test3

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```r
counts <- c(29,47,14,19,25,20,37,24)
x<-rep(c("Female","Male"),each=4)
y <- rep(c("Non-smoker", "Non-smoker", "Smoker", "Smoker"), times = 2)
z <- rep(c("Yes", "No", "Yes", "No"), times = 2)
cbind(x,y,z,counts)
```

```
##      x        y            z      counts
## [1,] "Female" "Non-smoker" "Yes" "29"
## [2,] "Female" "Non-smoker" "No"  "47"
## [3,] "Female" "Smoker"     "Yes" "14"
## [4,] "Female" "Smoker"     "No"  "19"
## [5,] "Male"   "Non-smoker" "Yes" "25"
## [6,] "Male"   "Non-smoker" "No"  "20"
## [7,] "Male"   "Smoker"     "Yes" "37"
## [8,] "Male"   "Smoker"     "No"  "24"
```

```r
m2 <- glm(counts ~    factor(x) * factor(y)
                  +factor(x) * factor(z)
                  +factor(y) * factor(z),family = "poisson")  #homogeneous association
summary(m2)
```

```
##
## Call:
## glm(formula = counts ~ factor(x) * factor(y) + factor(x) * factor(z) +
##     factor(y) * factor(z), family = "poisson")
##
## Deviance Residuals:
##       1        2        3        4        5        6        7        8
##  0.01771  -0.01389  -0.02541   0.02190  -0.01903   0.02134   0.01568  -0.01943
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                    3.8522     0.1411  27.307  < 2e-16 ***
## factor(x)Male                 -0.8612     0.2374  -3.627 0.000287 ***
## factor(y)Smoker               -0.9128     0.2406  -3.794 0.000148 ***
## factor(z)Yes                  -0.4882     0.2159  -2.261 0.023762 *
## factor(x)Male:factor(y)Smoker  1.1038     0.2908   3.796 0.000147 ***
## factor(x)Male:factor(z)Yes     0.7199     0.2881   2.499 0.012457 *
## factor(y)Smoker:factor(z)Yes   0.1946     0.2903   0.670 0.502619
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 28.312422  on 7  degrees of freedom
## Residual deviance:  0.003073  on 1  degrees of freedom
## AIC: 54.567
##
## Number of Fisher Scoring iterations: 3
```

```r
#Goodness-of-fit test:
G.2 <- m2$deviance
residual.df <- m2$df.residual
p.value <- pchisq(q = G.2, df = residual.df, lower.tail = FALSE)
c(G.2, residual.df, p.value)
```

```
## [1] 0.0030730 1.0000000 0.9557922
```

```r
#fitted count
round(m2$fitted.values,3)
```

```
##      1      2      3      4      5      6      7      8
## 28.905 47.095 14.095 18.905 25.095 19.905 36.905 24.095
```

```r
#loglinear model (XZ, YZ)
m1 <- glm(counts ~  factor(x) * factor(z)
                +factor(y) * factor(z),family = "poisson")#saturated model for three-way tables
summary(m1)
```

```
##
## Call:
## glm(formula = counts ~ factor(x) * factor(z) + factor(y) * factor(z),
##     family = "poisson")
##
## Deviance Residuals:
##      1      2      3      4      5      6      7      8
##  1.397   1.044  -1.603  -1.405  -1.268  -1.376   1.211   1.546
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)               3.6939     0.1449  25.499  < 2e-16 ***
## factor(x)Male            -0.4055     0.1946  -2.083  0.03722 *
## factor(z)Yes             -0.5976     0.2307  -2.590  0.00959 **
## factor(y)Smoker          -0.4435     0.1954  -2.270  0.02323 *
## factor(x)Male:factor(z)Yes    0.7714     0.2780   2.775  0.00552 **
## factor(z)Yes:factor(y)Smoker  0.3863     0.2762   1.399  0.16195
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 28.312  on 7  degrees of freedom
```

```
## Residual deviance: 14.945  on 2  degrees of freedom
## AIC: 67.509
##
## Number of Fisher Scoring iterations: 4
```

```
# Carry out a model comparison test.
anova(m1, m2, test = "Chisq")
```

```
## Analysis of Deviance Table
##
## Model 1: counts ~ factor(x) * factor(z) + factor(y) * factor(z)
## Model 2: counts ~ factor(x) * factor(y) + factor(x) * factor(z) + factor(y) *
##     factor(z)
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1         2    14.9448
## 2         1     0.0031  1   14.942 0.0001109 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
exp(m2$coefficients)
```

```
##                  (Intercept)           factor(x)Male
##                   47.0952929               0.4226475
##              factor(y)Smoker            factor(z)Yes
##                    0.4014139               0.6137494
## factor(x)Male:factor(y)Smoker  factor(x)Male:factor(z)Yes
##                    3.0156710               2.0542127
##  factor(y)Smoker:factor(z)Yes
##                    1.2148232
```

```
exp(0.7199)
```

```
## [1] 2.054228
```

```
exp(0.1946)
```

```
## [1] 1.214825
```