# ASTA

*The ASTA team*

## Contents

**1 Contingency tables** **2**

1.1 A contingency table . . . . . 2

**2 Independence** **3**

2.1 Independence . . . . . 3

2.2 The Chi-squared test for independence . . . . . 3

2.3 Calculation of expected table . . . . . 4

2.4 Chi-squared ($\chi^2$) test statistic . . . . . 4

2.5 $\chi^2$-test template. . . . . 5

2.6 The function `chisq.test`. . . . . 6

**3 The $\chi^2$-distribution** **6**

3.1 The $\chi^2$-distribution . . . . . 6

**4 Agresti - Summary** **7**

4.1 Summary . . . . . 7

**5 Standardized residuals** **8**

5.1 Residual analysis . . . . . 8

5.2 Residual analysis in `R` . . . . . 8

**6 Models for table data in `R`** **8**

6.1 Example . . . . . 8

6.2 Model specification . . . . . 9

6.3 Model specification in **R** . . . . . 9

6.4 Expected values and standardized residuals . . . . . 11

**7 Log-linear models** **12**

7.1 Model specification . . . . . 12

7.2 Example . . . . . 12

7.3 Model specification . . . . . 12

7.4 Example . . . . . 13

7.5 Model form . . . . . 13

7.6 Model comparison . . . . . 14

7.7 Deviance . . . . . 14

**8 Higher order interaction** **14**

8.1 Higher order interaction . . . . . 14

8.2 Bigger example . . . . . 15

8.3 Test of simple model against the saturated model . . . . . 17

8.4 Model reduction . . . . . 17

8.5 Final model and parameter estimates . . . . . 18

8.6 Predicted values . . . . . 18

**9 Graphical representation** **20**

9.1 Graphical representation . . . . . 20

9.2 Interpretation of graphical model . . . . . 20

9.3 Interpretation of graphical model . . . . . 21

9.4 Final model of the example . . . . . 22

# 1 Contingency tables

## 1.1 A contingency table

- We return to the dataset `popularKids`, where we study **association** between 2 **factors**: `Goals` and `Urban.Rural`.
- Based on a sample we make a cross tabulation of the factors and we get a so-called **contingency table** (krydstabel).

```
popKids <- read.delim("https://asta.math.aau.dk/datasets?file=PopularKids.txt")
library(mosaic)
tab <- tally(~Urban.Rural + Goals, data = popKids, margins = TRUE)
tab
```

```
##            Goals
## Urban.Rural Grades Popular Sports Total
##    Rural        57      50     42   149
##    Suburban     87      42     22   151
##    Urban       103      49     26   178
##    Total       247     141     90   478
```

### 1.1.1 A conditional distribution

- Another representation of data is the percent-wise distribution of `Goals` for each level of `Urban.Rural`, i.e. the sum in each row of the table is 100 (up to rounding):

```
tab <- tally(~Urban.Rural + Goals, data = popKids)
addmargins(round(100 * prop.table(tab, 1)),margin = 1:2)
```

```
##            Goals
## Urban.Rural Grades Popular Sports Sum
##    Rural        38      34     28 100
##    Suburban     58      28     15 101
##    Urban        58      28     15 101
##    Sum         154      90     58 302
```

- Here we will talk about the **conditional distribution** of `Goals` given `Urban.Rural`.
- An important question could be:
  - Are the goals of the kids different when they come from urban, suburban or rural areas? I.e. are the rows in the table significantly different?
- There is (almost) no difference between urban and suburban, but it looks like rural is different.

# 2 Independence

## 2.1 Independence

- Recall, that two factors are **independent**, when there is no difference between the population's distributions of one factor given the levels of the other factor.
- Otherwise the factors are said to be **dependent**.
- If we e.g. have the following conditional **population distributions** of `Goals` given `Urban.Rural`:

```
##            Goals
## Urban.Rural Grades Popular Sports
##    Rural       500     300    200
##    Suburban    500     300    200
##    Urban       500     300    200
```

- Then the factors `Goals` and `Urban.Rural` are independent.
- We take a sample and "measure" the factors $F_1$ and $F_2$. E.g. `Goals` and `Urban.Rural` for a random child.
- The hypothesis of interest today is:

$$H_0 : F_1 \text{ and } F_2 \text{ are independent}, \quad H_a : F_1 \text{ and } F_2 \text{ are dependent.}$$

## 2.2 The Chi-squared test for independence

- Our best guess of the distribution of `Goals` is the relative frequencies in the sample:

```
n <- margin.table(tab)
pctGoals <- round(100 * margin.table(tab, 2)/n, 1)
pctGoals
```

```
## Goals
##  Grades Popular  Sports
##    51.7    29.5    18.8
```

- If we assume independence, then this is also a guess of the conditional distributions of `Goals` given `Urban.Rural`.

- The corresponding expected counts in the sample are then:

```
##            Goals
## Urban.Rural Grades        Popular       Sports        Sum
##    Rural     77.0 (51.7%)  44.0 (29.5%)  28.1 (18.8%) 149.0 (100%)
##    Suburban  78.0 (51.7%)  44.5 (29.5%)  28.4 (18.8%) 151.0 (100%)
##    Urban     92.0 (51.7%)  52.5 (29.5%)  33.5 (18.8%) 178.0 (100%)
##    Sum      247.0 (51.7%) 141.0 (29.5%)  90.0 (18.8%) 478.0 (100%)
```

## 2.3 Calculation of expected table

```
pctexptab
```

```
##            Goals
## Urban.Rural Grades        Popular       Sports        Sum
##    Rural     77.0 (51.7%)  44.0 (29.5%)  28.1 (18.8%) 149.0 (100%)
##    Suburban  78.0 (51.7%)  44.5 (29.5%)  28.4 (18.8%) 151.0 (100%)
##    Urban     92.0 (51.7%)  52.5 (29.5%)  33.5 (18.8%) 178.0 (100%)
##    Sum      247.0 (51.7%) 141.0 (29.5%)  90.0 (18.8%) 478.0 (100%)
```

- We note that
  - The relative frequency for a given column is columnTotal divided by tableTotal. For example `Grades`, which is $\frac{247}{478} = 51.7\%$.
  - The expected value in a given cell in the table is then the cell's relative column frequency multiplied by the cell's rowTotal. For example `Rural` and `Grades`: $149 \times 51.7\% = 77.0$.
- This can be summarized to:
  - The expected value in a cell is the product of the cell's rowTotal and columnTotal divided by tableTotal.

## 2.4 Chi-squared ($\chi^2$) test statistic

- We have an **observed table**:

```
tab
```

```
##            Goals
## Urban.Rural Grades Popular Sports
##    Rural        57      50     42
##    Suburban     87      42     22
##    Urban       103      49     26
```

- And an **expected table**, if $H_0$ is true:

```
##            Goals
## Urban.Rural Grades Popular Sports Sum
##    Rural     77.0   44.0    28.1  149.0
##    Suburban  78.0   44.5    28.4  151.0
##    Urban     92.0   52.5    33.5  178.0
##    Sum      247.0  141.0    90.0  478.0
```

- If these tables are "far from each other", then we reject $H_0$. We want to measure the distance via the Chi-squared test statistic:
  - $X^2 = \sum \frac{(f_o - f_e)^2}{f_e}$: Sum over all cells in the table
  - $f_o$ is the frequency in a cell in the observed table
  - $f_e$ is the corresponding frequency in the expected table.
- We have:

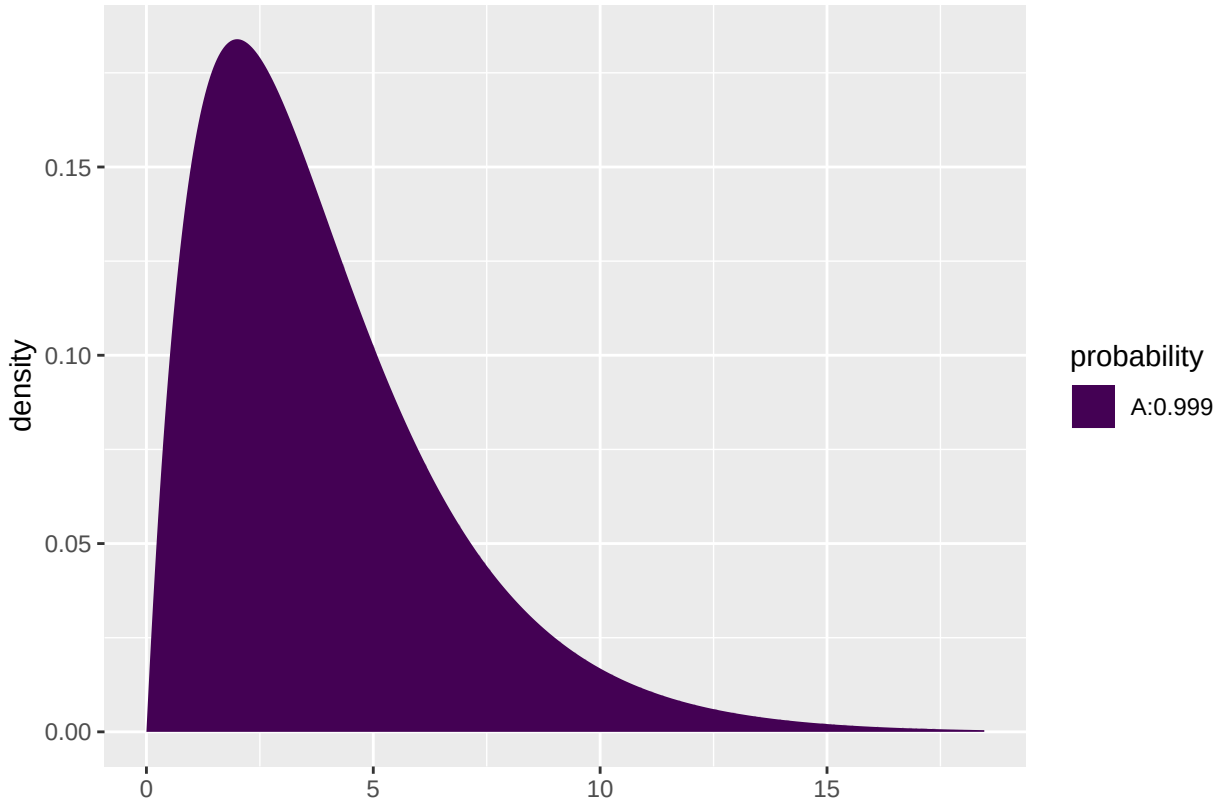
$$X^2_{obs} = \frac{(57-77)^2}{77} + \ldots + \frac{(26-33.5)^2}{33.5} = 18.8$$

- Is this a large distance??

## 2.5 $\chi^2$-test template.

- We want to test the hypothesis $H_0$ of independence in a table with $r$ rows and $c$ columns:
  - We take a sample and calculate $X^2_{obs}$ - the observed value of the test statistic.
  - p-value: Assume $H_0$ is true. What is then the chance of obtaining a larger $X^2$ than $X^2_{obs}$, if we repeat the experiment?
- This can be approximated by the **$\chi^2$-distribution** with $df = (r-1)(c-1)$ degrees of freedom.
- For `Goals` and `Urban.Rural` we have $r = c = 3$, i.e. $df = 4$ and $X^2_{obs} = 18.8$, so the p-value is:

```
1 - pdist("chisq", 18.8, df = 4)
```




```
## [1] 0.0008603303
```

- There is clearly a significant association between `Goals` and `Urban.Rural`.

### 2.6 The function `chisq.test`.

- All of the above calculations can be obtained by the function `chisq.test`.

```
tab <- tally(~ Urban.Rural + Goals, data = popKids)
testStat <- chisq.test(tab, correct = FALSE)
testStat
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab
## X-squared = 18.828, df = 4, p-value = 0.0008497
```

```
testStat$expected
```

```
##            Goals
## Urban.Rural   Grades  Popular   Sports
##    Rural    76.99372 43.95188 28.05439
##    Suburban 78.02720 44.54184 28.43096
##    Urban    91.97908 52.50628 33.51464
```

---

- The frequency data can also be put directly into a matrix.

```
data <- c(57, 87, 103, 50, 42, 49, 42, 22, 26)
tab <- matrix(data, nrow = 3, ncol = 3)
row.names(tab) <- c("Rural", "Suburban", "Urban")
colnames(tab) <- c("Grades", "Popular", "Sports")
tab
```

```
##          Grades Popular Sports
## Rural        57      50     42
## Suburban     87      42     22
## Urban       103      49     26
```

```
chisq.test(tab)
```

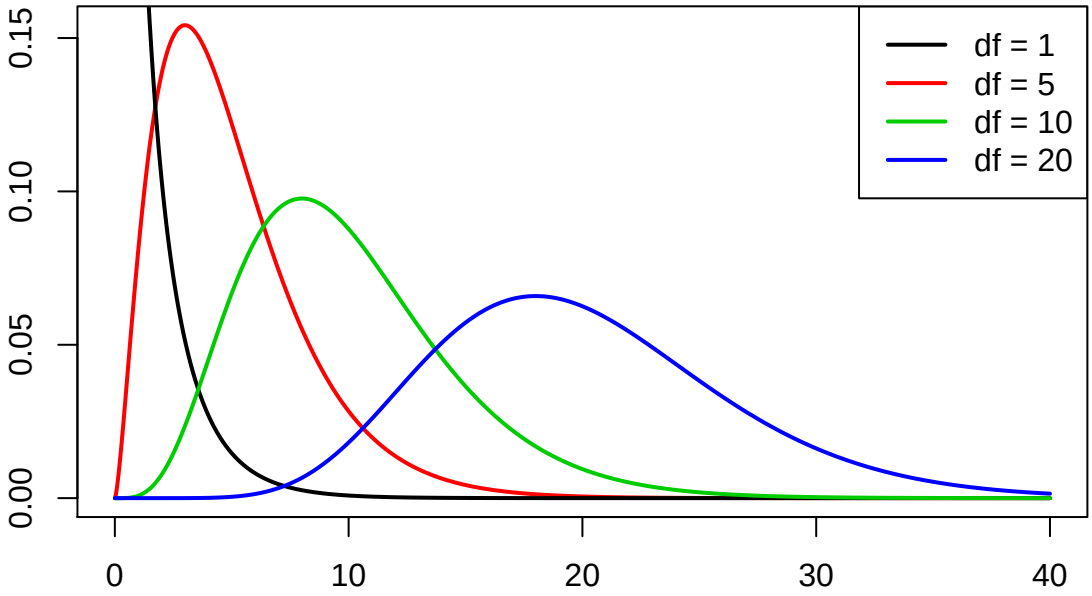
```
##
##  Pearson's Chi-squared test
##
## data:  tab
## X-squared = 18.828, df = 4, p-value = 0.0008497
```

# 3 The $\chi^2$-distribution

## 3.1 The $\chi^2$-distribution

- The $\chi^2$-distribution with $df$ degrees of freedom:

- Is never negative. And $X^2 = 0$ only happens if $f_e = f_o$.
- Has mean $\mu = df$
- Has standard deviation $\sigma = \sqrt{2df}$
- Is skewed to the right, but approaches a normal distribution when $df$ grows.




# 4 Agresti - Summary

## 4.1 Summary

- For the the Chi-squared statistic, $X^2$, to be appropriate we require that the expected values have to be $f_e \geq 5$.
- Now we can summarize the ingredients in the Chi-squared test for independence.

**TABLE 8.5:** The Five Parts of the Chi-Squared Test of Independence

1. Assumptions: Two categorical variables, random sampling, $f_e \geq 5$ in all cells
2. Hypotheses: $H_0$: Statistical independence of variables
   $H_a$: Statistical dependence of variables
3. Test statistic: $\chi^2 = \sum \frac{(f_o - f_e)^2}{f_e}$, where $f_e = \frac{(\text{Row total})(\text{Column total})}{\text{Total sample size}}$
4. $P$-value: $P$ = right-tail probability above observed $\chi^2$ value,
   for chi-squared distribution with $df = (r - 1)(c - 1)$
5. Conclusion: Report $P$-value
   If decision needed, reject $H_0$ at $\alpha$-level if $P \leq \alpha$

# 5 Standardized residuals

## 5.1 Residual analysis

- If we reject the hypothesis of independence it can be of interest to identify the significant deviations.
- In a given cell in the table, $f_o - f_e$ is the deviation between data and the expected values under the null hypothesis.
- We assume that $f_e \geq 5$.
- If $H_0$ is true, then the standard error of $f_o - f_e$ is given by

$$se = \sqrt{f_e(1 - \text{rowProportion})(1 - \text{columnProportion})}$$

- The corresponding $z$-score

$$z = \frac{f_o - f_e}{se}$$

  should in 95% of the cells be between $\pm 2$. Values above 3 or below -3 should not appear.
- In popKids table cell `Rural and Grade` we got $f_e = 77.0$ and $f_o = 57$. Here columnProportion= 51.7% and rowProportion= $149/478 = 31.2\%$.
- We can then calculate

$$z = \frac{57 - 77}{\sqrt{77(1 - 0.517)(1 - 0.312)}} = -3.95$$

  .
- Compared to the null hypothesis there are way too few rural kids who find grades important.
- In summary: The standardized residuals allow for cell-by-cell ($f_e$ vs $f_o$) comparision.

## 5.2 Residual analysis in R

- In R we can extract the standardized residuals from the output of `chisq.test`:

```
tab <- tally(~ Urban.Rural + Goals, data = popKids)
testStat <- chisq.test(tab, correct = FALSE)
testStat$stdres
```

```
##            Goals
## Urban.Rural     Grades    Popular     Sports
##    Rural    -3.9508449  1.3096235  3.5225004
##    Suburban  1.7666608 -0.5484075 -1.6185210
##    Urban     2.0865780 -0.7274327 -1.8186224
```

# 6 Models for table data in R

## 6.1 Example

- We will study the dataset `HairEyeColor`.

```
HairEyeColor <- read.delim("https://asta.math.aau.dk/datasets?file=HairEyeColor.txt")
head(HairEyeColor)
```

```
##    Hair   Eye  Sex Freq
## 1 Black Brown Male   32
## 2 Brown Brown Male   53
## 3   Red Brown Male   10
## 4 Blond Brown Male    3
## 5 Black  Blue Male   11
## 6 Brown  Blue Male   50
```

- Data is organized such that the variable `Freq` gives the frequency of each combination of the factors `Hair`, `Eye` and `Sex`.
- For example: 32 observations are men with black hair and brown eyes.
- We are interested in the association between eye color and hair color ignoring the sex
- We aggregate data, so we have a table with frequencies for each combination of `Hair` and `Eye`.

```
HairEye <- aggregate(Freq ~ Eye + Hair, FUN = sum, data = HairEyeColor)
HairEye
```

```
##      Eye  Hair Freq
## 1   Blue Black   20
## 2  Brown Black   68
## 3  Green Black    5
## 4  Hazel Black   15
## 5   Blue Blond   94
## 6  Brown Blond    7
## 7  Green Blond   16
## 8  Hazel Blond   10
## 9   Blue Brown   84
## 10 Brown Brown  119
## 11 Green Brown   29
## 12 Hazel Brown   54
## 13  Blue   Red   17
## 14 Brown   Red   26
## 15 Green   Red   14
## 16 Hazel   Red   14
```

## 6.2 Model specification

- We can write down a model for (the logarithm of) the expected frequencies by using dummy variables $z_{e1}, z_{e2}, z_{e3}$ and $z_{h1}, z_{h2}, z_{h3}$
- To denote the different levels of `Eye` and `Hair` (the reference level has all dummy variables equal to 0):

$$\log(f_e) = \alpha + \beta_{e1} z_{e1} + \beta_{e2} z_{e2} + \beta_{e3} z_{e3} + \beta_{h1} z_{h1} + \beta_{h2} z_{h2} + \beta_{h3} z_{h3}.$$

- Note that we haven't included an interaction term, which is this case implies, that we assume independence between `Eye` and `Hair` in the model.
- Since our response variable now is a count it is no longer a linear model (`lm`) as we have been used to (linear regression).
- Instead it is a so-called generalized linear model and the relevant `R` command is `glm`.

## 6.3 Model specification in R

```
model <- glm(Freq ~ Hair + Eye, family = poisson, data = HairEye)
```

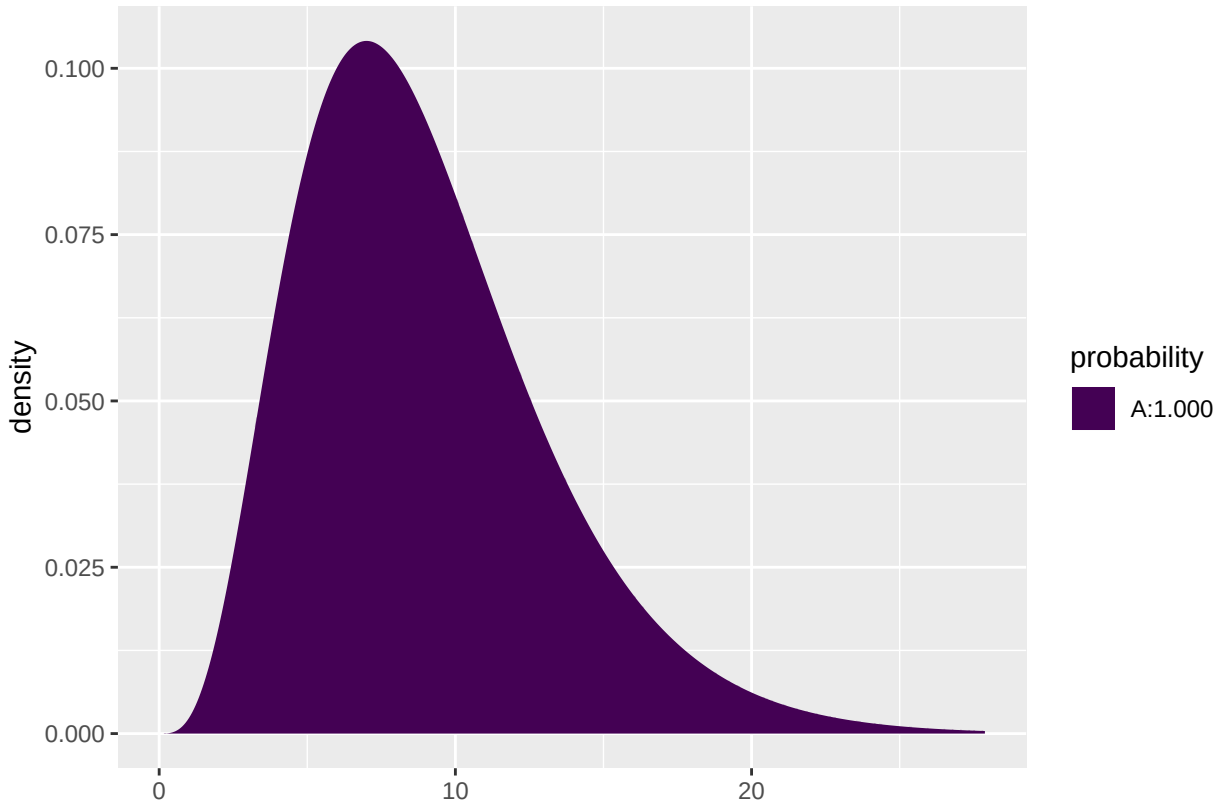
- The argument `family = poisson` ensures that `R` knows that data should be interpreted as discrete counts and not a continuous variable.

```
summary(model)
```

```
##
## Call:
## glm(formula = Freq ~ Hair + Eye, family = poisson, data = HairEye)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -7.326  -2.065  -0.212   1.235   6.172
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.66926    0.11055  33.191  < 2e-16 ***
## HairBlond    0.16206    0.13089   1.238  0.21569
## HairBrown    0.97386    0.11294   8.623  < 2e-16 ***
## HairRed     -0.41945    0.15279  -2.745  0.00604 **
## EyeBrown     0.02299    0.09590   0.240  0.81054
## EyeGreen    -1.21175    0.14239  -8.510  < 2e-16 ***
## EyeHazel    -0.83804    0.12411  -6.752 1.46e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 453.31  on 15  degrees of freedom
## Residual deviance: 146.44  on  9  degrees of freedom
## AIC: 241.04
##
## Number of Fisher Scoring iterations: 5
```

- A value of $X^2 = 146.44$ with $df = 9$ shows that there is very clear significance and we reject the null hypothesis of independence between hair and eye color.

```
1 - pdist("chisq", 146.44, df = 9)
```




```
## [1] 0
```

### 6.4 Expected values and standardized residuals

- We also want to look at expected values and standardized (studentized) residuals.
- The null hypothesis predicts $e^{3.67+0.02} = 40.1$ with brown eyes and black hair, but we have observed 68.
- This is significantly too many, since the standardized residual is 5.86.
- The null hypothesis predicts 47.2 with brown eyes and blond hair, but we have seen 7. This is significantly too few, since the standardized residual is -9.42.

```
HairEye$fitted <- fitted(model)
HairEye$resid <- rstudent(model)
HairEye
```

```
##      Eye  Hair Freq fitted  resid
## 1   Blue Black   20  39.22 -4.492
## 2  Brown Black   68  40.14  5.856
## 3  Green Black    5  11.68 -2.508
## 4  Hazel Black   15  16.97 -0.583
## 5   Blue Blond   94  46.12  9.368
## 6  Brown Blond    7  47.20 -9.423
## 7  Green Blond   16  13.73  0.719
## 8  Hazel Blond   10  19.95 -2.936
## 9   Blue Brown   84 103.87 -3.437
## 10 Brown Brown  119 106.28  2.151
## 11 Green Brown   29  30.92 -0.511
```

```
## 12 Hazel Brown   54  44.93  2.023
## 13  Blue   Red   17  25.79 -2.399
## 14 Brown   Red   26  26.39 -0.101
## 15 Green   Red   14   7.68  2.368
## 16 Hazel   Red   14  11.15  0.961
```

# 7 Log-linear models

## 7.1 Model specification

- We shall consider the data set `living`, which is a Danish survey on standard of living. The variables are
  - `B` (Housing, Bolig): bad/acceptable/good
  - `H` (Health, Helbred): bad/good
  - `I` (Isolated, Isoleret): yes/no
  - `A` (Anxiety, Angst): yes/no
- `N`: The number of respondents for each combination of the 4 factors above
- We want to order the factors such that the reference is "negative".

```
living <- read.delim("https://asta.math.aau.dk/datasets?file=living.txt", stringsAsFactors = TRUE)
```

```
living$B <- relevel(living$B,"Bad")
living$I <- relevel(living$I,"Yes")
living$A <- relevel(living$A,"Yes")
```

## 7.2 Example

- At first we study interaction between housing and health. So we aggregate data and only look at the association between `B` and `H` without controlling for `I` and `A`:

```
BH <- aggregate(N ~ B + H, FUN = sum, data = living)
BH
```

```
##            B    H    N
## 1        Bad  Bad  211
## 2 Acceptable  Bad  327
## 3       Good  Bad 1734
## 4        Bad Good  145
## 5 Acceptable Good  211
## 6       Good Good 1855
```

## 7.3 Model specification

- Like last time we can write down a model for (the logarithm of) the expected frequencies $f_e$ by using dummy variables.
- We let $z_{b1}, z_{b2}$ and $z_{h1}$ denote the different levels of `B` and `H` (the reference level has all dummy variables equal to 0):

$$\log(f_e) = \alpha + \beta_{b1} z_{b1} + \beta_{b2} z_{b2} + \beta_{h1} z_{h1} + \beta_{b1h1} z_{b1} z_{h1} + \beta_{b2h1} z_{b2} z_{h1}.$$

- Note that this time we have included an interaction term, which in this case implies, that we do not assume independence between `B` and `H` in the model.
- This model contains all possible terms and there are as many parameters(6) as there are cells(6) in the table. This is called the **saturated** model.

## 7.4 Example

- We fit the model using `glm`:

```
model <- glm(N ~ B * H, family = poisson, data = BH)
```

- The parameter estimates (of the contrasts, i.e. differences to the reference level (`B: Bad, H: Bad`) are

```
summary(model)
```

```
##
## Call:
## glm(formula = N ~ B * H, family = poisson, data = BH)
##
## Deviance Residuals:
## [1]  0  0  0  0  0  0
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)         5.3519     0.0688   77.74  < 2e-16 ***
## BAcceptable         0.4381     0.0883    4.96  7.0e-07 ***
## BGood               2.1063     0.0729   28.89  < 2e-16 ***
## HGood              -0.3751     0.1079   -3.48  0.00051 ***
## BAcceptable:HGood  -0.0630     0.1394   -0.45  0.65144
## BGood:HGood         0.4426     0.1129    3.92  8.9e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance:  4.2103e+03  on 5  degrees of freedom
## Residual deviance: -2.9532e-14  on 0  degrees of freedom
## AIC: 59.48
##
## Number of Fisher Scoring iterations: 2
```

- The combination `Good:Good` increases the response, i.e. an over representation of people with good housing conditions and good health.

## 7.5 Model form

- Log-linear models quickly become cumbersome to write down.
- For log-linear models the structure of the model is often more interesting than the value of the parameters.

- Therefore we typically just use the model form

$$\mathrm{B} + \mathrm{H} + \mathrm{B} : \mathrm{H}$$

where $\mathrm{B} + \mathrm{H}$ are the main effects and $\mathrm{B} : \mathrm{H}$ means that we have interaction between B and H.
- We shall stick to the **hierarchical principle**, which means that if $\mathrm{B} : \mathrm{H}$ is included then we must include $\mathrm{B} + \mathrm{H}$. For that reason we use the shorthand notation

$$\mathrm{B} * \mathrm{H} = \mathrm{B} + \mathrm{H} + \mathrm{B} : \mathrm{H}$$

## 7.6 Model comparison

- If we suggest a simpler model than the saturated model it will always provide a poorer fit to the given data.
- We need to find a model which is as simple (few parameters) as possible but which at the same time fits the data well.
- Last time we used the $\chi^2$ statistic to judge whether the model $\mathrm{B} + \mathrm{H}$ (independence between B and H) was good enough compared to the saturated model $\mathrm{B} * \mathrm{H}$. This is only possible for models with two variables.
- More generally we shall consider the **Deviance of a model**, which is - approximately - given by

$$\sum \frac{(\texttt{observed} - \texttt{expected})^2}{\texttt{expected}}$$

## 7.7 Deviance

- We look at the output from the function `drop1`:

```
drop1(model, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## N ~ B * H
##        Df Deviance  AIC  LRT Pr(>Chi)
## <none>         0.0 59.5
## B:H     2     40.8 96.3 40.8  1.4e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- The deviance for the saturated model ($\langle$none$\rangle$) is zero as observed=expected.
- Deviance is increased by 40.8, when we remove the interaction B:H.
- Removing B:H corresponds to the null hypothesis $H_0 : \beta_{b1h1} = \beta_{b2h1} = 0$.
- The deviance is compared with a $\chi^2(Df = 2)$ distribution to determine whether it is significant.
- Since the p-value is $1.4 \times 10^{-9}$ the interaction is significant and cannot be left out.

# 8 Higher order interaction

## 8.1 Higher order interaction

- We shall consider models with interaction between more that two variables.

- E.g. there may be a combined effect of adding water, fertilizer and light to a plant at the same time, i.e. the effect of adding water and fertilizer depends on whether the light is on.
- We call this a **3-way interaction**.
- We shall still respect the hierarchical principle:
  - If we include a 3-way interaction, then we must include all main effects and 2-way interactions of the 3 variables.
- Again we use short hand notation

$$B * H * A = B + H + A + B : H + B : A + H : A + B : H : A$$

- Similar considerations hold for 4-way interactions like $B * H * A * I$, etc.

## 8.2 Bigger example

- We fit the saturated model to the full dataset and look at the estimated parameters (only the last half of the values are printed to save space):

```
satmodel <- glm(N ~ B * H * A * I, family = poisson, data = living)
summary(satmodel)
```

```
##
## Call:
## glm(formula = N ~ B * H * A * I, family = poisson, data = living)
##
## Deviance Residuals:
##  [1]  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
## [24]  0
##
## Coefficients:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)                2.08e+00   3.54e-01    5.88  4.1e-09 ***
## BAcceptable                5.60e-01   4.43e-01    1.26  0.20671
## BGood                      1.42e+00   3.94e-01    3.60  0.00032 ***
## HGood                     -2.44e+01   4.22e+04    0.00  0.99954
## ANo                        4.86e-01   4.49e-01    1.08  0.27994
## INo                        1.75e+00   3.83e-01    4.57  5.0e-06 ***
## BAcceptable:HGood          2.28e+01   4.22e+04    0.00  0.99957
## BGood:HGood                2.27e+01   4.22e+04    0.00  0.99957
## BAcceptable:ANo            5.35e-02   5.61e-01    0.10  0.92408
## BGood:ANo                 -3.08e-02   5.01e-01   -0.06  0.95107
## HGood:ANo                  2.34e+01   4.22e+04    0.00  0.99956
## BAcceptable:INo            6.19e-03   4.80e-01    0.01  0.98971
## BGood:INo                  5.47e-01   4.24e-01    1.29  0.19716
## HGood:INo                  2.40e+01   4.22e+04    0.00  0.99955
## ANo:INo                    6.56e-01   4.80e-01    1.37  0.17214
## BAcceptable:HGood:ANo     -2.35e+01   4.22e+04    0.00  0.99956
## BGood:HGood:ANo           -2.25e+01   4.22e+04    0.00  0.99957
## BAcceptable:HGood:INo     -2.30e+01   4.22e+04    0.00  0.99957
## BGood:HGood:INo           -2.27e+01   4.22e+04    0.00  0.99957
## BAcceptable:ANo:INo       -2.52e-01   6.01e-01   -0.42  0.67537
## BGood:ANo:INo              2.83e-01   5.33e-01    0.53  0.59571
## HGood:ANo:INo             -2.34e+01   4.22e+04    0.00  0.99956
```

```
## BAcceptable:HGood:ANo:INo  2.36e+01   4.22e+04    0.00  0.99955
## BGood:HGood:ANo:INo        2.30e+01   4.22e+04    0.00  0.99957
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 1.0965e+04  on 23  degrees of freedom
## Residual deviance: 4.1199e-10  on  0  degrees of freedom
## AIC: 179.1
##
## Number of Fisher Scoring iterations: 20
```

- We see that the four-way interaction and all three-way interactions look like they could be left out.
- However, the p-values are related to removing one and leaving everything else in the model so we have to remove terms of the model one at a time and check against the new model.
- This can be done by successive use of `drop1` and `update` as explained in the following.

---

```
drop1(satmodel, test = "Chi")
```

```
## Single term deletions
##
## Model:
## N ~ B * H * A * I
##         Df Deviance AIC  LRT Pr(>Chi)
## <none>         0.00 179
## B:H:A:I  2     3.51 179 3.51     0.17
```

- The output of `drop1` reveals that the four-way interaction is insignificant and we remove it and save the updated model like this:

```
reducedmodel <- update(satmodel, .~.-B:H:A:I)
```

- We use `drop1` again:

```
drop1(reducedmodel, test = "Chi")
```

```
## Single term deletions
##
## Model:
## N ~ B + H + A + I + B:H + B:A + H:A + B:I + H:I + A:I + B:H:A +
##     B:H:I + B:A:I + H:A:I
##        Df Deviance AIC  LRT Pr(>Chi)
## <none>        3.51 179
## B:H:A   2     7.14 178 3.63     0.16
## B:H:I   2     3.53 175 0.02     0.99
## B:A:I   2     5.53 177 2.02     0.36
## H:A:I   1     4.59 178 1.07     0.30
```

- We see `B:H:I` could be removed and use `update` again:

```
reducedmodel <- update(reducedmodel, .~.-B:H:I)
```

- We can continue this way as long as we like.
- If instead we have a specific simple model in mind, we can define this model and test it against the saturated model with `anova` as shown in the following.

## 8.3 Test of simple model against the saturated model

- We fit the simpler model to the full dataset:

```
simplemodel <- glm(N ~ B*H + B*A + B*I + H*A + H*I + I*A, family = poisson, data = living)
```

- We compare the two models using `anova`:

```
anova(simplemodel, satmodel, test = "Chisq")
```

```
## Analysis of Deviance Table
##
## Model 1: N ~ B * H + B * A + B * I + H * A + H * I + I * A
## Model 2: N ~ B * H * A * I
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1         9       10.7
## 2         0        0.0  9     10.7      0.3
```

- The deviance between the two models is 10.697 with $df = 9$, which has a p-value of 29.7%. So we prefer the simpler model without four- and 3-way interactions.

## 8.4 Model reduction

- Let us check whether we can make further model reductions, where we again use the function `drop1`.

```
drop1(simplemodel, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## N ~ B * H + B * A + B * I + H * A + H * I + I * A
##        Df Deviance AIC  LRT Pr(>Chi)
## <none>        10.7 172
## B:H     2     38.2 195 27.5  1.1e-06 ***
## B:A     2     37.9 195 27.2  1.2e-06 ***
## B:I     2     35.2 192 24.5  4.7e-06 ***
## H:A     1     41.9 201 31.3  2.3e-08 ***
## H:I     1     56.0 215 45.4  1.6e-11 ***
## A:I     1     26.4 186 15.8  7.2e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Conclusion: All of the pairwise interaction terms are significant.

## 8.5 Final model and parameter estimates

- In conclusion our final model is `simplemodel`.

```
summary(simplemodel)
```

```
##
## Call:
## glm(formula = N ~ B * H + B * A + B * I + H * A + H * I + I *
##     A, family = poisson, data = living)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.7295  -0.4842  -0.0025   0.3166   1.2319
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)         2.1704     0.2296    9.45  < 2e-16 ***
## BAcceptable         0.6532     0.2632    2.48  0.01308 *
## BGood               1.1378     0.2336    4.87  1.1e-06 ***
## HGood              -1.7678     0.2103   -8.41  < 2e-16 ***
## ANo                 0.3507     0.1925    1.82  0.06849 .
## INo                 1.7480     0.2312    7.56  4.0e-14 ***
## BAcceptable:HGood  -0.0412     0.1412   -0.29  0.77037
## BGood:HGood         0.3777     0.1144    3.30  0.00096 ***
## BAcceptable:ANo    -0.1276     0.1583   -0.81  0.42035
## BGood:ANo           0.3941     0.1326    2.97  0.00297 **
## BAcceptable:INo    -0.1402     0.2587   -0.54  0.58788
## BGood:INo           0.7204     0.2280    3.16  0.00158 **
## HGood:ANo           0.4408     0.0794    5.55  2.8e-08 ***
## HGood:INo           1.1235     0.1798    6.25  4.2e-10 ***
## ANo:INo             0.6688     0.1628    4.11  4.0e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 10964.662  on 23  degrees of freedom
## Residual deviance:    10.697  on  9  degrees of freedom
## AIC: 171.8
##
## Number of Fisher Scoring iterations: 4
```

- We see that all significant interactions are positive - as expected(why?).
- `(Intercept)` is log of the expected number, when all factors are "bad". So the expected number is $\exp(2.17) = 8.76$, whereas the observed number is 8.

## 8.6 Predicted values

- What is the expected number of people without anxiety (A), with acceptable housing (B), good health (H) that are isolated (I)?

```
summary(simplemodel)
```

```
##
## Call:
## glm(formula = N ~ B * H + B * A + B * I + H * A + H * I + I *
##     A, family = poisson, data = living)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.7295  -0.4842  -0.0025   0.3166   1.2319
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)         2.1704     0.2296    9.45  < 2e-16 ***
## BAcceptable         0.6532     0.2632    2.48  0.01308 *
## BGood               1.1378     0.2336    4.87  1.1e-06 ***
## HGood              -1.7678     0.2103   -8.41  < 2e-16 ***
## ANo                 0.3507     0.1925    1.82  0.06849 .
## INo                 1.7480     0.2312    7.56  4.0e-14 ***
## BAcceptable:HGood  -0.0412     0.1412   -0.29  0.77037
## BGood:HGood         0.3777     0.1144    3.30  0.00096 ***
## BAcceptable:ANo    -0.1276     0.1583   -0.81  0.42035
## BGood:ANo           0.3941     0.1326    2.97  0.00297 **
## BAcceptable:INo    -0.1402     0.2587   -0.54  0.58788
## BGood:INo           0.7204     0.2280    3.16  0.00158 **
## HGood:ANo           0.4408     0.0794    5.55  2.8e-08 ***
## HGood:INo           1.1235     0.1798    6.25  4.2e-10 ***
## ANo:INo             0.6688     0.1628    4.11  4.0e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 10964.662  on 23  degrees of freedom
## Residual deviance:    10.697  on  9  degrees of freedom
## AIC: 171.8
##
## Number of Fisher Scoring iterations: 4
```

- Logarithm of the expected:

$$2.17042 + 0.65323 - 1.76785 + 0.35067 - 0.04121 - 0.12759 + 0.44076 = 1.67843$$

- so the expected number is $\exp(1.67843) = 5.36$, whereas the observed number is 5.

---

- We can of course make **R** calculate all the table values expected by the model and add them to the data:

```
living$expected <- fitted(simplemodel)
living[1:12,]
```

```
##             B    H   I   A   N expected
## 1         Bad Good Yes  No   5     3.30
## 2         Bad Good  No  No 107   113.78
## 3         Bad Good Yes Yes   0     1.50
## 4         Bad Good  No Yes  33    26.42
## 5         Bad  Bad Yes  No  13    12.44
## 6         Bad  Bad  No  No 144   139.47
## 7         Bad  Bad Yes Yes   8     8.76
## 8         Bad  Bad  No Yes  46    50.32
## 9  Acceptable Good Yes  No   5     5.36
## 10 Acceptable Good  No  No 155   160.54
## 11 Acceptable Good Yes Yes   3     2.76
## 12 Acceptable Good  No Yes  48    42.35
```

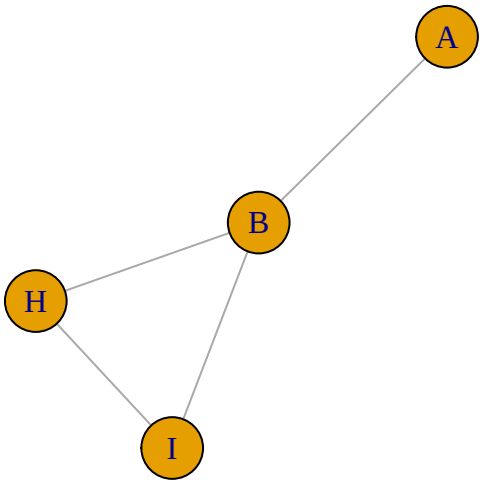
# 9 Graphical representation

## 9.1 Graphical representation

- We make a graphical representation by
  - drawing a circle for each variable.
  - connecting variables which enter the same model term.
- Example: Assume the model is

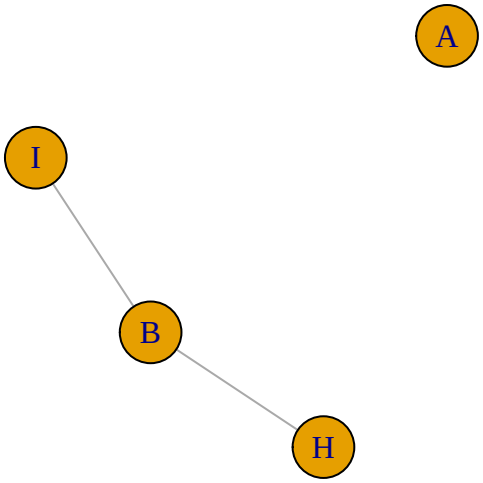
$$A * B + B * H * I$$

- Then the graphical representation is

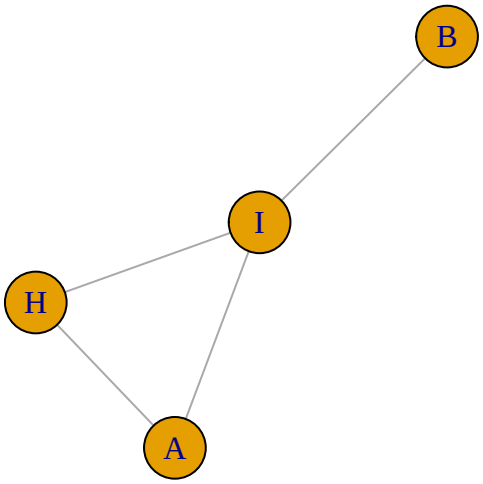



## 9.2 Interpretation of graphical model

- **Independence**: If A enters in the model formula, but A doesn't enter in any other terms (e.g. $A * B$, $A * H$, etc.), then A is independent of the other variables.
- E.g. $A + B * H + B * I$

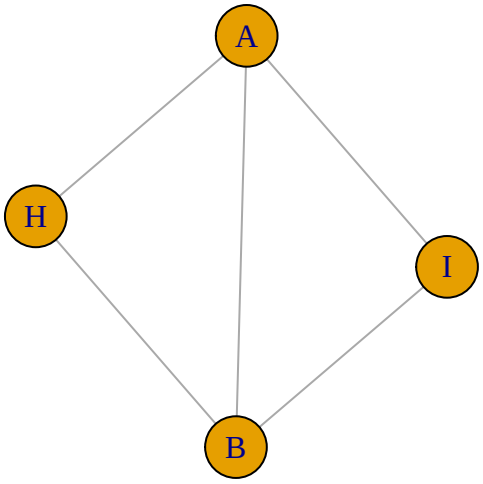



- **Explained association**. If B and H are "connected" via other terms, but don't enter the same term, then the association is explained by other variables. I.e. the model cannot include e.g. $B * H$, $B * H * A$ or $A * B * H * I$.
- E.g. $B * I + A * H * I$

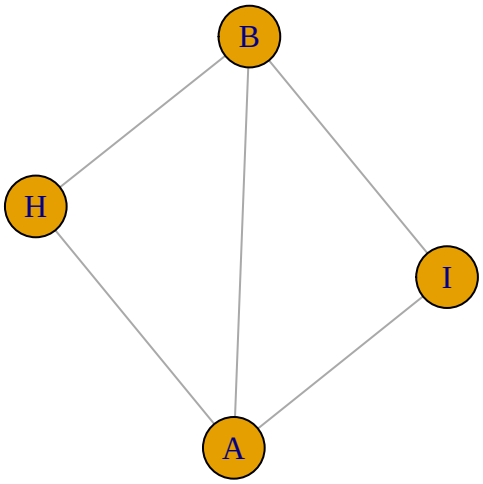



## 9.3 Interpretation of graphical model

- **Homogeneous association**: If $A * H$ enters the model, but $A * H$ doesn't enter more complicated terms, then the association between A and H is homogeneous.
- I.e. the model cannot contain $A * H * I$, $A * B * H$ or $A * B * H * I$.
- E.g. $A * H + A * I * B + B * H$



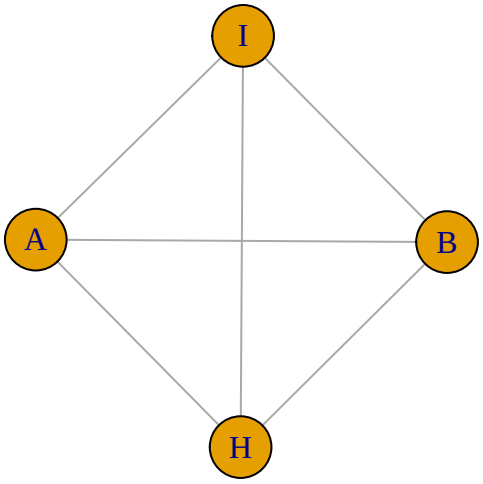

- **Heterogeneous association**: If $A * H$ enter the model as a part of a more complicated term, then the association between A and H is heterogeneous.
- I.e. the model *must* contain $A * H * I$, $A * B * H$ or $A * B * H * I$.
- E.g. $A * B * H + A * I * B$




## 9.4 Final model of the example

- In the example the final model was:

$$B * I + H * I + I * A + B * H + B * A + H * A$$




- We can directly see from the graph, that:
  - we don't have any independent variables since all variables are connected
  - we do not have an explained association.
- From the formula we have homogeneous association between all pairs of variables.