Section 5. Heart Disease Example

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```
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$Cholesterol
bloodsugar_T <- ifelse(heart_disease$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,
                                        mean(heart.disease$bloodsugar_T),
                                        mean(heart.disease$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 0.157028607 0.068767444 2.2834731 0.02240252  0.022246894 0.29181032
## tnie 0.009508400 0.009596119 0.9908589 0.32175448 -0.009299647 0.02831645
## tnde 0.160184996 0.069215344 2.3142989 0.02065133  0.024525415 0.29584458
## pnie 0.006352011 0.008795323 0.7222032 0.47016953 -0.010886506 0.02359053
## te   0.166537007 0.068633447 2.4264701 0.01524651  0.032017923 0.30105609
## pm   0.061687175 0.064985314 0.9492479 0.34249453 -0.065681700 0.18905605
##
## 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 0.1485149 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,
                                       mean(heart.disease$bloodsugar_T),
                                       mean(heart.disease$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
```

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```
##
## 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 0.17604305 0.10874790 1.6188180 0.10548644 -0.037098912 0.38918500
## tnie 0.02218435 0.02045352 1.0846229 0.27808872 -0.017903803 0.06227251
## tnde 0.18370690 0.10642803 1.7261138 0.08432694 -0.024888212 0.39230202
## pnie 0.01452050 0.02024783 0.7171383 0.47328879 -0.025164527 0.05420552
## te   0.19822740 0.10494154 1.8889317 0.05890098 -0.007454234 0.40390903
## pm   0.12201365 0.13032073 0.9362566 0.34914108 -0.133410291 0.37743758
##
## 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 0.1485149 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,
                                       mean(heart.disease$bloodsugar_T),
                                       mean(heart.disease$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 -0.007121690 0.28009136
## pnde 0.154212671 0.078167195 1.9728566 0.04851190  0.001007783 0.30741756
## tnie 0.004629623 0.009470917 0.4888252 0.62496547 -0.013933034 0.02319228
## tnde 0.156086098 0.075857222 2.0576300 0.03962566  0.007408675 0.30476352
## pnie 0.002756195 0.006546441 0.4210219 0.67373909 -0.010074593 0.01558698
## te   0.158842293 0.079348420 2.0018331 0.04530269  0.003322248 0.31436234
```

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```
## pm    0.031449245 0.063156534 0.4979571 0.61851427 -0.092335287 0.15523378
##
## 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 0.1485149 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:

```r
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,
                                       mean(heart.disease$bloodsugar_T),
                                       mean(heart.disease$maximumHR)),
                            mreg = "linear",
                            yreg = "loglinear",
                            interaction = TRUE,
                            casecontrol = FALSE,
                            na_omit = TRUE)
```

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

```r
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 0.1447268370 0.076815386 1.8840866 0.05955327 -0.005828553 0.29528223
## tnie 0.0006445522 0.004781363 0.1348051 0.89276596 -0.008726747 0.01001585
## tnde 0.1432056988 0.075390706 1.8995140 0.05749693 -0.004557369 0.29096877
## pnie 0.0021656904 0.006757399 0.3204917 0.74859562 -0.011078569 0.01540995
## te   0.1453713892 0.076589349 1.8980627 0.05768782 -0.004740977 0.29548376
## pm   0.0047623777 0.035430838 0.1344134 0.89307572 -0.064680788 0.07420554
##
## 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 0.1485149 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,
                                       mean(heart.disease$bloodsugar_T),
                                       mean(heart.disease$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 0.16376738 0.14188328 1.1542402 0.2484017 -0.11431873 0.4418535
## tnie 0.03002390 0.03868480 0.7761162 0.4376804 -0.04579692 0.1058447
## tnde 0.16221720 0.14196801 1.1426321 0.2531914 -0.11603499 0.4404694
## pnie 0.03157408 0.04102243 0.7696785 0.4414906 -0.04882840 0.1119766
## te   0.19379128 0.14625954 1.3249822 0.1851771 -0.09287214 0.4804547
## pm   0.16789256 0.21603052 0.7771706 0.4370581 -0.25551947 0.5913046
##
## 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 0.1485149 149.6073
##
## Note that effect estimates can vary over m_cde and c_cond values when interaction = TRUE.
```