

Section 5. Heart Disease Example

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```
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.1 --

## v ggplot2 3.3.5      v purrr 0.3.4
## v tibble 3.1.4       v dplyr 1.0.7
## v tidyr 1.1.3        v stringr 1.4.0
## v readr 2.0.1        v forcats 0.5.1

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

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

```
heart.disease <- mutate(heart_disease,
  sex_M = case_when(Sex == "Male" ~ 1,
    TRUE ~ 0),
  pain_non = case_when(ChestPain == "Non-anginal pain" ~ 1,
    TRUE ~ 0),
  bloodsugar_T = case_when(BloodSugar == TRUE ~ 1,
    TRUE ~ 0),
  HD = case_when(HeartDisease == "Yes" ~ 1,
    TRUE ~ 0))
```

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 = quantile(heart.disease$Cholesterol, 0.25),
                             a1 = quantile(heart.disease$Cholesterol, 0.75),
                             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 = quantile(heart.disease$Cholesterol, 0.25),
                           a1 = quantile(heart.disease$Cholesterol, 0.75),
                           m_cde = mean(heart.disease$BP),
                           c_cond = c(quantile(heart.disease$Age, 0.25),
                                       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 = quantile(heart.disease$Cholesterol, 0.25),
                             a1 = quantile(heart.disease$Cholesterol, 0.75),
                             m_cde = mean(heart.disease$BP),
                             c_cond = c(quantile(heart.disease$Age, 0.75),
                                         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

```

```
## tnde 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 = quantile(heart.disease$Cholesterol, 0.25),
                           a1 = quantile(heart.disease$Cholesterol, 0.75),
                           m_cde = mean(heart.disease$BP),
                           c_cond = c(mean(heart.disease$Age),
                                       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 0.1335840374 0.074406544 1.7953265 0.07260170 -0.012250108 0.27941818
## tnle 0.0006445522 0.004781363 0.1348051 0.89276596 -0.008726747 0.01001585
## tnle 0.1320628992 0.075467885 1.7499218 0.08013181 -0.015851438 0.27997724
## pnle 0.0021656904 0.006757399 0.3204917 0.74859562 -0.011078569 0.01540995
## te   0.1342285896 0.074690882 1.7971215 0.07231634 -0.012162850 0.28062003
## pm   0.0051297297 0.037890195 0.1353841 0.89230820 -0.069133688 0.07939315
##
## 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 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 = quantile(heart.disease$Cholesterol, 0.25),
                           a1 = quantile(heart.disease$Cholesterol, 0.75),
                           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_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 0.15262458 0.14666909 1.0406050 0.2980589 -0.13484154 0.4400907
## tnle 0.03002390 0.03868480 0.7761162 0.4376804 -0.04579692 0.1058447
## tnle 0.15107440 0.14805062 1.0204240 0.3075274 -0.13909947 0.4412483
## pnle 0.03157408 0.04102243 0.7696785 0.4414906 -0.04882840 0.1119766
## te 0.18264849 0.15080634 1.2111460 0.2258395 -0.11292650 0.4782235
## pm 0.17717639 0.23308921 0.7601227 0.4471813 -0.27967007 0.6340229
##
## 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.

```