# 8- Hypothesis testing with qualitative variables

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#### Readme

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#### Introduction

- Categorical variables represent facts that can be better described with labels than with numbers.
  - Example: Sex, better choose from  $\{Male, Female\}$  than from:  $\{1,2\}$ .
- Sometimes ordering of labels makes sense, although it is not reasonable to assign numbers to categories:
  - Example: Tumor stage:  $\{1,2,3,4\}$ , burt  $1+2 \neq 3!!!$
- Sex is an example of a categorical variable in nominal scale
- Stage is an example of a categorical variable in ordinal scale

```
sex <- factor(c("Female", "Male"))
stage <- factor(1:4, ordered=TRUE)</pre>
```

## **Example**

- Select one of the datasets that you have worked with during the course
  - diabetes.xls
  - osteopòrosis.csv
  - demora.xls
- Read the dataset and check that the categorical variables you are interested in are converted into factors.
- Confirm the conversion by summarizing the variables

## The analysis of categorical variables

- The analysis of categorical data proceeds as usual:
  - Start exploring the data with the tables and graphics
  - Proceed to estimation and testing if appropriate
- Estimation
  - Proportions: Point estimates, confidence intervals, Sample Size
- Testing
  - One variable (tests with proportions)
    - Does the proportion (% affected) match a given value?
    - Is the proportion (% affected) the same in two populations?
  - With two variables (chi-square and related)
    - Is there an association between two categorical variables?
    - Is there a relationship between the values of a categorical variable before and after treatment?

## **E**xample

#### Consider the following study relating smoking and cancer

Load data: "	dadesca	ncer.csv"			
		Smoking X	=1 Non g	smoking X=0	TOTAL
CANCER Y=1  NO CANCER Y=0  TOTAL		190		87 163 250	
		60			
		250			
0 0 0 0000000 0000000 0000000 0000000	0	00000000 00000000 00000000	0	00000000 00 00000000 00 00000000 00 000000	0000000 0000000 0000000 0000000 0000000

## **Crosstabulating a dataset**

```
dadescancer <- read.csv("datasets/dadescancer.csv", strings</pre>
```

```
attach(dadescancer)
mytable <-table(cancer, fumar)
mytable</pre>
```

```
## fumar

## cancer Fuma No fuma

## Cancer 190 87

## No cancer 60 163
```

# **Crosstabulation (2): Marginal tables**

```
margin.table(mytable, 1) # A frequencies (summed over B)
## cancer
##
     Cancer No cancer
##
        277
                  223
margin.table(mytable, 2) # B frequencies (summed over A)
## fumar
##
     Fuma No fuma
##
      250
              250
```

# Crosstabulation (2): In percentages

```
prop.table(mytable) # cell percentages
##
             fumar
  cancer Fuma No fuma
##
    Cancer 0.380 0.174
##
## No cancer 0.120 0.326
prop.table(mytable, 1) # row percentages
##
             fumar
##
  cancer
                   Fuma No fuma
    Cancer 0.6859206 0.3140794
##
##
    No cancer 0.2690583 0.7309417
# prop.table(mytable, 2) # column percentages
```

#### **Exercice**

- With the osteoporosis dataset repeat the crosstabulation done above using
  - Two categorical variables
  - Variable "MENOP" and a newly created variable "catBUA" created by properly categorizing variable BUA.

## One variable: Proportion tests

- According to medical literature, in the period 1950-1980, the proportion of obese individuals (defined by medical criteria: BMI  $\geq$  30) was 15% in the population of men over 55 years old.
- A random sample obtained from the same population between 2000 and 2003 showed that, over a total of 723 men older than 55, 142 were obese.
- Considering that the significance level that we use is 5%, can we say that the population of men older than 55 in 2000-2003 had the same proportion of obese cases than that population had in 50'-80'?

## Proportion tests with R

```
prop.test(x=142, n=723, p=0.15)
##
##
    1-sample proportions test with continuity correction
##
## data: 142 out of 723, null probability 0.15
## X-squared = 11.849, df = 1, p-value = 0.0005768
## alternative hypothesis: true p is not equal to 0.15
## 95 percent confidence interval:
## 0.1684325 0.2276606
## sample estimates:
##
           р
## 0.1964039
```

#### **Estimation comes with proportion test**

- prop.test does three distinct calculations
  - A test for the hypothesis  $H_0: p = p_0$  is performed
  - A confidence interval for *p* is built based on the sample
  - A point estimate for *p* is also provided.

```
> prop.test(x=142, n=723, p=0.15)

1-sample proportions test with continuity correction

data: 142 out of 723, null probability 0.15
X-squared = 11.849, df = 1, p-value = 0.0005768

alternative hypothesis: true p is not equal to 0.15
95 percent confidence interval:
0.1684325 0.2276606

Sample estimates:

p
0-1964039

Point estimate
```

#### **Exercise**

- In the osteoporosis dataset
  - Test the hypothesis that the proportion of women with osteoporosis is higher than 7%
    - In the global population of the study
    - Only in women with osteoporosis
  - Select a sample of size 100 and repeat the test. How do the results change?
  - What sample size should we have taken so that th precision of the confidence intervals would have been at most 3% with a probability of 95%?

## **Contingency tables**

- A contingency table (a.k.a cross tabulation or cross tab) is a matrix-like table that displays the (multivariate) frequency distribution of the variables.
- It is bidimensional, and classifies all observations according with two qualitative variables (A and B, rows and columns).

Clasif	$\mathbf{B}_{I}$	$B_2$	 $\mathbf{B}_{s}$	Total
$A_I$	$n_{II}$	$n_{12}$	 $n_{Is}$	$n_{I\bullet}$
$A_2$	$n_{21}$	n <sub>22</sub>	 $n_{2s}$	$n_{2\bullet}$
$A_r$	$n_{rl}$	$n_{r2}$	 $n_{rs}$	$n_{r\bullet}$
Total	$n_{\bullet I}$	n <sub>•2</sub>	$n_{\bullet s}$	N

## **Chi-squared test**

#### Chi squared independence test

 When the sample comes from a single population with 2 qualitative variables, the aim is to determine if there is relationship between vars:

#### Chi squared homogeneity test

 When each row is a sample from distinct populations (groups, subgroups...), the aim is to determine if both groups have significative differences in that variable

## **Chi-squared tests**

- When we have:
  - quantitative data,
  - one or more categories,
  - independent observations,
  - adequate sample size (>10)
- and our questions are like. . .
  - Do the number of individuals or objects that fall in each category differ significantly from the number you would expect?
  - Is this difference between the expected and observed due to sampling variation, or is it a real difference?

# Chi squared.test: Observed vs expected

Observades	Braf -	Braf+
Grau 1	97	5
Grau 2	81	7
Grau 3	32	18

Esperades	Braf -	Braf+
Grau 1	89.25	12.75
Grau 2	77.00	11.00
Grau 3	43.75	6.25

# Chi squared tests with R

```
mytable <-table(cancer, fumar)</pre>
chisq.test (mytable)
##
    Pearson's Chi-squared test with Yates' continuity corre
##
##
## data: mytable
## X-squared = 84.214, df = 1, p-value < 2.2e-16
Alternatively use Fisher test
fisher.test(mytable)
##
##
    Fisher's Exact Test for Count Data
##
## data: mytable
## p-value < 2.2e-16
## alternative hypothesis: true odds ratio is not equal to
```

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#### **Exercise**

- Use the osteoporosis dataset to study if it can be detected an association between the variables menop and classific in the osteoporosis dataset.
- Do not start with a test but with an appropriate summarization and visualization!