

## 24.

```
> X <- rep(c("Female", "Male"), each = 4)
> Y <- rep(rep(c("Non-smoker", "Smoker"), each = 2), times = 2)
> Z <- rep(c("Yes", "No"), times = 4)
> counts <- c(29,47,14,19,25,20,33,28)
> homogeneous.association <- glm(counts ~ factor(X) * factor(Y) + factor(X) * factor(Z) + factor(Y) * factor(Z), family = "poisson")
> summary(homogeneous.association)

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 
-0.1294  0.1030  0.1910 -0.1592  0.1419 -0.1553 -0.1214  0.1339 

Coefficients:
            Estimate Std. Error z value Pr(>|z|)    
(Intercept)  3.83509   0.14218  26.974 < 2e-16 ***
factor(X)Male -0.80483   0.23538 -3.419 0.000628 ***
factor(Y)Smoker -0.85434   0.23837 -3.584 0.000338 ***
factor(Z)Yes   -0.44385   0.21495 -2.065 0.038930 *  
factor(X)Male:factor(Y)Smoker  1.13087   0.28961  3.905 9.43e-05 ***
factor(X)Male:factor(Z)Yes    0.60396   0.28735  2.102 0.035568 *  
factor(Y)Smoker:factor(Z)Yes  0.05067   0.28942  0.175 0.861019  
---
Signif. codes:  0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 25.93086 on 7 degrees of freedom
Residual deviance: 0.16612 on 1 degrees of freedom
AIC: 54.769

Number of Fisher Scoring iterations: 3
```

We test the hypotheses

$H_0$  : Model M provides a good fit to the data.

$H_1$  : Model M does not provide a good fit to the data.

where the model M denotes the loglinear model of homogenous association.

Under the null hypothesis, the deviance is given by

$$G^2(M) \text{ approx.} = 0.1661$$

Which has approximately a  $\chi^2_1$  distribution. The p-value is given by

```
> p.value <- pchisq(0.1661, df = 1, lower.tail = FALSE)
> p.value
[1] 0.6836014
```

$$\text{p-value approx.} = P(\chi^2_1 > 0.1661) \text{ approx.} = 0.6836014$$

as the p-value is greater than any reasonable significance level ( $\alpha=0.1, \alpha=0.05, \alpha=0.01$ ), we do not reject  $H_0$ , and conclude that the loglinear model of homogeneous association provides a good fit to the data.

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