University of Toronto

Statistics: Making Sense of Data

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Chapter 1

Introduction

1 Making sense of data

1.1 Data categorization

An *observational unit* is the person or thing on which measurements are taken. Note that this can also be a case, object, a subject and so on. A *variable* is a characteristic measured on the observational unit. An instance of the variable we call the *observed value* or *observation*. Variables can be of three kind:

quantitive variable take numerical values for which arithmetic operations make sense. The height of the people is a such variable,

caterogical variable consist of records into which the observation falls into (one of several categories). For example the countries of the world may be classified into one of the five great continets: Europe, America, Africa, Asia and the Pacific,

ordinal variable have natural order, however the difference between two instance of the variables does nt always make sense. A good example is grades given by a teacher: A, B, C, D, E, F.

1.2 Quantative variables

One way of making sense of a quantitive variable is to use the *five number summary*. Given a collection of a observations we can calculate the:

Minimum is the lowest observation value.

Maximum is the highest observation value.

Median is the center observation, average point. To find it you'll need to sort the observations, and then take the observation in the middle position.

First quartile is the observation value at the $\frac{1}{4}$rd position in the sorted observation array.

Third quartile is the observation value at the $\frac{3}{4}$rd position in the sorted observation array.

A graphical representation of this five values is possible via the *boxplot* as shown on figure 1. On the boxplot the whiskers show the minimum and the maximum values.

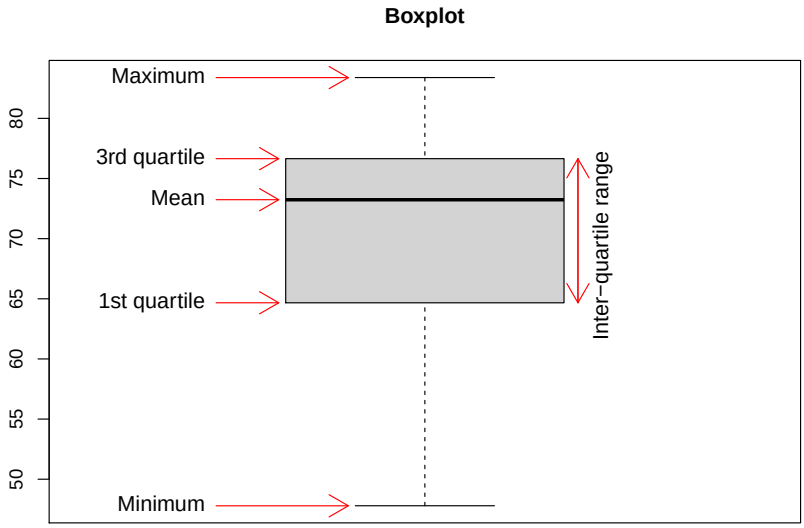

Figure 1: A simple way to represent the *five number summary*.

Note that the median, first or thrid quartile may result in a non–integer position. In this case these values are calcualted by interpolating them from the nearby observations, with the given percentage; therefore, it may happen that these values are not part of the variable instances.

Modified boxplots

Outliers (known as extreme values, or unusual observations) are hard to study on a classical boxplot, so for them we use the modified boxplot. In this case let us

first define the inter-quartile range (noted as IQR) as the difference between the 3rd and the 1st quartile. Then we can define the inner fences as the:

lower fence is = 1st quartile − 1.5·IQR, and the

upper fence is = 3st quartile + 1.5·IQR.

Now the lower whisker is noted as the lower fence, while the upper fence as the upper whisker. Observations smaller than the lower fence, or larger than the upper fence are drawn with their own circle on the plot as shown on figure 2.

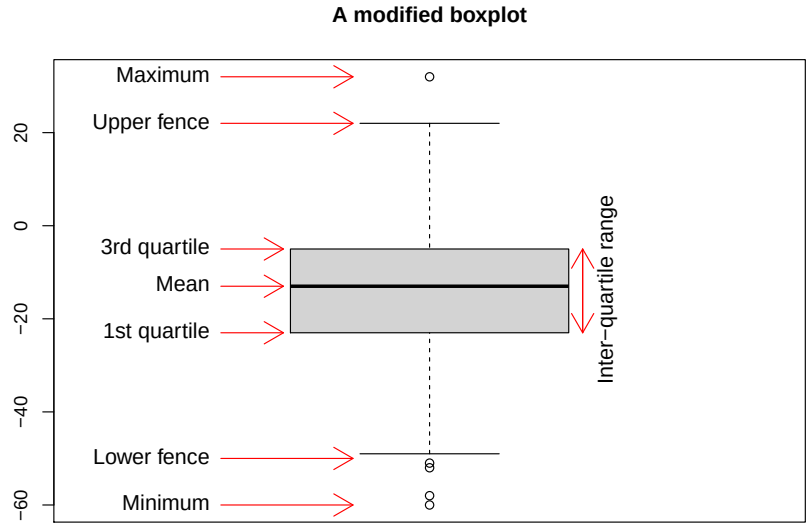

Figure 2: Modified boxplots help dealing with outliers.

Mean

Given a list of observations $(x_1, x_2, \ldots x_n)$, the mean of the variable is noted as $\bar{x}$ (or μ) and is calculated as:

$$\text{Mean} = \bar{x} = \frac{\sum \text{data values}}{\text{number of data points}} = \frac{\sum_{i=1}^{n} x_i}{n}.$$

However, this definition of mean is not robust, as it's easily influenced by outlier points. Note, that in contrast the median is robust. To alleviate this we can introduce the conept of trimmed mean, which exclude some percentage of

the lowest and highest values from the observations, before performing the same operation to calculate the *trimmed–mean*. The input of the trimmed mean is the percentage of outliers to remove.

Spread of the data

The range of the data is the difference between the maximum and the minimum. This is not a robust measurement. The same can be told about the IQR too. The deviation of an observation i is $x_i - \bar{x}$. A good show of the spread of the whole data is the:

$$\text{variance} = \frac{\sum_{i=1}^{n} (x_i - \bar{x})^2}{n - 1}$$

Note that we divide by one less than the count of observation points. An intuitive explanation for this is that the first observation does not tells us anything about deviation. The *standard deviation* (also noted as σ) is the square root of this ($\sqrt{\text{variance}}$), and shows the dispersion of a set of data from its mean.

The shape of the data - histogram

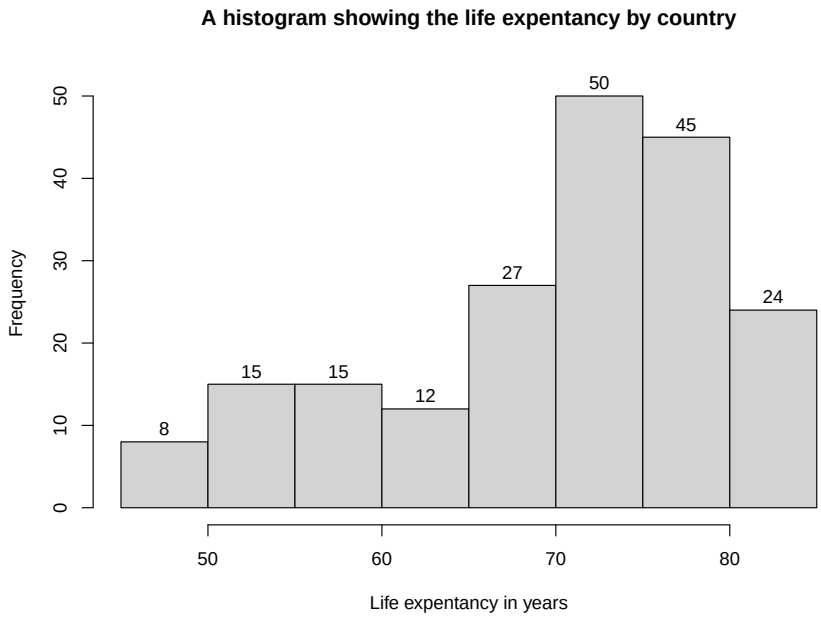

Figure 3: Histogram

The distribution is the pattern of values in the data, showing their frequency of occurance relative to each other. The histogram is a good way to show this graphically; you can see an example of this on figure 3.

Its key part is the number of *bin*s used, as observations must be separated into mutually exclusive and exhaustive bins. *Cutpoints* define where the bins start and where they end. Each bin has its own *frequency*, the number of observations in it. The largest bins define the *peaks* or *modes*. If a variable has a single peak we call it an unimodal, bimodal for two peaks and multiple peaks above that.

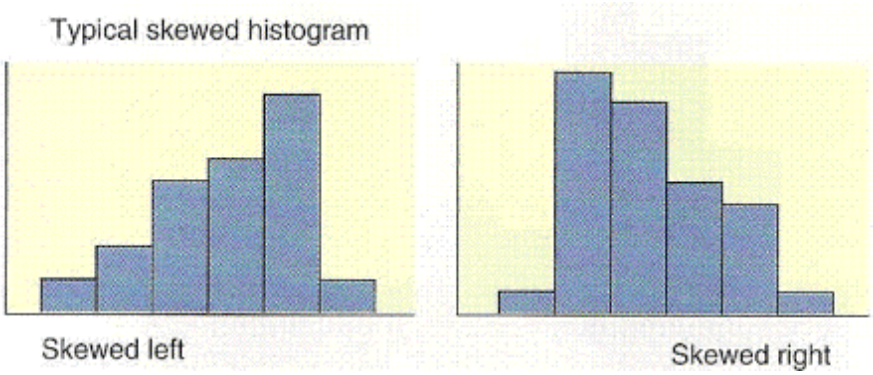

Figure 4: Skewed histograms

Uniform distribution is a case when all the data values occur around the same times, so we have no peaks, and such the variable has no mode. The tails of the histogram are on its left or right side, where its extreme values are. A histogram is left skewed if it has the left tail larger than the right, and right skewed if the right tail is larger than its left.

Empirical rule

The empirical rule (also know as three σ rule) states that for a normal distribution 68% of the data is within one standard deviation of the mean value, 95% is within two standard deviation, and 99.7% is within three standard deviation.

1.3 Categorical variables

Caterogical variables are not represented by numbers, so all of the earlier statistics no longer make sense. What does make sense is the frequency of the categories, which is graphically represented either by a barchart or a piechart.

Figure 5 shows an example of this. In case of barcharts we may choose to normalize the frequency, by dividing it with the total number of observations.

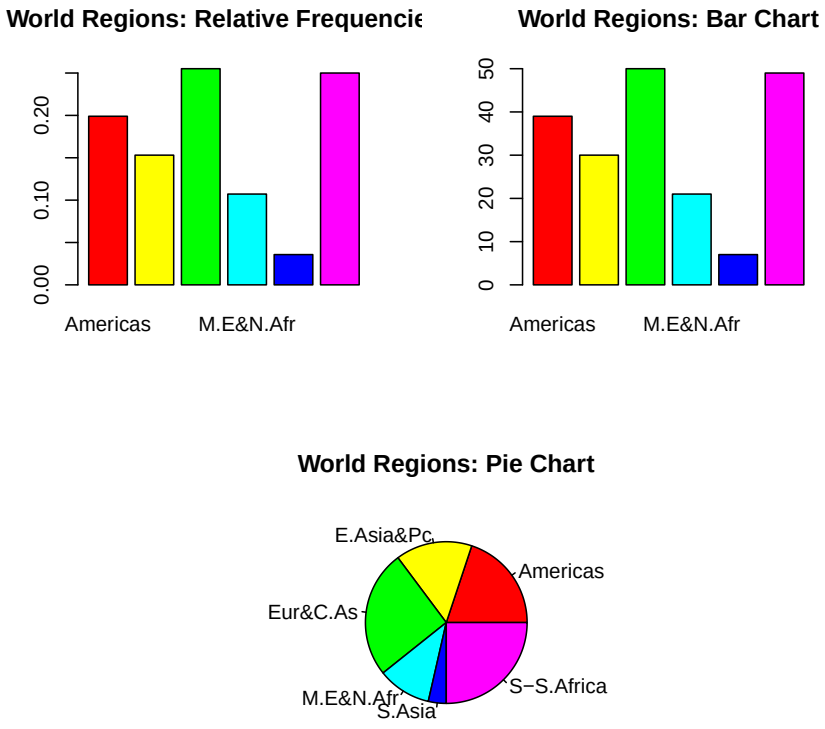

Figure 5: Skewed histograms

2 Releationships and data collections

2.1 Relationship between quantitive and categorical variables

Relationships are at the hearth of statistic. Let us consider an example. Let there be the unit of observation the worlds countries. Now we define on this two variables: a quantitive one – the life expentancy, and a caterogical one – in which of the six world regions they fall into. Now we want to check for instance if life expectancy in East Asia and Pacific tends to be larger than in the Sub-Saharan Africe.

One way of approach is to consider the median and mean per region, and to see where this it's larger. However, this does not tells the whole story as the highest in one of the regions can still be a lot higher than the lowest in another region. Box plot is a graphical way to make the comparision.

Examining the relationship between a quantitative variable and a categorical variable involves comparing the values of the quantitative variable among the groups defined by the categorical variable. We need to:

1. Examine the centre of the data in each group.
2. Examine the spread of the data in each group.
3. Examine the centre of the data in each group.

So create a boxplot (or summary) for each categorical observation and compare.

In the R language

In the R lanugage we can draw a new boxplot per category to make the comparision. To separate categories we can use the *split* function, and finally use non-modified boxplots (*range* is set to 0) to draw them, as seen on figure 6:

```
lifedata = read.table('LifeExpRegion.txt')
colnames(lifedata) = c('Country', 'LifeExp', 'Region')
attach(lifedata)
lifedata[Region=='EAP', ]
lifesplit = split(lifedata, Region)
lifeEAP = lifedata[Region=='EAP',]
lifeSSA = lifedata[Region == 'SSA', ]
boxplot(lifeEAP[,2], lifeSSA[,2], range=0, border=rainbow(2),
        names=c('EAP', 'SSA'), main="Life Expectancies: Box Plot")
```

```
boxplot(LifeExp~Region, range=0, border=rainbow(6),
                main='Life Expectancies: Box Plot (all 6 regions)')
```

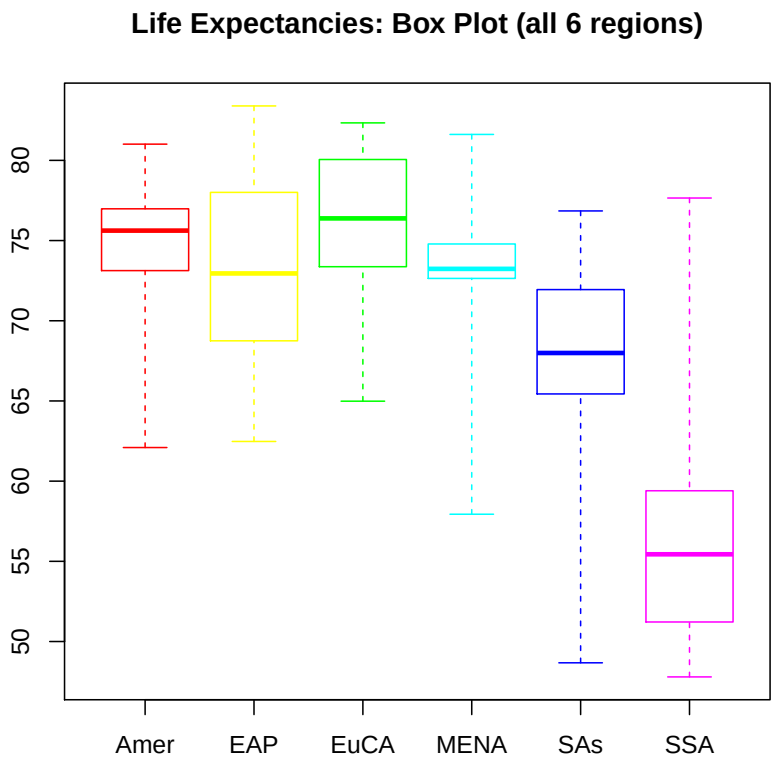

Figure 6: Boxplots to compare quantitive and categorical variables

2.2 Relationship between two categorical variables

For instance let there be the two observations the gender of persons and their body weight. One question we can ask is that are the same count of overweight female as man?

Distributions

Distribution types are:

joint distribution of two categorical variables is the frequency or relative frequency of the observations considered together as a combination. The graphical approach is to use bar plots per combination, or aggregate these into a stacked bar plot.

marginal distribution is the distribution of only one of the variables in a contingency table (so we take the total of the rows or of the columns in the table – essentially its the distribution by only one of the variables).

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conditional distribution of a categorical variable is its distribution within a fixed value of a second variable. This distribution is normalized by the count of the fixed value. For graphical approach a stacked plot is used, by using the percentage values. Two variables in a contingency table indedependent if the conditional distribution of one variable is the same for all values of other variable.

Simpson's paradox is when the conditional distributions within subgroups can differ from condition distributions for combined observations. The issue behind the paradox is that behind the two categorical variables ther is a third lurking variable which influences the study, like for a smoking study, to transform the age into age groups (if we study if the people die or not, having more old people in a group as observations may influence the result).

Categorical values in R

Categorical variables read into R are always sorted alphabetically, and therefore any statistics about it will be displayed on that order. However, sometimes there is a better order to this variables. In this case we can use the *factor* function and its *levels* paramter to set a different order for the categories:

```
allData <- read.table('SkeletonData.txt', header=TRUE) # dataset read
attach(allData) # now we can use the column header names as variables
BMI = factor(BMI, levels = c('underweight', 'normal', 'overweight',
                             'obese')) # reorder categories
```

We can even give to the categories nicer names, as we do in the following example for the sex categorical variable (which in the file is specified by the values 1 and 2):

```
Sex = factor(Sex, levels=c('1', '2'), labels=c('Male', 'Female'))
```

To find the number of items per category use the *table* command. You can divide tis with the number of observations to get the relative frequencies:

```
relfreqBMI = table(BMI)/length(BMI)
```

Which will result in the distribution of the data:

```
BMI
underweight      normal  overweight       obese
     0.1850      0.5625      0.2025      0.0500
```

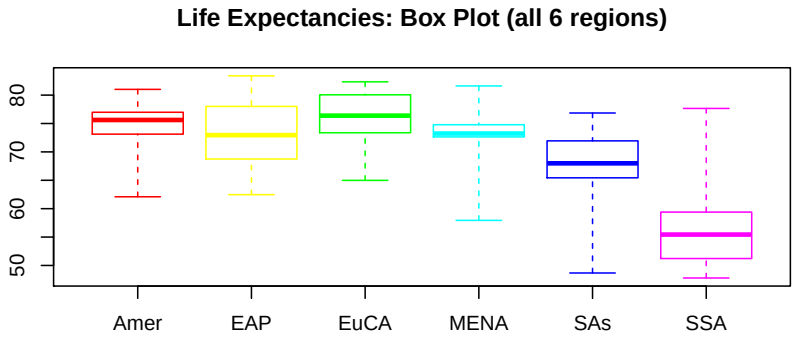
We can even combine the relative and non relative values in a single table:

```
cbind(freqBMI, relfreqBMI)
```

To get joint and the conditional distribution for two categorical variables we need to use the *CrossTable* function from the *gmodels* library.

```
library(gmodels)
joint = CrossTable(BMI, Sex, prop.chisq=FALSE)
  Cell Contents # legend for the table below
|-------------------------|
|                       N |
|           N / Row Total |
|           N / Col Total |
|         N / Table Total |
|-------------------------|
Total Observations in Table:  400
             | Sex
         BMI |      Male |    Female | Row Total |
-------------|-----------|-----------|-----------|
 underweight |        46 |        28 |        74 |
             |     0.622 |     0.378 |     0.185 |
             |     0.164 |     0.235 |           |
             |     0.115 |     0.070 |           |
-------------|-----------|-----------|-----------|
      normal |       166 |        59 |       225 |
             |     0.738 |     0.262 |     0.562 |
             |     0.591 |     0.496 |           |
             |     0.415 |     0.147 |           |
```

overweight	59	22	81
	0.728	0.272	0.203
	0.210	0.185	
	0.147	0.055	
obese	10	10	20
	0.500	0.500	0.050
	0.036	0.084	
	0.025	0.025	
Column Total	281	119	400
	0.703	0.297	



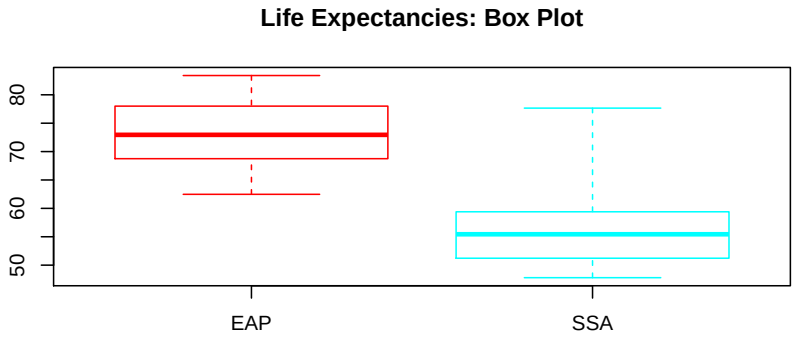


Figure 7: Relationship between two categorical variables

At this point the `joint` contains four tables: a contingency table (frequencies – `joint$t`), two conditional distribution (one per point of view – sex `joint$prop.col` or BMI `joint$prop.row`), and one displaying relative frequencies (joint distribution – `joint$prop.tbl`). We can use barplots to visualize this:

```
layout(matrix(c(2,2,1,1), 2, 2, byrow = TRUE))
# side by side barplot
barplot(joint$t, beside=TRUE, col=rainbow(4), ylab='Frequency',
                                              xlab='Sex')
# add legend information, 15 = plotting symbol, a little square
legend('topright', c('underweight', 'normal', 'overweight', 'obese'),
                                          pch = 15, col=rainbow(4))
#stacked barplot
barplot(joint$prop.col, beside=FALSE, col=rainbow(4),
                                      ylab='Frequency', xlab='Sex')
```

as you can see it on figure 7.

2.3 Relationship between two quantitive variables

One approach is to convert one (or both) of the quantitive variables into categorical variable and then just use the already seen methods. One way to create good groups is to use the quartile breakdown. However, this does not uses the full information of the quantitive variables.

One way to use it is to use a scatterplot (that is to use the quantitive variable pairs as points in the space). On this we can use regression techniques to fit a line on the points, effectively finding the relationship between the variables (correlation means a rising line)

A numerical representation of this is the *correlation*. Let there be two variables indicated by the series $x_1, x_2, \ldots, x_n$ and $y_1, y_2, \ldots y_n$, the correlation is calculated as:

$$\text{correlation} = \frac{\sum_{i=1}^{n}(x_i - \bar{x}) \cdot (y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n}(x_i - \bar{x})^2 \cdot \sum_{i=1}^{n}(y_i - \bar{y})^2}}$$

Correlation values are between $[-1, 1]$, where 1 is perfect match, and -1 is the perfect negative. If this is a positive value when one increases the other tends to follow. However, note that this only captures the linear aspects of the relationship.

In the R lanuage

For calculating the correlation we can use the *cor* function.

```
Countries = read.table('LifeGDPhiv.txt')
colnames(Countries) = c('Country', 'LifeExp', 'GDP', 'HIV')
attach(Countries)
plot(GDP, LifeExp, xlab='GDP(2000USD)', ylab='Life Expectancy (years)',
     main='Scatterplot: Life Expectancy versus GDP per capita')
cor(GDP, LifeExp)
[1] 0.6350906
cor(LifeExp, GDP)
```

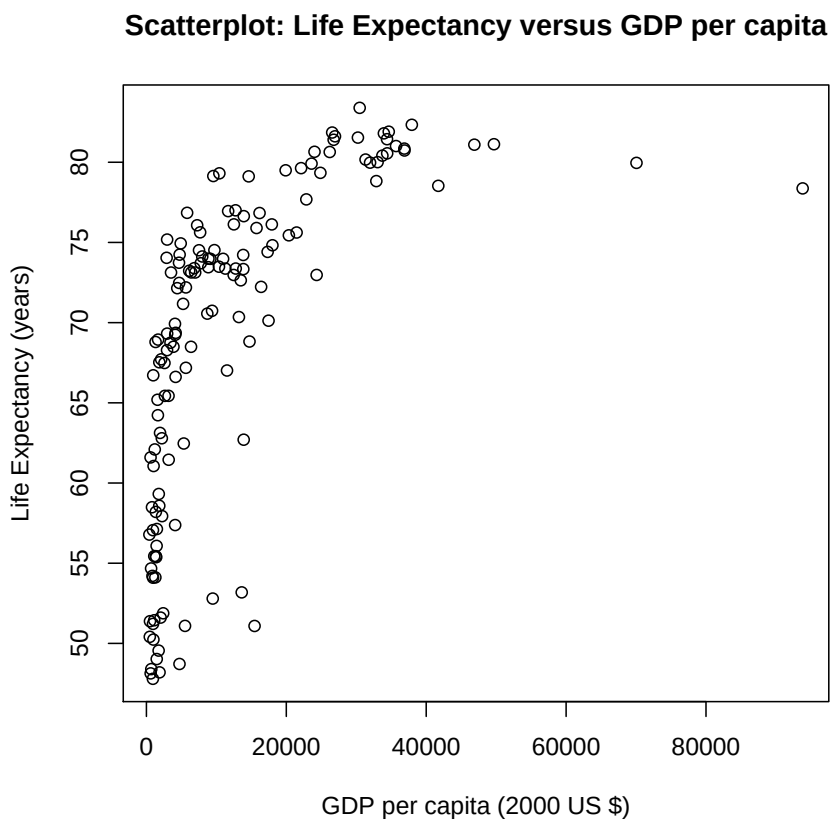


Figure 8: Relationship between two quantitive variables

Figure 8 shows the information visually, when drawn on a plot.

2.4 Sampling

The goal of the statistics is to make rational decision or conclusion based on the incomplete information that we have in our data. This process is knows as *statistical*

inference. The question is that if we see something in our date (like a relationship between two variables) is it due to chance or a real relationship? If it's not due to change then what broder conclusions we can make, like generalize them to a larger group, or does it supports a theoretical model? In this process the data collection has a major significance.

We collect data from the real world, however our scientific and statistical models are part of a theoretical world.

population the group we are interested in making conclusion about.

census a collection of data on the entire population. This would be the best, however it's impractical due to time and cost effectiveness; or it's straight up impossible if by observing the item we would destroy it. Therefore, in practice we sample the population; and infer conclusions from the sample group.

statistic is a value calculated from our observed data. It estimates a feature of the theoretical world.

paramter is a feature of the theoretical world. Statistics are used to estimate their values. In order to get a good estimation our sampling needs to be *representative*.

randomisation is the key to select representative samples. This ensures that we do not over– or under–sample any part of the population.

Methods to make random sampling:

Simple Random Sampling – SRS Each possibly sample size of n (the sample size) from the population is equally likely to be the sample that is choosen. A pratical example of this is taking out balls from a hat.

Stratified sampling Divide the population into non–overlapping subgroups called strata and choose a SRS within each subgroup. Provinces and states are a practical instances of stratas. This performs better when we may want to compare stratas, or can allow to better see traits if something is only characteristic to only some of the stratas (which otherwise would be hidden on the whole sample space).

Cluster sampling Divide the population into non–overlapping subgroups called clusters, select clusters at random, and include all individual inside the cluster for sampling. It's good when it's easier to select groups instead of members; for example if we want to study students we may choose to select random schools and use students inside those as samples. This does requires that each cluster to be representative for the whole population.

There are also non–random sampling techniques:

Systematic sampling Select every k–th individual from a list of the population, where the position of the first person choosen is randomly selected from the first k individuals. This will give a non–represenative sample if there is a structure to the list. This is fine if in the ordering of the population has no meaning.

Conveniance or Voluntar sampling Use the first n individuals that are available or the individuals who offer to participate. This is almost sure to give a non–representative sample which cannot be generalized to the population.

If the sample is not representative it can induce *bias* into our results, that is that it differs from its corresponding population in a systematic way. Bias types are:

Selection bias occurs when the sample is selected in such a way that it systematically excludes or under–represents part of the population. For instance poll by using only land line phones (misses the cellular population).

Measurement or Response bias occurs when the data are collected in such a way that it tend to result in observed values that are different from the actual value in some systematic way. In case of a poll this shows in terms of ill formed questions.

Nonresponse bias occurs when responses are not obtained from all individuals selected for inclusion in a sample. An example of this is in a poll working parents tend to not respond, so their sampling will be under represented.

2.5 Observational studies

Whenever we want to compare the effect of variables on each other we need to construct a study, for which sampling is really importat. Let us assume that we have two (or more) groups, and we want to compare a *response variable* (*outcome*) between them. An *explanatory variable* is a variable that can be used to possibly explain the differences in the response variable between groups (cause $\Rightarrow$ effect).

In the study we want to avoid *confounding variables*, which differ between groupsa and may effect the response variable so we can't tell what causes the differences between groups. For instance if one were to study the effect of pot on the IQ of the person, here a confounding variable is the social alternative (which governs the IQ better, than the pot itself).

Data collection methods include anecdotes (this are not representative), observational studies and experiments. Experiments differ from observational studie is the strength of the conclusion we can make, which is higher for the experiment.

In observational studies we just observe existing characteristics of a subset of individuals inside the population. The goal is to make conclusion about the population based on the samples, or to conclude the relationship between groups or variables in the sample.

In this scenario the investigator has no control on which individual in which group belongs or about any of their characteristic, as opposed to the experiment where he can add some kind of intervention.

The relationship between the outcome and the explanatory variable may be:

causes explanatory variable ⇒ outcome (drinking coffe results in a longer life)

reverse causation outcome ⇒ explanatory variable (people with health issues avoid drinking coffe, though the longer life)

coincidence pure chance

common cause both of them are effected by another variable (who have diabiates drink less coffee, however due to their sickness have shroter life)

confounding variable they vary with the explanatory variable. If one changes the other changes with it (smokers tend to drink more cofee, however this also effects the expected life outcome)

Lurking variables are variables that are not considered in the analysis, but may effect the natuer of relationship between the explenatory variable and the outcome. This may be a confounding variable, or the source of the common response , or another variable that, when considered, changes the nature of the relationship.

2.6 Experiments

Are the golden standard. Allows for making conlusions. Again the response variable (or also know as dependent variable – how it depends from other variables) is the outcome of interest, measured on each subject or entity participating in the study (this may be quantitive or categorical). Explanatory variable (predictor or independent variable) is a variable that we think might help to explain the value of the response variable (can also be quantitive or categorical).

Compared to the observation study now the researcher manipulates the explanatory variables to see the effect of them on the outcome. Tipically a researcher has finite time, and therefore he can study only a finit number of variable values,

and such the explanatory variable tends to be a categorical one, to which we can also refer as a *factor*. The values of the factor studied in the experiment are its *levels*.

A particular combination of values for the factors is called *treatment*. An *experimental unit* is the smallest unit to which the treatment is applied to. A treatment may not be applied to a single entity, like trying out a new study method for a class results in a single experimental unit (a class) instead of the count of the students inside the class.

extraneous factors are not of interest in the current study, but are thought to affect the reponse. They need to be controlled to avoid them effecting the outcome. For controlling we can:

- Hold it constant. This limits the generilization of the study, however it also eliminates turning the extraneous variable into a confounding one.
- Use blocking, where block are groups of experimental units that are similar. All treatments are assigned to experimental units within each block. So for instance in a vaccine testing we create age groups, and each group will have have members getting any one of treatments, however the group as a hole, receives all the vaccines.

However, this still does not solves the problem of extranous or unknown variables. To bypass this we need to use randomisation to assign experimental units to treatment groups.

Once we've eliminated other differences between the treatment groups, if the response variable is different among the groups, the only explanation is the treatment and casual conclusions can be made.

Fundamentals of experimental design:

1. *Control* the identified extraneous variables by blocking or holding them constant.
2. *Randomisation* – is to randomly assign expermintal units to treatment groups.
3. *Replication* – induce it. Not repeat the experiment, but to apply each treatment to more than one experimental unit. This allows to measure variability in the measurement of the response (which in turn also ensures that treatment groups are more comparable by extraneous factors, by having the oppurtunity of these to differ between groups).

Experiments also have a control group. This is used to make comparisions with a treatment of interest and either does not receives a treatment (what if the study itself causes the change to occur) or receives the current standard treatment. It's also refered to as the comparision group.

In conclusion we can say the randomised controlled experiments are needed to establish casual conclusion. Another technique to reduce the potential of bias is *blinding*:

1. the experimental units are blinded, so they do not know which treatment they have received.

2. the researcher is blinded if s/he does not know which treatment was given.

Experimetns can be single–blinded (only one type of blinding was used) or double–blind (if both types of blinding was used). You can also use the *placebo effect*. People often show change when participating in an experiment wheater or not they receive a treatment. It's given to the control group. A placebo is something that is identical to the treatment recevied by the treatment groups, except that it contains no active ingridients.

3 Introduction to Probability

3.1 The need for probability

Up to this point we've seen and focused on how to handle data available to us. Now it's time to see what the data in the real world corresponds in the theoretical world. The data of the real world, that we usually end up having, can be viewed as just a sampling of the theoretical world (which has an infinit number of data points). Even if it really isn't any more data points in the real world (so we have collected all the existing data points) we can still pretend that there is and construct a theoretical model around it.

We usually try to draw inferences about our theoretical world by using the data that we have, which represents the real world. Of course, the theoretical world may differ from the real world and we'll be interested in studying the relationship between two world. For instance let us consider a coin toss. In the theoretical world we *expect* to get 5 heads out of ten tosses, yet if we were to conduct a little experiment we may end up *getting* 6 heads out of ten tosses.

In some cases (like tossing a bottle cap) we may not even have a theoretical model, so the question arises that what we can conclude in this case?

3.2 Probability basics

Outcomes are possible data that our experiment may result in. The set of all possible outcomes is the *sample space* and it's noted as S.

Event is any subset of the sample space.

Probability – each event has it's own probability to turn true, and for event A:

$$0 \leq \mathrm{P}(A) \leq 1$$

For example, the probability of some outcome is 1, as we always end up having some result. The probability of the comploment event (meaning that event A is not true) is:

$$\mathrm{P}(\bar{A}) = 1 - \mathrm{P}(A)$$

The term probability may have multiple interpretations: applies to a theoretical world with a theoreticaal model where the probability for an event to occur is $\mathrm{P}(A)$; or we can look it as a long run, meaning that if we repeat the experiment over and over again for a long time the occurance of event A is $\mathrm{P}(A)$ fraction of all the events; another one is the subjective one: in my opinion the chance that the event to occur is $\mathrm{P}(A)$.

3.3 Probability distributions

For a coin or bear bottle fliping we use the binomial, not ass $\mathrm{B}(2, \frac{1}{2})$ distribution. If the exponential of the binomial is one, we refer to it as te Bernoulli distribution: Bernoulli$(\frac{1}{2})$ =$\mathrm{B}(1, \frac{1}{2})$. The rolling of a dice is a discrete uniform distribution.

Mean is the expected value, what it equales „on average"

$$\text{mean} = \mu = \sum_x x\mathrm{P}(x)$$

For instance in case of a rolling dice with six side:

$$\text{mean} = 1 \cdot \frac{1}{6} + 2 \cdot \frac{1}{6} + 3 \cdot \frac{1}{6} + 4 \cdot \frac{1}{6} + 5 \cdot \frac{1}{6} + 6 \cdot \frac{1}{6} = \frac{7}{2} = 3.5$$

For flipping two coins, with Y being the total number of heads:

$$\text{mean} = E(Y) = 0 \cdot \frac{1}{4} + 1 \cdot \frac{1}{2} + 2 \cdot \frac{1}{4} = 1$$

Variance in the theoretical world measures the spread of the values from their mean value. The formula is:

$$\text{variance} = \sum_x (x - \mu)^2 \cdot \mathrm{P}(x)$$

So for one coing flipping:

$$\text{variance} = \left(1 - \frac{1}{2}\right)^2 + \left(0 - \frac{1}{2}\right)^2 + = \frac{1}{4}$$

The *standard deviation* is:

$$\mathrm{SD} = \sqrt{\text{variance}} = \sqrt{\frac{1}{4}} = \frac{1}{2}$$

The mean is linear, so any linear combination of two random variables may be expressed with their means:

$$\mathrm{E}(aX + bY) = a \cdot \mathrm{E}(X) + b \cdot \mathrm{E}(Y)$$

For variance:

$$\begin{aligned} \mathrm{Var}(aX) &= a^2 \cdot \mathrm{Var}(X) \\ \mathrm{Var}(aX + b) &= a^2 \cdot \mathrm{Var}(X) \\ \mathrm{SD}(aX) &= |a| \cdot \mathrm{SD}(X) \end{aligned}$$

If X and Y are independent:

$$\mathrm{Var}(X+Y) = \mathrm{Var}(X) + \mathrm{Var}(Y)$$

Discrete random variables has a finit number of possible outcomes, and thus may be enumerated in a form of a list. Continous random varaibles can take any value inside an interval. An instance of this is the unifrom variable, for instance on the interval from zero to one, meaning it's equally likeley to be any number inside this interval.

So for example $\mathrm{P}(0 \leq X \leq 1) = 1$, and $\mathrm{P}(0 \leq X \leq \frac{1}{3}) = \frac{1}{3}$; generally speaking $\mathrm{P}(a \leq X \leq b) = b - a$, if $0 \leq a \leq b \leq 1$. This does mean that if $a = b$ the probability is zero, so it's easier to think of continous probability as the area under the graph of the density function. It's important that for any density function the total area of the entire graph to be equal with 1.

Uniform distributions are of a form of square function, however other functions exist to like the exponential(1) function has the form of:

$$f(x) = \begin{cases} e^{-x} & \text{if } x > 0 \\ 0 & \text{if } x \leq 0 \end{cases}$$

The standard normal (Gaussian) distribution (bell–curve):

$$f(x) = \frac{1}{\sqrt{2\pi}} \cdot e^{-\frac{x^2}{2}}$$

New bell–curves may be constructed by shifting the upper with μ (making it the new center point) and stretching it by a factor of σ, and is noted as Normal(μ, σ^2). If we have a random variable X from this newly constructed normal distribution we may transform it into a standard normal distribution by:

$$Z = \frac{X - \mu}{\sigma}, \quad \text{where } Z \sim \mathrm{Normal}(0, 1).$$

For expected values and standard deviation now we use integals instead of sums, for example the expected value of the uniform distribution between 0 and 1 is:

$$\mathrm{E}(X) = \int_0^1 x \mathrm{d}x = \frac{1}{2}$$

with it's variance:

$$\mathrm{Var}(X) = \int_0^1 \left(x - \frac{1}{2}\right)^2 \mathrm{d}x = \frac{1}{12}$$

For the exponential distribution it's expected value is:

$$\mathrm{E}(X) = \int_0^\infty x \cdot e^{-x} \mathrm{d}x = 1$$

with it's variance:

$$\mathrm{Var}(X) = \int_0^\infty (x-1)^2 \cdot e^{-x} \mathrm{d}x = 1$$

For the $X \sim$ Normal $(0, 1)$:

$$\mathrm{E}(X) = \int_{-\infty}^\infty x \cdot \frac{1}{\sqrt{2\pi}} \cdot e^{-\frac{x^2}{2}} \mathrm{d}x = 0$$

$$\mathrm{Var}(X) = \int_{-\infty}^\infty (x-0)^2 \cdot \frac{1}{\sqrt{2\pi}} \cdot e^{-\frac{x^2}{2}} \mathrm{d}x = 1$$

And in case of $Y \sim$ Normal (μ, σ^2) the mean is μ, variance of σ^2 and standard deviation of σ.

3.4 Long running averages

What happens if you repeat an experiment lots of times and you look at the average value you get. For example if you start flipping a coin a lot of times and you look at the fraction of times you get head, you expect that the more you do it, the more this comes closer to half. If you were to draw the probabilities of the coin flip on a graph, you'd observe that the shape starts to resemble the density function for the normal distribution. The same is the case for dice rolling at looking the average of the rolled numbers.

The Law of Large Numbers states that if an experiment is repeated over and over, then the average result will converge to the experiment's expected value.

The Central Limit Theorem states that if an experiment is repeated over and over, then the probabilities for the average result will converge to a Normal–distribution.

Suppose that an experiment is repeated over and over, with outcomes: $X_1, X_2, \ldots$ and suppose each mean is $\mathrm{E}(X_i) = m$, and each variance is is $\mathrm{Var}(X_i) = v$. Now let $\bar{X} = \frac{X_1 + X_2 + \ldots + X_n}{n}$ be the average outcome. In this case we can say that:

$$\mathrm{E}(\bar{X}) = \frac{\mathrm{E}(X_1) + \mathrm{E}(X_2) + \ldots + \mathrm{E}(X_n)}{n} = \frac{nm}{n} = m,$$

$$\mathrm{Var}(\bar{X}) = \frac{\mathrm{Var}(X_1) + \mathrm{Var}(X_2) + \ldots + \mathrm{Var}(X_n)}{n} = \frac{nv}{n^2} = \frac{v}{n},$$

so we can conclude as n rises to infinity the variance (uncerteinty) becomes smaller and smaller, tending to zero; with this the standard deviation too.

The centreal limit theorem also is responsible for the emparical rule; the percentages are true for the graph of the normal distribution. In conclusion we can say that all that is some kind of average, or is made up of lots and lots of small contributions usually has a normal distribution behind it.

3.5 Sampling distribution

From the real world we collect samples, which can be considered as part of the theoretical worlds population. We have scientific and statistical models in the theoretical world which have parameters of features that we do not know. We use the science of statistics to estimate them.

Let there be p our parameter of interest, what we are observing, and let it denote the number of heads of a coin flip sequence. From the real world (data) we get some result. With this we can esitmate the parameter as:

$$\hat{p} = \frac{\text{numbers of heads observed}}{\text{number of coin flips}}$$

.

The observed value of an estimator varies from sample of data to sample of data. The variability of this is called the *sampling variability*. The probability distributions of the possible value of an estimator is its sampling distribution.

A statistic used to estimate a paramters is *unbiased* if the expected value of its sampling distribution is equal to the value of the parameter being estimated (the sampling probability is the same as the theoretical probability). How close the distribution of the sampling gets to the parameter dependes on the varince of the sampling distribution. This decreases with the number of samples, so the more data we have the closer we get to the theoretical word.

Following the central limit theorem for large n the sampling distribution for a Bernoulli event (happens or not, with probability p) is $\mathrm{N}\left(p, \frac{p(1-p)}{n}\right)$ (sampling distribution of $\hat{p}$).

If we take a normal distribution as a sample distribution with a normal distribution theoretical model we can calculate the expected value of the theoretical model as the average of the sample we have, and the standard deviation of the theoretical model decreases with the number of data compared to the standard deviation of the sampling distribution ($\frac{\sigma}{\sqrt{n}}$). The sampling distribution of $\bar{X}$ is $\mathrm{N}\left(\mu, \frac{\sigma^2}{n}\right)$.

For calculating the variance dividing with $n-1$ is important to make the estimator unbiased, while dividing with n will result in a bias estimator.

4 Confidence interval

We observe the real world in order to understand the theoretical world; for this we'll use the scientific and statistical models divised in the theoretical world and use data from from the real world to estimate the paramters from the model. We do this in hope that what conclusions we can make from our models will also hold in the real world.

Now let us imagine the experiment of tossing a fair coin ten times. This experiment has a binomial distribution with probability $\frac{1}{2}$, however when amassing data from the real world we will not always get this proportion, due to the sampling having its own distribution: for example extreme events (like getting ten heads) are very unlikely, however getting half or close to half of them heads is likely to happen. The question arrises where do we draw the line, what are the values well likely to get most of the time?

Sometimes we will not have a model for our events: like in the case of flipping a beer cap. If we were to perform a single experiment and get m one side out of n events we can ask: was this a likely outcome? m may be a sample of any sample distribution (with its own parameters). For instance for the beer cap let $n = 1000$ and $m = 576$. Our statistical model is binomial with a 1000 samples, however we have no idea what's the probability of the model.

An estimation is $\hat{p} = \frac{n}{m} = \frac{576}{1000} = 0.576$. This may be a good estimate, however it may be some other number, and so we ask what also could p be? That is what is an interval that based on our existing experiments the probability of getting one side of the beer cap could be? We refer to this as the *confidence interval*.

The following methods are suppose that our data was taken in a form of simple random sampling, and that our variables are independent; something that statistical inference requires, otherwise we may need more complicated model.

So in conclusionwe can say that the goal of statistical inference is to draw conclusions about a population parameter based on the data in a sample (and statistics calculated from the data). A goal of statistical inference is to identify a range of plausible values for a population parameter. A goal of statistical inference is to identify a range of plausible values for a population parameter. Inferential procedures can be used on data that are collected from a random sample from a population.

4.1 Confidence intervals with proportions

Let us follow the example of the bottle cap. We are searching for the real p with the given estiamte $\hat{p}$. The expected value of $\hat{p}$ is $\mathrm{E}(\hat{p}) = p$ the variance is $\mathrm{Var}(\hat{p}) = \frac{p(1-p)}{n} = \frac{p(1-p)}{1000}$. Now according to the center limit theorem because p is

the addition of lots and lots of small flips, it approximately follows the normal distribution; that is $\hat{p} \approx \text{Normal}\left(p, \frac{p(1-p)}{1000}\right)$. Now by performing a reorganization:

$$\frac{\hat{p} - p}{\sqrt{p \cdot \frac{1-p}{n}}} \approx \text{Normal}(0, 1)$$

Now for a normal distribution (and according to the empirical rule) the area between $[-1.96, 1.96]$ covers 95% of the area, so most likely our sample is from this interval. In mathematical formula:

$$\text{P}\left(\left|\frac{\hat{p} - p}{\sqrt{p \cdot \frac{1-p}{n}}}\right| > 1.96\right) = 0.05 = 5\%$$

By writing up the reverse, and expanding we can conclude that, with $z_{\frac{\alpha}{2}} = 1.96$:

$$\text{P}\left(\underbrace{\hat{p} - \overbrace{z_{\frac{\alpha}{2}}\sqrt{p \cdot \frac{1-p}{n}}}^{\text{margin of error}}}_{\text{lower limit}} \leq p \leq \underbrace{\hat{p} + z_{\frac{\alpha}{2}}\sqrt{p \cdot \frac{1-p}{n}}}_{\text{upper limit}}\right) = 95\%$$

This means that we are 95% confident that the value of p is between is lower and upper limit. Now the true value of p is not random, however $\hat{p}$ is as we took a random sample. Now the problem with this formula is that while we do know $\hat{p}$, p is unknown. One solution is to make $\hat{p} = p$; or to make $p = \frac{1}{2}$ because that's the worst case, the widest interval we can get.

For a given confidence interval $[a, b]$ the margin of error may be calculated as:

$$\begin{aligned} a &= \hat{p} - \text{margin of error} \\ b &= \hat{p} - \text{margin of error} \\ \text{margin of error} &= \frac{b - a}{2} \end{aligned}$$

Now modifying the area under the normal distribution that we take we can get different confidence intervals for different probabilities. Now if you specify a bigger confidence value, like 99% you'll get a widder confidence interval. It's up to you the trade off you are willing to accept.

Now assume you want to achive an α probability that you're wrong. In this instance taken the graph of the normal distribution you want to find $z_{\frac{\alpha}{2}}$ (y axis) such that the area remaining at each and is only $\frac{\alpha}{2}$. In this case the area between

intervals $-z_{\frac{\alpha}{2}}$ to $z_{\frac{\alpha}{2}}$ is $1-\alpha$, which we are looking over, as now we're missing α of the full area.

4.2 Sample size for estimating a proportion

Now in order to get a proportion the size of the sample has a major impact. Let's see how we can determinate the sample size we need to find a given proportion. We do not want to go overboard with this as we may just waste resources or induce unrequired effort to collect it. We assume that data was collected with simple random sampling from a population.

So a margin of error is:

$$\text{margin of error} = z_{\frac{\alpha}{2}}\sqrt{p \cdot \frac{1-p}{n}}$$

For isntance, if our confidence interval is 95%, then $\frac{\alpha}{2} = \frac{1-0.95}{2} = 0.025$, and we want a margin of error of $\beta = 0.03$. The question is what n should be? For 95% our normal quantile is 1.96. So:

$$0.03 = 1.96\sqrt{p \cdot \frac{1-p}{n}}$$

But we do not know what p will be. To bypass this we plan for the worst case scenario, the expression $p \cdot (1-p)$ has its maximum at $p = \frac{1}{2}$, which also give our maximal margin of error for a given n. Now we resolve the equation:

$$n = \left(\frac{1.96 \cdot \frac{1}{2}}{0.03}\right)^2 = 1067$$

Confidence intervals are about our confidence in the procedure to give us correct results – 95% confidence intervals should contain the population parameter $p95\%$ of the time. If simple random samples are repeatedly taken from the population, due to the randomness of the sampling process the observed proportion of $\hat{p}$ will change from sample to sample and so will the confidence interval constructed around $\hat{p}$. Of these confidence intervals, 95% will include the true population proportion p.

Note that p is a population parameter and is therefore not a random variable. For any interval, p is either contained in the interval or not. Different margin of error will result in different number of events required, however the sample size increases quadratically as the margin of error decreases linearly.

4.3 Confidence intervals for means

In this case the data is not a categorical one, is instead a continous variable. In this case the expected value is $\mu = \bar{X}$, and this is also our estimation. The variance is equal to $\frac{\sigma^2}{n}$. Again if the data is made up of the sum of bunch of small measurements, we can assume according to the center limit theorem that $\bar{X} \approx \text{Normal}\left(\mu, \frac{\sigma^2}{n}\right)$. Again we reduce this to the standard normal distribution to get:

$$\frac{\bar{X} - \mu}{\sqrt{\frac{\sigma^2}{n}}} \approx \text{Normal}\,(0, 1)$$

Now the problem now is that we do not know the value of σ. What would be a good estimation for this? One solution is to use the standard deviation of X (calculated with dividing with $n - 1$), noted as s. However, while $\text{E}(s^2) = \sigma^2$, substituting this into upper formula does not gives a normal distribution; instead we'll have a t distribution with $n - 1$ degrees of freedom:

$$\frac{\bar{X} - \mu}{\sqrt{\frac{s^2}{n}}} \approx t_{n-1}$$

The t distribution is similar to the normal one, however not quite there. Increasing the degree of freedom reduces the difference between these two. With this the $z_{\frac{\alpha}{2}}$ changes also, so you'll need to use a table to get the correct number for a given number of freedom (which is $n-1$, where n is the sample size). The marginal error may be calculated as:

$$\text{marginal error} = z_{\frac{\alpha}{2}} \cdot \sqrt{\frac{s^2}{n}}$$

We can use this to calculate the true mean from a sample mean. That is with a given confidence we can say that our true mean is somewhere inside the calculated confidence interval, which depends from the sample mean with the calculated marginal error.

4.4 Robustness for confidence intervals

To use these methods many conditions must be satisfied, and an important part of the statistical inference is to determine if these hold. Here are what we need to make sure that they are true:

1. the n observations are independent,

2. n needs to be large enough, so that the central limit theorem may kick in and $\hat{p}$ to have a normal distribution,

For extreme theoretical p values larger counts of samples are required to achieve the same confidence interval. For instance in case of a coin flip if p is $\frac{1}{2}$ a hundred samples may be enough for the central limit theorem to kick in and achive a 95% confidence. However, if $p = 0.01$ we may need 1000 samples for the same confidence. An explanation for this is that the normal distribution is a continous model, and we are using it to estimate discrete values.

In order for the confidence interval procedure for the true proportion to provide reliable results, the total number of subjects surveyed should be large. If the true population proportion is close to 0.5 a sample of 100 may be adequate. However, if the true population proportion is closer to 0 or 1 a larger sample is required.

Increasing the sample size will not eliminate non-response bias. In the presence of non-response bias, the confidence interval may not cover the true population parameter at the specified level of confidence, regardless of the sample size. An assumption for the construction of confidence intervals is that respondents are selected independently.

In case of means the conditions are:

1. the n observations are independent

2. n needs to be large enough so that $\bar{X}$ is approximatly normally distributed.

The t distribution works extremly well with even a low number of samples ($n = 10$) if the theoretical model is a normal or skewed normal one. For this to not be true we need some really extreme distribution, like most of the time on one end, but has some chance for an outlier value. However, in these cases by just increasing the mean with a constant multiplier (like to 40) may already result in a 90% confidence value.

Nevertheless, we also need to consider if estimating the mean is a meaningful thing to do. Remeber that the mean is not a robust measurement, because it's effected by outliers, something that is true for the distribution too.

A method for constructing a confidence interval is robust if the resulting confidence intervals include the theoretical paramter approximately the percentage of time claimed by the confidence level, even if the necessary condition for the confidence interval isn't satisfied.