Data_Cleaning

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```
# Loading required packages
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(ggplot2)
library("vcdExtra")
```

```
## Loading required package: vcd
```

```
## Loading required package: grid
```

```
## Loading required package: gnm
```

```
##
## Attaching package: 'vcdExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     summarise
```

```
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
library(MASS)
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```r
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```r
library(patchwork)
```

```
##
## Attaching package: 'patchwork'
```

```
## The following object is masked from 'package:MASS':
##
##     area
```

```r
library(lattice)
```

```
##
## Attaching package: 'lattice'
```

```
## The following object is masked from 'package:gnm':
##
##     barley
```

Step 1 and 2: Data Cleaning and Descriptive Statistics

```r
# Load the CSV file
data_old <- read.csv("../Handout/final_cardiac_data.csv")

# Data Overview
head(data_old)
```

```
##     X   seqn event gender age ethnic1 educ sleep.hrs diabetes smoker  bmi
## 1 179 109441     0      2  20       3    4         9        2      2 18.0
## 2 323 109585     0      1  20       4    2         8        2      2 28.2
## 3 463 109726     0      1  20       4    4         5        2      2 26.2
## 4 546 109809     0      2  20       3    4         7        2      2 22.1
## 5 589 109852     0      2  20       2    2         6        2     NA 20.4
## 6 630 109893     0      2  20       4    3         8        2      1 30.3
```

```r
# Remove identifier columns
data <- data_old[, !(names(data_old) %in% c("X", "seqn"))]

# Run summary statistics to get overview
summary(data)
```

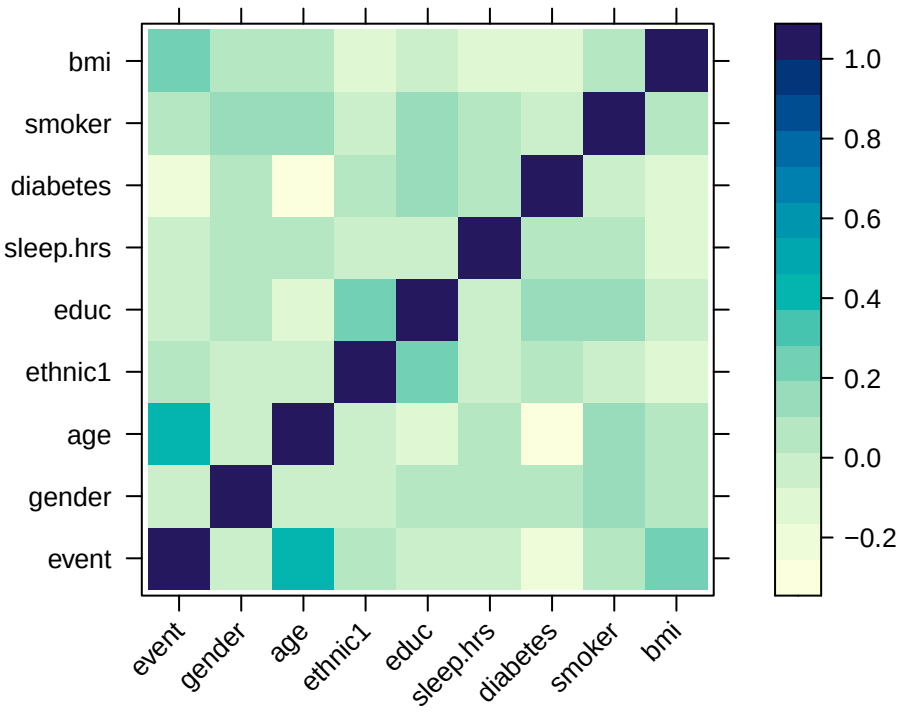
```
##      event            gender           age           ethnic1
##  Min.   :0.0000   Min.   :1.000   Min.   :20.00   Min.   :1.000
##  1st Qu.:0.0000   1st Qu.:1.000   1st Qu.:36.00   1st Qu.:3.000
##  Median :0.0000   Median :2.000   Median :52.00   Median :3.000
##  Mean   :0.4246   Mean   :1.516   Mean   :50.96   Mean   :3.279
##  3rd Qu.:1.0000   3rd Qu.:2.000   3rd Qu.:64.00   3rd Qu.:4.000
##  Max.   :1.0000   Max.   :2.000   Max.   :80.00   Max.   :5.000
##
```

```
##       educ         sleep.hrs         diabetes         smoker
##  Min.   :1.000   Min.   : 2.000   Min.   :1.000   Min.   :1.000
##  1st Qu.:3.000   1st Qu.: 6.500   1st Qu.:2.000   1st Qu.:2.000
##  Median :4.000   Median : 7.500   Median :2.000   Median :2.000
##  Mean   :3.557   Mean   : 7.551   Mean   :1.863   Mean   :1.763
##  3rd Qu.:4.000   3rd Qu.: 8.500   3rd Qu.:2.000   3rd Qu.:2.000
##  Max.   :9.000   Max.   :14.000   Max.   :9.000   Max.   :2.000
##                  NA's   :13       NA's   :72      NA's   :147
##       bmi
##  Min.   :14.20
##  1st Qu.:24.98
##  Median :29.10
##  Mean   :30.48
##  3rd Qu.:34.50
##  Max.   :86.20
##  NA's   :46
```

```r
# Find the correlation between each predictor
# Use it to check for collinearity when running regression models to predict missing values
cor_matrix <- cor(na.omit(data))
cor_matrix
```

```
##                 event      gender         age     ethnic1        educ
## event      1.00000000 -0.03829681  0.45808113  0.05271390 -0.04336137
## gender    -0.03829681  1.00000000 -0.06239729  0.01084565  0.02054031
## age        0.45808113 -0.06239729  1.00000000 -0.02250016 -0.09388666
## ethnic1    0.05271390  0.01084565 -0.02250016  1.00000000  0.26144749
## educ      -0.04336137  0.02054031 -0.09388666  0.26144749  1.00000000
## sleep.hrs -0.01610149  0.06277700  0.05518124 -0.03185989 -0.02145965
## diabetes  -0.24450494  0.05232879 -0.25758949  0.04338853  0.12825910
## smoker     0.02144489  0.12497939  0.13249983 -0.06804697  0.13381708
## bmi        0.20399110  0.08309773  0.01496912 -0.07913569 -0.01939811
##              sleep.hrs    diabetes      smoker         bmi
## event     -0.01610149 -0.24450494  0.02144489  0.20399110
## gender     0.06277700  0.05232879  0.12497939  0.08309773
## age        0.05518124 -0.25758949  0.13249983  0.01496912
## ethnic1   -0.03185989  0.04338853 -0.06804697 -0.07913569
## educ      -0.02145965  0.12825910  0.13381708 -0.01939811
## sleep.hrs  1.00000000  0.03917174  0.05190982 -0.08127697
## diabetes   0.03917174  1.00000000 -0.02345722 -0.13925171
## smoker     0.05190982 -0.02345722  1.00000000  0.07292136
## bmi       -0.08127697 -0.13925171  0.07292136  1.00000000
```

```r
# Use heat map to visualize correlation matrix
levelplot(cor_matrix,scale=list(x=list(rot=45)),xlab=NULL,ylab=NULL)
```



Event

```
table(data$event)
```

```
##
##    0    1
## 1099  811
```

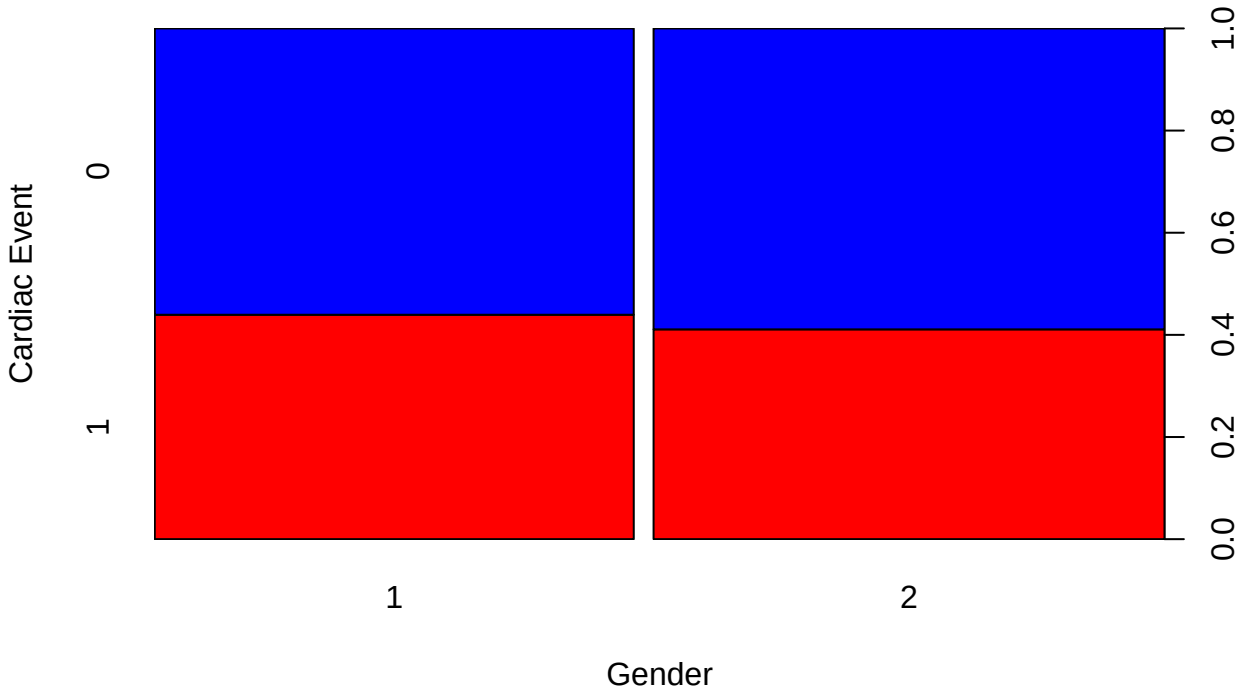
```
data$event <- as.factor(data$event)
```

Gender

```
table(data$gender)
```

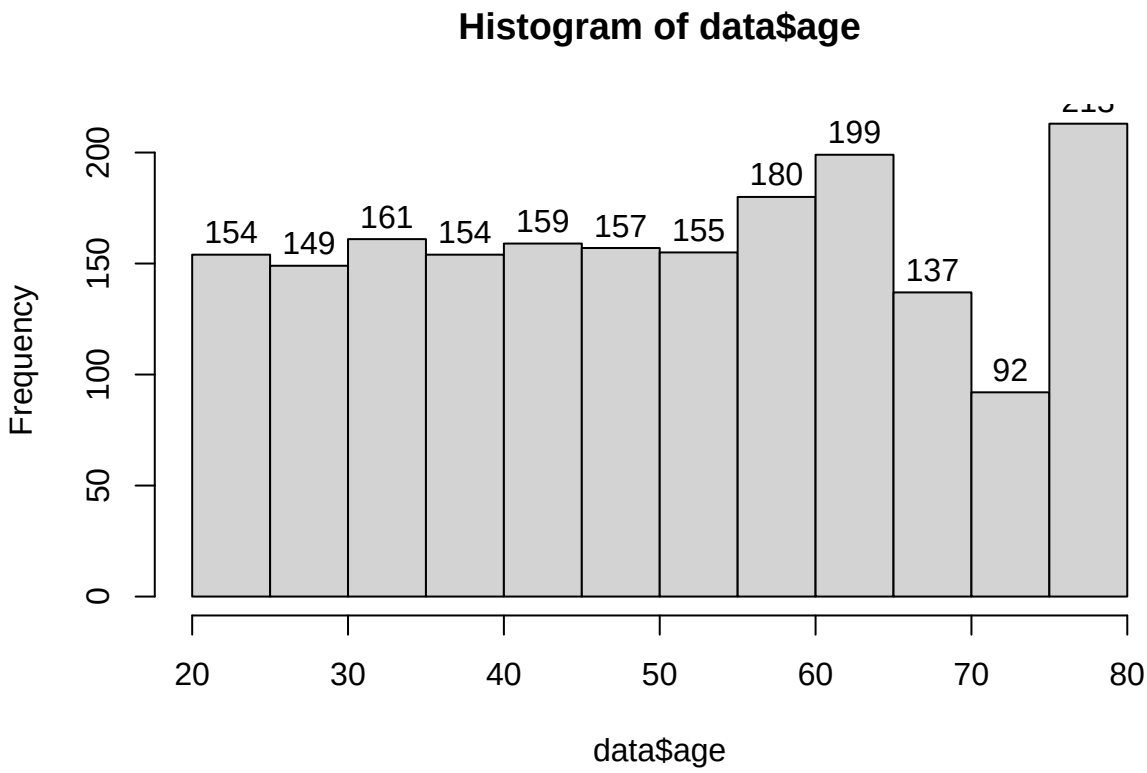
```
##
##   1   2
## 924 986
```

```
data$gender <- as.factor(data$gender)

gender_tab <- table(data$event, data$gender)

# Mosaic plot for gender
spineplot(t(gender_tab), main = "Gender and Cardiac Event",
          xlab="Gender", ylab="Cardiac Event", col=c("red","blue"))
```



Age

```
hist(data$age, labels = T)
```




```
# Slicing plot for age
age.fac = factor(cut(data$age, breaks=15),labels=1:15)
```

```r
table(age.fac)
```

```
## age.fac
##   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15
## 121 112 137 122 126 125 130 110 140 146 171 107  98  72 193
```

```r
# Empirical probs for each category
age.prob <- tapply(data$event, age.fac, mean)
```

```
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
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## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA
```
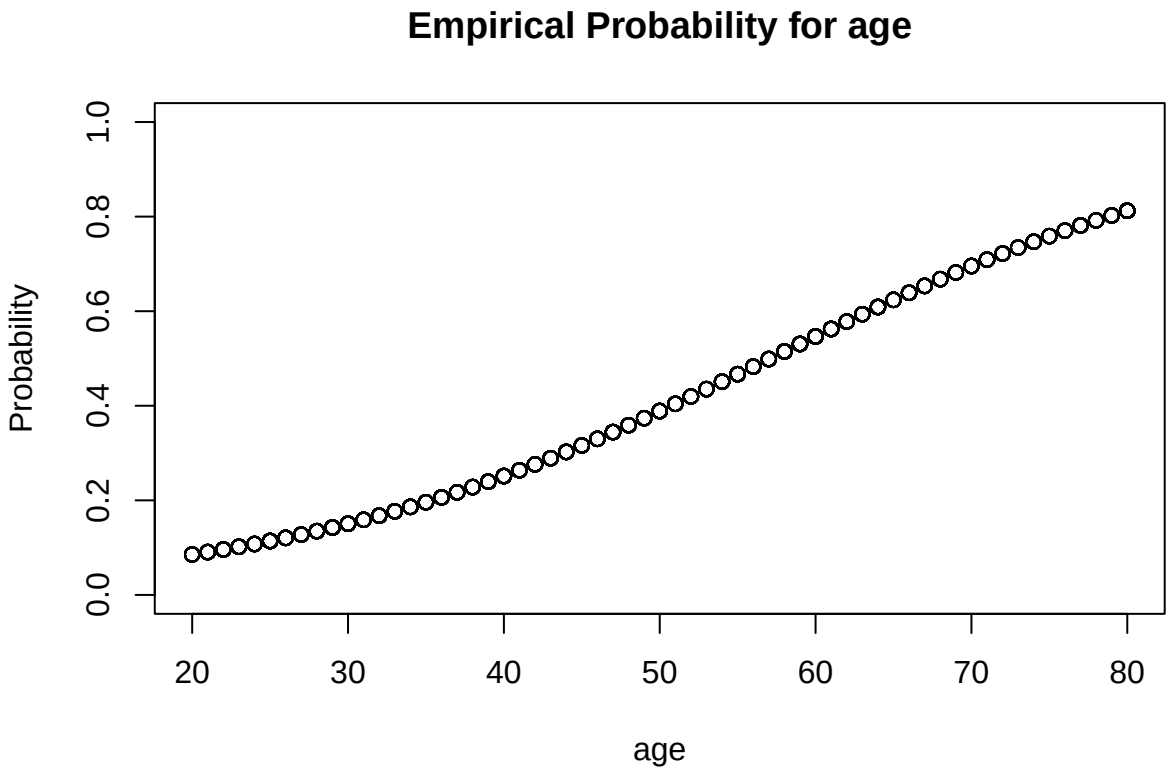
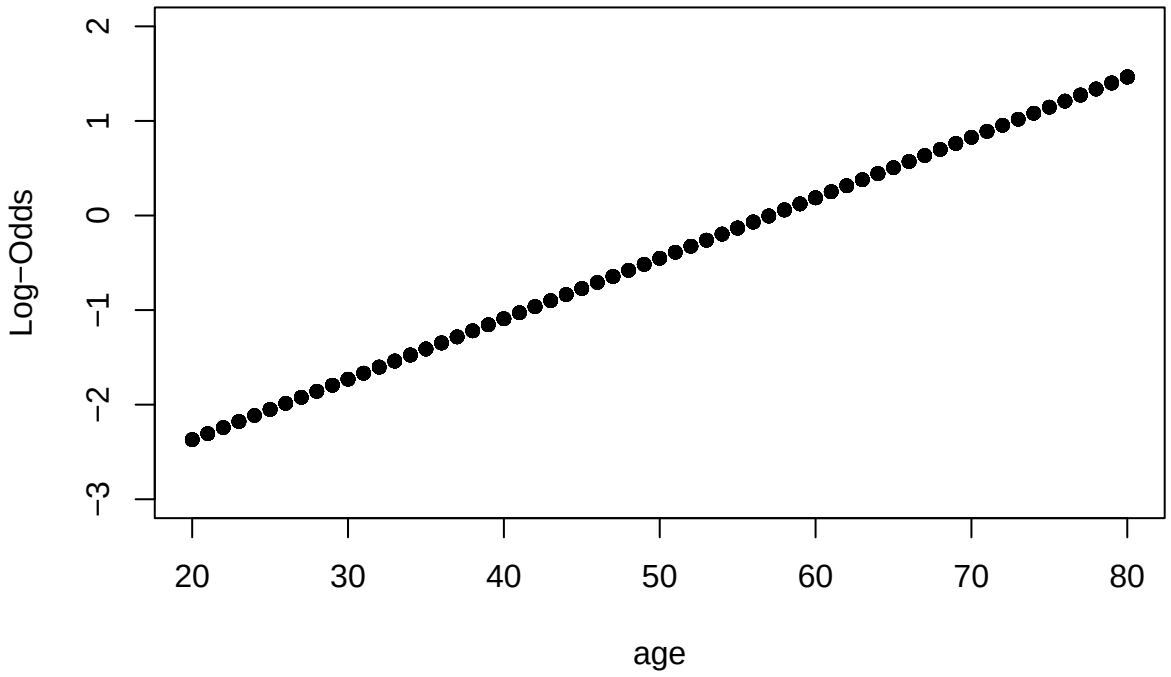

```
age.slice.avg <- tapply(data$age, age.fac, mean)
age.elogits <- log(age.prob/(1-age.prob))
# Run logistic regression on simulated data
age.out <- glm(event ~ age, data = data, family = 'binomial')

# Graph predicted and empirical probabilities
plot(data$age, age.out$fitted.values, ylab='Probability', ylim=c(0,1), xlab = 'age', main='Empirical Pr
points(age.slice.avg, age.prob, pch=16, col='blue')
```




```
age.pred <- age.out$fitted.value
age.plogits <- log(age.pred/(1-age.pred))
plot(data$age, age.plogits, pch=16, ylab='Log-Odds', ylim=c(-3, 2), xlab = 'age', main='Empirical Logit
points(age.slice.avg, age.elogits, pch=16, col='blue')
```

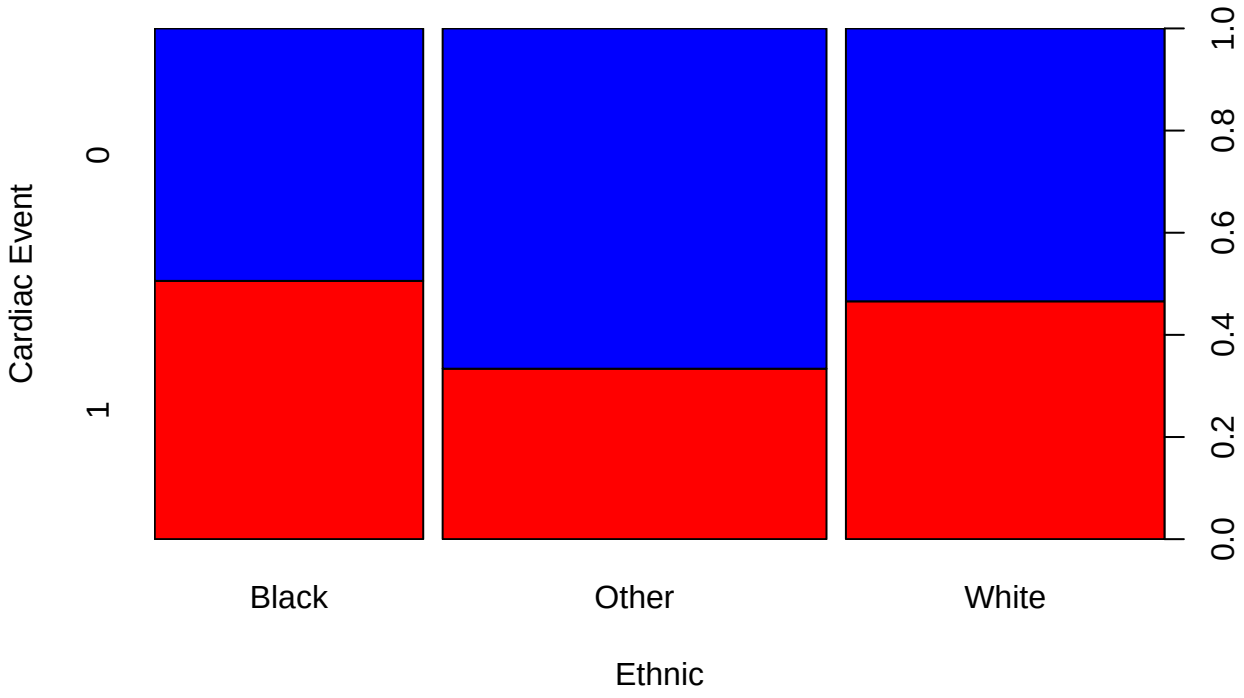


Ethnic

```
table(data$ethnic1)
```

```
##
##   1   2   3   4   5
## 230 195 627 528 330
```

```
data <- data %>%
  mutate(ethnic1 = case_when(
    ethnic1 == 1 ~ "Other",
    ethnic1 == 2 ~ "Other",
    ethnic1 == 3 ~ "White",
    ethnic1 == 4 ~ "Black",
    ethnic1 == 5 ~ "Other",
    TRUE ~ as.character(ethnic1)
  ))

ethnic_tab <- table(data$event, data$ethnic1)
spineplot(t(ethnic_tab), main = "Ethnic and Cardiac Event",
          xlab="Ethnic", ylab="Cardiac Event", col=c("red","blue"))
```



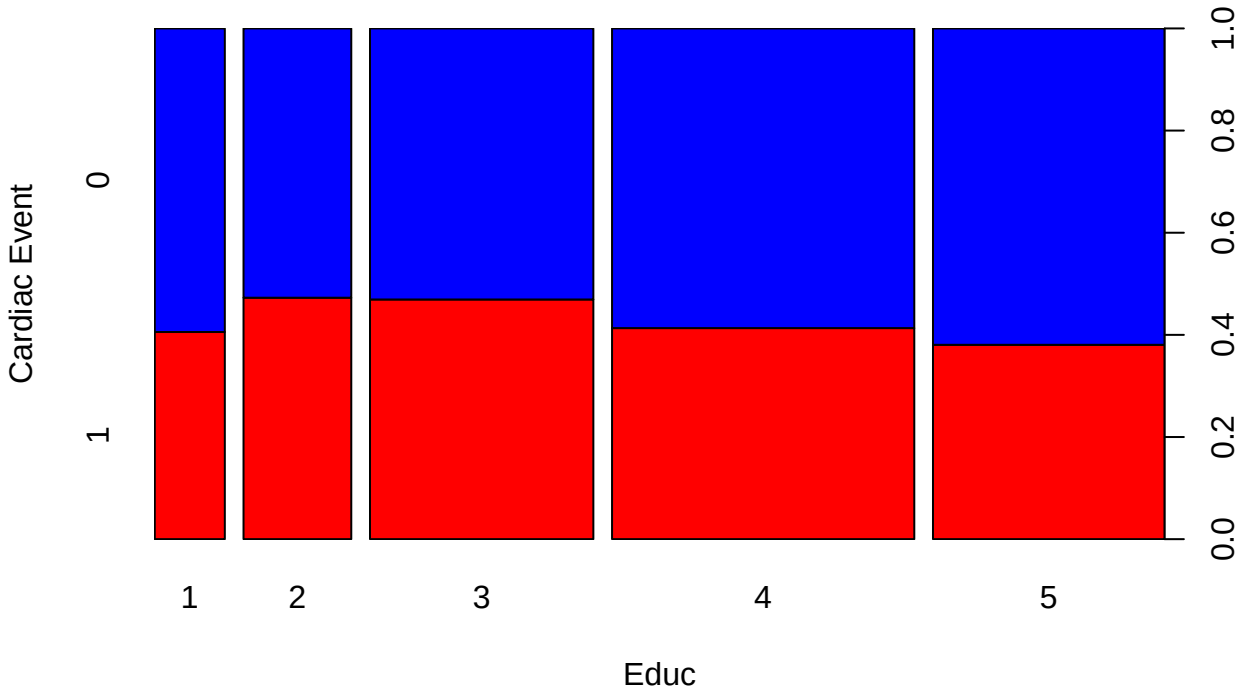

```
data$ethnic1 <- as.factor(data$ethnic1)
```

Educ

```
table(data$educ)
```

```
##
##   1   2   3   4   5   9
## 143 220 456 617 473   1
```

```
# Since educ = 9 means Don't know, it's hard to assign value and with only one record. Remove the recor
data <- data[data$educ != 9, ]

educ_tab <- table(data$event, data$educ)
spineplot(t(educ_tab), main = "Educ and Cardiac Event",
          xlab="Educ", ylab="Cardiac Event", col=c("red","blue"))
```




```
CMHtest(educ_tab)
```

```
## Cochran-Mantel-Haenszel Statistics for  by
##
##                   AltHypothesis   Chisq Df     Prob
## cor         Nonzero correlation  4.3993  1 0.035954
## rmeans   Row mean scores differ  4.3993  1 0.035954
## cmeans   Col mean scores differ 10.0988  4 0.038796
## general     General association 10.0988  4 0.038796
```

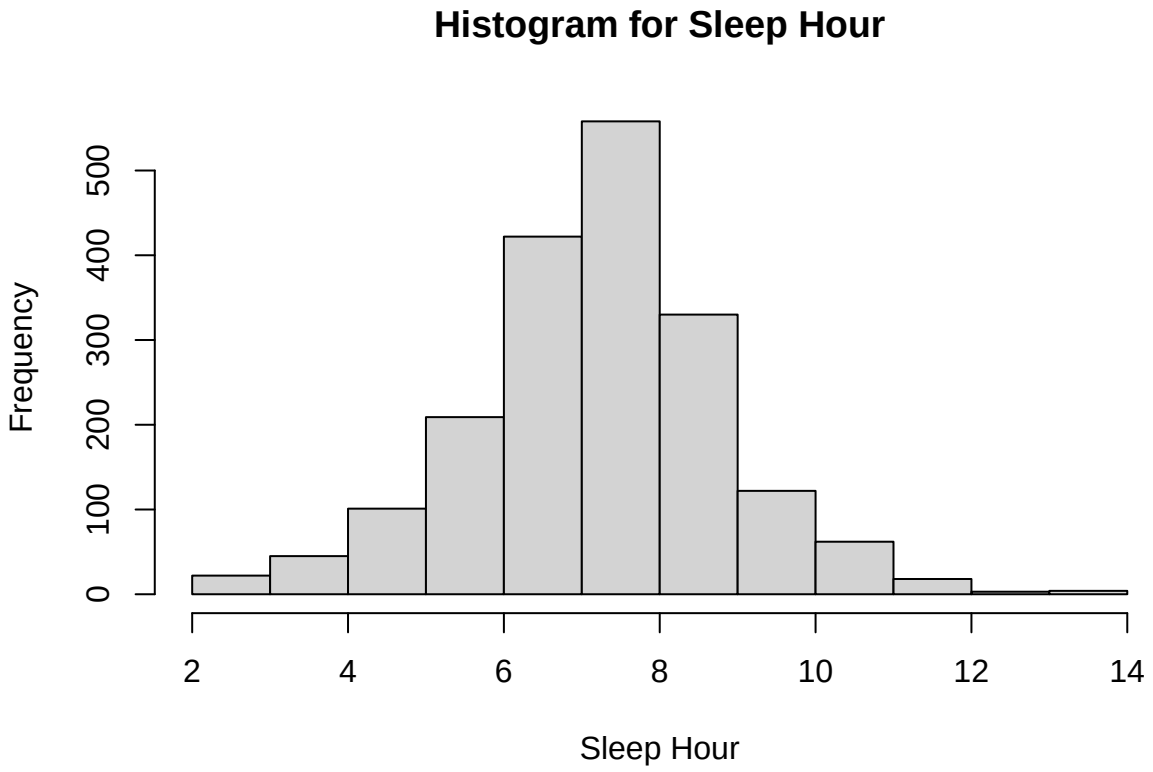
```
data$educ <- as.factor(data$educ)
```

Processing Variables with significant amount of missing values

```
# Only keep records without N/A value to do the predict
data_no_na <- na.omit(data)
```

Sleep hrs

```
# Sleep distribution
hist(data$sleep.hrs, main="Histogram for Sleep Hour", xlab="Sleep Hour")
```




```
# According to the correlation, use the highest possible predictors
# Use linear regression or logistic regression to predict the value of the NA
sleep_fit <- lm(sleep.hrs ~ gender+age+ethnic1+educ, data)
summary(sleep_fit)
```

```
##
## Call:
## lm(formula = sleep.hrs ~ gender + age + ethnic1 + educ, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.7567 -0.8773  0.0845  0.8807  6.8409
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   7.069670   0.213684  33.085  < 2e-16 ***
## gender2       0.224838   0.075323   2.985  0.00287 **
## age           0.004296   0.002233   1.924  0.05450 .
## ethnic1Other  0.231463   0.095843   2.415  0.01583 *
## ethnic1White  0.291135   0.098217   2.964  0.00307 **
## educ2        -0.033967   0.179713  -0.189  0.85011
## educ3        -0.048061   0.164188  -0.293  0.76977
## educ4        -0.066967   0.160005  -0.419  0.67561
## educ5        -0.010502   0.161354  -0.065  0.94811
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.635 on 1887 degrees of freedom
##   (13 observations deleted due to missingness)
## Multiple R-squared:  0.01241,    Adjusted R-squared:  0.008222
```

```
## F-statistic: 2.964 on 8 and 1887 DF,  p-value: 0.002674
```

```
# Based on first try, use the most significant predictors
sleep_fit1 <- lm(sleep.hrs ~ gender+ethnic1, data)
summary(sleep_fit1)
```

```
##
## Call:
## lm(formula = sleep.hrs ~ gender + ethnic1, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.7789 -0.7789  0.0422  0.9369  6.7580
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   7.24203    0.08253  87.753  < 2e-16 ***
## gender2       0.21574    0.07518   2.870 0.004157 **
## ethnic1Other  0.23540    0.09321   2.525 0.011639 *
## ethnic1White  0.32110    0.09695   3.312 0.000944 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.635 on 1892 degrees of freedom
##   (13 observations deleted due to missingness)
## Multiple R-squared:  0.01002,    Adjusted R-squared:  0.008453
## F-statistic: 6.385 on 3 and 1892 DF,  p-value: 0.0002651
```

```
# Evaluate Model Performance
# Predicted values from the model
predicted_sleep <- predict(sleep_fit1, newdata = data_no_na)

# R-squared (R²); low R^2 values, so regression model does not perform well. Thus, we decide to replace
rsquared <- 1 - (sum((data_no_na$sleep.hrs - predicted_sleep)^2) / sum((data_no_na$sleep.hrs - mean(data
```

```
## [1] 0.01105339
```

```
# Replace the missing value using the predict model
# Find rows with missing values
sleep_rows_with_na <- is.na(data$sleep.hrs)
data$sleep.hrs[sleep_rows_with_na] <- median(data_no_na$sleep.hrs)

# Check Result
sum(is.na(data$sleep.hrs))
```

```
## [1] 0
```

```
summary(data$sleep.hrs)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   2.000   6.500   7.500   7.552   8.500  14.000
```

```
# Creating Slicing plot for sleeping hrs

# Table to show distribution
table(data$sleep.hrs)
```

```
##
```

```
##    2    3  3.5    4  4.5    5  5.5    6  6.5    7  7.5    8  8.5    9  9.5   10
##    6   16    6   39   19   82   45  164  106  316  193  378  131  199   45   77
## 10.5   11 11.5   12   13   14
##   24   38    6   12    3    4
```

```
# According to data distribution, we can find the numbers of observation having sleep hours less than 5
data$sleep.hrs <- cut(data$sleep.hrs, breaks=c(-Inf, 5, 6, 7, 9, Inf), labels=c("<=5 hrs", "5-6 hrs", "
table(data$sleep.hrs)
```

```
##
## <=5 hrs 5-6 hrs 6-7 hrs 7-9 hrs  >9 hrs
##     168     209     422     901     209
```

```
sleep.fac = factor(data$sleep.hrs)

# Empirical probs for each category
sleep.prob <- tapply(data$event, sleep.fac, mean)
```

```
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
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## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA
```
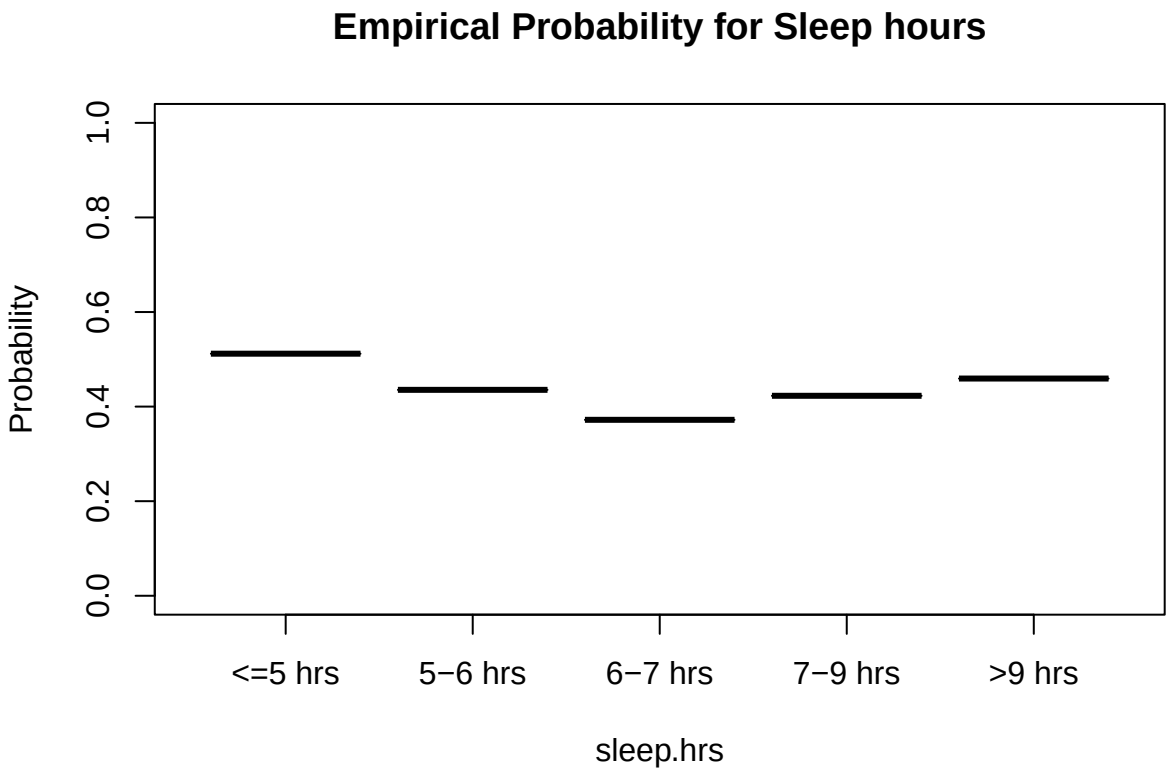

```
sleep.slice.avg <- tapply(data$sleep.hrs, sleep.fac, mean)
```

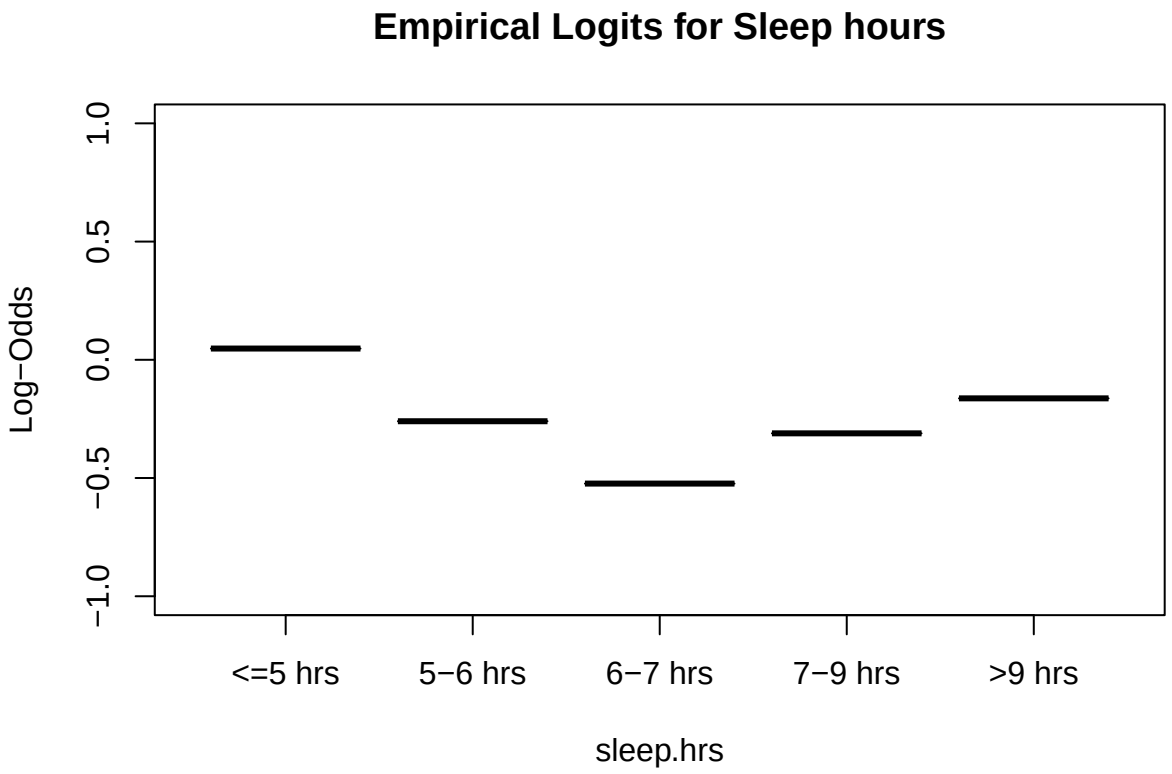
```
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA
```

```
sleep.elogits <- log(sleep.prob/(1-sleep.prob))

# Run logistic regression on simulated data
sleep.out <- glm(event ~ sleep.hrs, data = data, family = 'binomial')

# Graph predicted and empirical probabilities
plot(data$sleep.hrs, sleep.out$fitted.values, ylab='Probability', ylim=c(0,1), xlab = 'sleep.hrs', main=
```

```
points(sleep.slice.avg, sleep.prob, pch=16, col='blue')
```

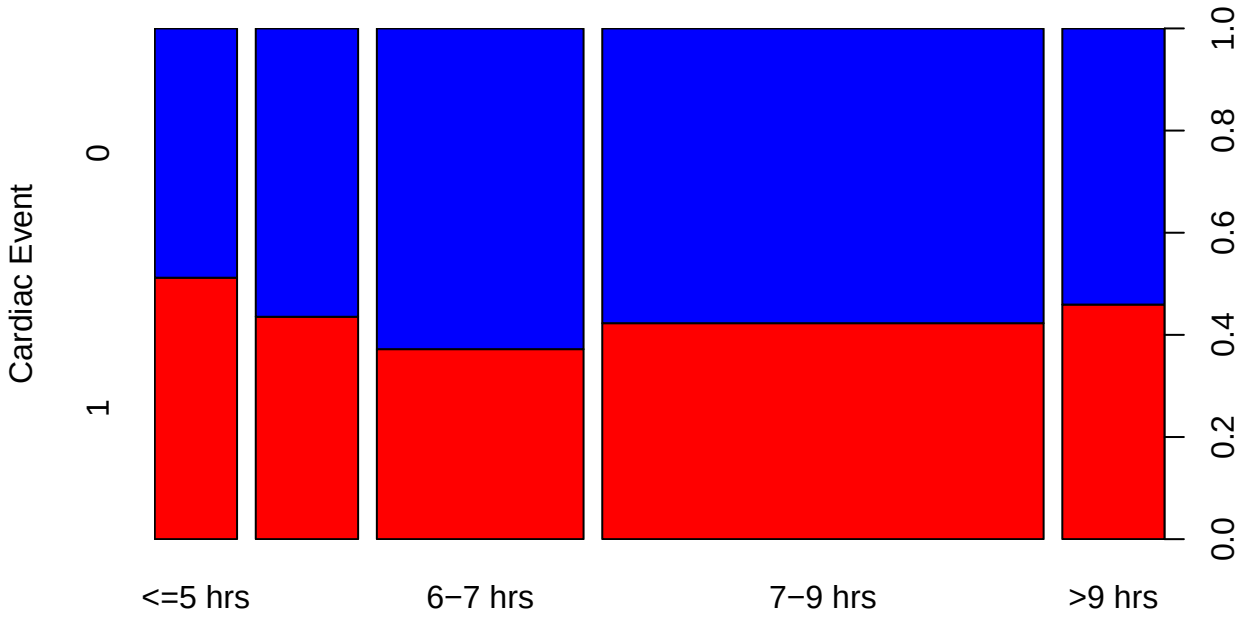



```
slepp.pred <- sleep.out$fitted.value
sleep.logits <- log(slepp.pred/(1-slepp.pred))
plot(data$sleep.hrs, sleep.logits, pch=16, ylab='Log-Odds', ylim=c(-1, 1), xlab = 'sleep.hrs', main='Em
points(sleep.slice.avg, sleep.elogits, pch=16, col='blue')
```




```
# Slicing plot shows that different steps instead of straight line, so code sleep hrs as categorical va
```

```
# Mosaic plot for sleep hrs
sleep_tab <- table(data$event, data$sleep.hrs)
spineplot(t(sleep_tab), main = "Sleep Hours and Cardiac Event",
          xlab="Sleep Hours", ylab="Cardiac Event", col=c("red","blue"))
```




```
CMHtest(sleep_tab) # The results shows that sleep hrs and cardiac event have no linear association
```

```
## Cochran-Mantel-Haenszel Statistics for  by
##
##                   AltHypothesis    Chisq Df     Prob
## cor         Nonzero correlation  0.62864  1 0.427855
## rmeans   Row mean scores differ  0.62864  1 0.427855
## cmeans   Col mean scores differ 11.14836  4 0.024946
## general     General association 11.14836  4 0.024946
```

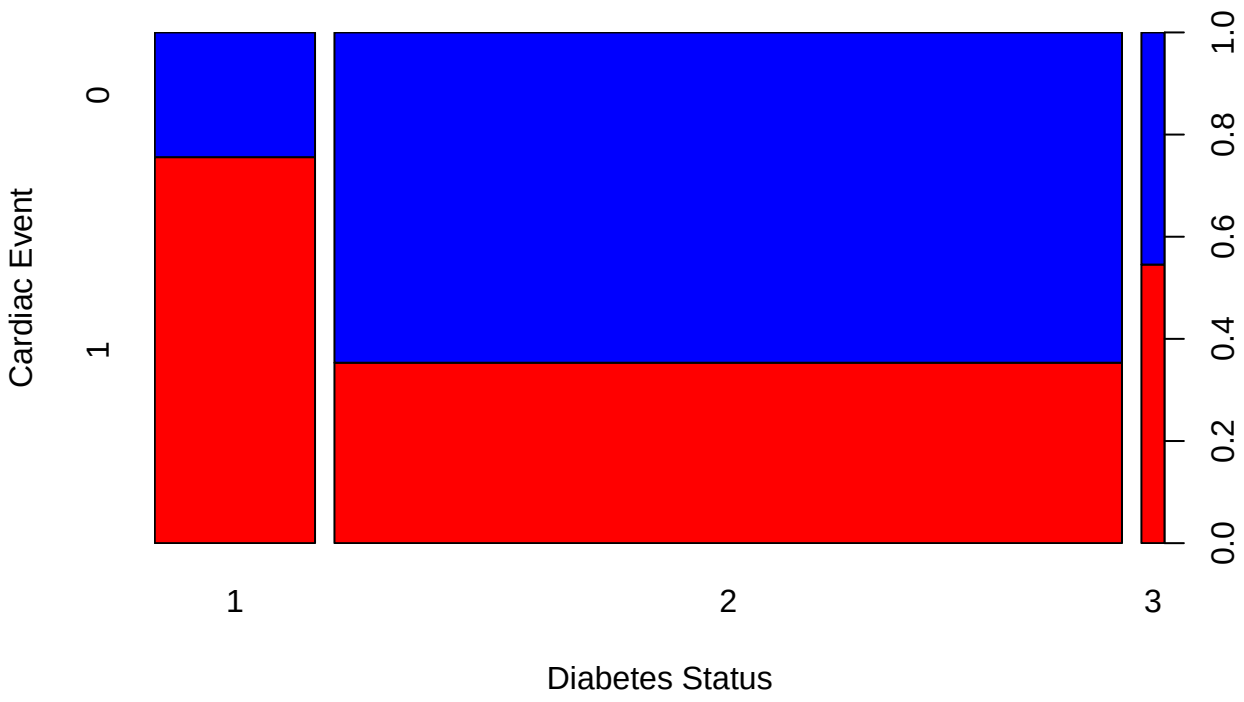
```
# Convert sleep to factor
data$sleep.hrs <- as.factor(data$sleep.hrs)
```

Diabetes

```
# Create a table to view the distribution of data
table(data$diabetes)
```

```
##
##    1    2    3    9
##  303 1489   44    1
```

```
# Change Don't know as NaN, which will be processed later.
data$diabetes[data$diabetes == 9] <- NaN

diabete_tab <- table(data$event, data$diabetes)
spineplot(t(diabete_tab), main = "Diabetes Status and Cardiac Event",
          xlab="Diabetes Status", ylab="Cardiac Event", col=c("red","blue"))
```




```
# Run trend data
CMHtest(diabete_tab)
```

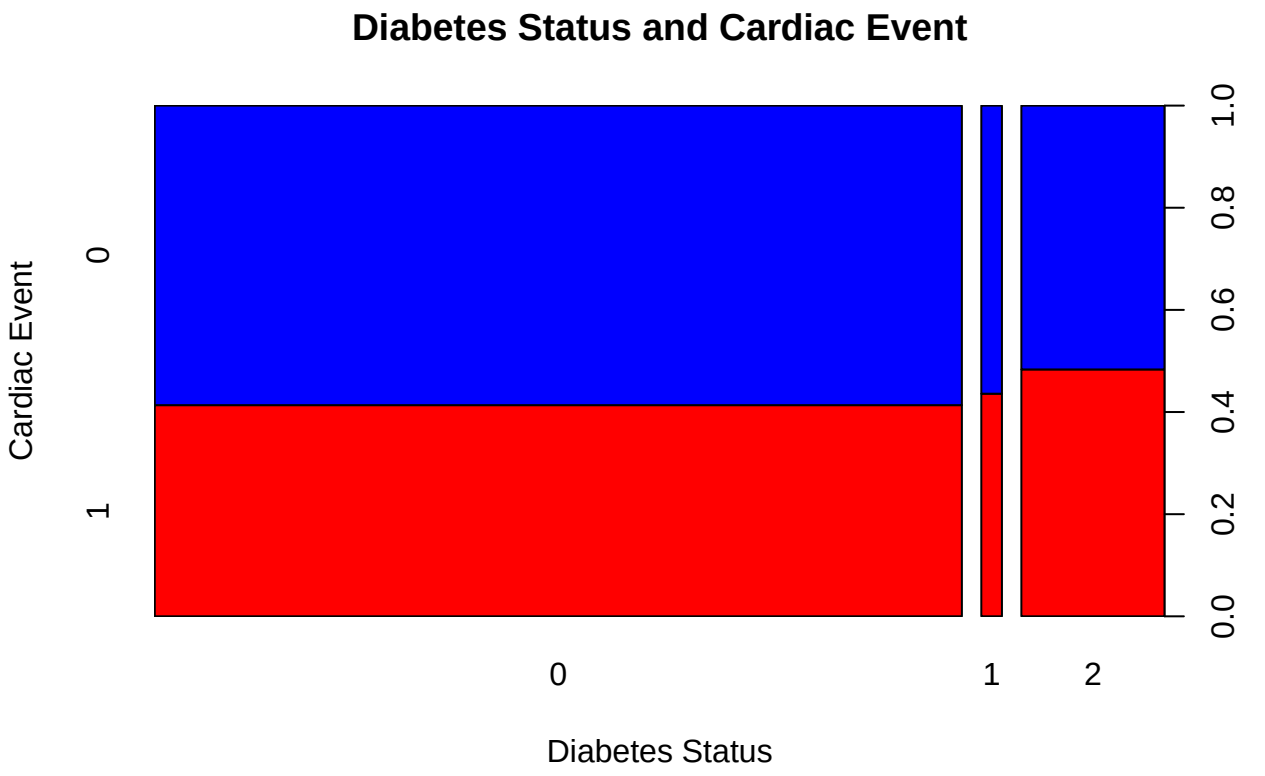
```
## Cochran-Mantel-Haenszel Statistics for  by
##
##                   AltHypothesis  Chisq Df       Prob
## cor         Nonzero correlation 119.21  1 9.4070e-28
## rmeans   Row mean scores differ 119.21  1 9.4070e-28
## cmeans   Col mean scores differ 169.61  2 1.4765e-37
## general     General association 169.61  2 1.4765e-37
```

```
# The trend test shows that there is a linear association, so keep borderline category
```

```
# Since diabetes has three categories, it is challenging to run logistic regression to predict diabetes
# Thus, we removed all NA
data<-subset(data, !is.na(diabetes))

# Recode diabete as ordinal categorical varaibles
data$diabetes[data_no_na$diabetes == 2] <- 0
data$diabetes[data_no_na$diabetes == 1] <- 2
data$diabetes[data_no_na$diabetes == 3] <- 1

# Check if na exists
table(data$diabetes,useNA = "ifany")
```

```
##
##    0    1    2
## 1526   39  271
```

```
diabete_tab <- table(data$event, data$diabetes)
spineplot(t(diabete_tab), main = "Diabetes Status and Cardiac Event",
          xlab="Diabetes Status", ylab="Cardiac Event", col=c("red","blue"))
```



Smoker

```
# check distribution for smoker
table(data$smoker)
```

```
##
##    1    2
##  402 1292
```

```
smoker_tab <- table(data$event, data$smoker)

# For Categorical response, first Categorize the result to (0-No smoke; 1-smoke)
# turn 2 into 0, which not only turns data to correct format of data for logistic regression but also m
data$smoker[data$smoker == 2] <- 0
smoke_pr <- glm(smoker ~ gender + educ + age, data = data, family = binomial)

# Model evaluation
summary(smoke_pr)
```

```
##
## Call:
## glm(formula = smoker ~ gender + educ + age, family = binomial,
##     data = data)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.096136   0.321853  -0.299  0.76517
## gender2     -0.664148   0.120470  -5.513 3.53e-08 ***
## educ2        0.880277   0.295409   2.980  0.00288 **
## educ3        0.577832   0.274894   2.102  0.03555 *
```

```
## educ4        0.322912   0.271656   1.189  0.23457
## educ5       -0.757818   0.298252  -2.541  0.01106 *
## age         -0.020030   0.003485  -5.748 9.03e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1856.5  on 1693  degrees of freedom
## Residual deviance: 1718.9  on 1687  degrees of freedom
##   (142 observations deleted due to missingness)
## AIC: 1732.9
##
## Number of Fisher Scoring iterations: 4
```

```
data_no_na$smoker[data_no_na$smoker == 2] <- 0
predicted_smoker <- ifelse(predict(smoke_pr, newdata = data_no_na) >= 0.5, 1, 0)
mean(data_no_na$smoker == predicted_smoker)
```

```
## [1] 0.7619048
```

```
# Missing value replace
rows_with_na <- is.na(data$smoker)
predicted_probabilities <- predict(smoke_pr, newdata = data[rows_with_na, ], type = "response")
data$smoker[rows_with_na] <- ifelse(predicted_probabilities >= 0.5, 1, 0)
data$smoker<-as.factor(data$smoker)
# Check Result
sum(is.na(data$smoker))
```

```
## [1] 0
```

```
summary(data$smoker)
```

```
##    0    1
## 1430  406
```

BMI

```
# According to the correlation, use the highest possible predictors
bmi_model = lm(bmi ~ educ + age + gender + ethnic1, data)
summary(bmi_model)
```

```
##
## Call:
## lm(formula = bmi ~ educ + age + gender + ethnic1, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -16.910  -5.259  -1.101   3.992  54.226
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  30.975054   1.052972  29.417  < 2e-16 ***
## educ2        -0.563561   0.896036  -0.629  0.52946
## educ3        -0.246001   0.815208  -0.302  0.76287
## educ4         0.768022   0.793910   0.967  0.33348
## educ5        -1.281855   0.801209  -1.600  0.10980
## age           0.006609   0.010992   0.601  0.54776
```

```
## gender2       1.082075   0.369375   2.929  0.00344 **
## ethnic1Other -2.243788   0.468925  -4.785 1.85e-06 ***
## ethnic1White -0.963150   0.479917  -2.007  0.04491 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.79 on 1784 degrees of freedom
##   (43 observations deleted due to missingness)
## Multiple R-squared:  0.03134,    Adjusted R-squared:  0.027
## F-statistic: 7.215 on 8 and 1784 DF,  p-value: 1.882e-09
```

```
# Based on first try, use the most significant predictors
bmi_model1 = lm(bmi ~ gender + ethnic1, data)
summary(bmi_model1)
```

```
##
## Call:
## lm(formula = bmi ~ gender + ethnic1, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -15.671  -5.371  -1.278   4.004  54.997
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   31.2027     0.4050  77.035  < 2e-16 ***
## gender2        1.0932     0.3699   2.955  0.00316 **
## ethnic1Other  -2.4248     0.4581  -5.293 1.35e-07 ***
## ethnic1White  -1.0177     0.4755  -2.140  0.03247 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.819 on 1789 degrees of freedom
##   (43 observations deleted due to missingness)
## Multiple R-squared:  0.02148,    Adjusted R-squared:  0.01984
## F-statistic: 13.09 on 3 and 1789 DF,  p-value: 1.853e-08
```

```
# Evaluate Model Performance
# Predicted values from the model

# R-squared (R²)

predicted_bmi <- predict(bmi_model1, newdata = data_no_na)

# R-squared (R²); low R^2 values, so regression model does not perform well.
rsquared <- 1 - (sum((data_no_na$bmi - predicted_bmi)^2) / sum((data_no_na$bmi - mean(data_no_na$bmi))^
```

```
## [1] 0.02483995
```

```
# Have terrible result in model, so we decided to use the median value to replace the missing value
rows_with_na <- is.na(data$bmi)
data$bmi[rows_with_na] <- median(data_no_na$bmi)
```

```
# Check Result
sum(is.na(data$bmi))
```

```
## [1] 0
```

```r
summary(data$bmi)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   14.20   25.10   29.20   30.45   34.20   86.20
```

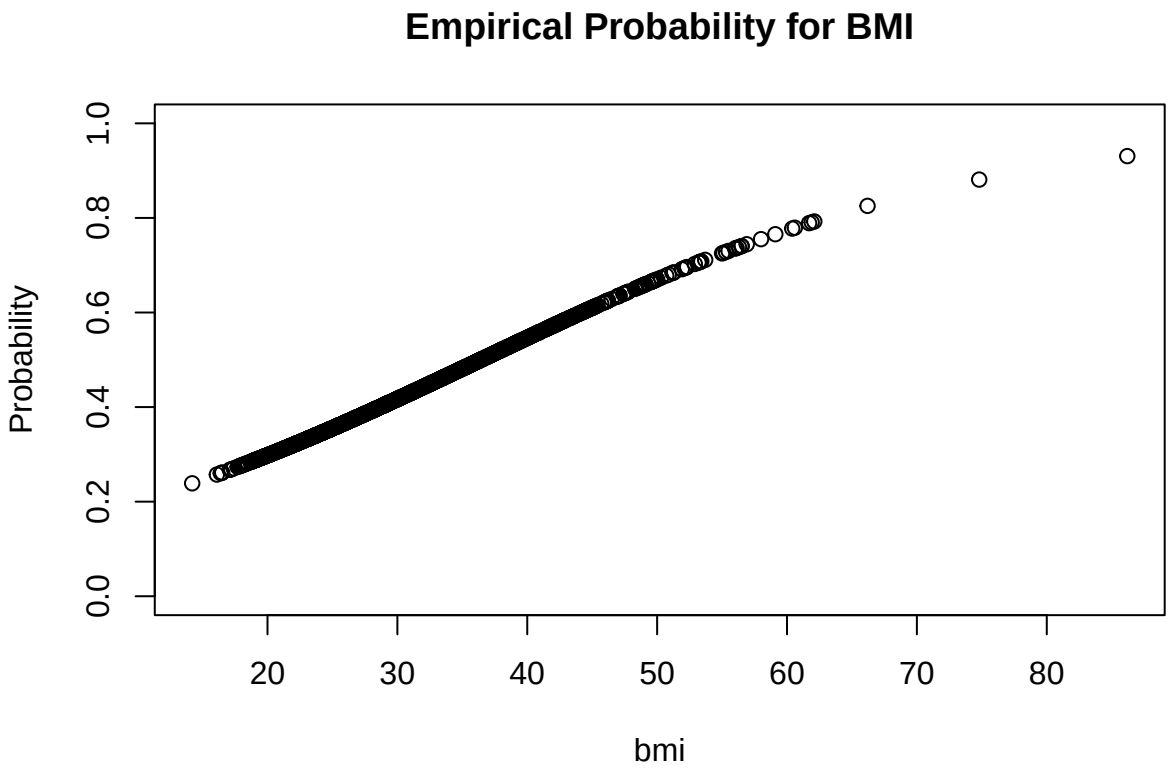
```r
# Slicing plot for BMI

bmi.fac = factor(cut(data$bmi, breaks=c(-Inf, 25, 30, 35, Inf)),labels=c("<=25, 25-30, 30-35, >35"))
table(bmi.fac)
```

```
## bmi.fac
## <=25, 25-30, 30-35, >351 <=25, 25-30, 30-35, >352 <=25, 25-30, 30-35, >353
##                      455                      585                      390
## <=25, 25-30, 30-35, >354
##                      406
```

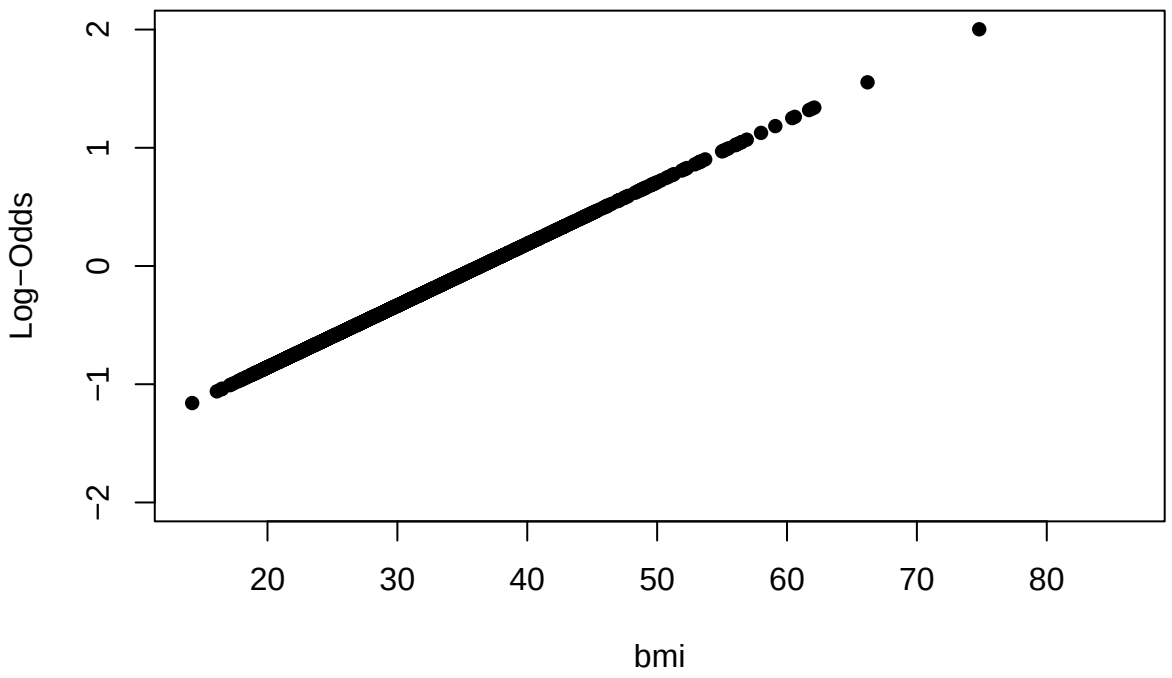
```r
# Empirical probs for each category
bmi.prob <- tapply(data$event, bmi.fac, mean)
```

```
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA

## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA
```

```r
bmi.slice.avg <- tapply(data$bmi, bmi.fac, mean)
bmi.elogits <- log(bmi.prob/(1-bmi.prob))
# Run logistic regression on simulated data
bmi.out <- glm(event ~ bmi, data = data, family = 'binomial')

# Graph predicted and empirical probabilities
plot(data$bmi, bmi.out$fitted.values, ylab='Probability', ylim=c(0,1), xlab = 'bmi', main='Empirical Pr
points(bmi.slice.avg, bmi.prob, pch=16, col='blue')
```




```
bmi.pred <- bmi.out$fitted.value
bmi.logits <- log(bmi.pred/(1-bmi.pred))
plot(data$bmi, bmi.logits, pch=16, ylab='Log-Odds', ylim=c(-2, 2), xlab = 'bmi', main='Empirical Logits
points(bmi.slice.avg, bmi.elogits, pch=16, col='blue')
```



```
# According to the slicing plot, the log-odds of bmi is strictly numerical, so we treat it numerical.
```

```
# Confirm that there's no NA left
anyNA(data)
```

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

Step 2: Descriptive Statistics

```
summary(data)
```

```
##  event    gender       age          ethnic1    educ      sleep.hrs
##  0:1057   1:885   Min.   :20.00   Black:511   1:137   <=5 hrs:162
##  1: 779   2:951   1st Qu.:36.00   Other:723   2:209   5-6 hrs:200
##                   Median :52.00   White:602   3:438   6-7 hrs:407
##                   Mean   :50.98               4:596   7-9 hrs:865
##                   3rd Qu.:64.00               5:456   >9 hrs :202
##                   Max.   :80.00
##     diabetes      smoker        bmi
##  Min.   :0.0000   0:1430   Min.   :14.20
##  1st Qu.:0.0000   1: 406   1st Qu.:25.10
##  Median :0.0000            Median :29.20
##  Mean   :0.3164            Mean   :30.45
##  3rd Qu.:0.0000            3rd Qu.:34.20
##  Max.   :2.0000            Max.   :86.20
```

Step 3: Two-Way Table

```
# Chi-sq test for categorical predictors

# gender
gender_tab <- table(data$event, data$gender)
chisq.test(gender_tab)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  gender_tab
## X-squared = 2.0098, df = 1, p-value = 0.1563
```

```
# ethnic
ethnic_tab <- table(data$event, data$ethnic1)
chisq.test(ethnic_tab)
```

```
##
##  Pearson's Chi-squared test
##
## data:  ethnic_tab
## X-squared = 41.875, df = 2, p-value = 8.071e-10
```

```
# sleep
sleep_tab <- table(data$event, data$sleep.hrs)
chisq.test(sleep_tab)
```

```
##
##  Pearson's Chi-squared test
##
## data:  sleep_tab
```

```
## X-squared = 8.6699, df = 4, p-value = 0.0699
```

```
# educ
educ_tab <- table(data$event, data$educ)
chisq.test(educ_tab)
```

```
##
##  Pearson's Chi-squared test
##
## data:  educ_tab
## X-squared = 8.9461, df = 4, p-value = 0.06246
```

```
# diabetes
diabetes_tab <- table(data$event, data$diabetes)
chisq.test(diabete_tab)
```

```
##
##  Pearson's Chi-squared test
##
## data:  diabete_tab
## X-squared = 4.6246, df = 2, p-value = 0.09903
```

```
# smoker
smoker_tab <- table(data$event, data$smoker)
chisq.test(smoker_tab)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  smoker_tab
## X-squared = 0.7801, df = 1, p-value = 0.3771
```

```
# Only ethnic seems to be associated with cardiac event.
```

```
# LR test for numerical predictors

# age
glm.age.null <- glm(event ~ 1, data = data, family = binomial)
glm.age <- glm(event ~ age, data = data, family = binomial)
lrtest(glm.age.null, glm.age)
```

```
## Likelihood ratio test
##
## Model 1: event ~ 1
## Model 2: event ~ age
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   1 -1251.5
## 2   2 -1028.5  1 445.98  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# bmi
glm.bmi.null <- glm(event ~ 1, data = data, family = binomial)
glm.bmi <- glm(event ~ bmi, data = data, family = binomial)
lrtest(glm.bmi.null, glm.bmi)
```

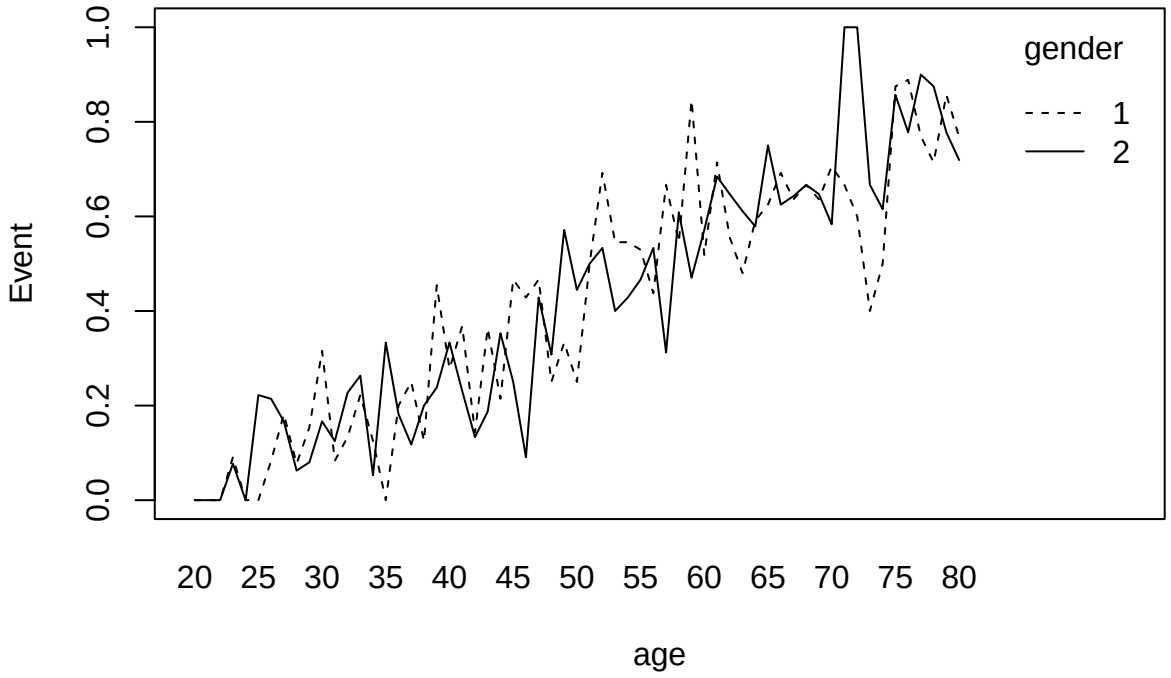
```
## Likelihood ratio test
##
```

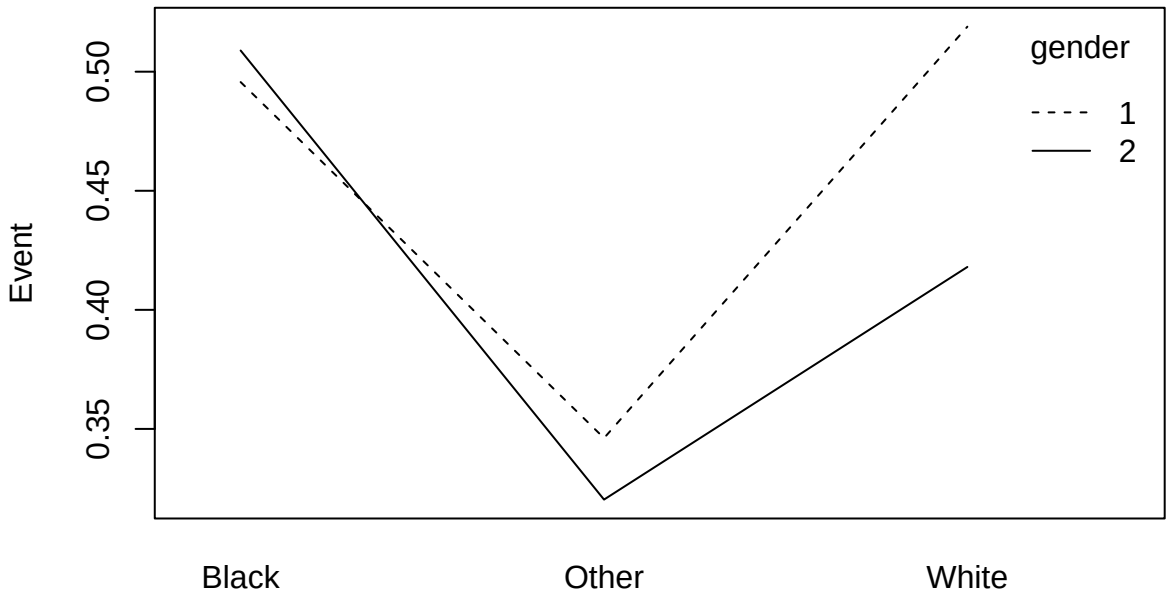
```
## Model 1: event ~ 1
## Model 2: event ~ bmi
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   1 -1251.5
## 2   2 -1216.4  1 70.186  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

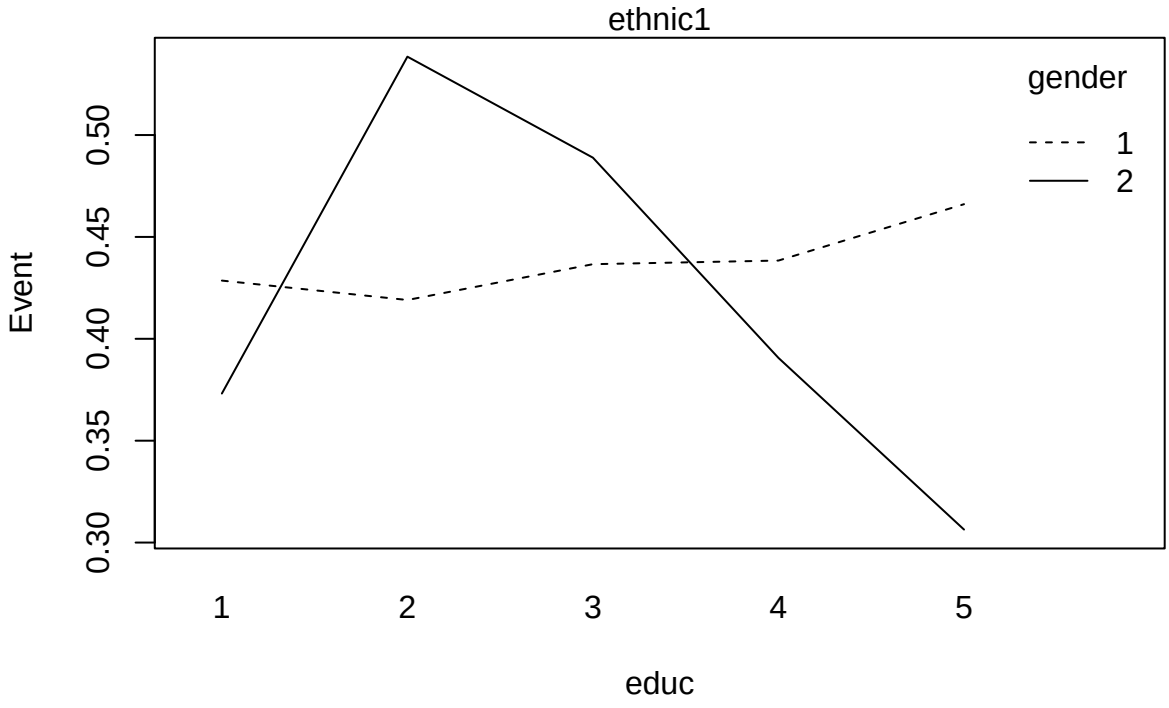
```
# Both age and bmi are good predictors of cardiac event.
```

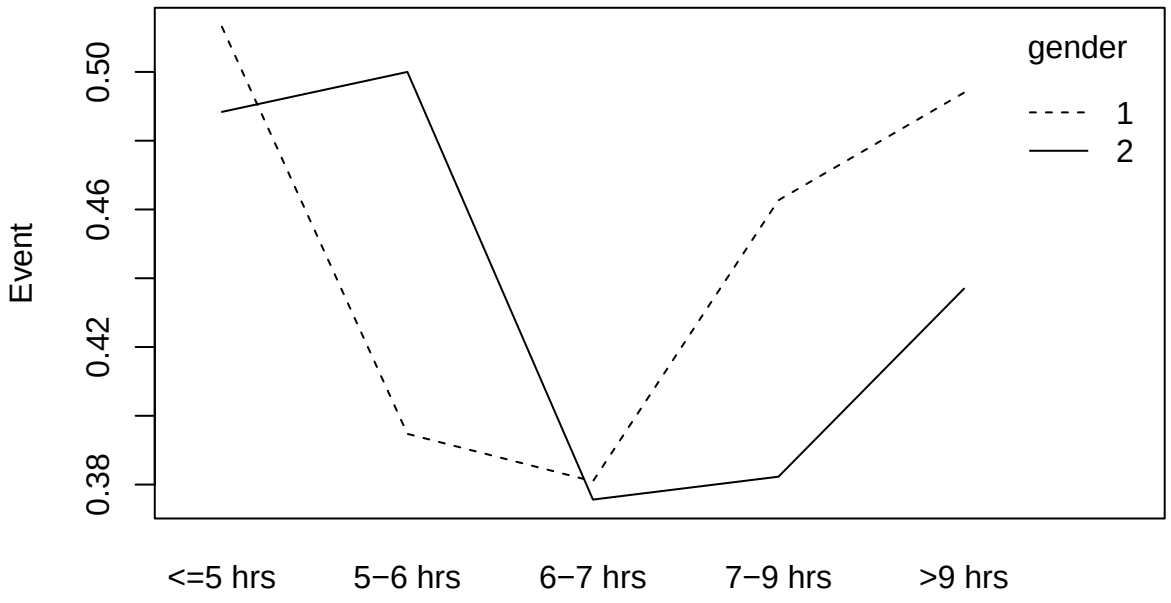
Step 4: Consider Model Option

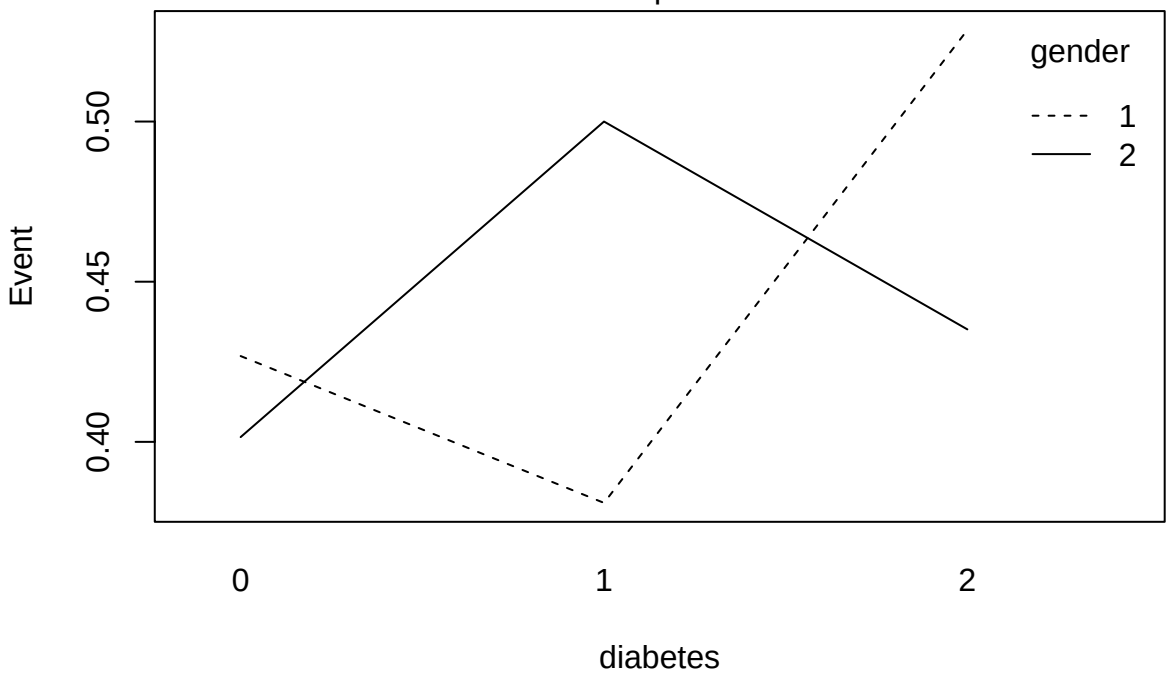
```
# Slicing plots from Step 2 shows that no transformation is needed
# We are focusing on exploring the interaction terms in this section.

# interaction.plot(data$diabetes, data$smoker, response = as.numeric(data$event), trace.label = "smoker
catv<-c("gender","diabetes","smoker","ethnic1","educ") # categorical
vars<-colnames(data)[!colnames(data)=="event"] # everything except response var.

for (i in catv){
  for (j in vars){
    if (i!=j){
      interaction.plot(
      x.factor = as.factor(data[[j]]),
      trace.factor = as.factor(data[[i]]),
      response = as.numeric(as.character(data$event)),
      type = "l", legend = TRUE,
      xlab=j,
      ylab="Event",
      trace.label = i
    )}
  }
}
```

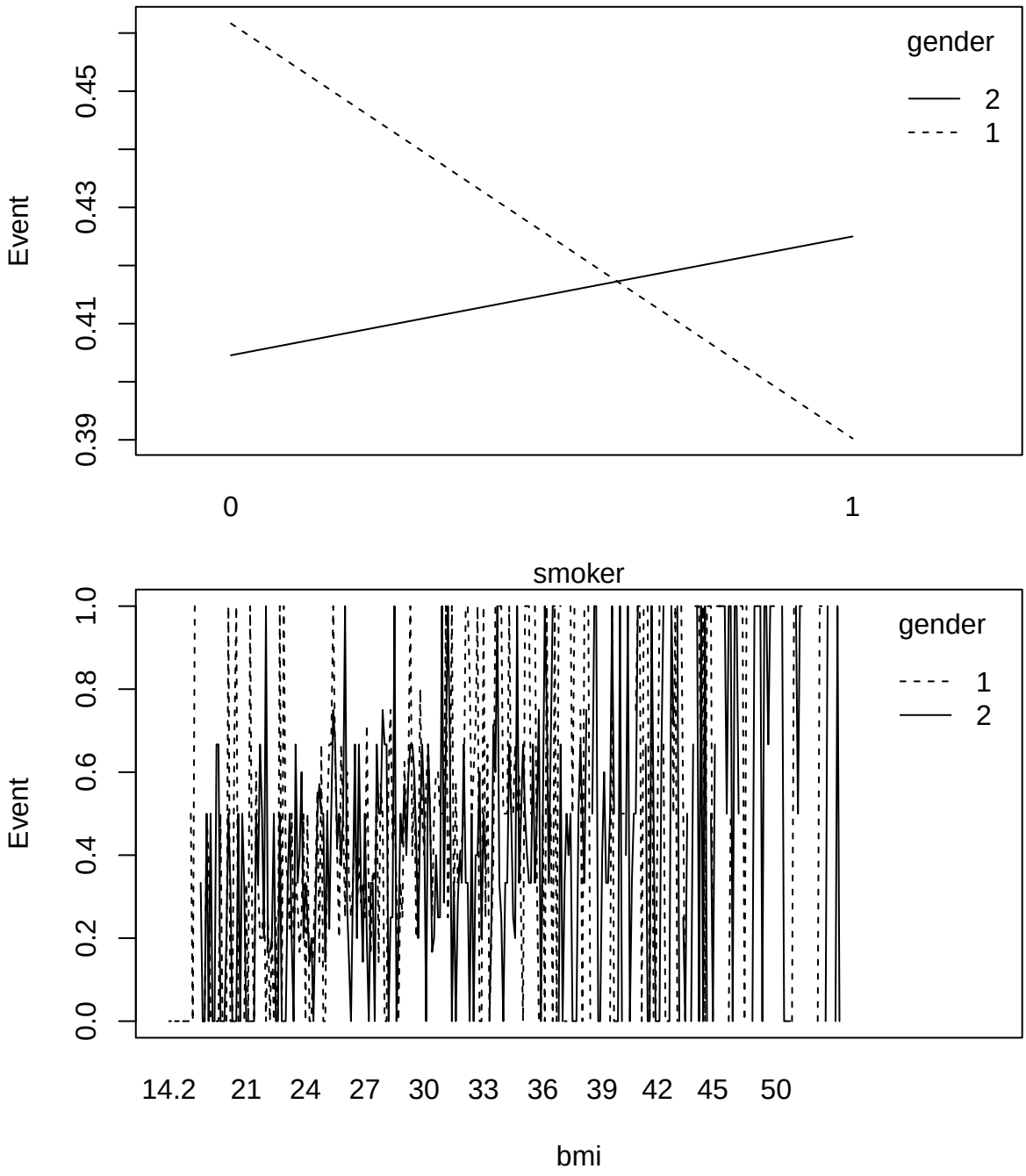


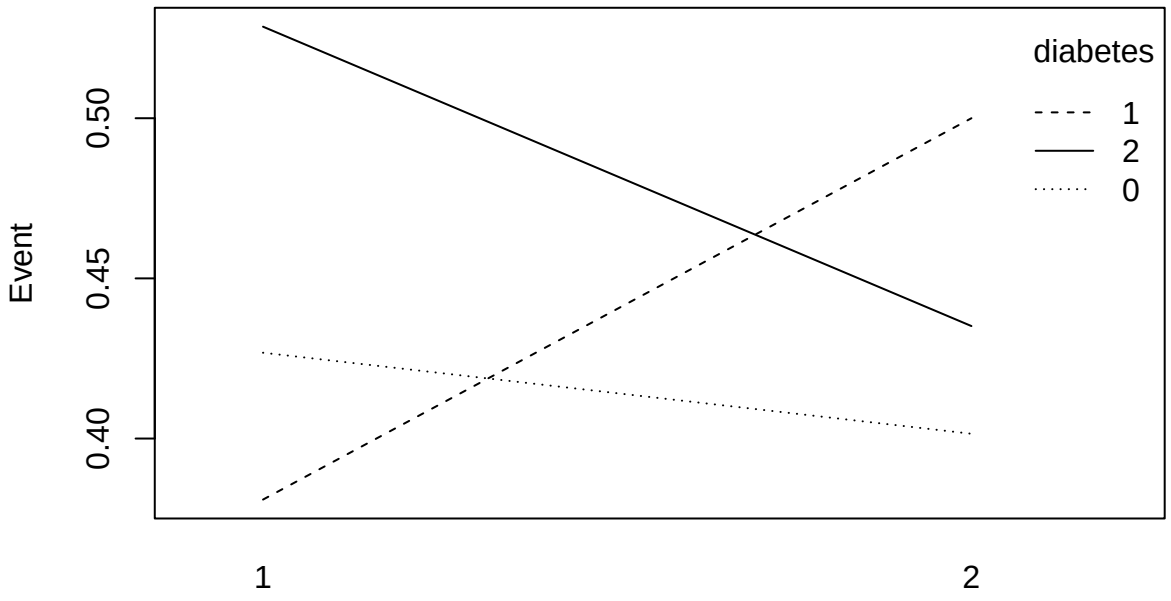

Event
0.35
0.40
0.45
0.50
gender
1
2
Black
Other
White
ethnic1

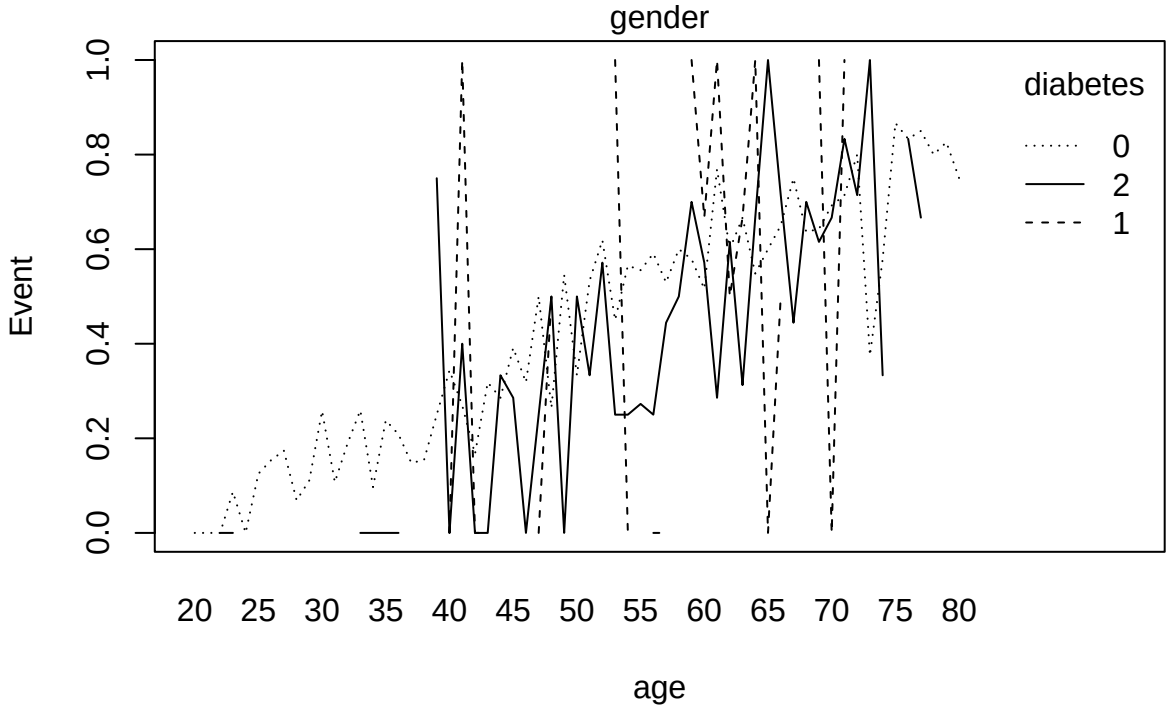

Event
0.30
0.35
0.40
0.45
0.50
gender
1
2
1
2
3
4
5
educ

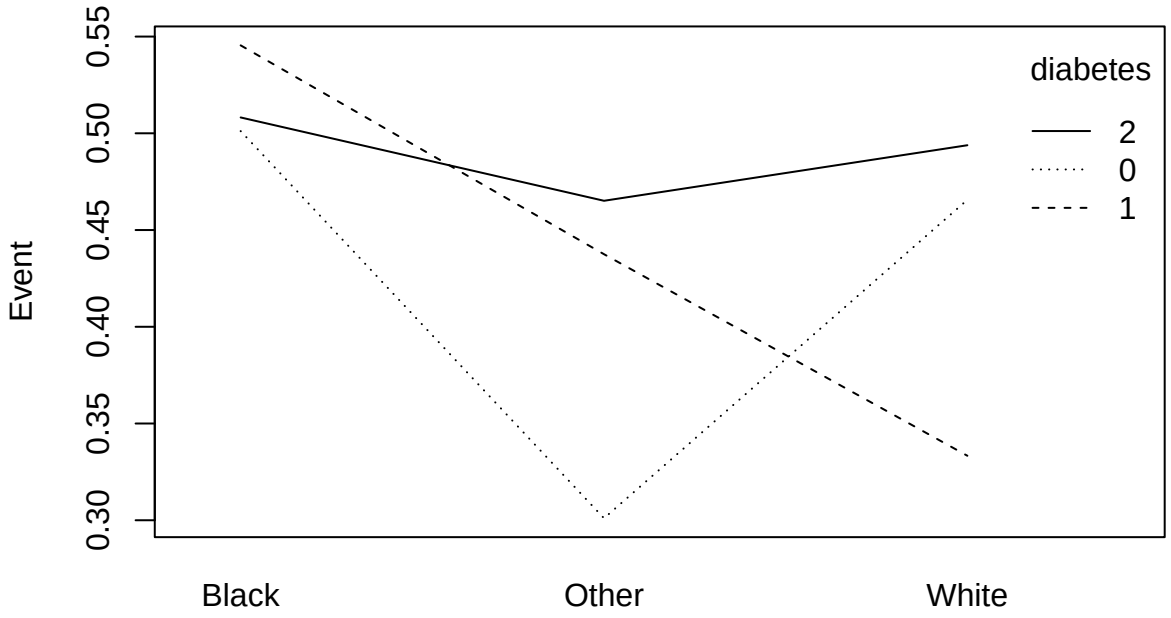

Event
0.38
0.42
0.46
0.50
gender
1
2
<=5 hrs
5−6 hrs
6−7 hrs
7−9 hrs
>9 hrs
sleep.hrs

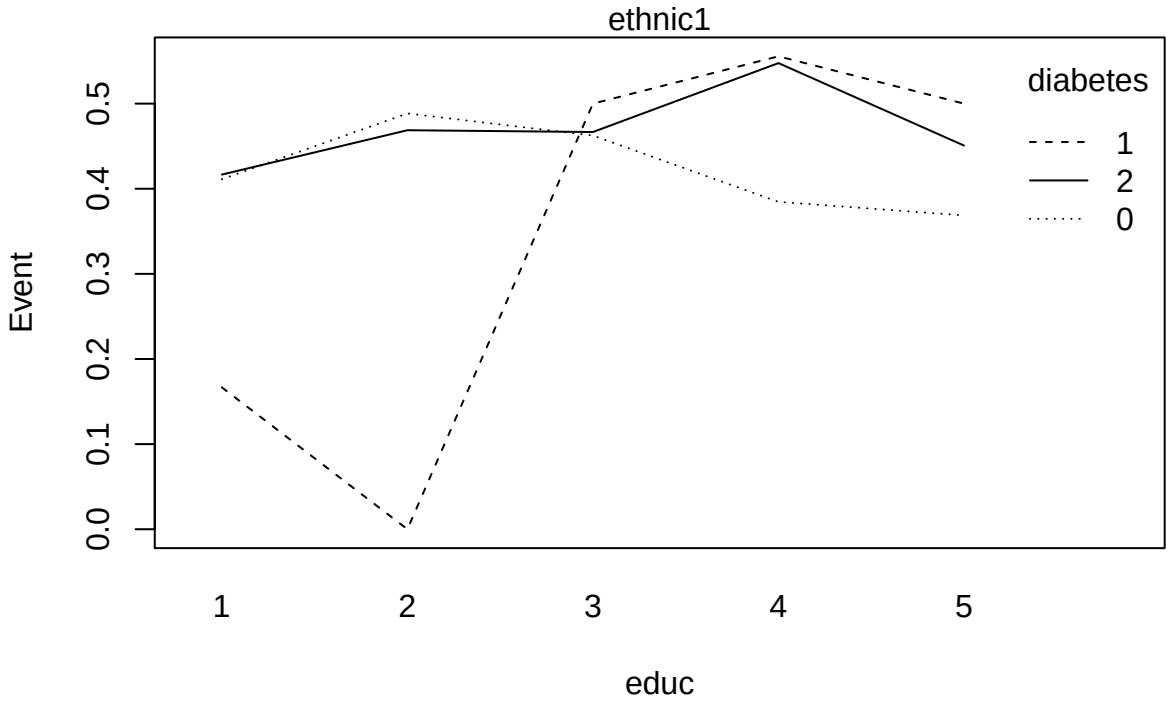

Event
0.40
0.45
0.50
gender
1
2
0
1
2
diabetes

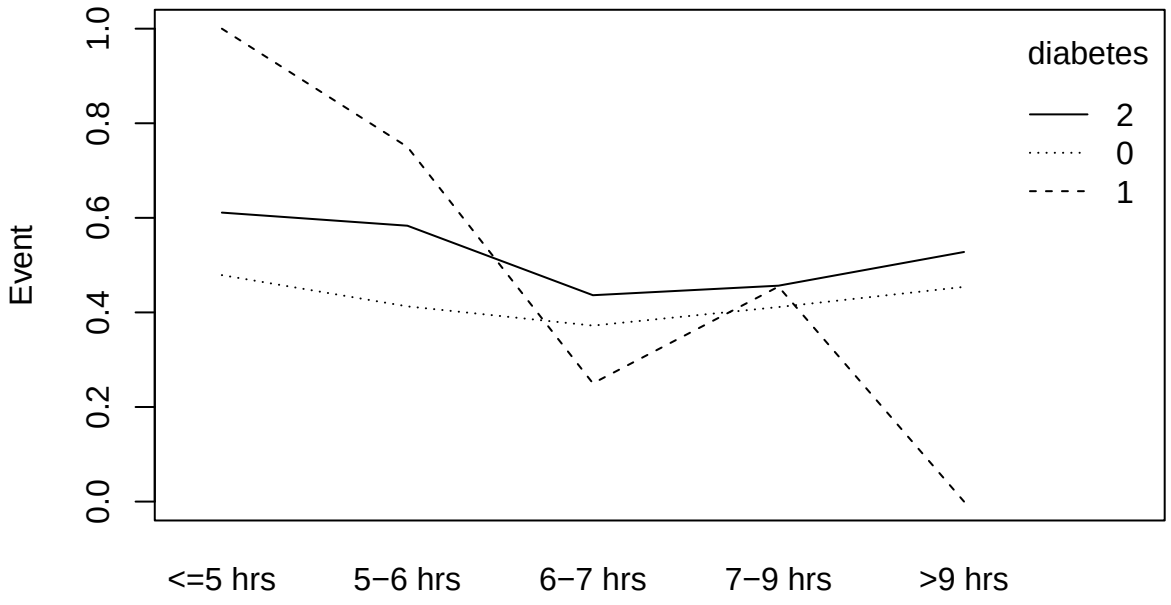

gender
2
1
Event
0.39
0.41
0.43
0.45
0
1
smoker
gender
1
2
Event
0.0
0.2
0.4
0.6
0.8
1.0
14.2
21
24
27
30
33
36
39
42
45
50
bmi

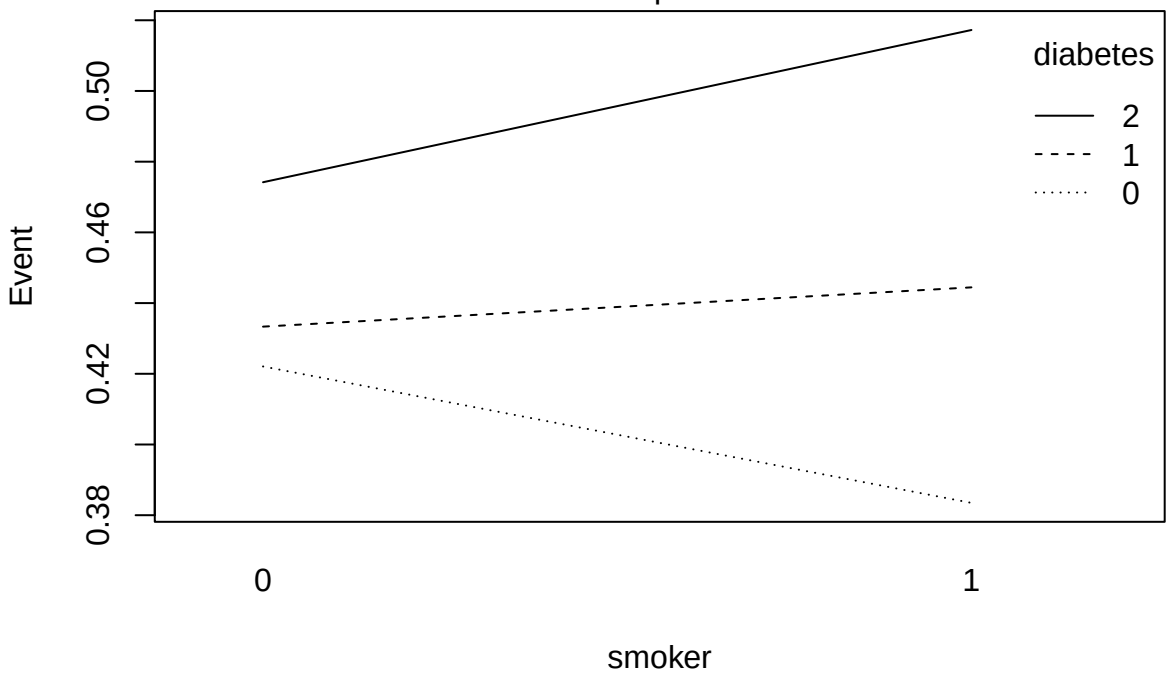

diabetes
1
2
0
Event
0.40
0.45
0.50
1
2
gender

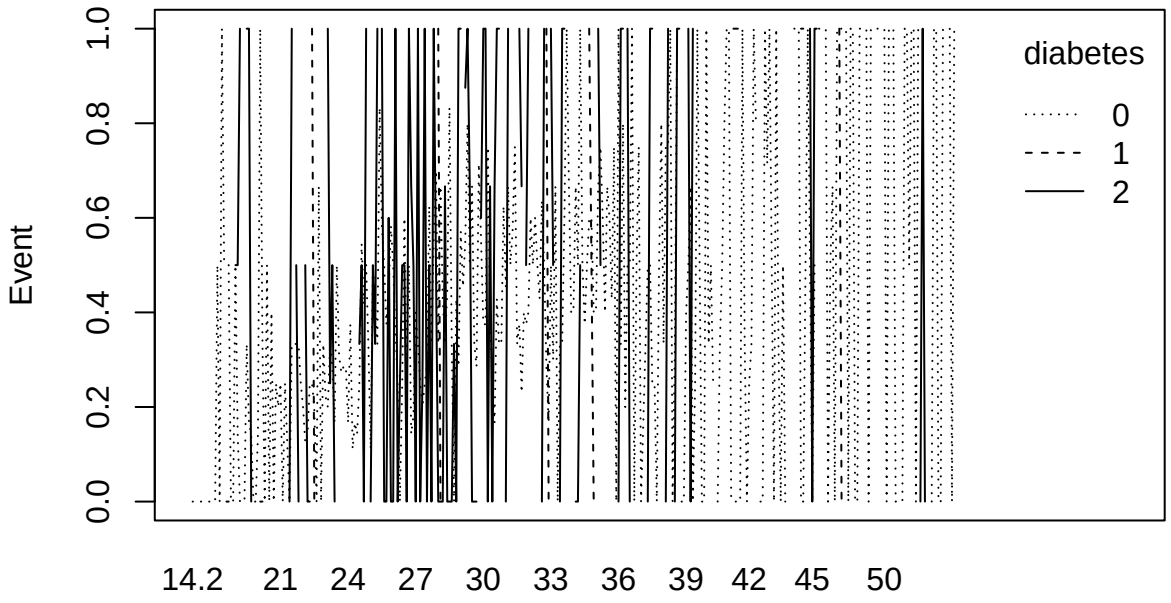

diabetes
0
2
1
Event
0.0
0.2
0.4
0.6
0.8
1.0
20
25
30
35
40
45
50
55
60
65
70
75
80
age

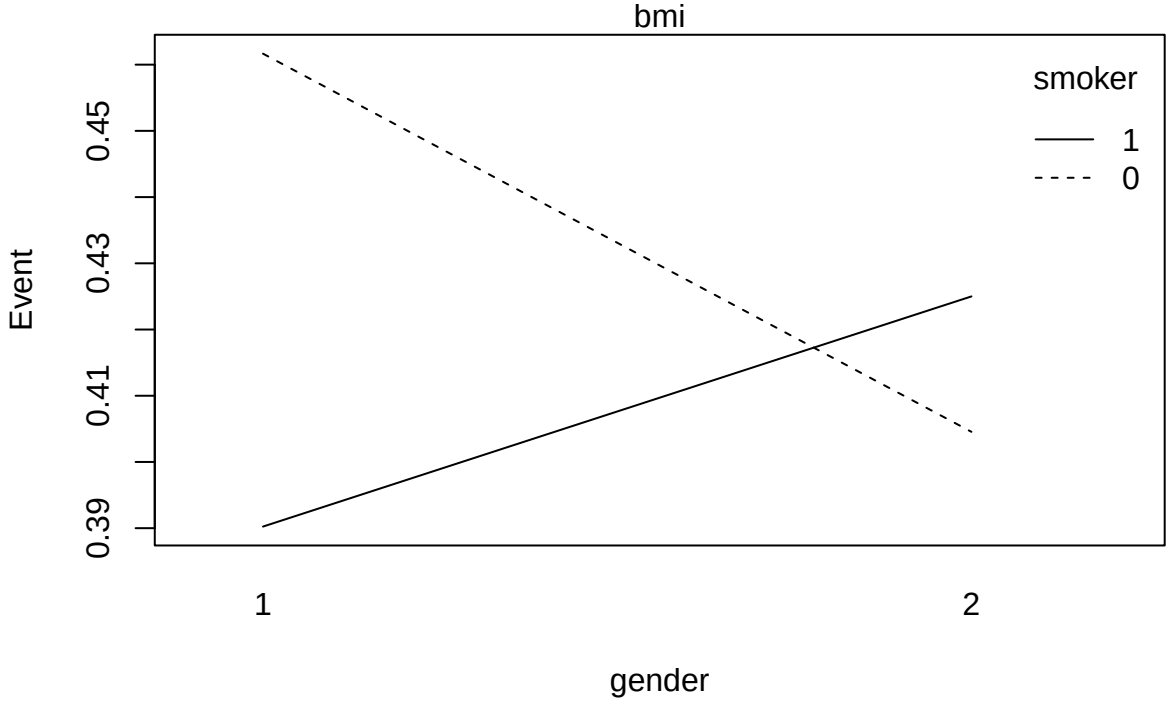

Event
0.30
0.35
0.40
0.45
0.50
0.55
diabetes
2
0
1
Black
Other
White
ethnic1

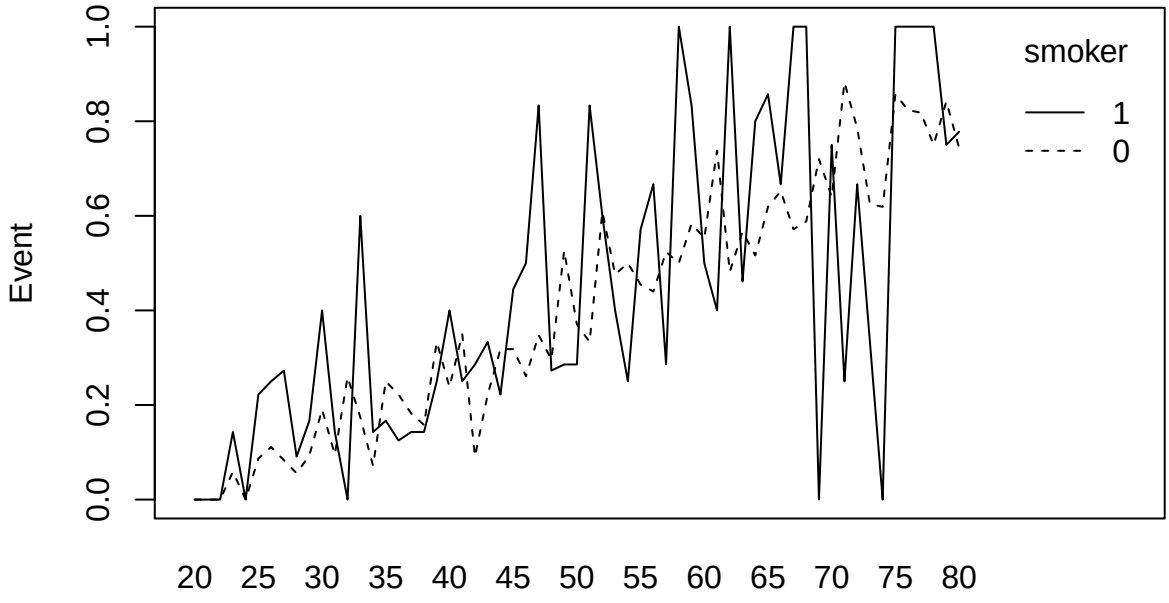

Event
0.0
0.1
0.2
0.3
0.4
0.5
diabetes
1
2
0
1
2
3
4
5
educ

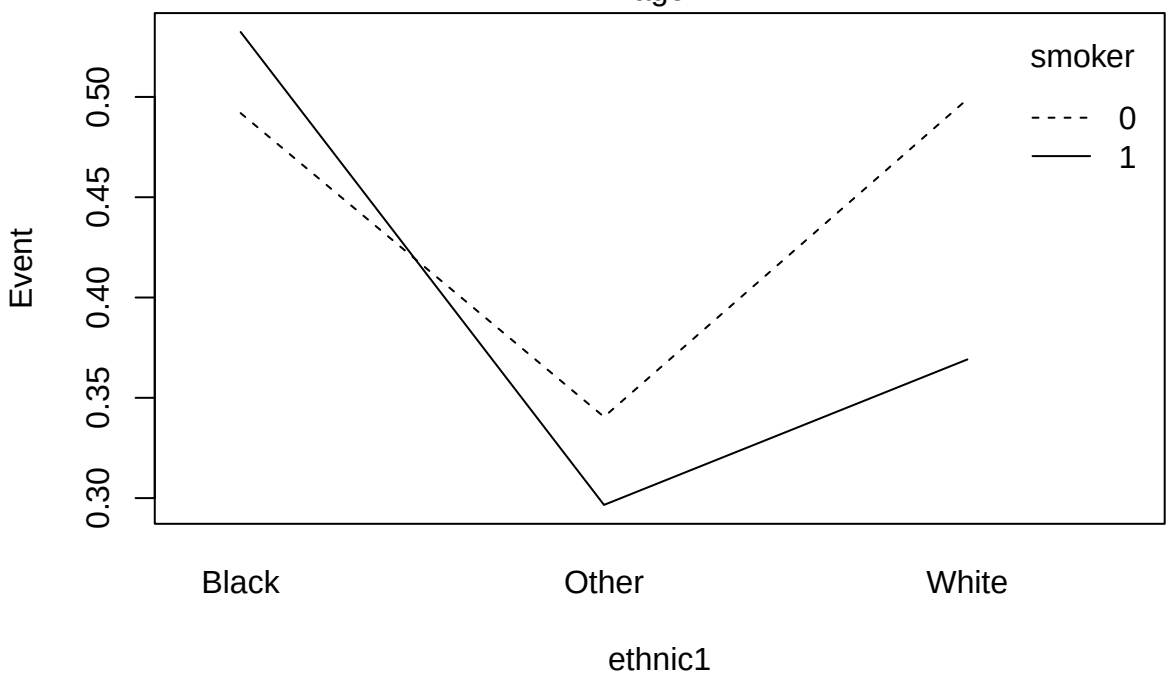

Event
0.0
0.2
0.4
0.6
0.8
1.0
diabetes
2
0
1
<=5 hrs
5−6 hrs
6−7 hrs
7−9 hrs
>9 hrs
sleep.hrs

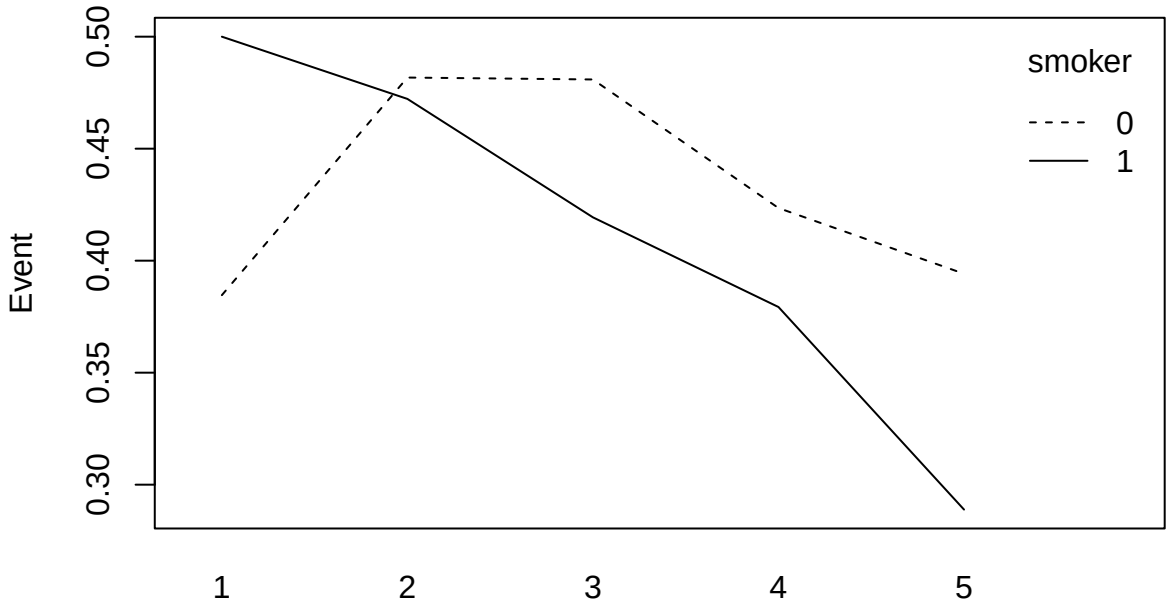

Event
0.38
0.42
0.46
0.50
diabetes
2
1
0
0
1
smoker

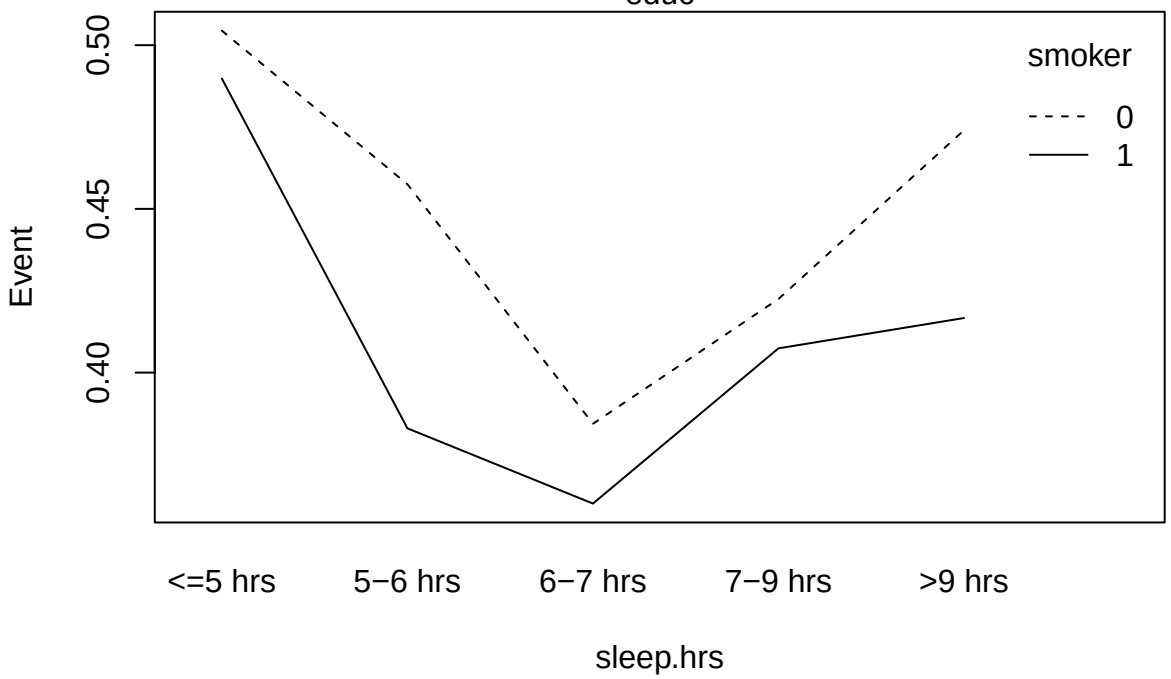

Event
0.0
0.2
0.4
0.6
0.8
1.0
diabetes
0
1
2
14.2
21
24
27
30
33
36
39
42
45
50
bmi

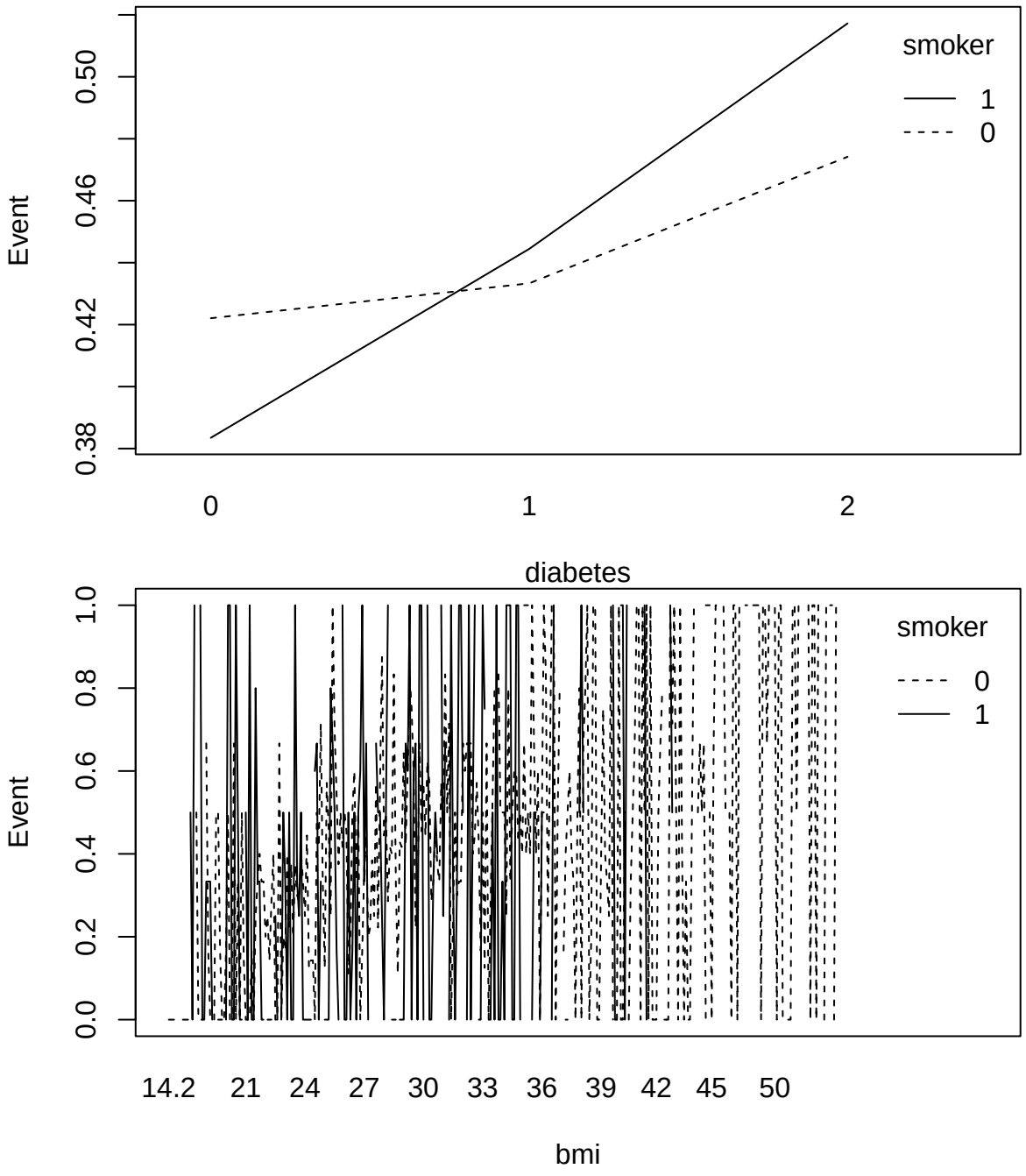

Event
0.39
0.41
0.43
0.45
smoker
1
0
1
2
gender

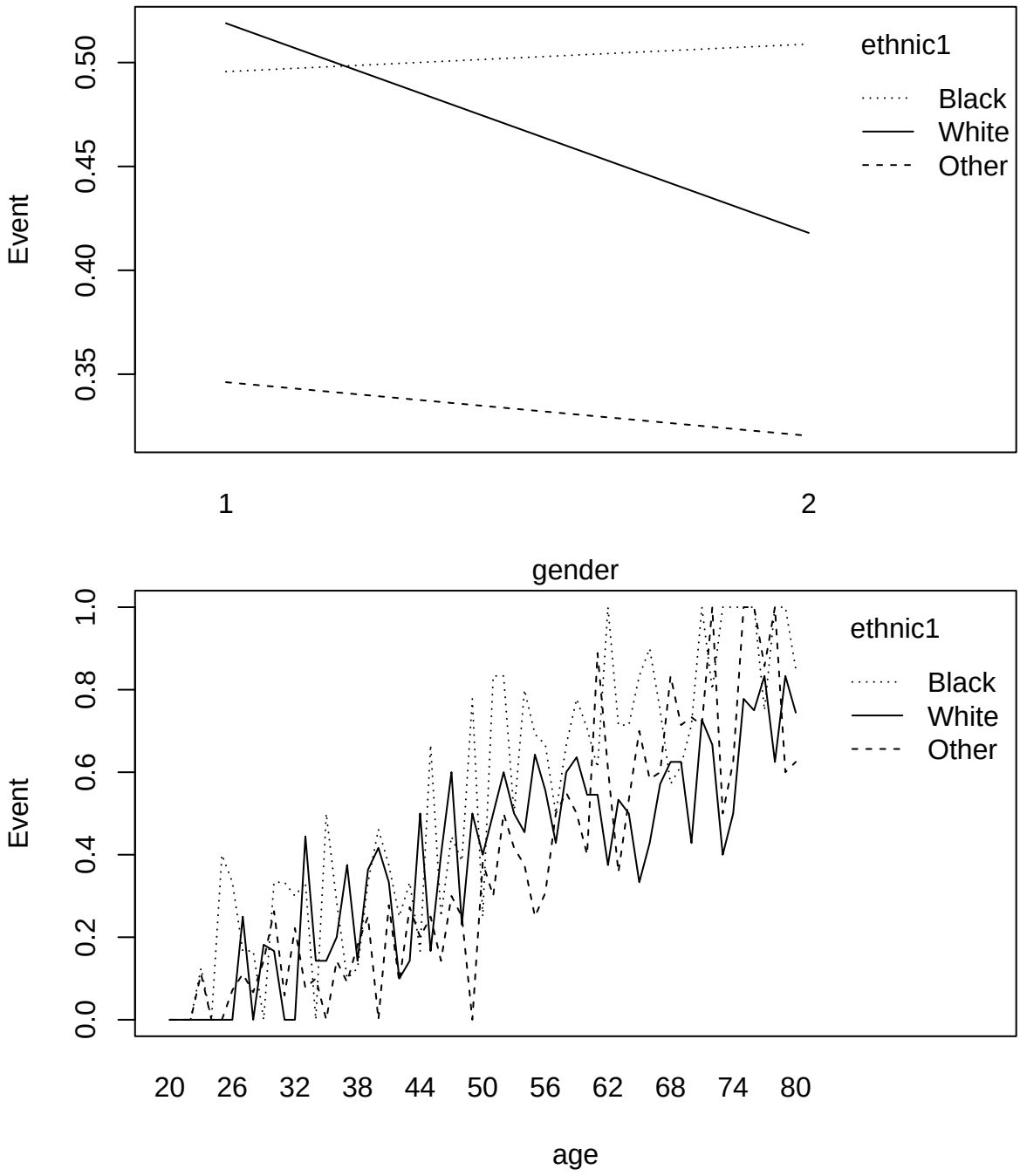

Event
0.0
0.2
0.4
0.6
0.8
1.0
smoker
1
0
20 25 30 35 40 45 50 55 60 65 70 75 80
age

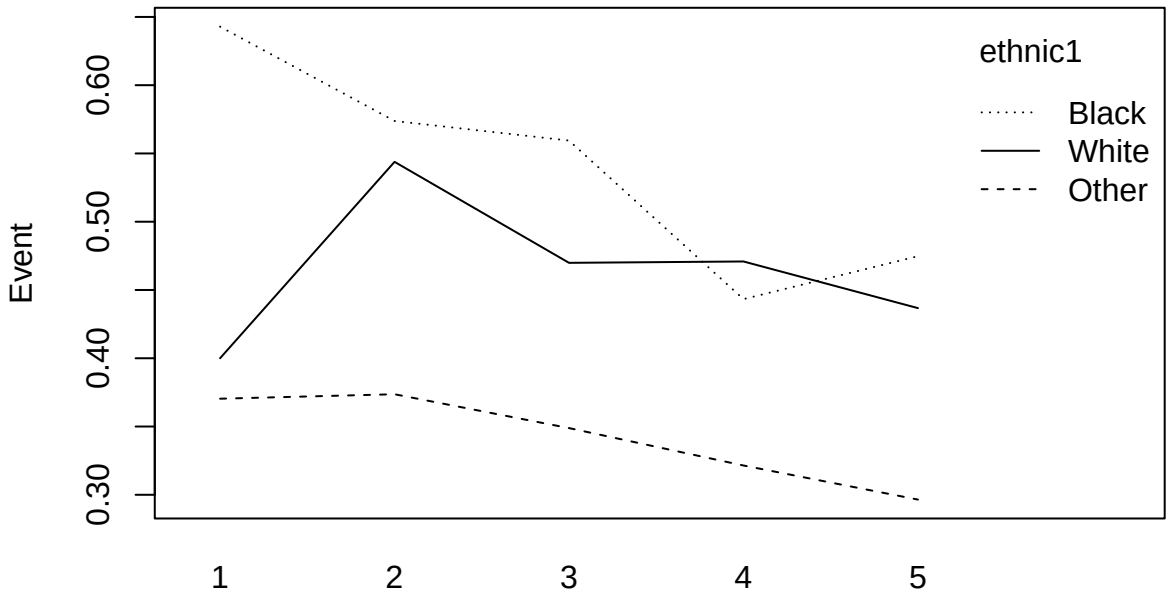

Event
0.30
0.35
0.40
0.45
0.50
smoker
0
1
Black
Other
White
ethnic1

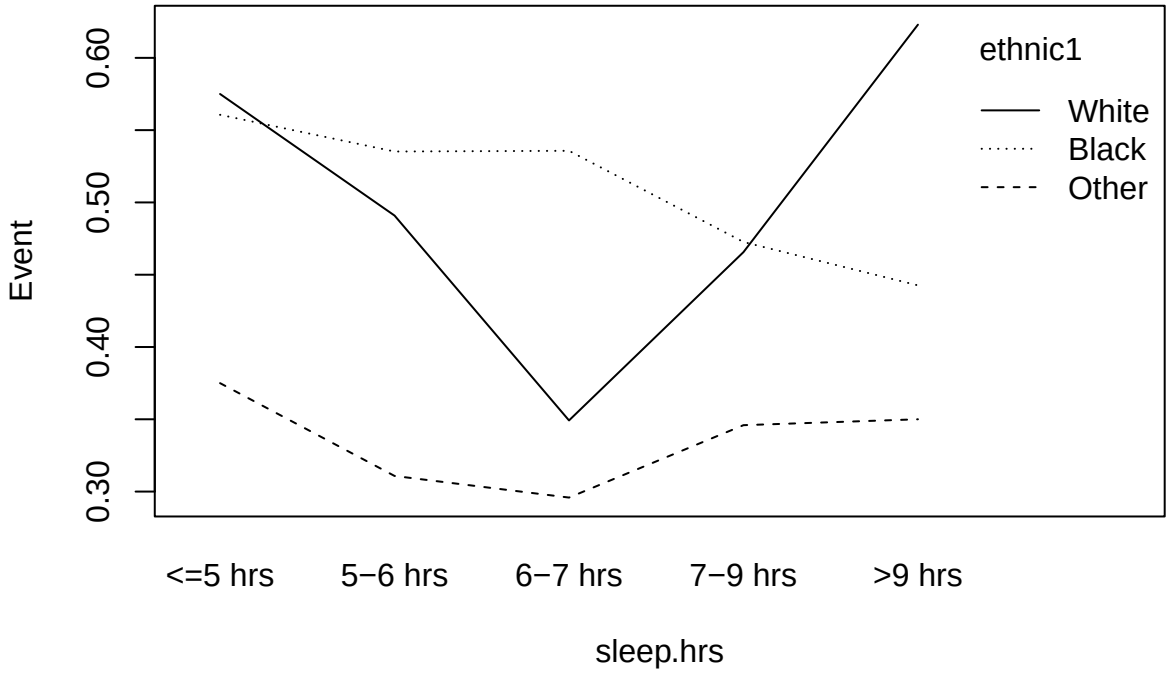

Event
0.30
0.35
0.40
0.45
0.50
smoker
0
1
1
2
3
4
5
educ

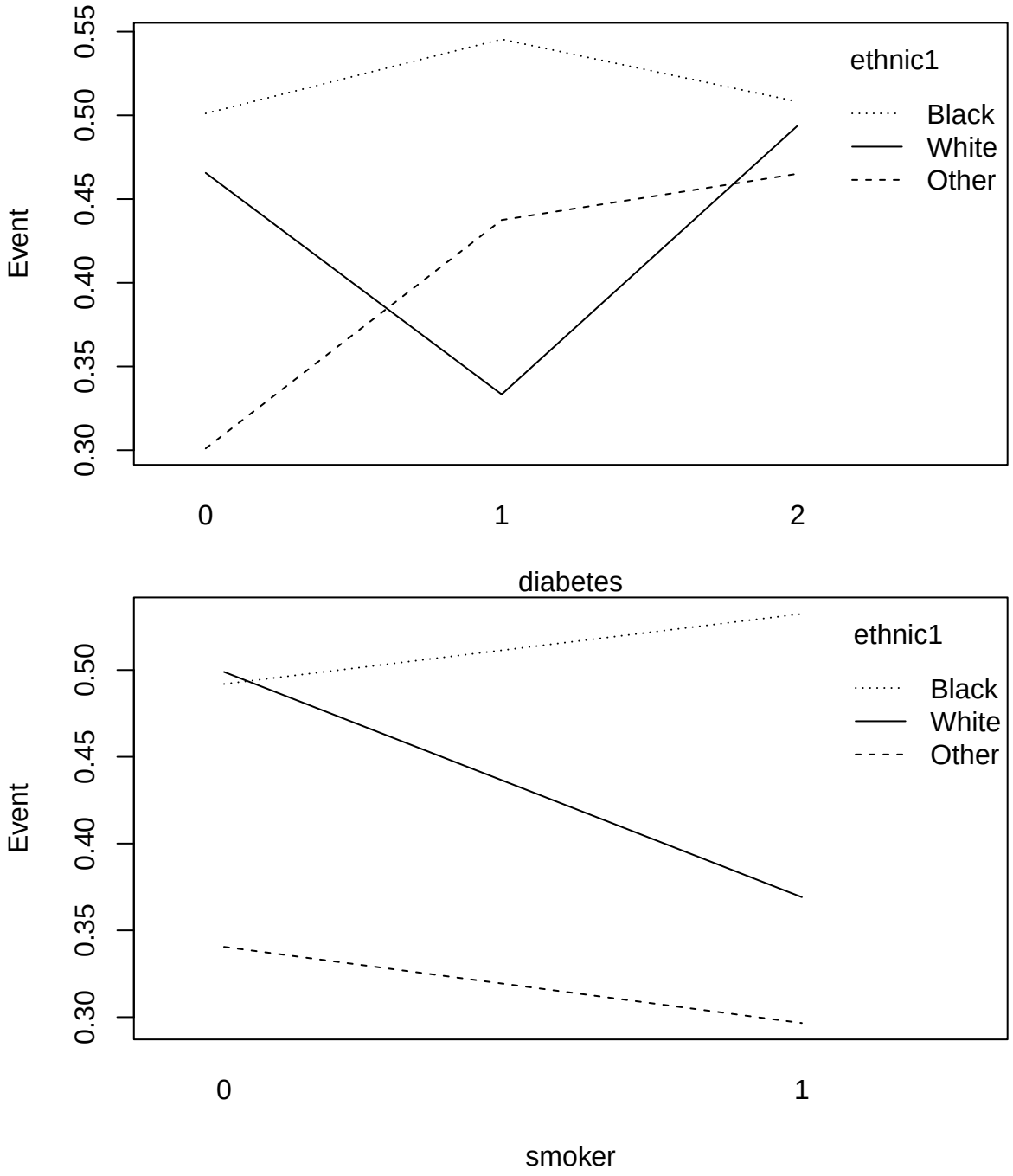

Event
0.40
0.45
0.50
smoker
0
1
<=5 hrs
5−6 hrs
6−7 hrs
7−9 hrs
>9 hrs
sleep.hrs

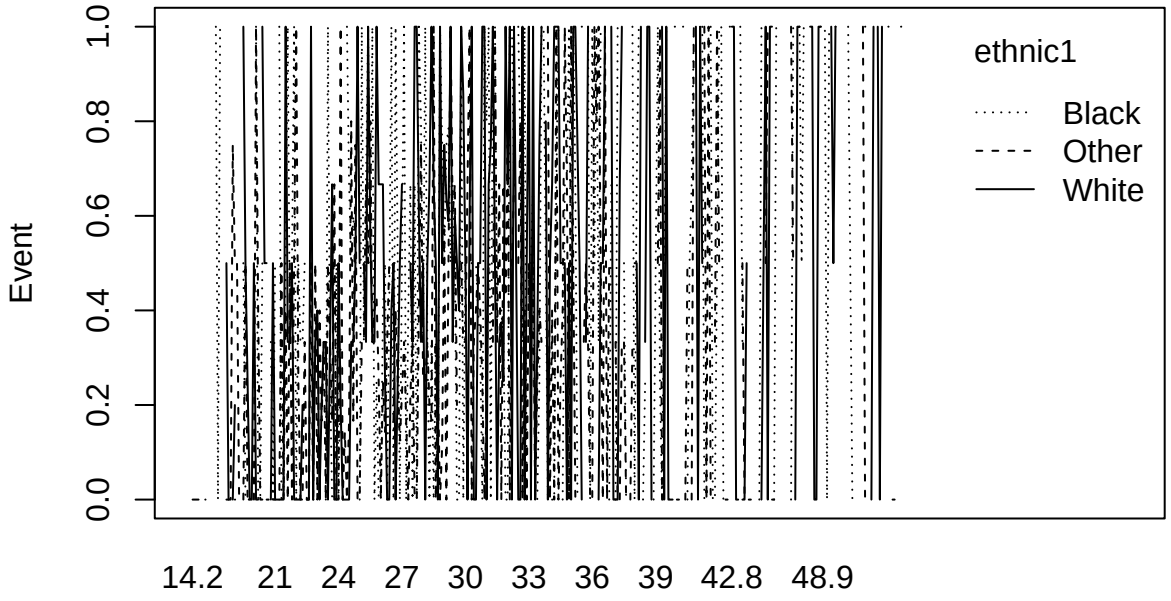

Event
0.38
0.42
0.46
0.50
0
1
2
diabetes
smoker
1
0
Event
0.0
0.2
0.4
0.6
0.8
1.0
14.2
21
24
27
30
33
36
39
42
45
50
bmi
smoker
0
1

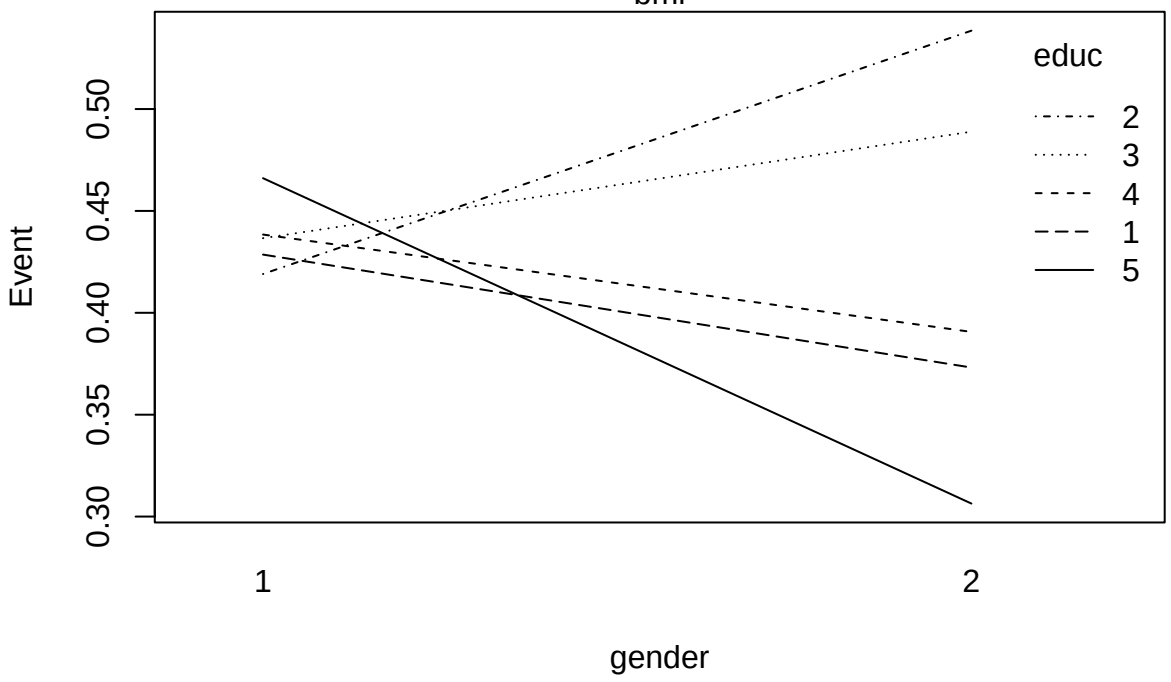

Event
0.35
0.40
0.45
0.50
ethnic1
Black
White
Other
1
2
gender
Event
0.0
0.2
0.4
0.6
0.8
1.0
ethnic1
Black
White
Other
20
26
32
38
44
50
56
62
68
74
80
age

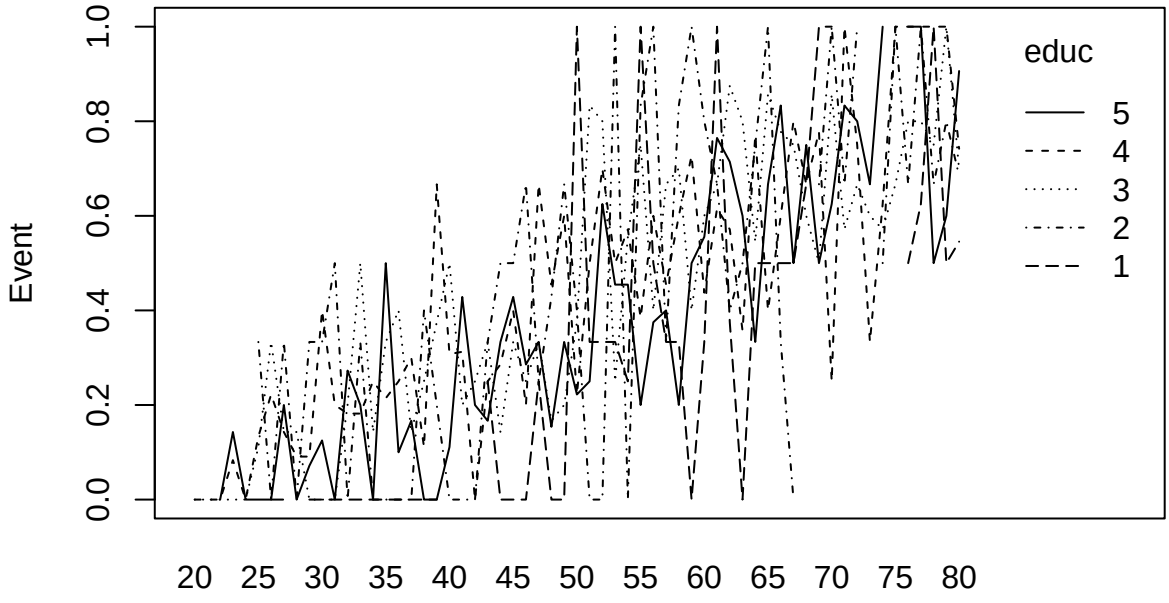

ethnic1
Black
White
Other
Event
0.30
0.40
0.50
0.60
1
2
3
4
5
educ

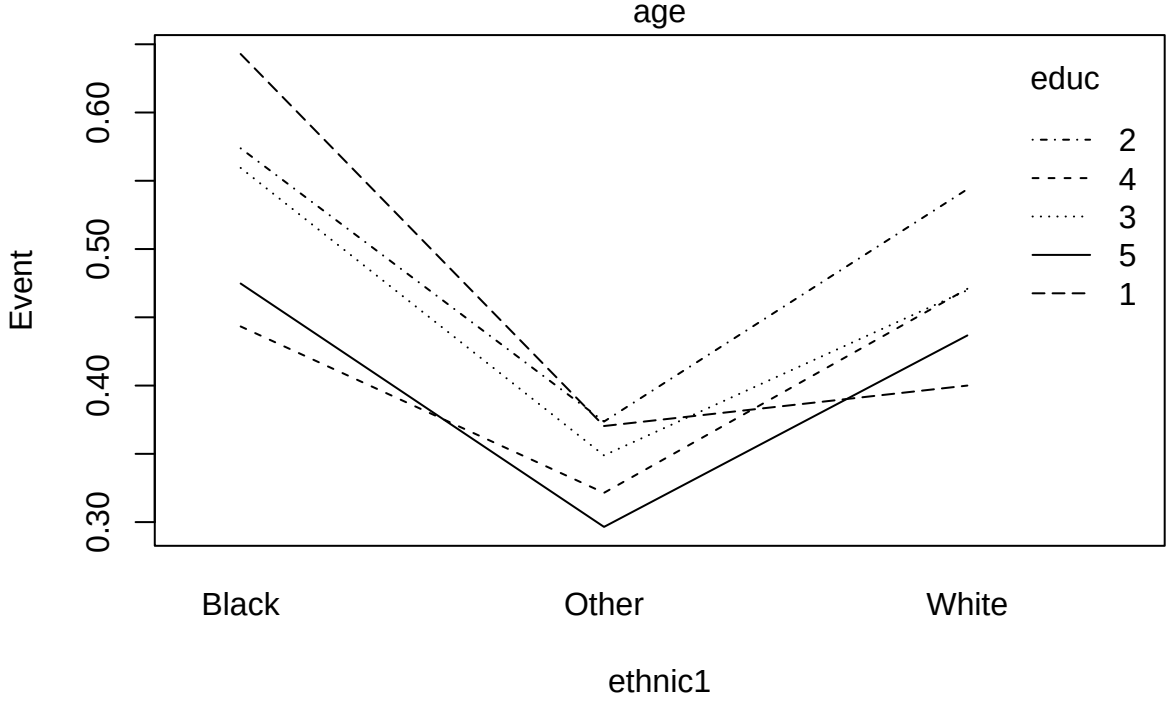

ethnic1
White
Black
Other
Event
0.30
0.40
0.50
0.60
<=5 hrs
5−6 hrs
6−7 hrs
7−9 hrs
>9 hrs
sleep.hrs

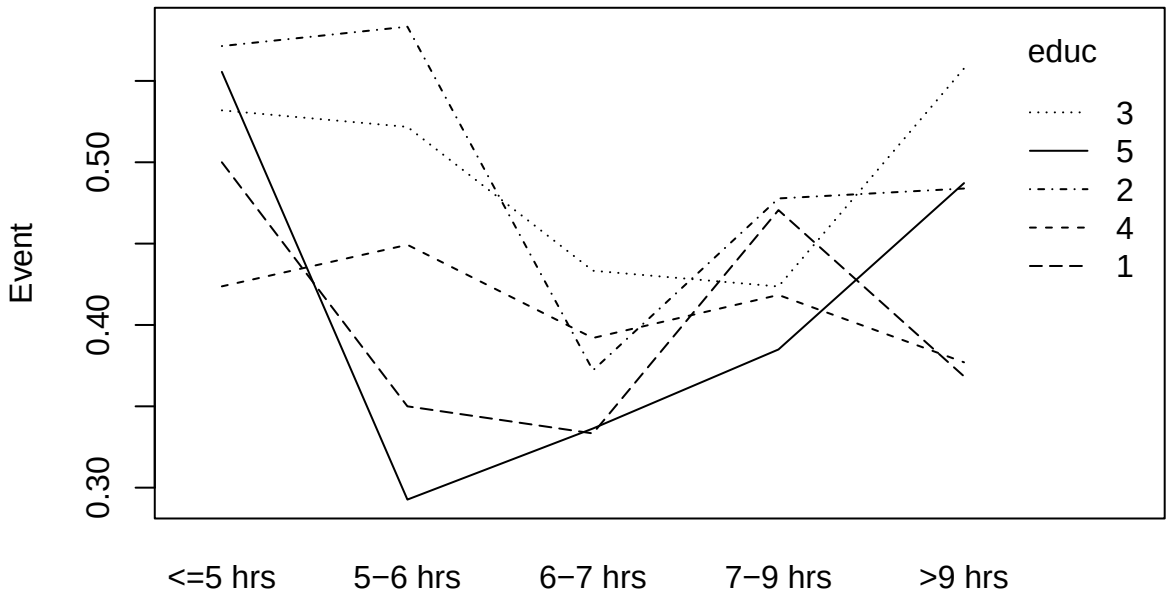

Event
0.30
0.35
0.40
0.45
0.50
0.55
0
1
2
diabetes
ethnic1
Black
White
Other
Event
0.30
0.35
0.40
0.45
0.50
0
1
smoker
ethnic1
Black
White
Other

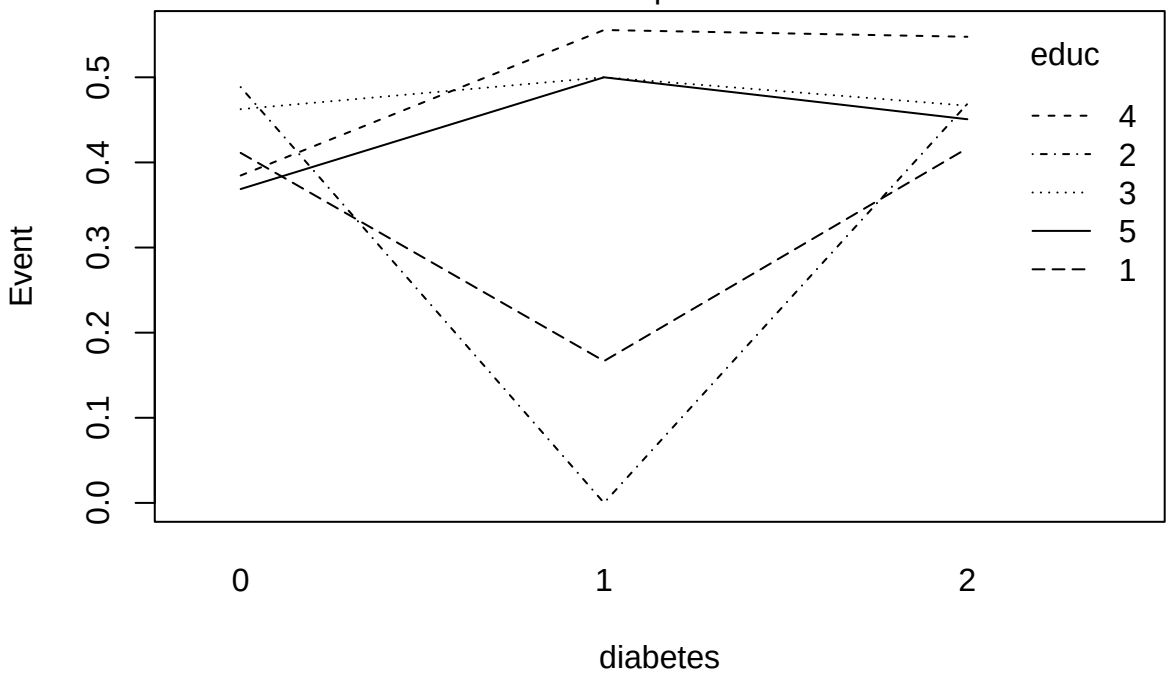

Event
0.0
0.2
0.4
0.6
0.8
1.0
ethnic1
Black
Other
White
14.2
21
24
27
30
33
36
39
42.8
48.9
bmi

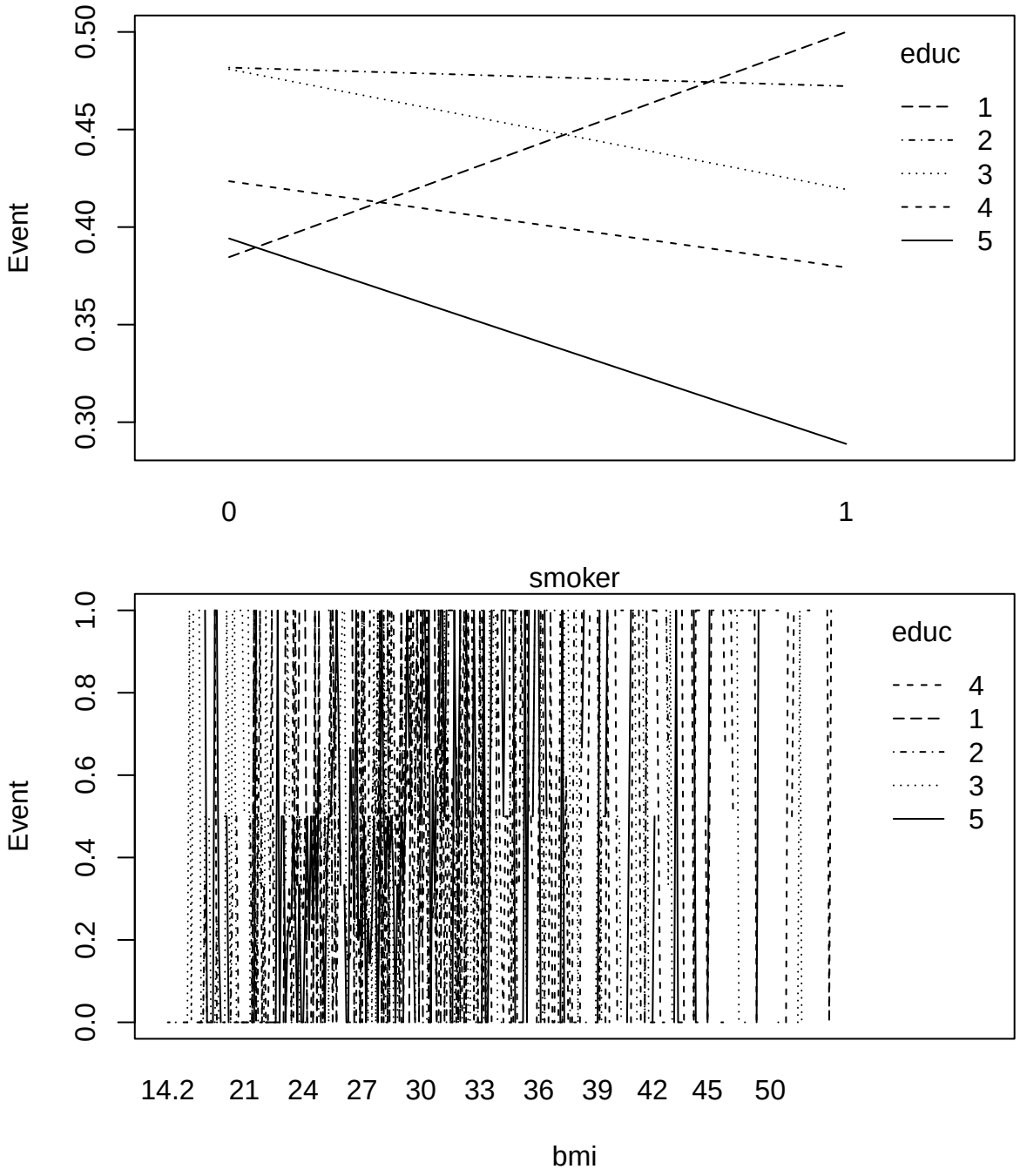

Event
0.30
0.35
0.40
0.45
0.50
educ
2
3
4
1
5
1
2
gender


Event
0.0
0.2
0.4
0.6
0.8
1.0
20
25
30
35
40
45
50
55
60
65
70
75
80
age
educ
5
4
3
2
1


Event
0.30
0.40
0.50
0.60
Black
Other
White
ethnic1
educ
2
4
3
5
1


Event
0.30
0.40
0.50
<=5 hrs
5−6 hrs
6−7 hrs
7−9 hrs
>9 hrs
sleep.hrs
educ
3
5
2
4
1


Event
0.0
0.1
0.2
0.3
0.4
0.5
0
1
2
diabetes
educ
4
2
3
5
1



Exploring Interaction Effect Through LR Test

```
# Prettified table with signif. indicator:
predictors<-c("gender" ,"age","ethnic1","educ" ,"sleep.hrs", "diabetes" ,"smoker"  ,"bmi")
lrfunction <- function(i, j, data) {
  formula_str <- paste("event ~", i, "+", j, "+", i, ":", j)
  model1 <- glm(formula_str, data = data, family = binomial)
  formula_str <- paste("event ~", i, "+", j)
  model2 <- glm(formula_str, data = data, family = binomial)
  lr_test <- lrtest(model1, model2)

  pvalue <- lr_test$Pr[2]
```

```
  significance <- ifelse(pvalue < 0.01, "**", ifelse(pvalue < 0.05, "*", ""))

  result <- data.frame(term1 = i, term2 = j, pvalue = pvalue, significance = paste0(round(pvalue, 3),sig
  return(result)
}

interaction_results <- data.frame(term1 = character(), term2 = character(), pvalue = numeric(), signifi

for (i in 1:(length(predictors))) {
  for (j in 1:(length(predictors))) {
    if (i == j) {
      pvalue <- NaN
      significance <- ""
    } else {
      result <- lrfunction(predictors[[i]], predictors[[j]], data)
      pvalue <- result$pvalue
      significance <- result$significance
    }
    interaction_results <- rbind(interaction_results, data.frame(term1 = predictors[[i]], term2 = predi
  }
}

interaction_matrix <- reshape2::acast(interaction_results, term1 ~ term2, value.var = "significance")

interaction_matrix
```

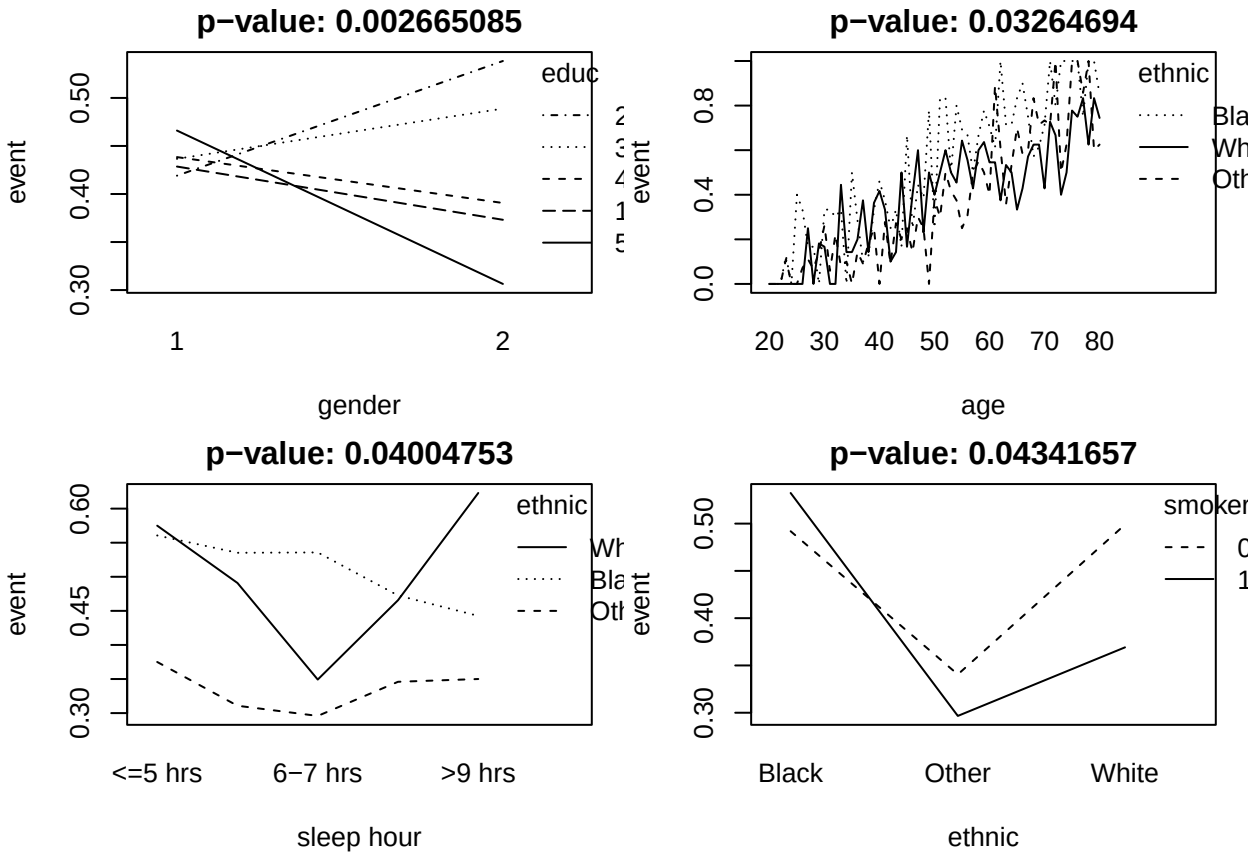
```
##           age      bmi     diabetes educ      ethnic1  gender    sleep.hrs
## age       ""       "0.358" "0.554"  "0.154"   "0.033*" "0.834"   "0.972"
## bmi       "0.358"  ""      "0.097"  "0.314"   "0.679"  "0.496"   "0.399"
## diabetes  "0.554"  "0.097" ""       "0.206"   "0.05*"  "0.38"    "0.74"
## educ      "0.154"  "0.314" "0.206"  ""        "0.849"  "0.003**" "0.729"
## ethnic1   "0.033*" "0.679" "0.05*"  "0.849"   ""       "0.152"   "0.102"
## gender    "0.834"  "0.496" "0.38"   "0.003**" "0.152"  ""        "0.184"
## sleep.hrs "0.972"  "0.399" "0.74"   "0.729"   "0.102"  "0.184"   ""
## smoker    "0.468"  "0.912" "0.293"  "0.583"   "0.043*" "0.106"   "0.968"
##           smoker
## age       "0.468"
## bmi       "0.912"
## diabetes  "0.293"
## educ      "0.583"
## ethnic1   "0.043*"
## gender    "0.106"
## sleep.hrs "0.968"
## smoker    ""
```

```
write.csv(interaction_matrix, ".\\interaction_result.csv", row.names=TRUE)
```

Select 4 significant interaction terms:

```
par(mfrow = c(1, 1))
par(mfrow = c(2, 2), mar = c(4, 4, 2, 1))
#options(repr.plot.width = 50, repr.plot.height = 20)


interaction.plot(
```

```
  x.factor = as.factor(data$gender),
  trace.factor = as.factor(data$educ),
  response =as.numeric(as.character(data$event))
  , type = "l", legend = TRUE,
  xlab="gender",
  ylab="event",
  trace.label = "educ",
  main="p-value: 0.002665085")

interaction.plot(
  x.factor = as.factor(data$age),
  trace.factor = as.factor(data$ethnic1),
  response = as.numeric(as.character(data$event))
  , type = "l", legend = TRUE,
  xlab="age",
  ylab="event",
  trace.label = "ethnic",
  main="p-value: 0.03264694")

interaction.plot(
x.factor = as.factor(data$sleep.hrs),
trace.factor = as.factor(data$ethnic1),
response =as.numeric(as.character(data$event))
, type = "l", legend = TRUE,
xlab="sleep hour",
ylab="event",
trace.label = "ethnic",
main="p-value: 0.04004753")

interaction.plot(
x.factor = as.factor(data$ethnic1),
trace.factor = as.factor(data$smoker),
response =as.numeric(as.character(data$event))

, type = "l", legend = TRUE,
xlab="ethnic",
ylab="event",
trace.label = "smoker",
main="p-value: 0.04341657")
```




```
# Set a higher threshold (alpha = 0.01), so only the interaction term between gender and education is s
```

Step 5: Fit, Compare, Select Models

```
# Evaluate Full Model
full.model <- glm(event ~.+educ*gender, data = data, family = binomial)
summary(full.model)
```

```
##
## Call:
## glm(formula = event ~ . + educ * gender, family = binomial, data = data)
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -5.978707   0.521941 -11.455  < 2e-16 ***
## gender2          -0.372400   0.402913  -0.924 0.355346
## age               0.075137   0.004129  18.197  < 2e-16 ***
## ethnic1Other     -0.495992   0.145565  -3.407 0.000656 ***
## ethnic1White     -0.638080   0.149327  -4.273 1.93e-05 ***
## educ2             0.291036   0.369643   0.787 0.431081
## educ3             0.361929   0.331783   1.091 0.275335
## educ4             0.331388   0.322932   1.026 0.304804
## educ5             0.581796   0.326390   1.783 0.074665 .
## sleep.hrs5-6 hrs -0.225793   0.249162  -0.906 0.364825
## sleep.hrs6-7 hrs -0.445424   0.220324  -2.022 0.043210 *
## sleep.hrs7-9 hrs -0.238886   0.203224  -1.175 0.239801
## sleep.hrs>9 hrs  -0.285829   0.251464  -1.137 0.255681
## diabetes         -0.143095   0.075153  -1.904 0.056906 .
```

```
## smoker1           0.285674   0.142676   2.002 0.045257 *
## bmi               0.067162   0.007803   8.607  < 2e-16 ***
## gender2:educ2     0.709475   0.519313   1.366 0.171883
## gender2:educ3     0.422549   0.461811   0.915 0.360201
## gender2:educ4     0.362424   0.450508   0.804 0.421121
## gender2:educ5    -0.266648   0.463800  -0.575 0.565346
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2503.0  on 1835  degrees of freedom
## Residual deviance: 1907.2  on 1816  degrees of freedom
## AIC: 1947.2
##
## Number of Fisher Scoring iterations: 4
```

```
# AIC Backward Selection
step(full.model,direction="backward", k=2)
```

```
## Start:  AIC=1947.17
## event ~ gender + age + ethnic1 + educ + sleep.hrs + diabetes +
##     smoker + bmi + educ * gender
##
##               Df Deviance    AIC
## - sleep.hrs    4   1911.7 1943.7
## <none>             1907.2 1947.2
## - gender:educ  4   1915.5 1947.5
## - diabetes     1   1910.8 1948.8
## - smoker       1   1911.2 1949.2
## - ethnic1      2   1927.6 1963.6
## - bmi          1   1988.6 2026.6
## - age          1   2355.7 2393.7
##
## Step:  AIC=1943.66
## event ~ gender + age + ethnic1 + educ + diabetes + smoker + bmi +
##     gender:educ
##
##               Df Deviance    AIC
## - gender:educ  4   1919.7 1943.7
## <none>             1911.7 1943.7
## - diabetes     1   1915.5 1945.5
## - smoker       1   1915.8 1945.8
## - ethnic1      2   1933.1 1961.1
## - bmi          1   1994.4 2024.4
## - age          1   2363.6 2393.6
##
## Step:  AIC=1943.66
## event ~ gender + age + ethnic1 + educ + diabetes + smoker + bmi
##
##            Df Deviance    AIC
## - gender    1   1921.0 1943.0
## - educ      4   1927.5 1943.5
## <none>          1919.7 1943.7
## - diabetes  1   1923.3 1945.3
```

```
## - smoker    1   1924.1 1946.1
## - ethnic1   2   1940.7 1960.7
## - bmi       1   2005.6 2027.6
## - age       1   2377.6 2399.6
##
## Step:  AIC=1942.96
## event ~ age + ethnic1 + educ + diabetes + smoker + bmi
##
##            Df Deviance    AIC
## - educ      4   1928.8 1942.8
## <none>          1921.0 1943.0
## - diabetes  1   1924.5 1944.5
## - smoker    1   1926.0 1946.0
## - ethnic1   2   1941.7 1959.7
## - bmi       1   2005.8 2025.8
## - age       1   2383.6 2403.6
##
## Step:  AIC=1942.79
## event ~ age + ethnic1 + diabetes + smoker + bmi
##
##            Df Deviance    AIC
## <none>          1928.8 1942.8
## - diabetes  1   1932.2 1944.2
## - smoker    1   1934.9 1946.9
## - ethnic1   2   1951.9 1961.9
## - bmi       1   2015.1 2027.1
## - age       1   2394.1 2406.1
##
## Call:  glm(formula = event ~ age + ethnic1 + diabetes + smoker + bmi,
##     family = binomial, data = data)
##
## Coefficients:
##  (Intercept)           age  ethnic1Other  ethnic1White      diabetes
##     -5.88095       0.07408      -0.56346      -0.63579      -0.13747
##      smoker1           bmi
##      0.34201       0.06741
##
## Degrees of Freedom: 1835 Total (i.e. Null);  1829 Residual
## Null Deviance:       2503
## Residual Deviance: 1929  AIC: 1943
```

```
# BIC Backward Selection
step(full.model,direction="backward", k=log(nrow(data)), k.out=log(nrow(data)))
```

```
## Start:  AIC=2057.48
## event ~ gender + age + ethnic1 + educ + sleep.hrs + diabetes +
##     smoker + bmi + educ * gender
##
##               Df Deviance    AIC
## - sleep.hrs    4   1911.7 2031.9
## - gender:educ  4   1915.5 2035.8
## - diabetes     1   1910.8 2053.6
## - smoker       1   1911.2 2054.0
## <none>             1907.2 2057.5
```

```
## - ethnic1      2   1927.6 2062.9
## - bmi          1   1988.6 2131.4
## - age          1   2355.7 2498.5
##
## Step:  AIC=2031.91
## event ~ gender + age + ethnic1 + educ + diabetes + smoker + bmi +
##     gender:educ
##
##               Df Deviance    AIC
## - gender:educ  4   1919.7 2009.8
## - diabetes     1   1915.5 2028.2
## - smoker       1   1915.8 2028.5
## <none>             1911.7 2031.9
## - ethnic1      2   1933.1 2038.3
## - bmi          1   1994.4 2107.1
## - age          1   2363.6 2476.3
##
## Step:  AIC=2009.85
## event ~ gender + age + ethnic1 + educ + diabetes + smoker + bmi
##
##            Df Deviance    AIC
## - educ      4   1927.5 1987.7
## - gender    1   1921.0 2003.6
## - diabetes  1   1923.3 2006.0
## - smoker    1   1924.1 2006.7
## <none>          1919.7 2009.8
## - ethnic1   2   1940.7 2015.8
## - bmi       1   2005.6 2088.2
## - age       1   2377.6 2460.3
##
## Step:  AIC=1987.67
## event ~ gender + age + ethnic1 + diabetes + smoker + bmi
##
##            Df Deviance    AIC
## - gender    1   1928.8 1981.4
## - diabetes  1   1931.1 1983.7
## - smoker    1   1933.0 1985.6
## <none>          1927.5 1987.7
## - ethnic1   2   1951.0 1996.0
## - bmi       1   2015.0 2067.6
## - age       1   2388.1 2440.7
##
## Step:  AIC=1981.39
## event ~ age + ethnic1 + diabetes + smoker + bmi
##
##            Df Deviance    AIC
## - diabetes  1   1932.2 1977.3
## - smoker    1   1934.9 1980.0
## <none>          1928.8 1981.4
## - ethnic1   2   1951.9 1989.4
## - bmi       1   2015.1 2060.2
## - age       1   2394.1 2439.2
##
## Step:  AIC=1977.31
```

```
## event ~ age + ethnic1 + smoker + bmi
##
##           Df Deviance    AIC
## - smoker   1   1938.0 1975.6
## <none>         1932.2 1977.3
## - ethnic1  2   1956.0 1986.1
## - bmi      1   2017.7 2055.3
## - age      1   2400.3 2437.8
##
## Step:  AIC=1975.6
## event ~ age + ethnic1 + bmi
##
##           Df Deviance    AIC
## <none>         1938.0 1975.6
## - ethnic1  2   1964.0 1986.5
## - bmi      1   2020.1 2050.2
## - age      1   2401.6 2431.6
##
## Call:  glm(formula = event ~ age + ethnic1 + bmi, family = binomial,
##     data = data)
##
## Coefficients:
##  (Intercept)           age  ethnic1Other  ethnic1White           bmi
##     -5.60878       0.07119      -0.63061      -0.63284       0.06523
##
## Degrees of Freedom: 1835 Total (i.e. Null);  1831 Residual
## Null Deviance:       2503
## Residual Deviance: 1938  AIC: 1948
```

Final model(`final.model`):age+ethnic+smoker+bmi:

$$\begin{aligned}\text{logit}(\pi_E) &= \ln\left(\frac{\mathbb{P}(\text{event})}{1-\mathbb{P}(\text{event})}\right)\\ &= \beta_0 + \beta_{\text{age}}\text{age} + \beta_{\text{Ethnic:Other}}\text{Ethnic:Other} + \beta_{\text{Ethnic:White}}\text{Ethnic:White}\\ &+ \beta_{\text{Ethnic:White}}\text{Ethnic:White} + \beta_{\text{Smoker}}\text{Smoker} + \beta_{\text{BMI}}\text{BMI}\end{aligned}$$

Step 6: Assess the model's overall fit

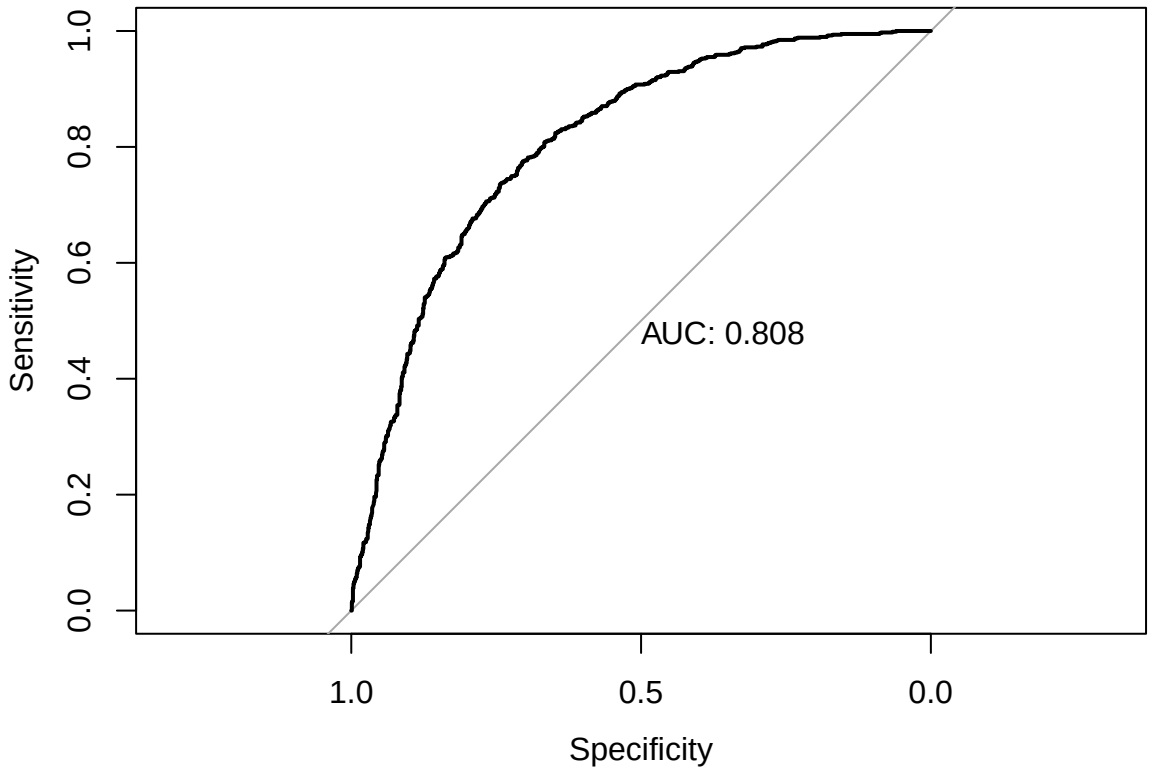
ROC Curve

```
## ROC curve:
final.model<-glm(event~age+ethnic1+smoker+bmi,data,family=binomial)
probs <- predict(final.model

                 , type = "response")

roc <- roc(data$event, probs)
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

```r
plot(roc, print.auc = TRUE)
```



Confusion matrix

```r
# install.packages(caret)
library(caret)
predicted_classes <- ifelse(probs > 0.5, 1, 0)
confusion_matrix <- caret::confusionMatrix(factor(data$event), factor(predicted_classes))

# Full results:
# print(confusion_matrix)

# Table only:
confusion_matrix$table
```

```
##           Reference
## Prediction   0   1
##          0 833 224
##          1 252 527
```

Probability plot:

```r
## Age+smoker
mean_bmi <- mean(data$bmi)
mean_age <- mean(data$age)

plot_data <- expand.grid(
  age = seq(min(data$age), max(data$age), length.out = 100),  # Adjust the length.out as needed
```

```
  smoker = as.factor(c(0, 1)),
  ethnic1= "Other",
  bmi = mean_bmi
)

plot_data$predicted_prob <- predict(final.model, newdata = plot_data, type = "response")

plot.as<-ggplot(plot_data, aes(x = age, y = predicted_prob, color = factor(smoker))) +
  geom_line() +
  labs(title = "Probability Plot (age:smoker)") +
  scale_color_manual(values = c("blue", "red"))

## Age+ethnic
plot_data <- expand.grid(
  age = seq(min(data$age), max(data$age), length.out = 100),
  smoker = as.factor(0),
  ethnic1= as.factor(c("Black","Other", "White" )),
  bmi = mean_bmi
)

plot_data$predicted_prob <- predict(final.model, newdata = plot_data, type = "response")
plot.ae<-ggplot(plot_data, aes(x = age, y = predicted_prob, color = factor(ethnic1))) +
  geom_line() +
  labs(title = "Probability Plot (age:ethnicity)") +
  scale_color_manual(values = c("black", "red","blue"))

## bmi+smoker
plot_data <- expand.grid(
  bmi = seq(min(data$bmi), max(data$bmi), length.out = 100),  # Adjust the length.out as needed
  smoker = as.factor(c(0, 1)),
  ethnic1= "Other",
  age = mean_age
)

plot_data$predicted_prob <- predict(final.model, newdata = plot_data, type = "response")

plot.bs<-ggplot(plot_data, aes(x = bmi, y = predicted_prob, color = factor(smoker))) +
  geom_line() +
  labs(title = "Probability Plot (bmi:smoker)") +
  scale_color_manual(values = c("blue", "red"))

## bmi+ethnic
plot_data <- expand.grid(
  bmi = seq(min(data$bmi), max(data$bmi), length.out = 100),
  smoker = as.factor(0),
  ethnic1= as.factor(c("Black","Other", "White" )),
  age = mean_age
)

plot_data$predicted_prob <- predict(final.model, newdata = plot_data, type = "response")
plot.be<-ggplot(plot_data, aes(x = bmi, y = predicted_prob, color = factor(ethnic1))) +
  geom_line() +
  labs(title = "Probability Plot (bmi:ethnicity)") +
```

```
  scale_color_manual(values = c("black", "red","blue"))

combined_plot_h1 <- plot.as + plot.ae
combined_plot_h2 <-plot.bs + plot.be
combined_plot_h1/combined_plot_h2
```