6 I COMMON STATISTICAL TEST

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Script for importing data from the following spreadsheet:

```
Workbook: /Users/juanheinklopper/Documents/MATLAB/MATLAB for Data Science/Data/heart.xlsx
Worksheet: heart
```

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Set up the Import Options and import the data

```
clear global
clearvars
opts = spreadsheetImportOptions("NumVariables", 12);

% Specify sheet and range
opts.Sheet = "heart";
opts.DataRange = "A2:L919";

% Specify column names and types
opts.VariableNames = ["Age", "Sex", "ChestPainType", "RestingBP",
"Cholesterol", "FastingBS", "RestingECG", "MaxHR", "ExerciseAngina",
"Oldpeak", "ST_Slope", "HeartDisease"];
opts.VariableTypes = ["double", "categorical", "categorical", "double",
"double", "double", "categorical", "double", "categorical", "double",
"categorical", "categorical"];

% Specify variable properties
opts = setvaropts(opts, ["Sex", "ChestPainType", "RestingECG",
"ExerciseAngina", "ST_Slope", "HeartDisease"], "EmptyFieldRule", "auto");

% Import the data
```

```
heart = readtable("/Users/juanheinklopper/Documents/MATLAB/MATLAB for Data
Science/Data/heart.xlsx", opts, "UseExcel", false);
clear opts
```

Introduction

In this final chapter we explore commonly used statistical tests and models. As in the previous chapter we start by importing the `heart.csv` spreadsheet file using the built-in app for data import.

We start with tests applicable to continuous numerical variables such as comparing two means.

Common statistical tests for numerical variables

Comparing the mean of a numerical variable grouped by the classes of a binary variable

Any data analysis starts with exploratory data analysis (EDA) in the form of summary statistics and data visualization. We use the `groupsummary` function to calculate summary statistics of the Age variable grouped by the two classes of the Sex variable.

```
% Compute group summary of Age observations grouped by classes of Sex
% variable
age_by_sex = groupsummary(heart,"Sex",["mean","median","mode","max","min",
...
    "range","std","var","nummissing"],"Age")
```

```
age_by_sex = 2×11 table
```

	Sex	GroupCount	mean_Age	median_Age	mode_Age	max_Age	min_Age
1	F	193	52.4922	53	54	76	30
2	M	725	53.7821	55	54	77	28

There is a small difference in the mean age of the two classes. Below we create column vectors separately for the ages of the two classes and assign the vectors to the variables `age_female` and `age_male`.

```
% Create an array of Age values for female subjects named "age_female"
age_female = table2array(heart(heart.Sex == "F", "Age"));
% Create an array of Age values for male subjects named "age_male"
age_male = table2array(heart(heart.Sex == "M", "Age"));
```

The difference between mean age for each group is calculated using simple subtraction.

```
% Calculate difference in means
mean(age_female) - mean(age_male)
```

```
ans = -1.2898
```

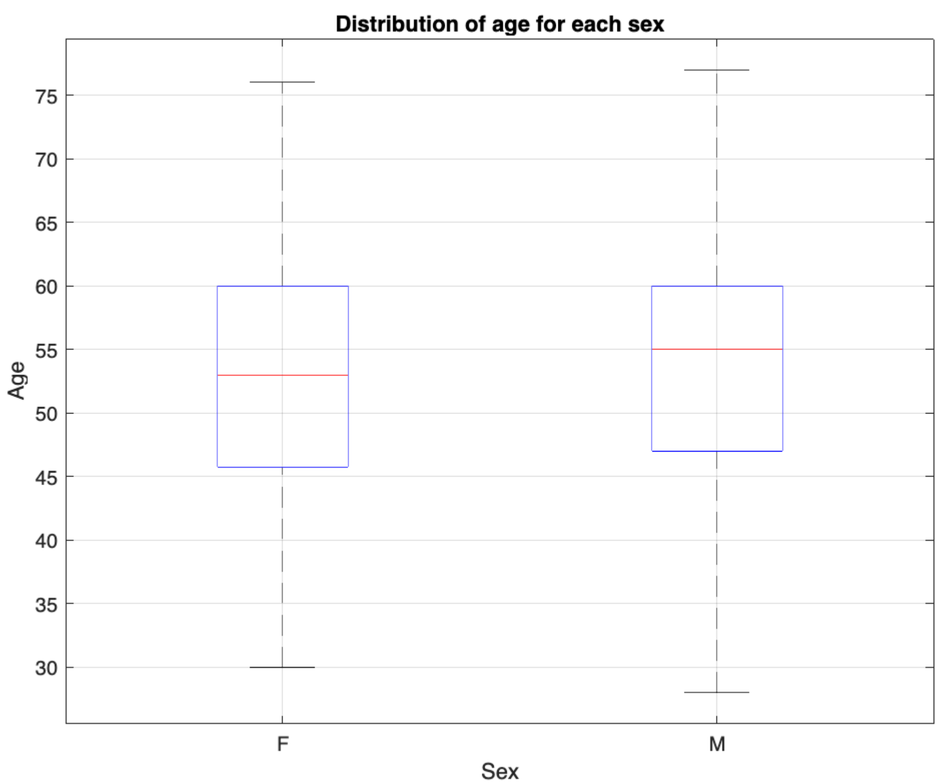
To compare the two age vectors we can use a t test. There are two two-sample t tests. The equal and the unequal variance t tests. While there are statistical tests to determine equal variance, we use a simple variance fraction here. We divided the two variances. It does not matter which group is in the numerator and which is in the denominator.

```
% Variance ratio
var(age_female) / var(age_male)
```

```
ans = 1.0256
```

If the fraction is on the interval $\left[\frac{1}{2}, 2\right]$, we consider an equal variance t test. Otherwise we use an unequal variance t tests. In this case, we use the former. Before doing so, though, we complete the EDA and create a box-and-whisker plot of the age distribution of each of the classes of the Sex variable.

```
% Create a box plot of the Age variable for each of the classes in the Sex
% variable
boxplot(heart.Age, heart.Sex)
grid on
title("Distribution of age for each sex")
xlabel("Sex")
ylabel("Age")
hold off
```



From the summary statistics and the data visualization, it seems that there will not ne a difference between the mean ages. Below, we perform an equal variance t test. The null hypothesis is that there is no difference between the mean ages in the population. We might write $H_0 : \mu_{\text{female}} - \mu_{\text{male}} = 0$. The two-tailed alternative hypothesis states that there is a difference and we might write $H_0 : \mu_{\text{female}} - \mu_{\text{male}} \neq 0$.

```
% Two-tailed equal variance t test at 5% level of significance (use
% 'Vartype','unequal' for unequal variance t-test)
[h, p, ci, stats] = ttest2(age_female,age_male, "Alpha", 0.05, "Tail",
"both")
```

```
h = 0
p = 0.0914
ci = 2×1
   -2.7878
    0.2081
stats = struct with fields:
    tstat: -1.6899
       df: 916
       sd: 9.4231
```

We see the result h=0 and this means that we fail to reject the null hypothesis and we must state that there is not enough evidence at the 5% level of significance to show that there is a difference in the mean age of women and men. We see a *p* value that is more than a chosen level of significance of $\alpha = 0.05$. The confidence interval for the difference in means contains the value 0 under the null hypothesis. All of these values indicate that we fail to reject the null hypothesis.

The results can be visualized for a better understanding, especially if we include out test statistic value T and the critical T value.. Under the null hypothesis or test statistic T is described by the t distribution given the degrees of freedom, which we write as $T \sim t(\nu)$ under H_0. We can calculate the latter for the t test using the `df` attribute of our `stats` variable. Below, we assign this to the variable `nu`.

```
% Calculate the degrees of freedom
nu = stats.df
```

```
nu = 916
```

The results shows that $\nu = 916$. Next, we create a vector of values to populate the x axis in our probability density plot. We create 300 values on the interval $[-5, 5]$ and assign it to the variable k.

```
% Create a vector of values to populate the x-axis
k = linspace(-5,5,300);
```

Now we use the vector of values in the variable k to calculate y axis values representing the probability density function (PDF) of the t distribution given ν. For this we use the `tpdf` function. The PDF value are assigned to the variable `tdistpdf`.

```
% Calculate values for the PDF
tdistpdf = tpdf(k,nu);
```

The T statistic for our test can be returned using the `tstat` attribute of our `stats` variable. We assign this to the variable `tval`.

```
% Return the test statistic and assign it to the variable tval
tval = stats.tstat
```

```
tval = -1.6899
```

The `tpdf` function can be used to calculate the value of the T statistic for the given degrees of freedom. This is assigned to the variable `tvalpdf`.

```
% Calculate the PDF for the given test statistic
tvalpdf = tpdf(tval,nu);
```

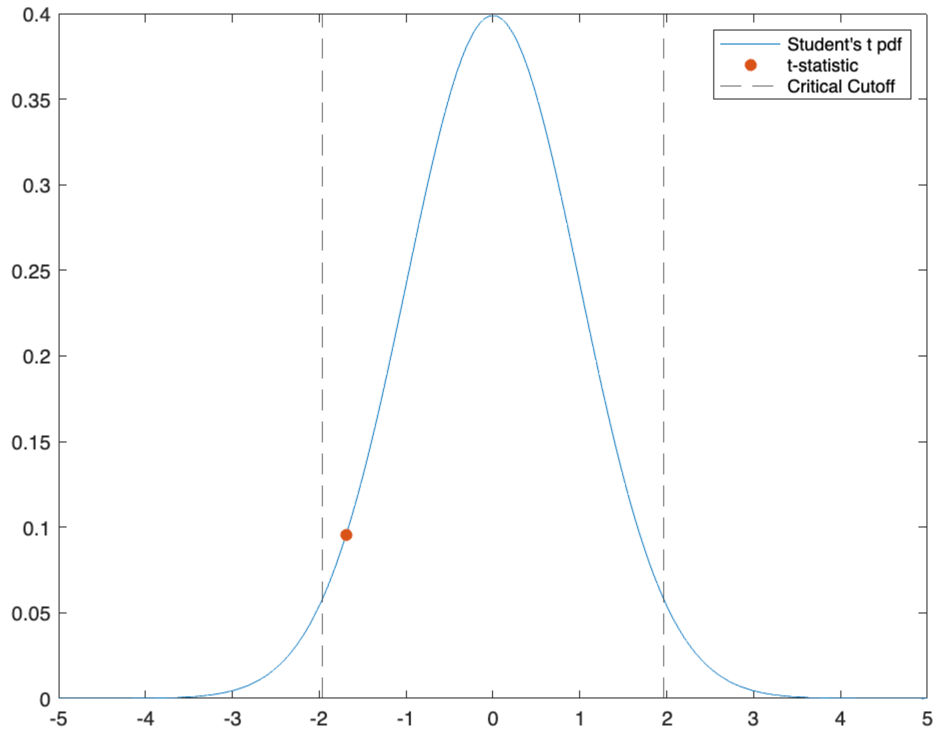
The (upper tail) critical value is calculated using the `tinv` function. The first argument is $1 - \frac{\alpha}{2}$ and the second is the degrees of freedom.

```
% Calculate the upper tail critical value
tcrit = tinv(0.975,nu)
```

```
tcrit = 1.9626
```

We can now plot the PDF of the t distribution under 916 degrees of freedom. We draw vertical dashed lines at the critical values and note that the T statistic is not in the upper or lower tails of rejection.

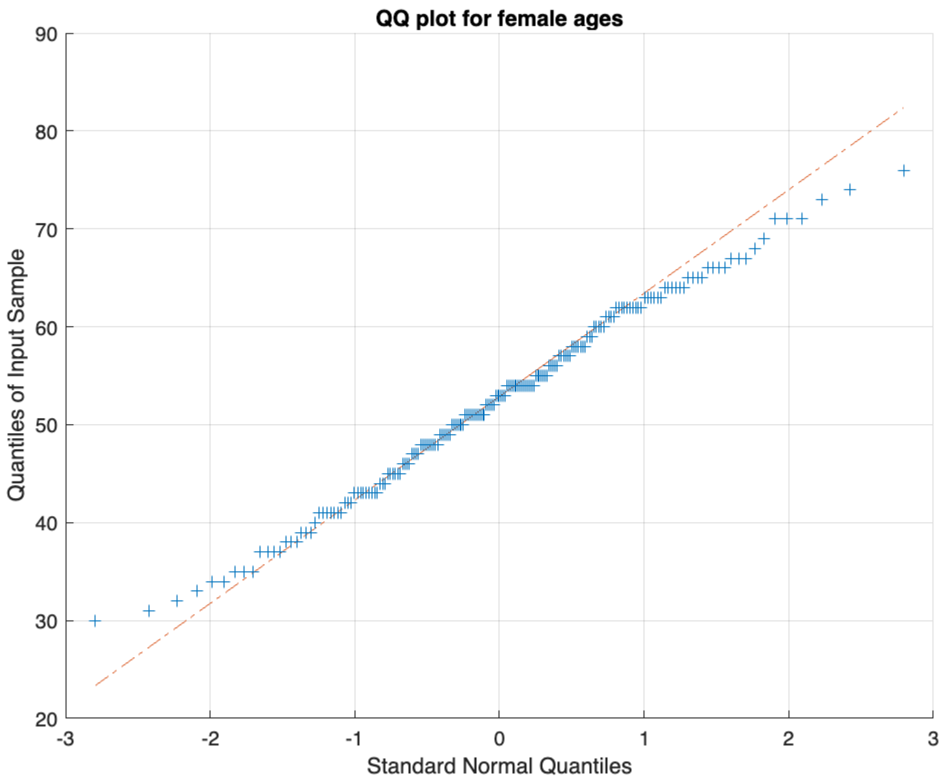
```
% Plot the PDF, the T statistic and the critical values
plot(k,tdistpdf)
hold on
scatter(tval,tvalpdf,"filled")
xline(tcrit,"--")
xline(-tcrit,"--")
legend(["Student's t pdf","t-statistic", ...
    "Critical Cutoff"])
hold off
```



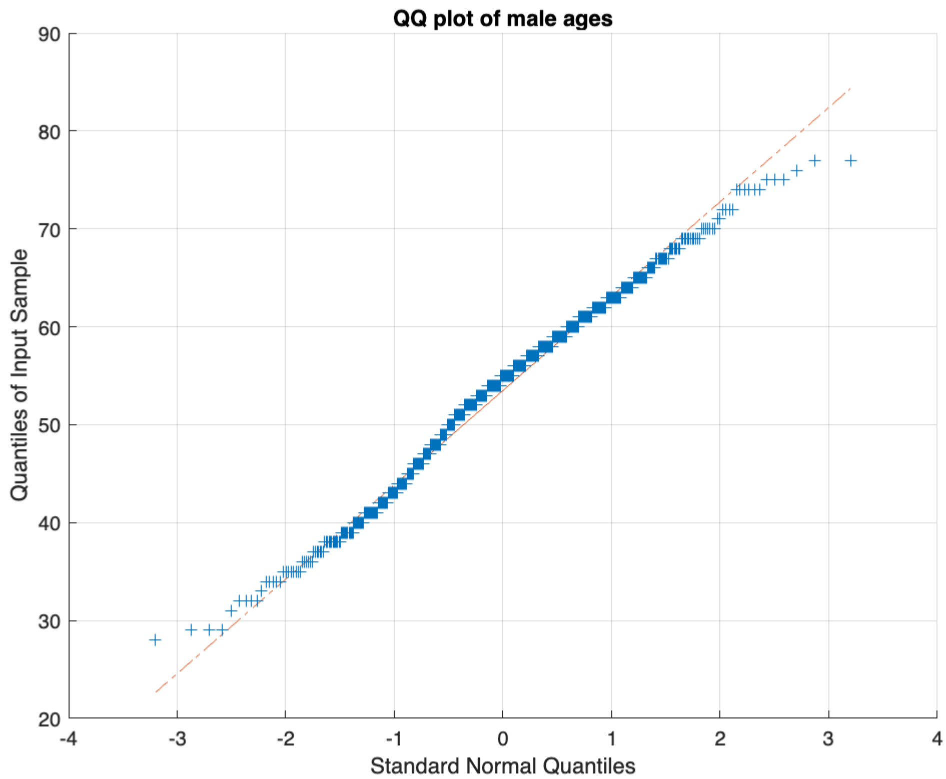
Performing the t test we assumed that the random variables were independent and identically distributed. In other words, we assumed that all subjects were independent of each other and assumed that the ages of both classes were from a population in which these values are normally distributed. Since we had at least 30 samples in each group, these assumptions were not all critical and we could still invoke the Central Limit Theorem and use the probability density function of t distribution to determine the distribution of T statistic values under the null hypothesis and specific degrees of freedom.

There are statistical tests and data visualization that can be used to determine the assumption of normality. These include the Shapiro-Wilk tests and quantile-quantile plots or QQ plots. The latter plots the standard normal quantiles on the x axis and the quantiles of the observations on the y axis of a scatter plot. A line of normality is added. If the markers of the scatter plot fall roughly on this line, we assume that the values are from a population in which the variable is normally distributed. Below, we create QQ plots for both groups.

```
% Show QQ plots for female samples
qqplot(age_female)
grid on
title('QQ plot for female ages')
hold off
```




```
% QQQ plot of male ages
qqplot(age_male)
grid on
title('QQ plot of male ages')
hold off
```



In both cases it seems that we can assume normality. We should also verify that there are no significant statistical outliers. the box-and-whisker plot showed no suspected outliers. We could also use a rule of thumb such as looking for values that are more than 3 standard deviations from the mean.

If the assumptions for the use of a parametric tests (such as the t tests) are not met, we use a non-parametric tests such as the Mann-Whitney-U test. Under the null hypothesis of this test the medians are equal and under the alternative hypothesis, they are not. The `ranksum` test is used for the test.

```
% Compute Mann-Whitney-U test
[p, h, stats] = ranksum(age_female, age_male)
```

```
p = 0.0695
h = logical
   0
stats = struct with fields:
       zval: -1.8149
    ranksum: 82745
```

We find a similar result here and fail to reject the null hypothesis.

Comparing the mean of a numerical variable grouped by the classes of a multi-level variable

We consider summary statistics and data visualization of the Age variable for each of the classes of the `ChestPainType` variable.

```
% Compute group summary
```

```
newTable = groupsummary(heart,"ChestPainType",["mean","median","max","min", ...
    "range","std","var"],"Age")
```

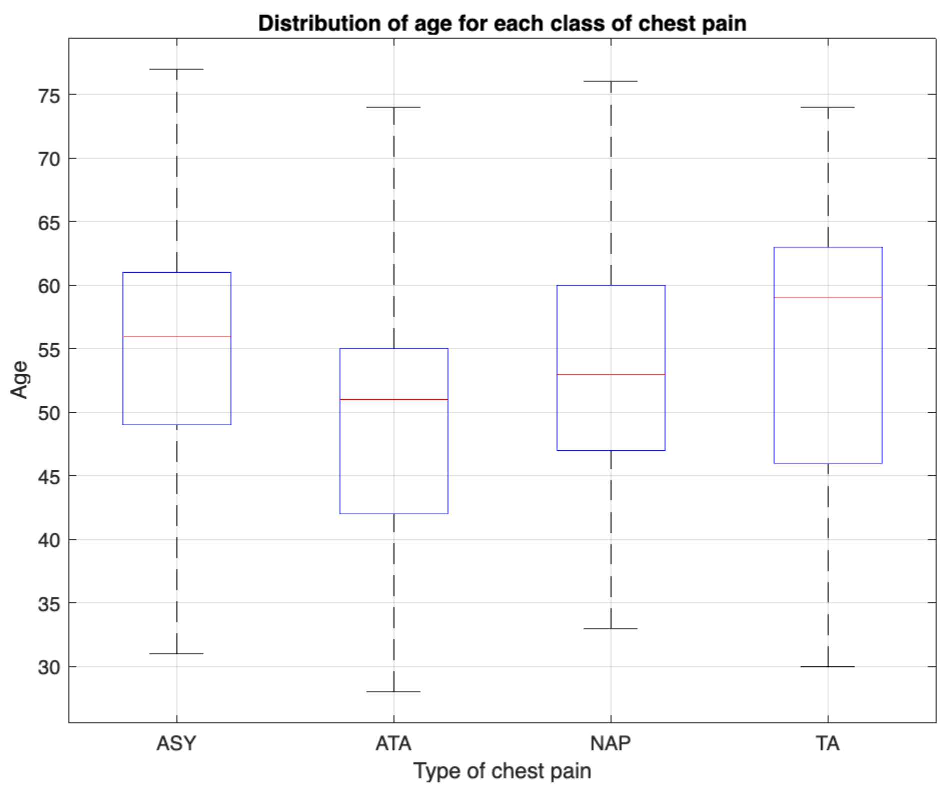
newTable = 4×9 table

...

	ChestPainType	GroupCount	mean_Age	median_Age	max_Age	min_Age
1	ASY	496	54.9597	56	77	31
2	ATA	173	49.2428	51	74	28
3	NAP	203	53.3103	53	76	33
4	TA	46	54.8261	59	74	30

As part of our EDA we also create a box-and-whisker plot.

```
% Create a box plot of the Age variable for each of the classes in the
% ChestPainType variable
boxplot(heart.Age,heart.ChestPainType)
grid on
title("Distribution of age for each class of chest pain")
xlabel("Type of chest pain")
ylabel("Age")
```



Under the null hypothesis all population mean ages are equal. Under the alternative hypothesis, not all mean age are equal. To test this hypothesis, we can select a base class of the `ChestPainType` variable after constructing dummy variables for the variable. A linear model compares the ages for each group. We use the

TASK button on the LIVE EDITOR tab and create a pivot table to see the classes of the `ChestPainType` variable and their frequencies.

```
% Create pivoted table
pivotedData = pivot(heart, Rows="ChestPainType",
RowLabelPlacement="rownames")
```

pivotedData = 4×1 table

	count
1 ASY	496
2 ATA	173
3 NAP	203
4 TA	46

We now need to create a design matrix for the predictor variables and a vector for the response variable.

```
% Create a vector of the ChestPainType column and assign it to the variable
chestPainType
chestPainType = heart.ChestPainType
```

```
chestPainType = 918×1 categorical
ATA
NAP
ATA
ASY
NAP
NAP
ATA
ATA
ASY
ATA
      ⋮
```

```
% Create dummy variables for a design matrix
dummyChestPainType = dummyvar(chestPainType)
```

```
dummyChestPainType = 918×4
     0     1     0     0
     0     0     1     0
     0     1     0     0
     1     0     0     0
     0     0     1     0
     0     0     1     0
     0     1     0     0
     0     1     0     0
     1     0     0     0
     0     1     0     0
     ⋮
```

Take very careful note of the order of the dummy variables from the pivot table code above. The order can be rearranged as required, for instance setting the second column as the first would be `dummyChestPainType(:, [2 1 3 4])`. The base category must be the first column. The first column (the base class) is removed. The result is the final design matrix such that we have the linearity $\widehat{\beta}_0 + \widehat{\beta}_1 x_1 + \widehat{\beta}_2 x_2 + \widehat{\beta}_3 x_3$ Where x_1 is the ATA class, x_2 is the NAP class, and x_3 is the TA class.

```
% Remove the first column
dummyChestPainType = dummyChestPainType(:, [2 3 4])
```

```
dummyChestPainType = 918×3
     1     0     0
     0     1     0
     1     0     0
     0     0     0
     0     1     0
     0     1     0
     1     0     0
     1     0     0
     0     0     0
     1     0     0
     :
```

Now we extract a response vector, in this case the `Age` variable.

```
% Extract the Age column as a response vector assigned to the variable age
age = heart.Age
```

```
age = 918×1
    40
    49
    37
    48
    54
    39
    45
    54
    37
    48
     :
```

Now we can create a linear model using the `fitlm` function and assign the model to the variable `model`.

```
% Create a linear model assigned to the variable model
model = fitlm(dummyChestPainType, age)
```

```
model = 
Linear regression model:
    y ~ 1 + x1 + x2 + x3

Estimated Coefficients:
                   Estimate      SE        tStat        pValue  
                   ________    _______    ________    __________

    (Intercept)       54.96    0.41295      133.09             0
    x1              -5.7169    0.81207     -7.0399    3.7758e-12
    x2              -1.6493    0.76629     -2.1524       0.03163
    x3             -0.13359     1.4175   -0.094244       0.92494
```

```
Number of observations: 918, Error degrees of freedom: 914
Root Mean Squared Error: 9.2
R-squared: 0.0525,  Adjusted R-Squared: 0.0494
F-statistic vs. constant model: 16.9, p-value = 1.14e-10
```

Note that the intercept estimate is 54.96. This is the mean age of the ASY chest pain type class. The $x1$ estimate is -5.7169 and if we calculate $54.96 - 5.7169$ we get the mean of the ATA class age. The intercept estimate plus any specific other estimate is the mean for the age of that class. This shows that the linear model is a comparison of the four mean ages.

We see a large F statistic value of 16.9 with a *p* value of less than 0.01. We reject the null hypothesis and state that there is enough evidence at the 5% level of significance to show that there is a difference in the mean age between the four groups of chest pain type. We can also use the `anova` function to see the results of analysis of variance for these results.

```
% Calculate ANOVA results
anova(model,'summary')
```

ans = 3×5 table

	SumSq	DF	MeanSq	F	pValue
1 Total	8.1589e+04	917	88.9743	NaN	NaN
2 Model	4.2803e+03	3	1.4268e+03	16.8683	1.1368e-10
3 Residual	7.7309e+04	914	84.5832	NaN	NaN

From the ANOVA table we see the same F statistic and *p* value. Note that the mean squared error due to the regression 1426.8 and the mean squared error due to the residual is 84.5832. We need to perform *post hoc* analysis to examine the pairwise differences in means. We have $k = 4$ groups and can for ${}_kC_2 = 6$ pairwise tests. There are many *post hoc* tests. Here we use the pairwise t statistic and the Bonferroni adjusted *p* value. The latter divided the originally chosen α by the number of pairwise comparison so as not to compound the type I error. The adjusted *p* value is calculated below.

```
% Bonferroni alpha value
0.05/6
```

ans = 0.0083

We create a function to calculate the t statistic.

```
% Pairwise t statistic
function t = pairwise_t(x1, x2, n1, n2, sse)
    t = (x1 - x2) / (sqrt((sse) * ((1/n1) + (1/n2))));
end
```

The sum of squared errors due to the residual is assigned to the variable `sw`.

```
% Assign the mean squared error due to the residual to the variable sw
sw = 84.5832
```

sw = 84.5832

The mean age of those with chest pain class ASY is compared to those with the class ATA.

```
% Calculate the t statistic for the first pairwise comparison
pairwise_t(54.9597, 49.2428, 496, 173, sw)
```

```
ans = 7.0399
```

The degrees of freedom is the sample size minus the number of groups, i.e. $N - k = 918 - 4 = 914$. This is used to calculate the critical t value.

```
% Calculate the critical t value
tinv(1-(0.0083/2),914)
```

```
ans = 2.6454
```

The first t statistic is larger than the critical value and we reject the null hypothesis. There is a difference in the mean age between these two classes. The *p* value for the t statistic is calculated.

```
% Calculate the two-tailed p value
2 * (1-tcdf(7.0399, 914))
```

```
ans = 3.7770e-12
```

Note that there are functions in MATLAB to conduct an analysis of variance test to compare the means of a numerical variable across more than two groups. The `anova1` function requires each group to have the same sample size, though. Instead, we used a linear regression model above, which is the same task. We can also use a non-parametric test such as the Kruskal-Wallis test. For the Kruskal-Wallist test we have that H_0: all medians are the same, and H_1: all medians are not the same. Below, we create four separate arrays to hold the Age variable values for each of the four classes of the `ChestPainType` variable.

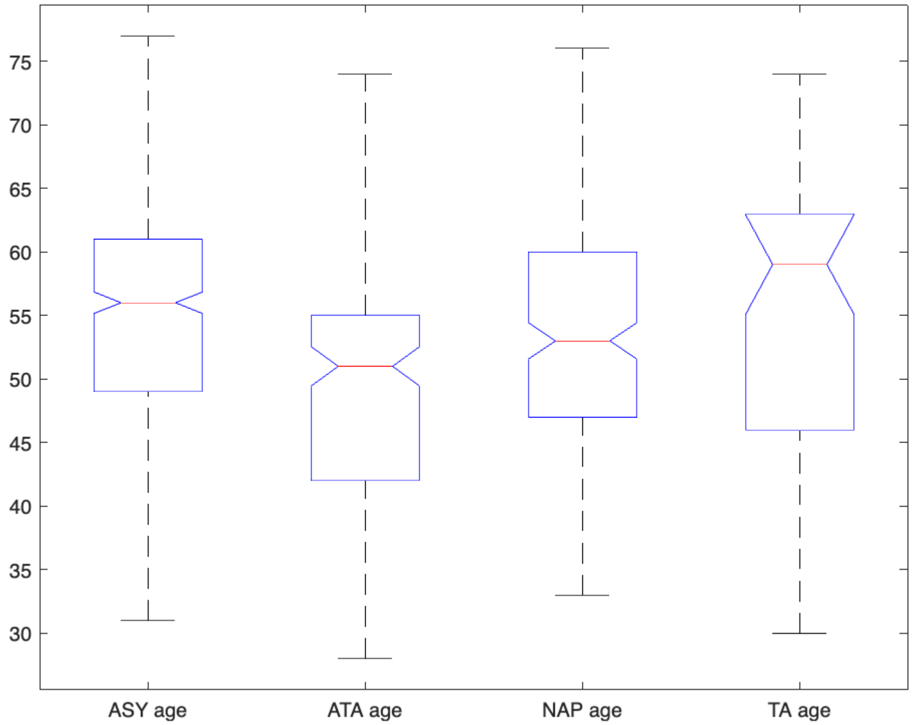
```
% Create vectors of age values for each group
age_ASY = table2array(heart(heart.ChestPainType=='ASY',"Age"));
age_ATA = table2array(heart(heart.ChestPainType=='ATA',"Age"));
age_NAP = table2array(heart(heart.ChestPainType=='NAP',"Age"));
age_TA = table2array(heart(heart.ChestPainType=='TA',"Age"));
```

The `kruskalwallis` function performs the Kruskal-Wallis test. The first argument creates a table of columns where each column is an array of the ages for a specific group. The second is an array that generates a group name for each observation in each group. The `repelem` function is used to repeat the name of each group. Note the use of the `'` to transpose the output of each `repelem` function, which returns a row vector by default. The `kruskalwallis` function returns three objects, which we assign to the variables p_kw (returns a *p* value), `tbl_kw` (returns an analysis of variance table), and `stats_hw` (returns a statistics object that we can use for *post-hoc* analysis). The last argument is `"on"` which prints the results as output.

```
% Perform the Kruskal-Wallis test
[p_kw, tbl_kw, stats_kw] = kruskalwallis([age_ASY;age_ATA;age_NAP;age_TA],
[repelem("ASY age", length(age_ASY))'; repelem("ATA age",
length(age_ATA))'; repelem("NAP age", length(age_NAP))'; repelem("TA age",
length(age_TA))'],"on")
```

Kruskal-Wallis ANOVA Table

```
Source        SS          df        MS        Chi-sq    Prob>Chi-sq
---------------------------------------------------------------------
Groups     3.4129e+06      3    1137633.4     48.6      1.58809e-10
Error     6.09846e+07    914      66722.8
Total     6.43975e+07    917
```




```
p_kw = 1.5881e-10
tbl_kw = 4×6 cell
```

	1	2	3	4	5	6
1	'Source'	'SS'	'df'	'MS'	'Chi-sq'	'Prob>Chi-sq'
2	'Groups'	3.4129e+06	3	1.1376e+06	48.5986	1.5881e-10
3	'Error'	6.0985e+07	914	6.6723e+04	[ ]	[ ]
4	'Total'	64397522	917	[ ]	[ ]	[ ]

```
stats_kw = struct with fields:
        gnames: {4×1 cell}
             n: [496 173 203 46]
        source: 'kruskalwallis'
     meanranks: [500.5373 342.1705 445.9163 518.2174]
          sumt: 849450
```

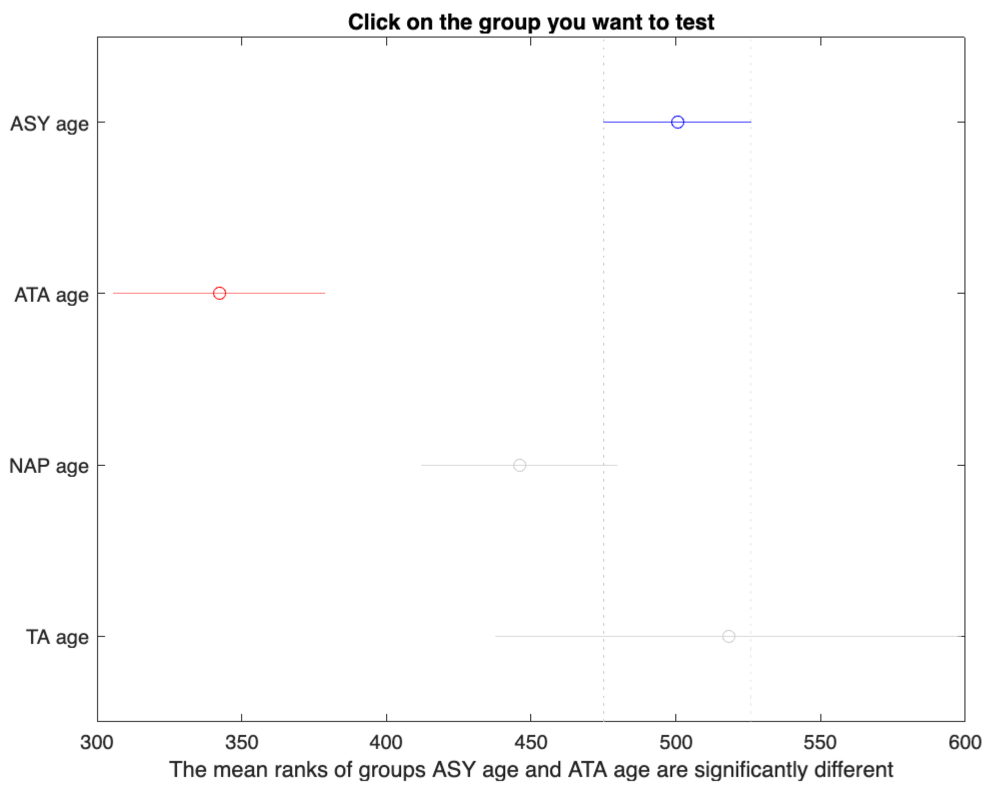
From the box-and-whisker plot is seems that the ATA group ages are different from all three other groups, but that they, in turn, are all very similar. The results show a *p* value that is less than a level of significance of 0.05

and we state that there is enough evidence at the 5% level of significance to show that there is a difference in the mean ages between the four chest pain types. We can now conduct *post-hoc* analysis.

The `multcompare` function can perform the analysis. We use it below with the first argument being the `stats_kw` objects from the Kruskal-Wallis test. By default, the critical value type is from Tukey's honestly significant difference procedure. Instead, we use the Bonferroni procedure here. Four object are returned. We assign them to the variables `c_b` (returns a matrix of pairwise comparison results), `m_b` (returns the estimated values of the means (or whatever statistics are being compared) for each group and the corresponding standard errors), `h_b` (returns a handle for the comparison graph), and `gnames_b` (returns the groups names). By default, the first group is used as the control group. The `ControlGroup` argument can be used to select a different groups as control.

```
% Perform a multi-comparison test
[c_b, m_b, h_b, gnames_b] =
multcompare(stats_kw,'CriticalValueType','bonferroni');
```

```
Note: Intervals can be used for testing but are not simultaneous confidence intervals.
```



The plot is not that helpful in determining all the pairwise comparisons. Below, we create a table to summarize the mean and standard error of the ages for each group.

```
% Print a summary of the mean and standard errors for the age of each
% group
tbl_summary = array2table(m_b,"RowNames",gnames_b,"VariableNames",
["Mean","Standard Error"])
```

tbl_summary = 4×2 table

	Mean	Standard Error
1 ASY age	500.5373	11.8990
2 ATA age	342.1705	20.1478
3 NAP age	445.9163	18.5995
4 TA age	518.2174	39.0725

We can also print a summary of all six pairwise comparisons.

```
% Print a summary of the pairwise comparisons
tbl_pw = array2table(c_b,"VariableNames",["Group","Control Group","Lower
Limit","Difference","Upper Limit","p-value"]);
tbl_pw.("Group") = gnames_b(tbl_pw.("Group"));
tbl_pw.("Control Group") = gnames_b(tbl_pw.("Control Group"))
```

tbl_pw = 6×6 table

	Group	Control Group	Lower Limit	Difference	Upper Limit	p-value
1	'ASY age'	'ATA age'	96.6339	158.3668	220.0996	7.8306e-11
2	'ASY age'	'NAP age'	-3.6318	54.6210	112.8738	0.0802
3	'ASY age'	'TA age'	-125.4375	-17.6801	90.0773	1
4	'ATA age'	'NAP age'	-176.0876	-103.7457	-31.4038	9.2771e-04
5	'ATA age'	'TA age'	-292.0279	-176.0469	-60.0658	3.7275e-04
6	'NAP age'	'TA age'	-186.4679	-72.3011	41.8657	0.5686

A suspected from the box-and-whisker plot, the significant differences are between the ATA group and all three other groups.

Common tests for categorical variables

Pearson's χ^2 test for association between two categorical variables

Pearson's χ^2 test for association requires a table of observed data (contingency table). We consider the `Sex` and `ChestPainType` variables. Under the null hypothesis there is no association between these two variables (the variables are independent).

```
% Create pivot table
sex_chestpaintype = pivot(heart, Rows="Sex", Columns="ChestPainType")
```

sex_chestpaintype = 2×5 table

	Sex	ASY	ATA	NAP	TA
1	F	70	60	53	10
2	M	426	113	150	36

The table values as assigned to a matrix.

```
% Matrix of values
sex_chestpaintype_matrix = [70 60 53 10; 426 113 150 36]
```

```
sex_chestpaintype_matrix = 2×4
    70    60    53    10
   426   113   150    36
```

We create a user-defined function named `chi2square` to conduct Pearson's χ^2 test.

```
% Create a function to conduct the test at the 5% level of significance
function [e, df, h, p, X2, X2crit] = chi2square(x) % To return table of
expected values, degrees of freedom, test decision rule, p value, X2 and
critical X2 values
% Compute expectation and chi-square statistic, and determine p value.

    e = sum(x,2)*sum(x)/sum(x(:)); % Calculate the expected values
(independent variables)
    X2 = (x-e).^2./e; % Calculate square of observed value value minus
expected divided by expected value
    X2 = sum(X2(:)); % Sum over all
    df = prod(size(x)-[1 1]); % Calculate the degrees of freedom
    p = 1-chi2cdf(X2,df); % Calculate p value of X2 statistic
    X2crit = icdf('chisquare', [1 - 0.05], df); % Calculate critical X2
value
    h = double(p <= 0.05); % Decision rule based on p value
end
% Use table values as input
[e, df, h, p, X2, X2crit] = chi2square(sex_chestpaintype_matrix)
```

```
e = 2×4
  104.2789   36.3715   42.6786    9.6710
  391.7211  136.6285  160.3214   36.3290
df = 3
h = 1
p = 4.8803e-08
X2 = 36.8792
X2crit = 7.8147
```

The table of observed data meets the size sample size assumption for the test. The h=1 indicates that we reject the null hypothesis. The *p* value is less than the chosen $\alpha = 0.05$. As confirmation we see that the X^2 test statistic is larger than the critical X^2 value for 3 degrees of freedom. There is enough evidence at the 5% level of significance to show that there is an association between the `Sex and ChestPainType variables.`

Statistical models

Correlation between two numerical variables

The linear association between two continuous numerical variables can be evaluated using correlation. A scatter plot shows the correlation between the `Age` and `Cholesterol` variables.

```
% Create a scatter plot of Age vs Cholesterol
scatter(heart.Age,heart.Cholesterol)
```

```
grid on
title("Age vs cholesterol levels")
xlabel("Age [years]")
ylabel("Cholesterol [mg/dL]")
hold off
```

We note all the values in the `Cholesterol` variable that are 0. A new table is created for the two variables and all observations that are 0 are omitted.

```
% Create a new table
age_cholesterol_sex_data = heart(heart.Cholesterol ~= 0,{'Age',
'Cholesterol','Sex'})
```

age_cholesterol_sex_data = 746×3 table

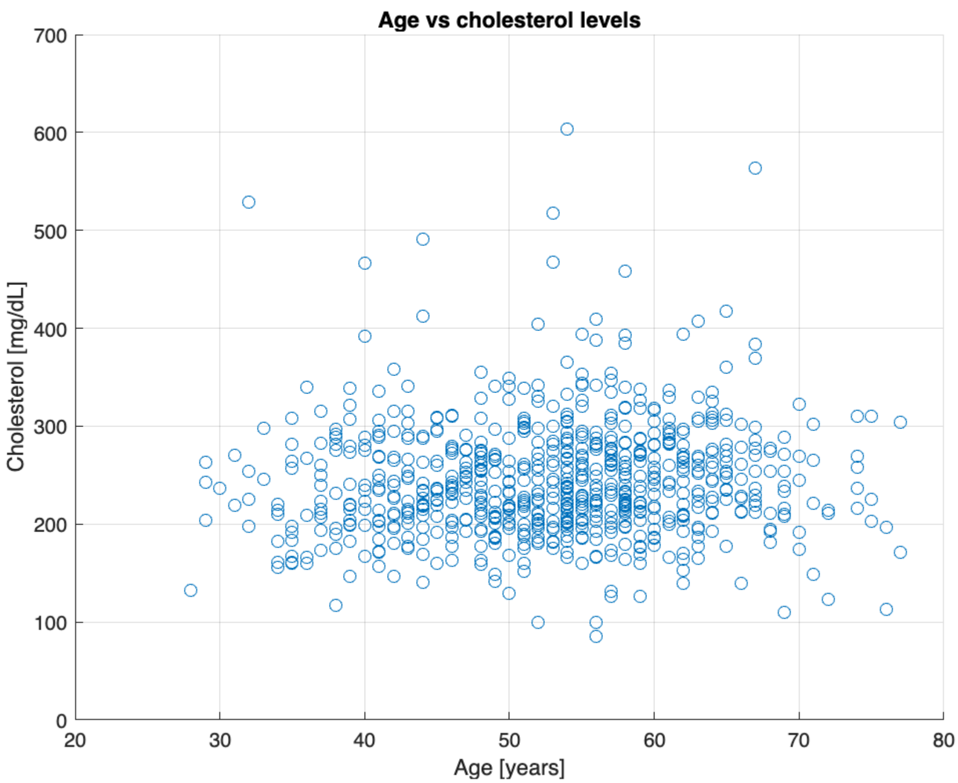
	Age	Cholesterol	Sex
1	40	289	M
2	49	180	F
3	37	283	M
4	48	214	F
5	54	195	M
6	39	339	M
7	45	237	F
8	54	208	M

	Age	Cholesterol	Sex
9	37	207	M
10	48	284	F
11	37	211	F
12	58	164	M
13	39	204	M
14	49	234	M

⋮

The scatter plot is recreated.

```
% Create a scatter plot of Age vs Cholesterol
scatter(age_cholesterol_sex_data.Age, age_cholesterol_sex_data.Cholesterol)
grid on
title("Age vs cholesterol levels")
xlabel("Age [years]")
ylabel("Cholesterol [mg/dL]")
hold off
```



The `corr` function returns Pearson's correlation coefficient r and the p value.

```
% Correlation between Age and Cholesterol variables
```

```
[rho, pval] = corr(age_cholesterol_sex_data.Age,
age_cholesterol_sex_data.Cholesterol, "Tail", "both")
```

```
rho = 0.0588
pval = 0.1088
```

There is poor linear association (or correlation) between the two variables.

Linear regression

We use the Curve Fitter app in the APPS tab. The model can be exported to the workspace and the plots can be opened in the Plot Editor. We create two vectors to use in the app.

```
% Create vectors
age = age_cholesterol_sex_data.Age;
cholesterol = age_cholesterol_sex_data.Cholesterol;
```

We create the model using the app. The app returns a named model to the workspace.

The `fitlm` function can be used to create the model manually/

```
% Create a linear model
age_cholesterol_model = fitlm(age, cholesterol, "linear")
```

```
age_cholesterol_model =
Linear regression model:
    y ~ 1 + x1

Estimated Coefficients:
                   Estimate      SE        tStat       pValue
                   ________    _______    ______    __________

    (Intercept)      225.3      12.236    18.412    1.1457e-62
    x1             0.36564     0.22775    1.6055       0.10881


Number of observations: 746, Error degrees of freedom: 744
Root Mean Squared Error: 59.1
R-squared: 0.00345,  Adjusted R-Squared: 0.00211
F-statistic vs. constant model: 2.58, p-value = 0.109
```

The model $\widehat{y} = \widehat{\beta}_0 + \widehat{\beta}_1 x = 225.3 + 0.36564 \times \text{age}$.

The results are the same as for the Curve Fitter app. The F statistic is 0.258 with a *p* value of 0.109. The coefficient of determination is a low 0.00345 meaning that the model explains less than 0.3% of the variability in the cholesterol value.

```
% Create vectors
sex = categorical(age_cholesterol_sex_data.Sex);
sex(1:5)
```

```
ans = 5×1 categorical
M
F
M
F
```

```
M
```

We add another explanatory variable, Sex. This is a binary variable and we choose M as the base class.

```
% Create dummy variables for a design matrix
dummySex = dummyvar(sex);
% Create a design matrix
X = [age dummySex]
```

```
X = 746×3
    40     0     1
    49     1     0
    37     0     1
    48     1     0
    54     0     1
    39     0     1
    45     1     0
    54     0     1
    37     0     1
    48     1     0
     ⋮
```

```
% Create design matrix choosing columns 1 and 2 (by choosing column 2 we
% have M as the base class
X = X(:, [1 2]);
% Fit a model with two predictor variable (numerical and binary)
fittedmodel_age_sex_cholesterol = fitlm(X, cholesterol, 'linear')
```

```
fittedmodel_age_sex_cholesterol = 
Linear regression model:
    y ~ 1 + x1 + x2

Estimated Coefficients:
                   Estimate      SE        tStat       pValue  
                   ________    _______    ______    __________

    (Intercept)     220.14      12.291    17.911    6.5791e-60
    x1             0.39356     0.22671    1.7359      0.082991
    x2               15.09      5.0147    3.0092     0.0027079


Number of observations: 746, Error degrees of freedom: 743
Root Mean Squared Error: 58.8
R-squared: 0.0155,  Adjusted R-Squared: 0.0128
F-statistic vs. constant model: 5.83, p-value = 0.00307
```

Logistic regression

If the outcome variable is binary, we can create logistic regression model.

```
X = dummySex;
X = X(:, 1);
glm_data = table(X, age, cholesterol,'VariableNames',{'Sex', 'Age',
'Cholesterol'})
```

```
glm_data = 746×3 table
```

	Sex	Age	Cholesterol
1	0	40	289
2	1	49	180
3	0	37	283
4	1	48	214
5	0	54	195
6	0	39	339
7	1	45	237
8	0	54	208
9	0	37	207
10	1	48	284
11	1	37	211
12	0	58	164
13	0	39	204
14	0	49	234

⋮

```
% Create a logistic regression model
predict_sex = fitglm(glm_data, 'Sex ~ Age + Cholesterol', 'Distribution',
'binomial')
```

```
predict_sex =
Generalized linear regression model:
    logit(Sex) ~ 1 + Age + Cholesterol
    Distribution = Binomial

Estimated Coefficients:
                   Estimate       SE        tStat       pValue  
                   _________    _________    _______    _________

    (Intercept)      -1.5353      0.57776    -2.6574    0.0078753
    Age            -0.011775    0.0090923    -1.2951      0.19529
    Cholesterol    0.0041299    0.0014002     2.9494    0.0031834


746 observations, 743 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 9.91, p-value = 0.00705
```

The estimates, $\widehat{\beta}_1$ and $\widehat{\beta}_2$, of the model are log odds ratios and we have to calculate $e^{\widehat{\beta}_i}$ to write the model.

```
% Exponential each of the coefficients
exp(predict_sex.Coefficients.Estimate)
```

```
ans = 3×1
    0.2154
    0.9883
```

1.0041