

Section 5. Heart Disease Example

Yi Li

22/07/2022

```
library(regmedint)
```

```
## Warning: package 'regmedint' was built under R version 4.1.2
```

```
# install.packages("cheese")  
require(cheese)
```

```
## Loading required package: cheese
```

```
# dataset 'heart_disease':  
# A: Cholesterol  
# M: BP  
# Y: HeartDisease
```

1. Pre-process data to convert all variables to numeric type

```
age <- heart_disease$Age  
sex_M <- ifelse(heart_disease$Sex == "Male", 1, 0)  
pain_typical <- ifelse(heart_disease$ChestPain == "Typical angina", 1, 0)  
pain_atypical <- ifelse(heart_disease$ChestPain == "Atypical angina", 1, 0)  
pain_non <- ifelse(heart_disease$ChestPain == "Non-anginal pain", 1, 0)  
bp <- heart_disease$BP  
cholesterol <- heart_disease$Cholesterol  
# fasting blood sugar > 120 mg/dl:  
bloodsugar_T <- ifelse(heart_disease$BloodSugar == TRUE, 1, 0)  
maximumHR <- heart_disease$MaximumHR  
HD <- ifelse(heart_disease$HeartDisease == "Yes", 1, 0)  
  
heart.disease <- cbind.data.frame(age, sex_M, pain_typical, pain_atypical, pain_non,  
                                bp, cholesterol, bloodsugar_T, maximumHR, HD)
```

2. Fit regmedint()

(1) No EMM terms

```

regmedint_noEMM <- regmedint(data = heart.disease,
                             yvar = "HD",
                             avar = "cholesterol",
                             mvar = "bp",
                             cvar = c("age", "sex_M", "pain_non",
                                       "bloodsugar_T", "maximumHR"),
                             emm_ac_mreg = NULL,
                             emm_ac_yreg = NULL,
                             emm_mc_yreg = NULL,
                             eventvar = NULL,
                             a0 = summary(heart.disease$cholesterol)[2],
                             a1 = summary(heart.disease$cholesterol)[5],
                             m_cde = mean(heart.disease$bp),
                             c_cond = c(mean(heart.disease$age),
                                         0, 0, 1,
                                         mean(heart.disease$maximumHR)),
                             mreg = "linear",
                             yreg = "loglinear",
                             interaction = TRUE,
                             casecontrol = FALSE,
                             na_omit = TRUE)

```

loglinear is implemented as modified Poisson (Zou 2004).

```
summary(regmedint_noEMM)
```

```

## ### Mediator model
##
## Call:
## lm(formula = bp ~ cholesterol + age + sex_M + pain_non + bloodsugar_T +
##     maximumHR, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -37.323 -11.853  -1.564  10.521  59.618
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   89.31699    11.86603   7.527 6.29e-13 ***
## cholesterol    0.02103     0.01942   1.083  0.27972
## age           0.53800     0.12038   4.469 1.12e-05 ***
## sex_M        -1.35956     2.13286  -0.637  0.52433
## pain_non     -2.44490     2.18569  -1.119  0.26422
## bloodsugar_T  7.39882     2.74156   2.699  0.00736 **
## maximumHR     0.05626     0.04662   1.207  0.22848
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.72 on 296 degrees of freedom
## Multiple R-squared:  0.1152, Adjusted R-squared:  0.09726
## F-statistic: 6.423 on 6 and 296 DF, p-value: 2.236e-06
##

```

```

## ### Outcome model
##
## Call:
## glm(formula = HD ~ cholesterol + bp + cholesterol:bp + age +
##      sex_M + pain_non + bloodsugar_T + maximumHR, family = poisson(link = "log"),
##      data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5292  -0.7409  -0.4741   0.4306   1.2822
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.320e-01  2.306e+00  -0.101  0.919877
## cholesterol  -2.464e-03  8.446e-03  -0.292  0.770457
## bp           -3.012e-03  1.746e-02  -0.173  0.862988
## age           1.271e-02  7.055e-03   1.802  0.071621 .
## sex_M         7.440e-01  1.705e-01   4.363  1.28e-05 ***
## pain_non      -7.281e-01  2.044e-01  -3.563  0.000367 ***
## bloodsugar_T   6.338e-02  1.516e-01   0.418  0.675857
## maximumHR     -1.304e-02  2.211e-03  -5.896  3.72e-09 ***
## cholesterol:bp 3.665e-05  6.297e-05   0.582  0.560619
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 216.63  on 302  degrees of freedom
## Residual deviance: 161.84  on 294  degrees of freedom
## AIC: 457.84
##
## Number of Fisher Scoring iterations: 5
##
## ### Mediation analysis
##      est      se      Z      p      lower      upper
## cde  0.151129223 0.068988477 2.1906444 0.02847753 0.015914293 0.28634415
## pnde 0.171804155 0.074720938 2.2992773 0.02148920 0.025353808 0.31825450
## tnle 0.009508400 0.009596119 0.9908589 0.32175448 -0.009299647 0.02831645
## tnle 0.174960544 0.076945045 2.2738377 0.02297575 0.024151028 0.32577006
## pnle 0.006352011 0.008795323 0.7222032 0.47016953 -0.010886506 0.02359053
## te   0.181312555 0.074644944 2.4289998 0.01514054 0.035011154 0.32761396
## pm   0.057068081 0.060053885 0.9502813 0.34196936 -0.060635371 0.17477153
##
## Evaluated at:
## avar: cholesterol
## a1 (intervened value of avar) = 275
## a0 (reference value of avar) = 211
## mvar: bp
## m_cde (intervend value of mvar for cde) = 131.6898
## cvar: age sex_M pain_non bloodsugar_T maximumHR
## c_cond (covariate vector value) = 54.43894 0 0 1 149.6073
##
## Note that effect estimates can vary over m_cde and c_cond values when interaction = TRUE.

```

(2) EMM by age

(a) Age is set to the 1st quartile:

```
regmedint_age1 <- regmedint(data = heart.disease,
                           yvar = "HD",
                           avar = "cholesterol",
                           mvar = "bp",
                           cvar = c("age", "sex_M", "pain_non",
                                     "bloodsugar_T", "maximumHR"),
                           emm_ac_mreg = c("age"),
                           emm_ac_yreg = c("age"),
                           emm_mc_yreg = c("age"),
                           eventvar = NULL,
                           a0 = summary(heart.disease$cholesterol)[2],
                           a1 = summary(heart.disease$cholesterol)[5],
                           m_cde = mean(heart.disease$bp),
                           c_cond = c(summary(heart.disease$age)[2],
                                       0, 0, 1,
                                       mean(heart.disease$maximumHR)),
                           mreg = "linear",
                           yreg = "loglinear",
                           interaction = TRUE,
                           casecontrol = FALSE,
                           na_omit = TRUE)
```

loglinear is implemented as modified Poisson (Zou 2004).

```
summary(regmedint_age1)
```

```
## ### Mediator model
##
## Call:
## lm(formula = bp ~ cholesterol + age + sex_M + pain_non + bloodsugar_T +
##     maximumHR + cholesterol:age, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -35.831 -11.798  -1.519   10.134   59.499
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   54.384088   31.211681    1.742  0.08248 .
## cholesterol    0.165108    0.120651    1.368  0.17221
## age           1.145709    0.516471    2.218  0.02729 *
## sex_M        -1.507966    2.134715   -0.706  0.48050
## pain_non     -2.207722    2.192755   -1.007  0.31484
## bloodsugar_T    7.209900    2.743863    2.628  0.00905 **
## maximumHR      0.060403    0.046706    1.293  0.19694
## cholesterol:age -0.002532    0.002093   -1.210  0.22728
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 16.71 on 295 degrees of freedom
## Multiple R-squared:  0.1196, Adjusted R-squared:  0.09867
## F-statistic: 5.723 on 7 and 295 DF,  p-value: 3.197e-06
##
## ### Outcome model
##
## Call:
## glm(formula = HD ~ cholesterol + bp + cholesterol:bp + age +
##      sex_M + pain_non + bloodsugar_T + maximumHR + cholesterol:age +
##      bp:age, family = poisson(link = "log"), data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5274  -0.7412  -0.4724   0.4248   1.2775
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -1.408e+00  4.145e+00  -0.340  0.734017
## cholesterol   -3.862e-04  1.118e-02  -0.035  0.972443
## bp             4.435e-04  3.065e-02   0.014  0.988456
## age            3.716e-02  6.423e-02   0.579  0.562850
## sex_M          7.436e-01  1.702e-01   4.370  1.24e-05 ***
## pain_non      -7.202e-01  2.063e-01  -3.491  0.000481 ***
## bloodsugar_T   6.271e-02  1.503e-01   0.417  0.676578
## maximumHR     -1.297e-02  2.224e-03  -5.831  5.50e-09 ***
## cholesterol:bp  4.295e-05  6.324e-05   0.679  0.497053
## cholesterol:age -5.142e-05  1.251e-04  -0.411  0.680998
## bp:age        -8.953e-05  4.617e-04  -0.194  0.846254
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 216.63  on 302  degrees of freedom
## Residual deviance: 161.75  on 292  degrees of freedom
## AIC: 461.75
##
## Number of Fisher Scoring iterations: 5
##
## ### Mediation analysis
##      est      se      Z      p      lower      upper
## cde  0.17926959 0.10754420 1.6669388 0.09552658 -0.031513163 0.39005235
## pnde 0.19291688 0.10903116 1.7693738 0.07683151 -0.020780268 0.40661403
## tnle 0.02218435 0.02045352 1.0846229 0.27808872 -0.017903803 0.06227251
## tnle 0.20058074 0.10924364 1.8360862 0.06634492 -0.013532865 0.41469434
## pnle 0.01452050 0.02024783 0.7171383 0.47328879 -0.025164527 0.05420552
## te   0.21510123 0.10550127 2.0388496 0.04146504  0.008322532 0.42187993
## pm   0.11336192 0.11822174 0.9588923 0.33761300 -0.118348434 0.34507227
##
## Evaluated at:
## avar: cholesterol
## a1 (intervened value of avar) = 275
## a0 (reference value of avar) = 211
## mvar: bp

```

```
## m_cde (intervend value of mvar for cde) = 131.6898
## cvar: age sex_M pain_non bloodsugar_T maximumHR
## c_cond (covariate vector value) = 48 0 0 1 149.6073
##
## Note that effect estimates can vary over m_cde and c_cond values when interaction = TRUE.
```

(b) Age is set to the 3rd quartile:

```
regmedint_age2 <- regmedint(data = heart.disease,
                           yvar = "HD",
                           avar = "cholesterol",
                           mvar = "bp",
                           cvar = c("age", "sex_M", "pain_non",
                                     "bloodsugar_T", "maximumHR"),
                           emm_ac_mreg = c("age"),
                           emm_ac_yreg = c("age"),
                           emm_mc_yreg = c("age"),
                           eventvar = NULL,
                           a0 = summary(heart.disease$cholesterol)[2],
                           a1 = summary(heart.disease$cholesterol)[5],
                           m_cde = mean(heart.disease$bp),
                           c_cond = c(summary(heart.disease$age)[5],
                                       0, 0, 1,
                                       mean(heart.disease$maximumHR)),
                           mreg = "linear",
                           yreg = "loglinear",
                           interaction = TRUE,
                           casecontrol = FALSE,
                           na_omit = TRUE)
```

```
## loglinear is implemented as modified Poisson (Zou 2004).
```

```
summary(regmedint_age2)
```

```
## ### Mediator model
##
## Call:
## lm(formula = bp ~ cholesterol + age + sex_M + pain_non + bloodsugar_T +
##     maximumHR + cholesterol:age, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -35.831 -11.798  -1.519   10.134   59.499
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   54.384088   31.211681   1.742  0.08248 .
## cholesterol    0.165108    0.120651    1.368  0.17221
## age           1.145709    0.516471    2.218  0.02729 *
## sex_M        -1.507966    2.134715   -0.706  0.48050
## pain_non     -2.207722    2.192755   -1.007  0.31484
## bloodsugar_T   7.209900    2.743863    2.628  0.00905 **
```

```

## maximumHR      0.060403   0.046706   1.293  0.19694
## cholesterol:age -0.002532   0.002093  -1.210  0.22728
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.71 on 295 degrees of freedom
## Multiple R-squared:  0.1196, Adjusted R-squared:  0.09867
## F-statistic: 5.723 on 7 and 295 DF,  p-value: 3.197e-06
##
## ### Outcome model
##
## Call:
## glm(formula = HD ~ cholesterol + bp + cholesterol:bp + age +
##      sex_M + pain_non + bloodsugar_T + maximumHR + cholesterol:age +
##      bp:age, family = poisson(link = "log"), data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5274  -0.7412  -0.4724   0.4248   1.2775
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.408e+00  4.145e+00  -0.340  0.734017
## cholesterol  -3.862e-04  1.118e-02  -0.035  0.972443
## bp           4.435e-04  3.065e-02   0.014  0.988456
## age          3.716e-02  6.423e-02   0.579  0.562850
## sex_M        7.436e-01  1.702e-01   4.370  1.24e-05 ***
## pain_non     -7.202e-01  2.063e-01  -3.491  0.000481 ***
## bloodsugar_T  6.271e-02  1.503e-01   0.417  0.676578
## maximumHR    -1.297e-02  2.224e-03  -5.831  5.50e-09 ***
## cholesterol:bp  4.295e-05  6.324e-05   0.679  0.497053
## cholesterol:age -5.142e-05  1.251e-04  -0.411  0.680998
## bp:age       -8.953e-05  4.617e-04  -0.194  0.846254
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 216.63  on 302  degrees of freedom
## Residual deviance: 161.75  on 292  degrees of freedom
## AIC: 461.75
##
## Number of Fisher Scoring iterations: 5
##
## ### Mediation analysis
##      est      se      Z      p      lower      upper
## cde  0.136484835  0.073269982  1.8627661  0.06249519 -0.0071216903  0.28009136
## pnde 0.171086504  0.087534090  1.9545129  0.05064060 -0.0004771598  0.34265017
## tnle 0.004629623  0.009470917  0.4888252  0.62496547 -0.0139330338  0.02319228
## tnle 0.172959932  0.086187562  2.0067853  0.04477253  0.0040354144  0.34188445
## pnle 0.002756195  0.006546441  0.4210219  0.67373909 -0.0100745933  0.01558698
## te   0.175716126  0.088584387  1.9836015  0.04730028  0.0020939186  0.34933833
## pm   0.028663337  0.057827175  0.4956724  0.62012554 -0.0846758440  0.14200252
##

```

```
## Evaluated at:
## avar: cholesterol
## a1 (intervened value of avar) = 275
## a0 (reference value of avar) = 211
## mvar: bp
## m_cde (intervend value of mvar for cde) = 131.6898
## cvar: age sex_M pain_non bloodsugar_T maximumHR
## c_cond (covariate vector value) = 61 0 0 1 149.6073
##
## Note that effect estimates can vary over m_cde and c_cond values when interaction = TRUE.
```

(3) EMM by sex

(a) Sex is set to male:

```
regmedint_sex1 <- regmedint(data = heart.disease,
                           yvar = "HD",
                           avar = "cholesterol",
                           mvar = "bp",
                           cvar = c("age", "sex_M", "pain_non",
                                     "bloodsugar_T", "maximumHR"),
                           emm_ac_mreg = c("sex_M"),
                           emm_ac_yreg = c("sex_M"),
                           emm_mc_yreg = c("sex_M"),
                           eventvar = NULL,
                           a0 = summary(heart.disease$cholesterol)[2],
                           a1 = summary(heart.disease$cholesterol)[5],
                           m_cde = mean(heart.disease$bp),
                           c_cond = c(summary(heart.disease$age)[2],
                                       1, 0, 1,
                                       mean(heart.disease$maximumHR)),
                           mreg = "linear",
                           yreg = "loglinear",
                           interaction = TRUE,
                           casecontrol = FALSE,
                           na_omit = TRUE)
```

loglinear is implemented as modified Poisson (Zou 2004).

```
summary(regmedint_sex1)
```

```
## ### Mediator model
##
## Call:
## lm(formula = bp ~ cholesterol + age + sex_M + pain_non + bloodsugar_T +
##     maximumHR + cholesterol:sex_M, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -37.311 -11.846  -1.579   10.516   59.614
##
## Coefficients:
```



```

##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    89.2725104 12.6330995   7.067 1.15e-11 ***
## cholesterol    0.0212201  0.0268045   0.792  0.42919
## age            0.5379639  0.1206327   4.460 1.17e-05 ***
## sex_M          -1.2601997  9.7947227  -0.129  0.89771
## pain_non       -2.4458242  2.1911778  -1.116  0.26524
## bloodsugar_T    7.3966098  2.7543987   2.685  0.00765 **
## maximumHR       0.0562368  0.0467361   1.203  0.22983
## cholesterol:sex_M -0.0003975  0.0382464  -0.010  0.99171
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.75 on 295 degrees of freedom
## Multiple R-squared:  0.1152, Adjusted R-squared:  0.0942
## F-statistic: 5.487 on 7 and 295 DF,  p-value: 6.077e-06
##
## ### Outcome model
##
## Call:
## glm(formula = HD ~ cholesterol + bp + cholesterol:bp + age +
##      sex_M + pain_non + bloodsugar_T + maximumHR + cholesterol:sex_M +
##      bp:sex_M, family = poisson(link = "log"), data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5544  -0.7264  -0.4121   0.4396   1.5537
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -4.434e+00  2.422e+00  -1.831  0.067149 .
## cholesterol    4.975e-03  8.368e-03   0.594  0.552188
## bp             2.701e-02  1.778e-02   1.520  0.128607
## age            1.311e-02  7.037e-03   1.863  0.062479 .
## sex_M          3.874e+00  1.132e+00   3.421  0.000625 ***
## pain_non      -6.756e-01  2.066e-01  -3.271  0.001072 **
## bloodsugar_T   2.294e-02  1.519e-01   0.151  0.879985
## maximumHR     -1.308e-02  2.267e-03  -5.771  7.86e-09 ***
## cholesterol:bp -1.784e-05  5.948e-05  -0.300  0.764292
## cholesterol:sex_M -4.297e-04  2.472e-03  -0.174  0.861986
## bp:sex_M       -2.162e-02  6.592e-03  -3.281  0.001036 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 216.63  on 302  degrees of freedom
## Residual deviance: 157.75  on 292  degrees of freedom
## AIC: 457.75
##
## Number of Fisher Scoring iterations: 5
##
## ### Mediation analysis
##               est           se           Z           p           lower           upper
## cde  0.1405561671 0.073737493 1.9061696 0.05662820 -0.003966663 0.28507900

```

```
## pnde 0.1375379062 0.073164896 1.8798347 0.06013062 -0.005862654 0.28093847
## tnle 0.0006445522 0.004781363 0.1348051 0.89276596 -0.008726747 0.01001585
## tnle 0.1360167680 0.073341458 1.8545686 0.06365785 -0.007729849 0.27976338
## pnle 0.0021656904 0.006757399 0.3204917 0.74859562 -0.011078569 0.01540995
## te 0.1381824584 0.073266201 1.8860328 0.05929053 -0.005416656 0.28178157
## pm 0.0049925874 0.036973104 0.1350330 0.89258582 -0.067473365 0.07745854
##
## Evaluated at:
## avar: cholesterol
## a1 (intervened value of avar) = 275
## a0 (reference value of avar) = 211
## mvar: bp
## m_cde (intervend value of mvar for cde) = 131.6898
## cvar: age sex_M pain_non bloodsugar_T maximumHR
## c_cond (covariate vector value) = 48 1 0 1 149.6073
##
## Note that effect estimates can vary over m_cde and c_cond values when interaction = TRUE.
```

(b) Sex is set to female:

```
regmedint_sex2 <- regmedint(data = heart.disease,
                           yvar = "HD",
                           avar = "cholesterol",
                           mvar = "bp",
                           cvar = c("age", "sex_M", "pain_non",
                                     "bloodsugar_T", "maximumHR"),
                           emm_ac_mreg = c("sex_M"),
                           emm_ac_yreg = c("sex_M"),
                           emm_mc_yreg = c("sex_M"),
                           eventvar = NULL,
                           a0 = summary(heart.disease$cholesterol)[2],
                           a1 = summary(heart.disease$cholesterol)[5],
                           m_cde = mean(heart.disease$bp),
                           c_cond = c(summary(heart.disease$age)[2],
                                       0, 0, 1,
                                       mean(heart.disease$maximumHR)),
                           mreg = "linear",
                           yreg = "loglinear",
                           interaction = TRUE,
                           casecontrol = FALSE,
                           na_omit = TRUE)
```

loglinear is implemented as modified Poisson (Zou 2004).

```
summary(regmedint_sex2)
```

```
## ### Mediator model
##
## Call:
## lm(formula = bp ~ cholesterol + age + sex_M + pain_non + bloodsugar_T +
##     maximumHR + cholesterol:sex_M, data = data)
##
```

```

## Residuals:
##      Min       1Q   Median       3Q      Max
## -37.311 -11.846  -1.579  10.516  59.614
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   89.2725104  12.6330995   7.067 1.15e-11 ***
## cholesterol    0.0212201   0.0268045   0.792  0.42919
## age           0.5379639   0.1206327   4.460 1.17e-05 ***
## sex_M         -1.2601997   9.7947227  -0.129  0.89771
## pain_non      -2.4458242   2.1911778  -1.116  0.26524
## bloodsugar_T   7.3966098   2.7543987   2.685  0.00765 **
## maximumHR      0.0562368   0.0467361   1.203  0.22983
## cholesterol:sex_M -0.0003975  0.0382464  -0.010  0.99171
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.75 on 295 degrees of freedom
## Multiple R-squared:  0.1152, Adjusted R-squared:  0.0942
## F-statistic: 5.487 on 7 and 295 DF, p-value: 6.077e-06
##
## ### Outcome model
##
## Call:
## glm(formula = HD ~ cholesterol + bp + cholesterol:bp + age +
##      sex_M + pain_non + bloodsugar_T + maximumHR + cholesterol:sex_M +
##      bp:sex_M, family = poisson(link = "log"), data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5544  -0.7264  -0.4121   0.4396   1.5537
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -4.434e+00  2.422e+00  -1.831 0.067149 .
## cholesterol    4.975e-03  8.368e-03   0.594 0.552188
## bp            2.701e-02  1.778e-02   1.520 0.128607
## age           1.311e-02  7.037e-03   1.863 0.062479 .
## sex_M         3.874e+00  1.132e+00   3.421 0.000625 ***
## pain_non      -6.756e-01  2.066e-01  -3.271 0.001072 **
## bloodsugar_T   2.294e-02  1.519e-01   0.151 0.879985
## maximumHR     -1.308e-02  2.267e-03  -5.771 7.86e-09 ***
## cholesterol:bp -1.784e-05  5.948e-05  -0.300 0.764292
## cholesterol:sex_M -4.297e-04  2.472e-03  -0.174 0.861986
## bp:sex_M       -2.162e-02  6.592e-03  -3.281 0.001036 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 216.63  on 302  degrees of freedom
## Residual deviance: 157.75  on 292  degrees of freedom
## AIC: 457.75
##

```

```

## Number of Fisher Scoring iterations: 5
##
## ### Mediation analysis
##      est      se      Z      p      lower      upper
## cde  0.16805614 0.14239468 1.1802136 0.2379153 -0.11103230 0.4471446
## pnde 0.15657845 0.14390898 1.0880381 0.2765783 -0.12547796 0.4386349
## tnle 0.03002390 0.03868480 0.7761162 0.4376804 -0.04579692 0.1058447
## tnle 0.15502827 0.14484890 1.0702758 0.2844952 -0.12887035 0.4389269
## pnle 0.03157408 0.04102243 0.7696785 0.4414906 -0.04882840 0.1119766
## te   0.18660235 0.14814734 1.2595727 0.2078235 -0.10376110 0.4769658
## pm   0.17375487 0.22622296 0.7680691 0.4424461 -0.26963399 0.6171437
##
## Evaluated at:
## avar: cholesterol
## a1 (intervened value of avar) = 275
## a0 (reference value of avar) = 211
## mvar: bp
## m_cde (intervend value of mvar for cde) = 131.6898
## cvar: age sex_M pain_non bloodsugar_T maximumHR
## c_cond (covariate vector value) = 48 0 0 1 149.6073
##
## Note that effect estimates can vary over m_cde and c_cond values when interaction = TRUE.

```