Contingency tables

The ASTA team

Contents

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 = 2)
```

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

- 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

- The relative frequencies in the sample gives an estimate of the unconditional distribution of `Goals`:

```
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 (χ^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:

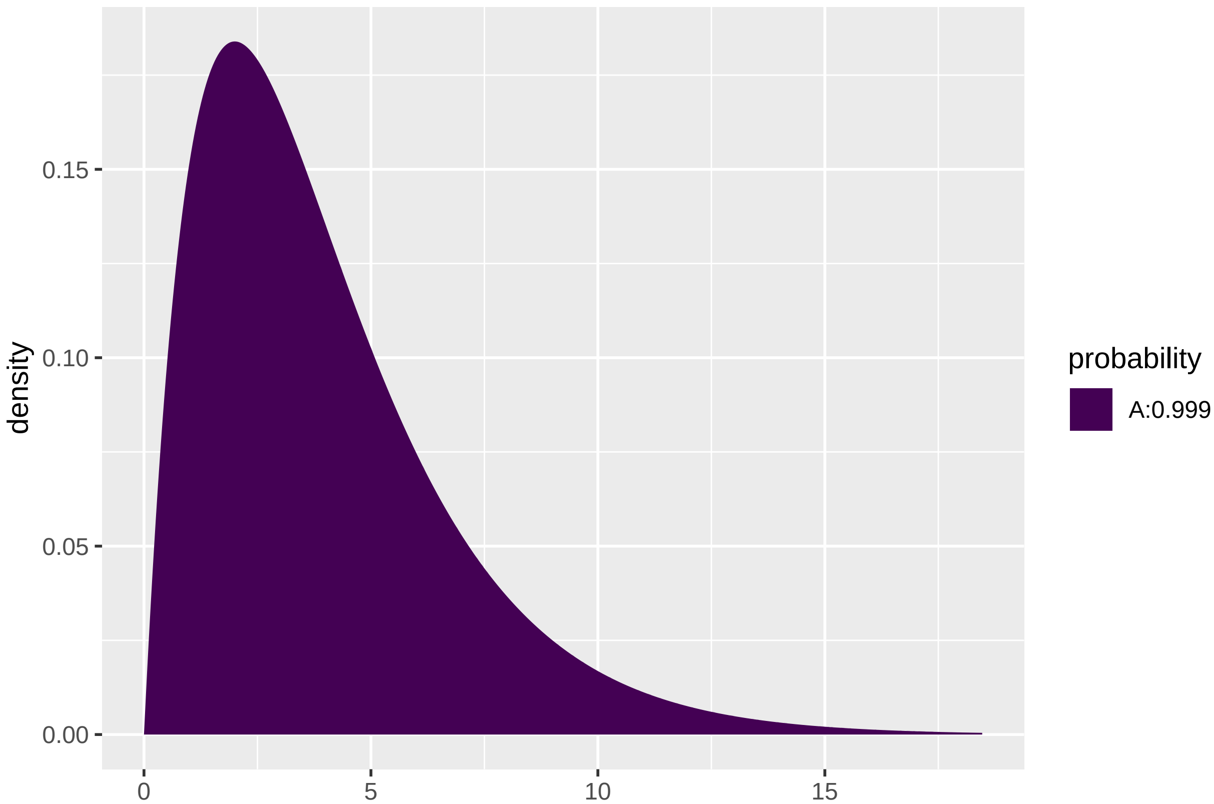
$$X^2_{obs} = \frac{(57-77)^2}{77} + \ldots + \frac{(26-33.5)^2}{33.5} = 18.8$$

- Is this a large distance??

2.5 χ^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 χ^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] 0.00086
```

- 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 = 20, df = 4, p-value = 8e-04
```

```
testStat$expected
```

```
##             Goals
## Urban.Rural Grades Popular Sports
##    Rural        77    44.0   28.1
##    Suburban     78    44.5   28.4
##    Urban        92    52.5   33.5
```

- 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
```

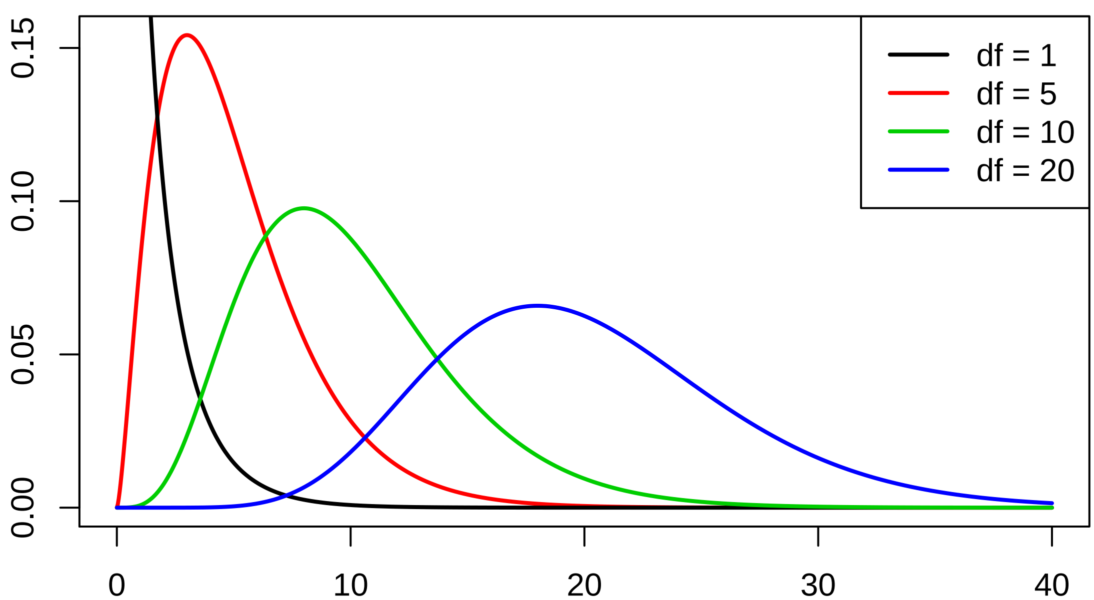
```
chisq.test(tab)
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab
## X-squared = 20, df = 4, p-value = 8e-04
```

3 The χ^2-distribution

3.1 The χ^2-distribution

- The χ^2-distribution with df degrees of freedom:
  - Is never negative.
  - 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 $f_e = \frac{\text{(Row total)(Column total)}}{\text{Total sample size}}$
4. P-value: P = right-tail probability above observed χ^2 value,
   for chi-squared distribution with $df = (r - 1)(c - 1)$
5. Conclusion: Report P-value
   If decision needed, reject H_0 at α-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 ± 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    -3.951   1.310  3.523
##    Suburban  1.767  -0.548 -1.619
##    Urban     2.087  -0.727 -1.819
```

5.3 Why not just use two-way ANOVA ?

- number of persons in different categories are *not* normally distributed
- variance typically larger the larger expected frequency
- underlying data are discrete (for each person, which column and row category does person belong to)
- these discrete variables are naturally modelled in terms of probabilies for different categories
- therefore hypothesis of independence becomes natural null hypothesis
- it is possible to model table frequencies as dependent variable using a regression model but then we need the framework of *generalized linear models* (see last slides)

Contingency table:

- *counts* of how many individuals fall within different categories for two (or more) categorical variables

Two-way ANOVA:

- a number of individuals/objects/... available for each combination of two categorical variables
- next a continuous variable is measured for each individual or object (this becomes the response variable)

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)
```

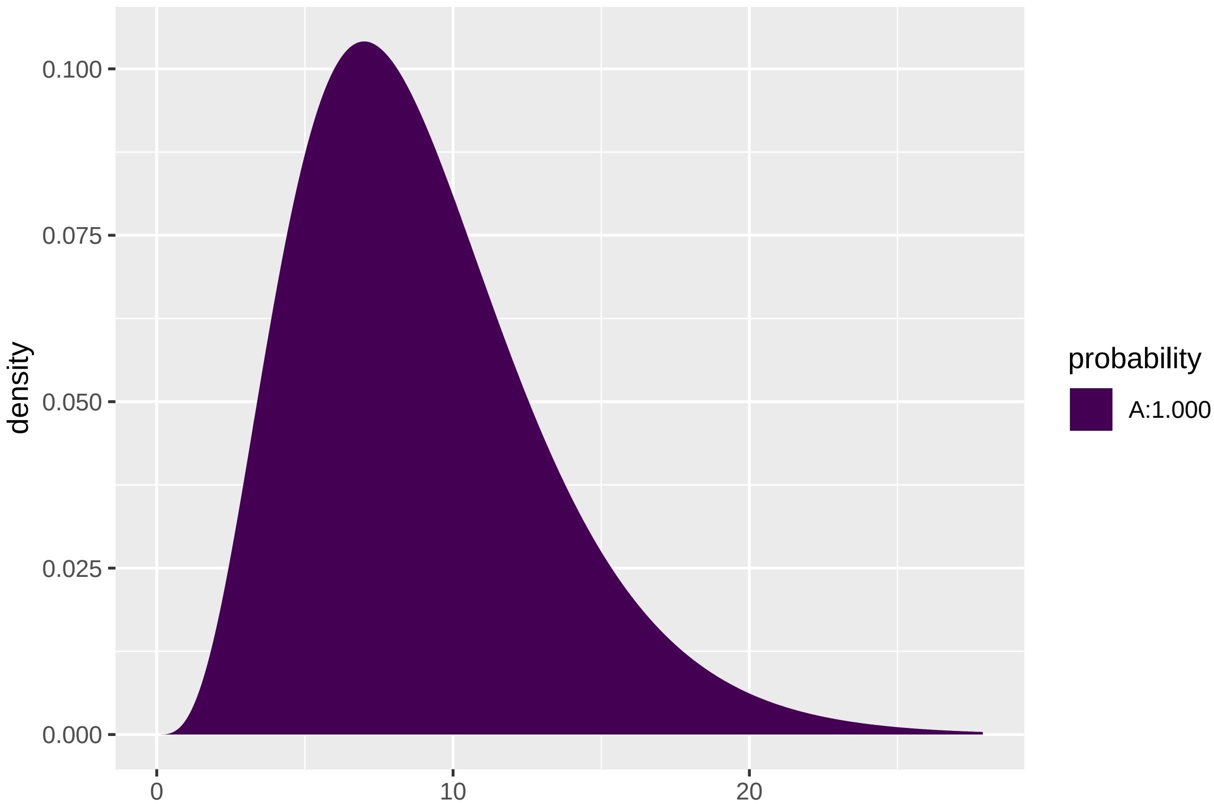
- The argument `family = poisson` ensures that `R` knows that data should be interpreted as discrete counts and not a continuous variable.

```r
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)   3.6693     0.1105   33.19  < 2e-16 ***
## HairBlond     0.1621     0.1309    1.24    0.216
## HairBrown     0.9739     0.1129    8.62  < 2e-16 ***
## HairRed      -0.4195     0.1528   -2.75    0.006 **
## EyeBrown      0.0230     0.0959    0.24    0.811
## EyeGreen     -1.2118     0.1424   -8.51  < 2e-16 ***
## EyeHazel     -0.8380     0.1241   -6.75  1.5e-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
##
## 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.

```r
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
```