,5) ~ 3),
         DMDEDUC2 = case_when(DMDEDUC2 == 1 ~ 1, # 1: Less Than 9th Grade
                              DMDEDUC2 %in% c(2,3,4,5,7,9) ~ 2),
         DMDMARTL = case_when(DMDMARTL == 1 ~ 1, #1: married
                              DMDMARTL %in% c(2,3,4,5,6,77,99) ~ 2),
         SMQ040 = case_when(SMQ040 %in% c(1,2) ~ 1,
                             SMQ040 %in% c(3,9) ~ 2))

data = data %>%
  mutate(BPQ020 = case_when(BPQ020 == 1 ~ 1,
                             BPQ020 == 2 ~ 2,
                             BPQ020 == 9 ~ 3),
         BPQ080 = case_when(BPQ080 == 1 ~ 1,
                             BPQ080 == 2 ~ 2,
                             BPQ080 %in% c(7,9) ~ 3),
         BPQ090A = case_when(BPQ090A == 1 ~ 1,
                              BPQ090A == 2 ~ 2,
                              BPQ090A == 9 ~ 3))

data = data %>%
  mutate(MCQ160F = case_when(MCQ160F == 1 ~ 1,
                              MCQ160F == 2 ~ 2,
                              MCQ160F == 9 ~ 3),
         MCQ160C = case_when(MCQ160C == 1 ~ 1,
                              MCQ160C == 2 ~ 2,
                              MCQ160C %in% c(7,9) ~ 3),
         MCQ160E = case_when(MCQ160E == 1 ~ 1,
                              MCQ160E == 2 ~ 2,
                              MCQ160E %in% c(7,9) ~ 3),
         MCQ160L = case_when(MCQ160L == 1 ~ 1,
                              MCQ160L == 2 ~ 2,
                              MCQ160L == 9 ~ 3))

data = data %>%
  mutate(DIQ010 = case_when(DIQ010 == 1 ~ 1,
                             DIQ010 == 2 ~ 2,
```

```

        DIQ010 %in% c(3,7,9) ~3),
  DIQ050 = case_when(DIQ050 == 1 ~ 1,
                     DIQ050 ==2 ~ 2,
                     DIQ050 %in% c(7,9) ~3),
  DIQ070 = case_when(DIQ070 == 1 ~ 1,
                     DIQ070 ==2 ~ 2,
                     DIQ070 ==9 ~3))

data$RIAGENDR <- factor(data$RIAGENDR, levels = 1: 2, labels =c("Male", "Female"))
data$RIDRETH1 <- factor(data$RIDRETH1, levels = 1: 3, labels =c("Black", "White", "other"))
data$DMDEDUC2 <- factor(data$DMDEDUC2, levels = 1: 2, labels =c("Less Than 9th Grade", "9th Grade or above"))
data$DMDMARTL <- factor(data$DMDMARTL, levels = 1: 2, labels =c("Married", "Non-Married"))
data$SMQ040 <- factor(data$SMQ040, levels = 1: 2, labels =c("smoked", "Non-smoked"))

data$BPQ020 <- factor(data$BPQ020, levels = 1: 3, labels =c("Yes", "No", "other"))
data$BPQ080 <- factor(data$BPQ080, levels = 1: 3, labels =c("Yes", "No", "other"))
data$BPQ090A <- factor(data$BPQ090A, levels = 1: 3, labels =c("Yes", "No", "other"))

data$MCQ160F <- factor(data$MCQ160F, levels = 1: 3, labels =c("Yes", "No", "other"))
data$MCQ160C <- factor(data$MCQ160C, levels = 1: 3, labels =c("Yes", "No", "other"))
data$MCQ160E <- factor(data$MCQ160E, levels = 1: 3, labels =c("Yes", "No", "other"))
data$MCQ160L <- factor(data$MCQ160L, levels = 1: 3, labels =c("Yes", "No", "other"))

data$DIQ010 <- factor(data$DIQ010, levels = 1: 3, labels =c("Yes", "No", "other"))
data$DIQ050 <- factor(data$DIQ050, levels = 1: 3, labels =c("Yes", "No", "other"))
data$DIQ070 <- factor(data$DIQ070, levels = 1: 3, labels =c("Yes", "No", "other"))

data$outcome = NULL
data$outcome[data$LBXGLU>=126] = 1
data$outcome[data$DIQ010=='Yes'] = 1
data$outcome[data$DIQ050=='Yes'] = 1
data$outcome[data$DIQ070=='Yes'] = 1
data$outcome[data$LBXGLU<=126 & data$DIQ010!='Yes'&data$DIQ010!='Yes'&data$DIQ010!='Yes'] = 0
data$outcome = as.factor(data$outcome)
data1 = data %>%
  drop_na(outcome) %>%
  filter(RIDAGEYR>=20) %>%
  filter(MCQ160L!= 'Yes')
# exclusion criteria: no missing value in outcome, age >=20, no history of liver disease.
data1 = data1 %>%
  mutate(age = case_when(RIDAGEYR<=39 ~ 1,
                         RIDAGEYR>=40 & RIDAGEYR <=59 ~2,
                         RIDAGEYR>=60 ~ 3))
data1$age <- factor(data1$age, levels = 1: 3, labels =c("20-39", "40-59", "60 and above"))

data1$hypten = NULL # definition of hypertension is : mean systolic blood pressure
# of 140 mm Hg, a mean diastolic blood pressure of 90 mm Hg OR have been told by doctor

data1$hypten[data1$BPXDAR>=90&data1$BPXSAR>=140] =1
data1$hypten[data1$BPXDAR<=90|data1$BPXSAR<=140] =0
data1$hypten[data1$BPQ020 == 'Yes'] = 1
table(data1$hypten)

```

```
##
##      0      1
## 3052 3450
```

```
data1$hypten = as.factor(data1$hypten)
```

```
data1$totalcho = NULL # Total cholesterol: reporting that a physician had diagnosed that person with h
# reporting that a physician had advised that person to take cholesterol lowering medications
data1$totalcho[data1$BPQ080 == 'Yes'|data1$BPQ090 == 'Yes'] = 1
data1$totalcho[data1$BPQ080 != 'Yes'| data1$BPQ090 != 'Yes'] = 0
table(data1$totalcho)
```

```
##
##      0      1
## 4374 2267
```

```
data1$totalcho = as.factor(data1$totalcho)
```

```
data1$cardiov = NULL # cardiovascular disease was defined as a self-reported history of coronary heart
data1$cardiov[data1$MCQ160F== 'Yes'|data1$MCQ160C== 'Yes'|data1$MCQ160E== 'Yes']=1
data1$cardiov[data1$MCQ160F!= 'Yes'&data1$MCQ160C!= 'Yes'& data1$MCQ160E!= 'Yes']=0
table(data1$cardiov)
```

```
##
##      0      1
## 8542 1046
```

```
data1$cardiov = as.factor(data1$cardiov)
data1$bilirudin = NULL
data1$bilirudin[data1$LBDSTBSI>=10]=1
data1$bilirudin[data1$LBDSTBSI<=10]=0
table(data1$bilirudin)
```

```
##
##      0      1
## 2849 6347
```

```
data1$bilirudin = as.factor(data1$bilirudin)
```

```
# recalculate the weight in 8 yrs
```

```
data1$INT8YR = NULL
data1$INT8YR[data1$SDDSRVYR==1|data1$SDDSRVYR==2] = 2/4 * data1$WTINT4YR[data1$SDDSRVYR==1|data1$SDDSRV
data1$INT8YR[data1$SDDSRVYR==3|data1$SDDSRVYR==4] = 1/4 * data1$WTINT2YR[data1$SDDSRVYR==3|data1$SDDSRV
```

```
write.csv(data1, 'analysis.csv')
```

```
# data cleaning
```

```
data1 = read.csv("analysis.csv")
```

```

data1 = data1 %>%
  mutate(bmi = case_when (BMXBMI<25 ~ 1,
    (BMXBMI>=25 & BMXBMI<29) ~ 2,
    BMXBMI>=30 ~ 3))
data1$bmi <- factor(data1$bmi, levels = 1: 3, labels =c("less than 25", "25-29", "30 and above"))

data1$waist[data1$RIAGENDR=="Male" & data1$BMXWAIST < 102] = "lower"
data1$waist[data1$RIAGENDR=="Male" & data1$BMXWAIST >= 102] = "higher"
data1$waist[data1$RIAGENDR=="Female" & data1$BMXWAIST < 88] = "lower"
data1$waist[data1$RIAGENDR=="Female" & data1$BMXWAIST >= 88] = "higher"
data1$waist = as.factor(data1$waist)

data1$tri[data1$LBXTR < 90] = "low"
data1$tri[data1$LBXTR >= 90] = "high"
data1$tri = as.factor(data1$tri)

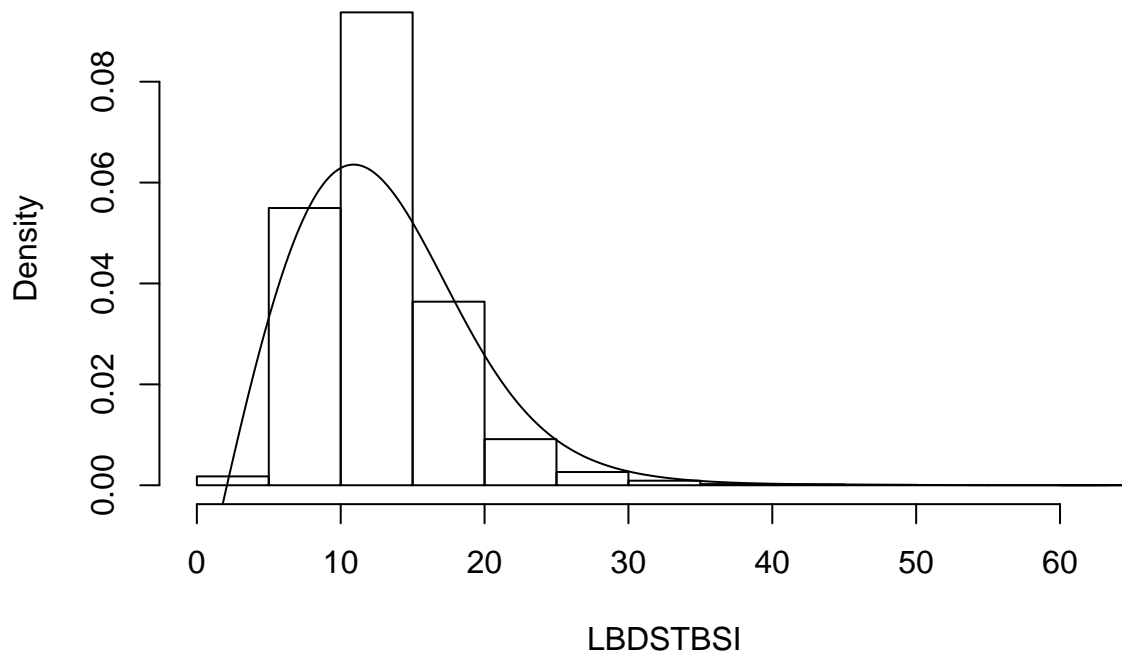
data1$al[data1$RIAGENDR=="Male" & data1$ALQ130 > 4] = "heavy consumption"
data1$al[data1$RIAGENDR=="Male" & data1$ALQ130 <= 4] = "moderate or no consumption"
data1$al[data1$RIAGENDR=="Female" & data1$ALQ130 > 3] = "heavy consumption"
data1$al[data1$RIAGENDR=="Female" & data1$ALQ130 <= 3] = "moderate or no consumption"
data1$al = as.factor(data1$al)

# survey design
dstrat <- svydesign(id = ~SDMVPSU, strata = ~SDMVSTRA, weights = ~INT8YR, data = data1, nest= T)

# figure 1
svyhist(~LBDSTBSI,design=dstrat,main="Histogram with kernel density")
den =svysmooth(~LBDSTBSI, dstrat,bandwidth = 5)
lines(den)

```

## Histogram with kernel density



```
# age
age = svyby(~bilirudin, ~age, design = dstrat, svymean, na.rm = TRUE)
age
```

```
##           age bilirudin      se
## 20-39      20-39 0.6981508 0.01487740
## 40-59      40-59 0.7239031 0.01014965
## 60 and above 60 and above 0.7326492 0.01285297
```

```
confint(age)
```

```
##           2.5 %    97.5 %
## 20-39      0.6689916 0.7273099
## 40-59      0.7040101 0.7437960
## 60 and above 0.7074579 0.7578406
```

```
# gender
gender = svyby(~bilirudin, ~factor(RIAGENDR), design = dstrat, svymean, na.rm = TRUE)
gender
```

```
##           factor(RIAGENDR) bilirudin      se
## Female      Female 0.6185947 0.01106139
## Male        Male 0.8195233 0.00965585
```

```
confint(gender)
```

```
##           2.5 %    97.5 %  
## Female 0.5969147 0.6402746  
## Male   0.8005982 0.8384484
```

```
# education
```

```
edu = svyby(~bilirudin, ~factor(DMDEDUC2), design = dstrat, svymean, na.rm = TRUE)  
edu
```

```
##           factor(DMDEDUC2) bilirudin      se  
## 9th Grade or above    9th Grade or above 0.7205259 0.00920115  
## Less Than 9th Grade Less Than 9th Grade 0.6661506 0.01850784
```

```
confint(edu)
```

```
##           2.5 %    97.5 %  
## 9th Grade or above 0.7024920 0.7385598  
## Less Than 9th Grade 0.6298759 0.7024253
```

```
# race
```

```
race = svyby(~bilirudin, ~factor(RIDRETH1), design = dstrat, svymean, na.rm = TRUE)  
race
```

```
##           factor(RIDRETH1) bilirudin      se  
## Black           Black 0.6114524 0.02235191  
## other           other 0.6861098 0.02297137  
## White           White 0.7408065 0.01060867
```

```
confint(race)
```

```
##           2.5 %    97.5 %  
## Black 0.5676434 0.6552613  
## other 0.6410867 0.7311329  
## White 0.7200139 0.7615991
```

```
# smoke
```

```
smoke = svyby(~bilirudin, ~factor(SMQ040), design = dstrat, svymean, na.rm = TRUE)  
smoke
```

```
##           factor(SMQ040) bilirudin      se  
## Non-smoked    Non-smoked 0.7365148 0.01349653  
## smoked        smoked 0.6642354 0.01648430
```

```
confint(smoke)
```

```
##           2.5 %    97.5 %  
## Non-smoked 0.7100621 0.7629676  
## smoked     0.6319268 0.6965441
```

```
# alcohol
al = svyby(~bilirudin, ~factor(al), design = dstrat, svymean, na.rm = TRUE)
al
```

```
##                factor(al) bilirudin          se
## heavy consumption          heavy consumption 0.7275852 0.01755101
## moderate or no consumption moderate or no consumption 0.7285306 0.01041782
```

```
confint(al)
```

```
##                2.5 %    97.5 %
## heavy consumption    0.6931859 0.7619846
## moderate or no consumption 0.7081120 0.7489491
```

```
# triclycerides
tri = svyby(~bilirudin, ~factor(tri), design = dstrat, svymean, na.rm = TRUE)
tri
```

```
##      factor(tri) bilirudin          se
## high      high 0.7197541 0.01018127
## low       low 0.7385510 0.01302811
```

```
confint(tri)
```

```
##          2.5 %    97.5 %
## high 0.6997992 0.7397090
## low  0.7130163 0.7640856
```

```
# waist circumference
waist = svyby(~bilirudin, ~factor(waist), design = dstrat, svymean, na.rm = TRUE)
waist
```

```
##      factor(waist) bilirudin          se
## higher      higher 0.6791497 0.012486971
## lower      lower 0.7575596 0.009566348
```

```
confint(waist)
```

```
##          2.5 %    97.5 %
## higher 0.6546756 0.7036237
## lower  0.7388099 0.7763093
```

```
# bmi
bmi = svyby(~bilirudin, ~factor(bmi), design = dstrat, svymean, na.rm = TRUE)
bmi
```

```
##      factor(bmi) bilirudin          se
## less than 25 less than 25 0.7304532 0.01186527
## 25-29      25-29 0.7451276 0.01176859
## 30 and above 30 and above 0.6694125 0.01507449
```

```
confint(bmi)
```

```
##           2.5 %    97.5 %
## less than 25 0.7071977 0.7537087
## 25-29        0.7220616 0.7681937
## 30 and above 0.6398670 0.6989579
```

```
# logistic regression without covariates
```

```
model1 <- svyglm(bilirudin ~ factor(hypten) + factor(totalcho) + factor(cardiov) + factor(tri) + factor
summary(model1)
```

```
##
## Call:
## svyglm(formula = bilirudin ~ factor(hypten) + factor(totalcho) +
##       factor(cardiov) + factor(tri) + factor(al) + factor(bmi) +
##       factor(waist), design = dstrat, family = quasibinomial)
##
## Survey design:
## svydesign(id = ~SDMVPSU, strata = ~SDMVSTRA, weights = ~INT8YR,
##       data = data1, nest = T)
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   0.324671   0.247937   1.309   0.1962
## factor(hypten)1                 0.383153   0.152443   2.513   0.0152 *
## factor(totalcho)1               0.026706   0.120839   0.221   0.8260
## factor(cardiov)1               -0.022284   0.174713  -0.128   0.8990
## factor(tri)low                 -0.067074   0.137608  -0.487   0.6280
## factor(al)moderate or no consumption 0.008003   0.167252   0.048   0.9620
## factor(bmi)25-29                0.232062   0.167499   1.385   0.1719
## factor(bmi)30 and above         0.172522   0.180198   0.957   0.3429
## factor(waist)lower              0.519501   0.198660   2.615   0.0117 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 1.147372)
##
## Number of Fisher Scoring iterations: 4
```

```
# logistic regression with covariates
```

```
model2 <- svyglm(bilirudin ~ factor(hypten) + factor(totalcho) + factor(cardiov) + factor(tri) + factor
summary(model2)
```

```
##
## Call:
## svyglm(formula = bilirudin ~ factor(hypten) + factor(totalcho) +
##       factor(cardiov) + factor(tri) + factor(al) + factor(bmi) +
##       factor(waist) + factor(age) + factor(RIAGENDR) + factor(DMDEDUC2) +
##       factor(RIDRETH1) + factor(SMQ040) + factor(DMDMARTL), design = dstrat,
##       family = quasibinomial)
##
## Survey design:
```

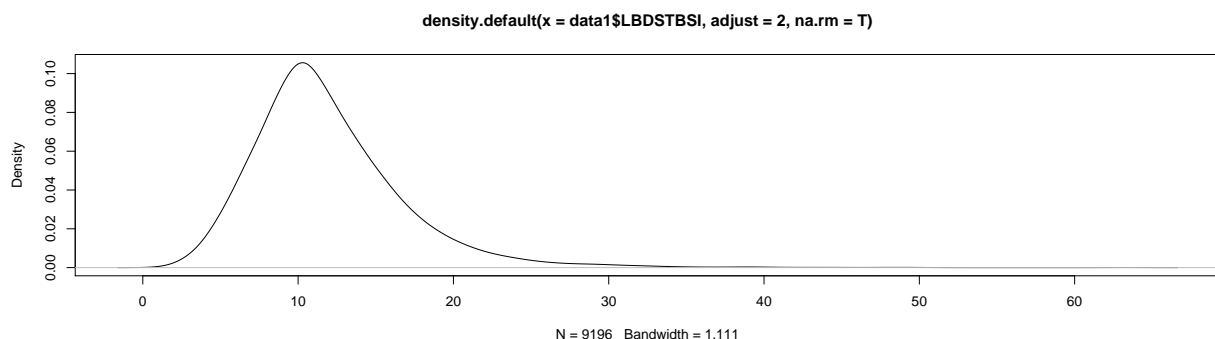


```
## svydesign(id = ~SDMVPSU, strata = ~SDMVSTRA, weights = ~INT8YR,
##       data = data1, nest = T)
##
## Coefficients:
##
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -0.291995   0.552556  -0.528   0.5999
## factor(hypten)1       0.322703   0.198092   1.629   0.1106
## factor(totalcho)1     0.039096   0.176575   0.221   0.8258
## factor(cardiov)1     -0.186440   0.183346  -1.017   0.3149
## factor(tri)low        0.147376   0.218775   0.674   0.5041
## factor(al)moderate or no consumption -0.008046   0.245233  -0.033   0.9740
## factor(bmi)25-29       0.117536   0.196004   0.600   0.5519
## factor(bmi)30 and above 0.179466   0.252741   0.710   0.4815
## factor(waist)lower     0.144293   0.258873   0.557   0.5802
## factor(age)40-59      -0.010170   0.214659  -0.047   0.9624
## factor(age)60 and above 0.223206   0.280565   0.796   0.4307
## factor(RIAGENDR)Male   0.849238   0.159352   5.329 3.42e-06 ***
## factor(DMDEDUC2)Less Than 9th Grade -0.015983   0.353143  -0.045   0.9641
## factor(RIDRETH1)other  0.624456   0.332404   1.879   0.0671 .
## factor(RIDRETH1)White  0.554830   0.239258   2.319   0.0252 *
## factor(SMQ040)smoked  -0.274210   0.227548  -1.205   0.2348
## factor(DMDMARTL)Non-Married -0.096574   0.194437  -0.497   0.6219
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 1.122213)
##
## Number of Fisher Scoring iterations: 4
```

additional analysis : bivariate analysis and introducing interaction terms in regression

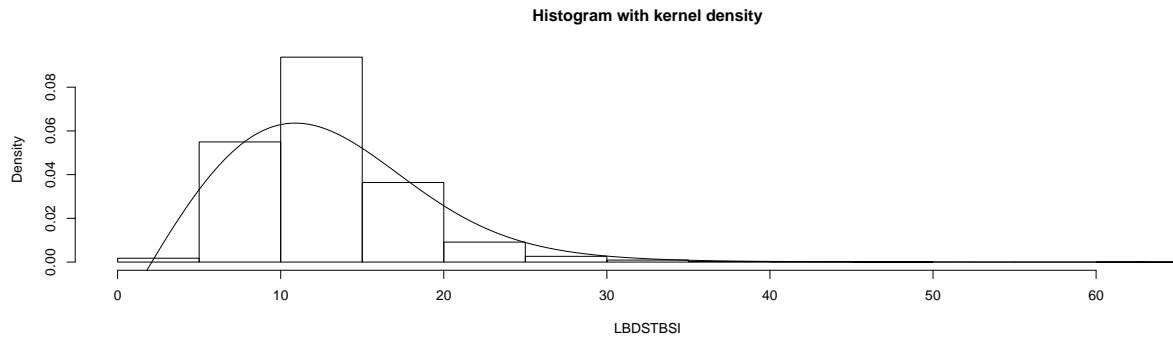
```
#exploring potential relationship between two covariates in predicting the outcome by bivariate analysis.
des = svydesign(ids = ~SDMVPSU, weights = ~INT8YR, strata = ~SDMVSTRA, nest = T, data = data1)
options( survey.lonely.psu = "adjust" )

plot(density(data1$LBDSTBSI, na.rm = T, adjust = 2))
```

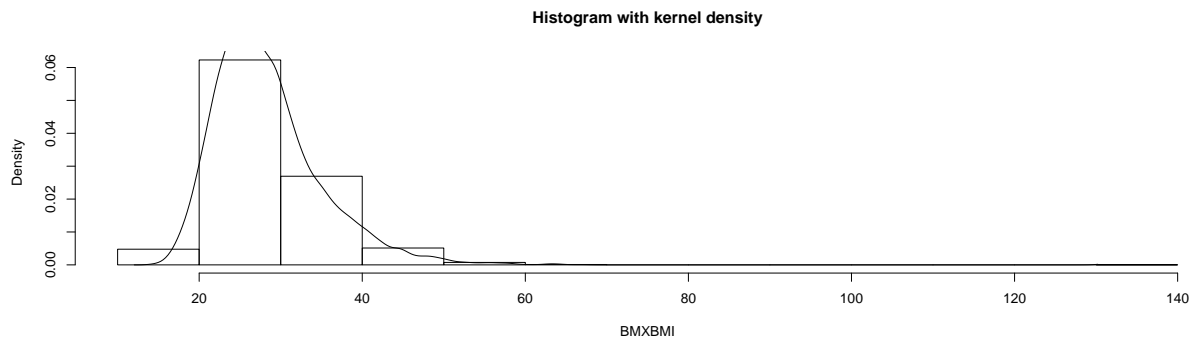


```
svyhist(~LBDSTBSI,design=des,main="Histogram with kernel density")

den  =svysmooth(~LBDSTBSI, des,bandwidth = 5)
lines(den)
```

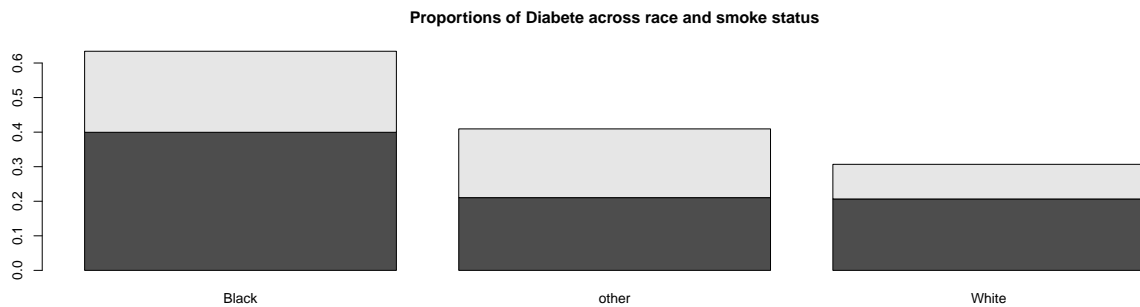


```
svyhist(~BMXBMI,design=des,main="Histogram with kernel density")
den  =svysmooth(~BMXBMI, des)
lines(den)
```



```
b = svyby(~outcome,~SMQ040+RIDRETH1,design=des,svymean)

barplot(b,beside=F,main="Proportions of Diabete across race and smoke status")
```

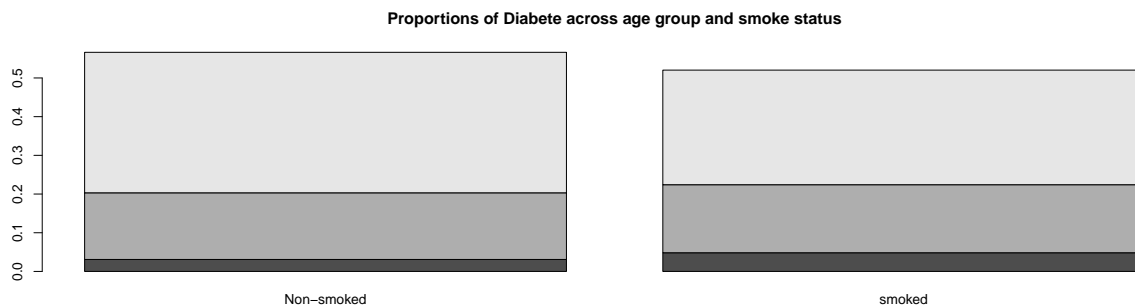


```
svychisq(~SMQ040+RIDRETH1,des,statistic = 'F') # Rao-Scott F-statistic test shows association between s
```

```
##
## Pearson's X^2: Rao & Scott adjustment
##
## data: svychisq(~SMQ040 + RIDRETH1, des, statistic = "F")
## F = 20.423, ndf = 1.7636, ddf = 104.0495, p-value = 1.296e-07
```

```
c = svyby(~outcome,~age+SMQ040,design=des,svymean)
```

```
barplot(c,beside=F,main="Proportions of Diabete across age group and smoke status")
```



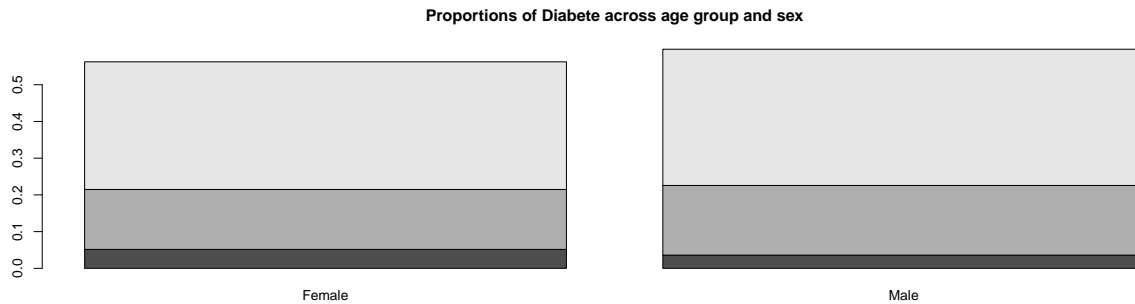
```
d = svyby(~outcome,~age+RIDRETH1,design=des,svymean)
```

```
barplot(d,beside=F,main="Proportions of Diabete across age group and race")
```

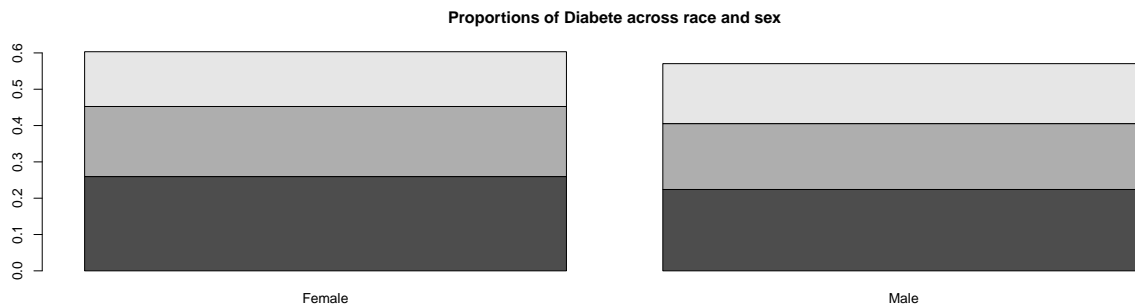


```
e = svyby(~outcome,~age+RIAGENDR,design=des,svymean)
```

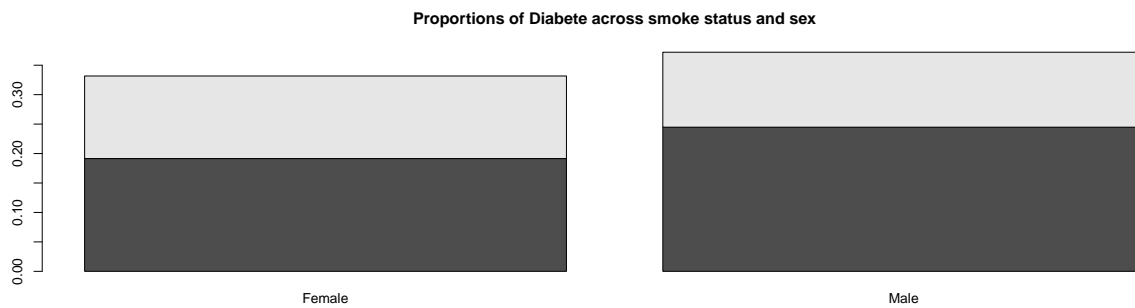
```
barplot(e,beside=F,main="Proportions of Diabete across age group and sex")
```



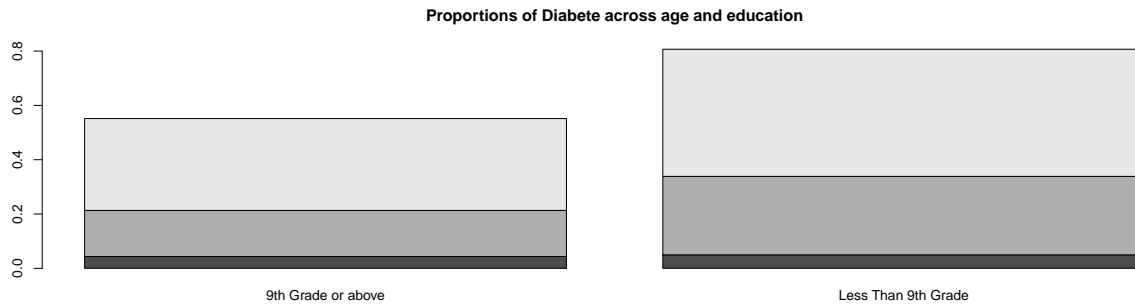
```
f = svyby(~outcome, ~RIDRETH1+RIAGENDR, design=des, svymean)
barplot(f, beside=F, main="Proportions of Diabetes across race and sex")
```



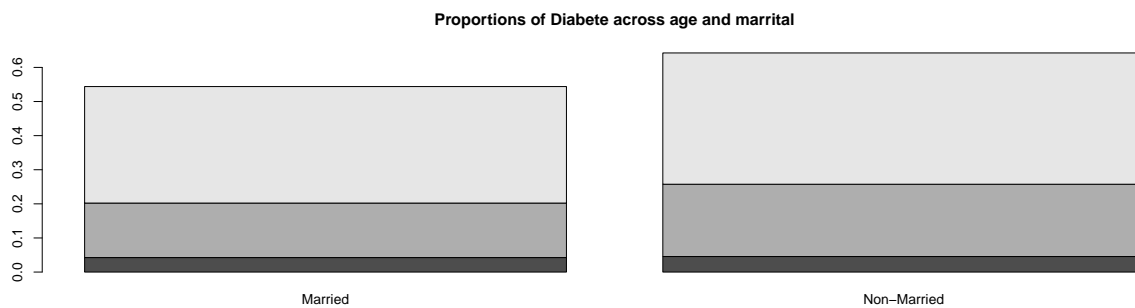
```
g = svyby(~outcome, ~SMQ040+RIAGENDR, design=des, svymean)
barplot(g, beside=F, main="Proportions of Diabetes across smoke status and sex")
```



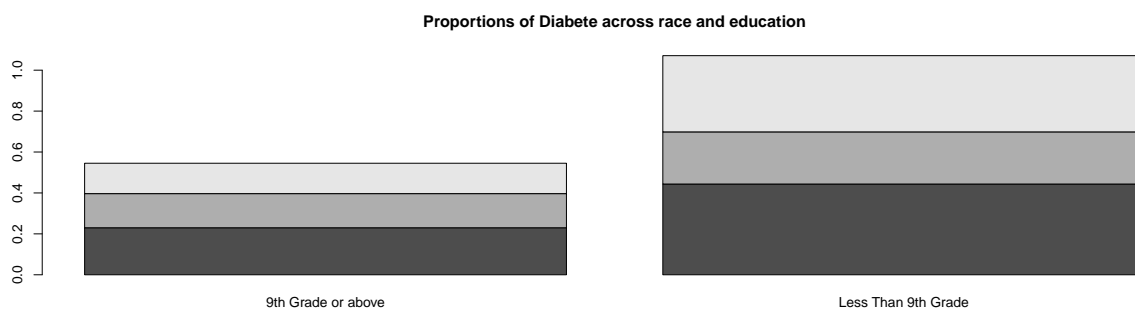
```
h = svyby(~outcome, ~age+DMDEDUC2, design=des, svymean)
barplot(h, beside=F, main="Proportions of Diabetes across age and education")
```



```
i = svyby(~outcome,~age+DMDMARTL,design=des,svymean)
barplot(i,beside=F,main="Proportions of Diabetes across age and marital")
```



```
j = svyby(~outcome,~RIDRETH1+DMDEDUC2,design=des,svymean)
barplot(j,beside=F,main="Proportions of Diabetes across race and education")
```

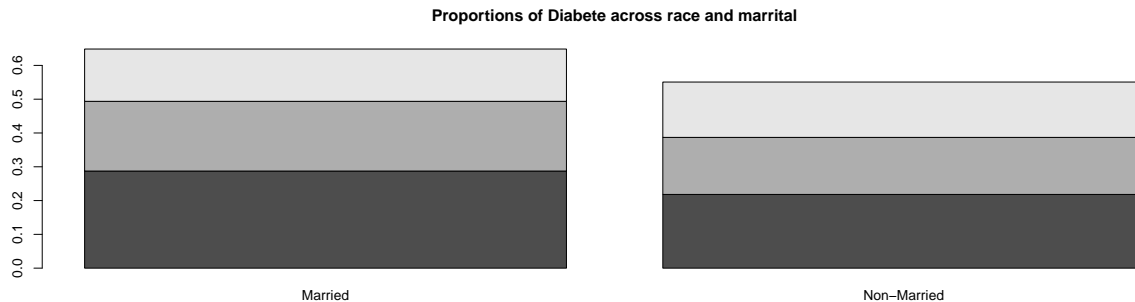


```
svychisq(~RIDRETH1+DMDEDUC2,des,statistic = 'F') # Rao-Scott F-statistic test shows association between

##
## Pearson's X^2: Rao & Scott adjustment
##
## data: svychisq(~RIDRETH1 + DMDEDUC2, des, statistic = "F")
## F = 246.4, ndf = 1.7875, ddf = 105.4606, p-value < 2.2e-16
```

```
k = svyby(~outcome, ~RIDRETH1+DMDMARTL, design=des, svymean)

barplot(k, beside=F, main="Proportions of Diabete across race and marrital")
```



```
# add interaction terms in covariates adjusted model
```

```
model3 <- svyglm(bilirudin ~ factor(hypten) + factor(totalcho) + factor(cardiov) + factor(tri) + factor
summary(model3)
```

```
##
## Call:
## svyglm(formula = bilirudin ~ factor(hypten) + factor(totalcho) +
##   factor(cardiov) + factor(tri) + factor(al) + factor(bmi) +
##   factor(waist) + factor(age) + factor(RIAGENDR) + factor(DMDEDUC2) +
##   factor(RIDRETH1) + factor(SMQ040) + factor(DMDMARTL) + factor(SMQ040) *
##   factor(RIDRETH1), design = dstrat, family = quasibinomial)
##
## Survey design:
## svydesign(id = ~SDMVPSU, strata = ~SDMVSTRA, weights = ~INT8YR,
##   data = data1, nest = T)
##
## Coefficients:
##
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.50891 0.59384 -0.857 0.396
## factor(hypten)1 0.31599 0.19887 1.589 0.120
## factor(totalcho)1 0.03710 0.17687 0.210 0.835
## factor(cardiov)1 -0.18358 0.18492 -0.993 0.327
## factor(tri)low 0.14254 0.21954 0.649 0.520
## factor(al)moderate or no consumption -0.01145 0.24900 -0.046 0.964
## factor(bmi)25-29 0.11729 0.19462 0.603 0.550
## factor(bmi)30 and above 0.17930 0.25461 0.704 0.485
## factor(waist)lower 0.13921 0.25778 0.540 0.592
## factor(age)40-59 -0.01861 0.21021 -0.089 0.930
## factor(age)60 and above 0.21246 0.28194 0.754 0.455
## factor(RIAGENDR)Male 0.85475 0.16063 5.321 3.97e-06
## factor(DMDEDUC2)Less Than 9th Grade -0.00956 0.35342 -0.027 0.979
## factor(RIDRETH1)other 0.75544 0.45718 1.652 0.106
## factor(RIDRETH1)White 0.81418 0.38380 2.121 0.040
## factor(SMQ040)smoked 0.12660 0.42151 0.300 0.765
```

```
## factor(DMDMARTL)Non-Married -0.09619 0.19295 -0.499 0.621
## factor(RIDRETH1)other:factor(SMQ040)smoked -0.23802 0.55924 -0.426 0.673
## factor(RIDRETH1)White:factor(SMQ040)smoked -0.46895 0.50611 -0.927 0.360
##
## (Intercept)
## factor(hypten)1
## factor(totalcho)1
## factor(cardiov)1
## factor(tri)low
## factor(al)moderate or no consumption
## factor(bmi)25-29
## factor(bmi)30 and above
## factor(waist)lower
## factor(age)40-59
## factor(age)60 and above
## factor(RIAGENDR)Male ***
## factor(DMDEDUC2)Less Than 9th Grade
## factor(RIDRETH1)other
## factor(RIDRETH1)White *
## factor(SMQ040)smoked
## factor(DMDMARTL)Non-Married
## factor(RIDRETH1)other:factor(SMQ040)smoked
## factor(RIDRETH1)White:factor(SMQ040)smoked
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 1.121433)
##
## Number of Fisher Scoring iterations: 4
```

```
regTermTest(model3, ~bilirudin ~ factor(hypten) + factor(totalcho) + factor(cardiov) + factor(tri) + fa
```

```
## Working (Rao-Scott+F) LRT for factor(hypten) factor(totalcho) factor(cardiov) factor(tri) factor(al)
## in svyglm(formula = bilirudin ~ factor(hypten) + factor(totalcho) +
## factor(cardiov) + factor(tri) + factor(al) + factor(bmi) +
## factor(waist) + factor(age) + factor(RIAGENDR) + factor(DMDEDUC2) +
## factor(RIDRETH1) + factor(SMQ040) + factor(DMDMARTL) + factor(SMQ040) *
## factor(RIDRETH1), design = dstrat, family = quasibinomial)
## Working 2logLR = 2941.053 p= 0.061179
## (scale factors: 2.9 2.3 2.1 1.9 1.3 0.98 0.85 0.73 0.65 0.53 0.45 0.4 0.35 0.28 0.2 0.18 ); denomi
```

```
model4 <- svyglm(bilirudin ~ factor(hypten) + factor(totalcho) + factor(cardiov) + factor(tri) + factor
summary(model4)
```

```
##
## Call:
## svyglm(formula = bilirudin ~ factor(hypten) + factor(totalcho) +
## factor(cardiov) + factor(tri) + factor(al) + factor(bmi) +
## factor(waist) + factor(age) + factor(RIAGENDR) + factor(DMDEDUC2) +
## factor(RIDRETH1) + factor(SMQ040) + factor(DMDMARTL) + factor(DMDEDUC2) *
## factor(RIDRETH1), design = dstrat, family = quasibinomial)
##
```

```
## Survey design:
## svydesign(id = ~SDMVPSU, strata = ~SDMVSTRA, weights = ~INT8YR,
##   data = data1, nest = T)
##
## Coefficients:
##
##                                     Estimate Std. Error
## (Intercept)                      -2.707e-01  5.603e-01
## factor(hypten)1                   3.229e-01  2.002e-01
## factor(totalcho)1                 3.607e-02  1.768e-01
## factor(cardiov)1                 -1.956e-01  1.857e-01
## factor(tri)low                    1.466e-01  2.192e-01
## factor(al)moderate or no consumption -7.888e-05  2.446e-01
## factor(bmi)25-29                  1.229e-01  1.968e-01
## factor(bmi)30 and above           1.892e-01  2.513e-01
## factor(waist)lower                1.572e-01  2.591e-01
## factor(age)40-59                 -1.248e-02  2.156e-01
## factor(age)60 and above           2.284e-01  2.826e-01
## factor(RIAGENDR)Male              8.482e-01  1.598e-01
## factor(DMDEDUC2)Less Than 9th Grade -1.243e+00  7.233e-01
## factor(RIDRETH1)other             5.401e-01  3.261e-01
## factor(RIDRETH1)White            5.181e-01  2.380e-01
## factor(SMQ040)smoked             -2.680e-01  2.281e-01
## factor(DMDMARTL)Non-Married       -9.942e-02  1.940e-01
## factor(DMDEDUC2)Less Than 9th Grade:factor(RIDRETH1)other 1.602e+00  9.228e-01
## factor(DMDEDUC2)Less Than 9th Grade:factor(RIDRETH1)White 1.163e+00  7.807e-01
##
##                                     t value Pr(>|t|)
## (Intercept)                      -0.483    0.6315
## factor(hypten)1                   1.613    0.1144
## factor(totalcho)1                 0.204    0.8394
## factor(cardiov)1                 -1.053    0.2984
## factor(tri)low                    0.669    0.5073
## factor(al)moderate or no consumption 0.000    0.9997
## factor(bmi)25-29                  0.625    0.5358
## factor(bmi)30 and above           0.753    0.4558
## factor(waist)lower                0.607    0.5473
## factor(age)40-59                 -0.058    0.9541
## factor(age)60 and above           0.808    0.4237
## factor(RIAGENDR)Male              5.308 4.14e-06 ***
## factor(DMDEDUC2)Less Than 9th Grade -1.718    0.0933 .
## factor(RIDRETH1)other             1.656    0.1053
## factor(RIDRETH1)White            2.177    0.0353 *
## factor(SMQ040)smoked             -1.175    0.2468
## factor(DMDMARTL)Non-Married       -0.512    0.6111
## factor(DMDEDUC2)Less Than 9th Grade:factor(RIDRETH1)other 1.736    0.0901 .
## factor(DMDEDUC2)Less Than 9th Grade:factor(RIDRETH1)White 1.490    0.1438
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 1.121369)
##
## Number of Fisher Scoring iterations: 4
```

```
regTermTest(model4, ~bilirudin ~ factor(hypten) + factor(totalcho) + factor(cardiov) + factor(tri) + fa
```



```

## Working (Rao-Scott+F) LRT for factor(hypten) factor(totalcho) factor(cardiov) factor(tri) factor(al)
## in svyglm(formula = bilirudin ~ factor(hypten) + factor(totalcho) +
##   factor(cardiov) + factor(tri) + factor(al) + factor(bmi) +
##   factor(waist) + factor(age) + factor(RIAGENDR) + factor(DMDEDUC2) +
##   factor(RIDRETH1) + factor(SMQ040) + factor(DMDMARTL) + factor(DMDEDUC2) *
##   factor(RIDRETH1), design = dstrat, family = quasibinomial)
## Working 2logLR = 6394.498 p= 0.041855
## (scale factors: 2.7 2.2 2 1.8 1.7 0.95 0.89 0.79 0.75 0.58 0.49 0.38 0.29 0.24 0.18 0.12 ); denomi

```