

Topic 5 – Introduction to hypothesis testing

ENVX1002 Statistics in Life and Environmental Sciences

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Outline

- Inferential statistics
- Confidence intervals
- Hypothesis testing
- 1-sample tests

Inferential statistics

- You should be familiar with **EDA** by now
- Now we are going to take the next step into the world of **inferential statistics**
- This is an important and sometimes difficult step in statistics
- We are going to draw conclusions about a population from a “smaller” sample of that population

Hypothesis testing

- A hypothesis consists either of a suggested explanation for a phenomenon or of a reasoned proposal suggesting possible relationships between multiple phenomena

Why?

- To make evidence based decisions, we need to evaluate the evidence
- Hypothesis testing is a scientific method for weighing up the evidence given the data against the given hypothesis (model)

Evidence?

- The data is not consistent with the hypothesis if the gap between the observed value (data) and the expected value is too big (> 2 or 3 Standard Errors)

Hypothesis testing

Framework

- Null Hypothesis (H_0) vs Alternative Hypothesis (H_1)
- Is the data consistent with H_0 ? Wait, but I'm interested in if there is a difference?
 - ▶ Falsifiability: only takes one contrary observation to falsify a statement (Karl Popper)
 - Can we falsify this statement? "There are invisible and undetectable fairies in my garden." - it is non-falsifiable so we cannot test it with empirical data.
 - Can we falsify this statement? "All swans are black" - if we observe a single white swan, then the statement is falsified.



Figure 1: a counterexample. DAU 1, E 3

Hypothesis testing

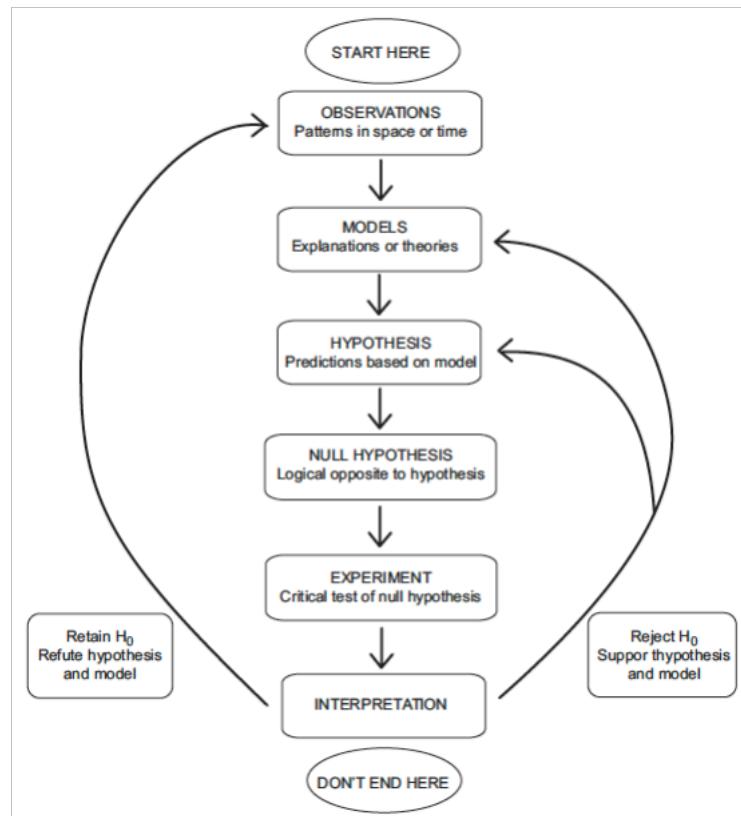


Figure 2: Underwood, A.J., 2009, April. Components of design in ecological field experiments. In *Annales Zoologici Fennici* (Vol. 46, No. 2, pp. 93-111). Finnish Zoological and Botanical Publishing Board.

Hypothesis testing

We will follow the steps in hypothesis testing

- Choose level of significance (usually 0.05)
- Write null and alternate hypotheses
- Check assumptions
- Calculate test statistic
- Obtain P-value or critical value
- Make statistical conclusion
- Write a scientific (biological) conclusion

Hypothesis testing

Acronyms

Sometimes we use HATPC to remember these steps - HAT Prevent Cancer - come up with your own

- **H:** Hypothesis
- **A:** Assumptions
- **T:** Test statistic
- **P:** P-Value
- **C:** Conclusion

Hypothesis (H)

- The **null hypothesis** (H_0) assumes that the difference between the observation (data) and the expected value is due to chance
- The **alternative hypothesis** (H_1) assumes that the difference between the observed value (data) and expected value is NOT due to chance alone.

Assumptions (A)

- We need to check the assumptions of the test we are using.
- For example, if we are using a one sample t-test we need to check the assumption of normality.
- This is done by 1) looking at the distribution of our data (EDA) and 2) using a hypothesis test such as the Shapiro-Wilk test.
- If the assumptions are not met, we may need to transform the data or use a non-parametric test.

Test Statistic (T)

Measures the difference between what is observed in the data and what is expected from the null hypothesis.

$$\text{Test statistic} = \frac{\text{Observed value} - \text{Expected value}}{\text{Standard error}}$$

P-Value (P)

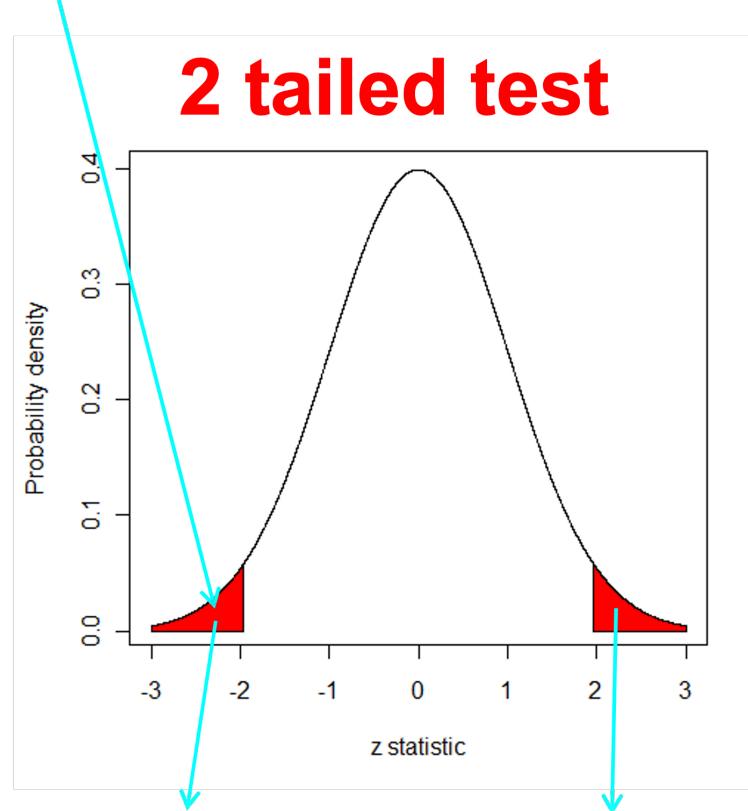
What is P-value?

- The P-value is a way of weighing up whether the sample (data) is consistent with H_0
More formally:
 - The P-value is the chance of observing the test statistic (or something more extreme) if the H_0 is true.

P-value (P)

What does this have to do with sampling distributions??

Sample mean



P-Value (P)

“If the P-value is low the Null hypothesis must go.”

- So we calculate the P-value to assess the level of evidence against the Null hypothesis.
 - Generally if a P-value > 0.05 we say there is **no strong** evidence to reject the null hypothesis (we fail to reject it)
 - We never say we accept the null hypothesis!!
 - 0.05 is called the significance level
 - We may choose other significance levels such as 0.2, 0.01, 0.001 (for this course we will use 0.05)

P-Value (P)

Common mistakes

- The p-value is not the chance that the NULL hypothesis is true
- A large p-value does not mean that H_0 is true

Size of p-value	What not to say	What to say
Small	H_0 is not true	There is evidence against H_0
	H_0 is false	We reject H_0
Large	We accept H_0	Data is consistent with H_0
		We retain H_0

- The use of 0.05 is not mandatory, it is a convention.

P-value (P)

Controversy

Nature article 1

Nature article 2

- Should we move away from an over reliance on p-values towards more robust statistical methods and a greater emphasis on the size and reproducibility of effects?
- Look up terms like “**P Hacking**”...

A little more on the P-value

Why is the p-value 0.05?

- The p-value is the probability of observing a test statistic as extreme as the one calculated, assuming the null hypothesis is true.
- It is based on the idea we 1 in 20 times we will reject the null hypothesis when it is true.

Conclusion (C)

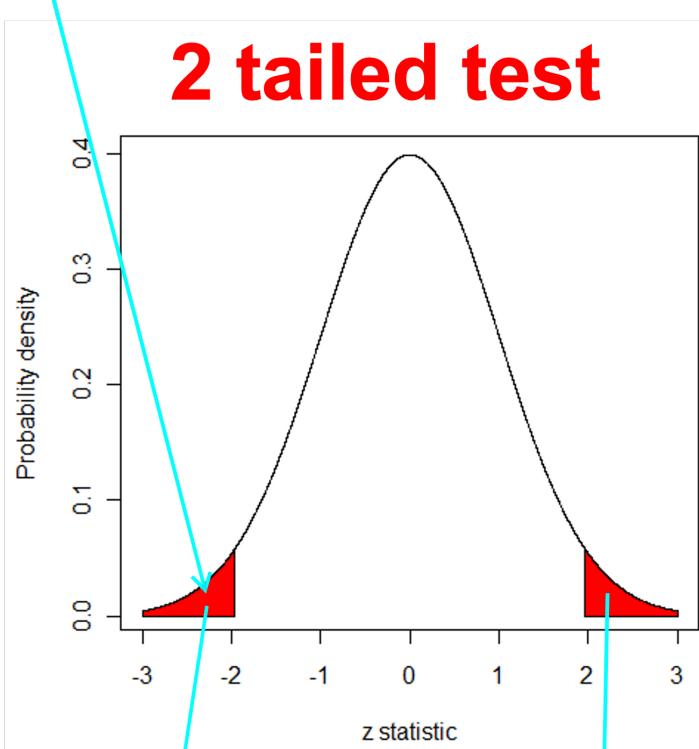
- We make a statistical conclusion based on the p-value and the level of significance.
- We also make a scientific (biological) conclusion based on the statistical conclusion.

Tails

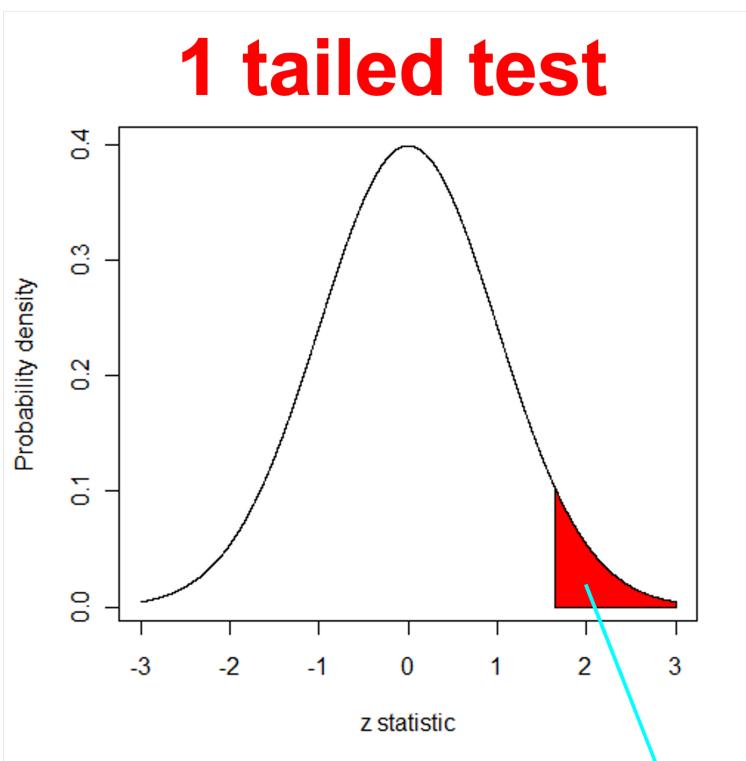
Tails??

Sample mean

2 tailed test



1 tailed test



One tailed tests are used when we are specifically interested in whether the observed value is greater or less than the

- In this course we will mostly use two-tailed tests because we are interested in whether the observed value is different to the expected value. Examples are quality control and production processes.

$P = 0.025$

$P = 0.025$

$P = 0.05$

Tails

- Let say we would like to test whether a sample or population behaves according to a known or expected value. For example, ENVX1002 students have a mean heart rate of 70 beats per minute (c). We could test the relationship between our population or sample mean (μ) or (y) and our expected mean (c).
 - ▶ $H_0 : \mu = c$ Two tailed
 - ▶ $H_1 : \mu \neq c$ Two tailed
 - ▶ $H_0 : \mu \geq c$ One tailed - greater than
 - ▶ $H_1 : \mu < c$ One tailed - greater than
 - ▶ $H_0 : \mu \leq c$ One tailed - less than
 - ▶ $H_1 : \mu > c$ One tailed - less than
- We usually use the first (two tailed) form unless we are specifically interested in testing whether the difference is in one direction or the means of two variables are equivalent (i.e. equivalence testing in production)
- In this course we are assuming that the population/sample is normally distributed.

Type error??

Type I error

- False positive: we reject H_0 when it is true

Type II error

- False negative: we accept H_0 when it is false

		DECISION
		H_0 rejected H_0 accepted / retained
H_0 is false	Correct decision $1-\beta$	False negative Type II Error ($P = \beta$ usually unknown)
H_0 is true	False positive Type I Error ($P = \alpha$ usually 0.05)	Correct decision $1-\alpha$

Note: Decreasing the significance level (α) to say 0.01 will increase the probability of type II error

Sample size and power

Sample size & Power

- While we won't do these calculations, it is important to think about sample size and power. For example, when comparing two means we can estimate the sample size required using the following

$$n = \left(\frac{(Z_{\alpha/2} + Z_{\beta})^2 \cdot (SD_1^2 + SD_2^2)}{\delta^2} \right)$$

- n represents the required sample size for each group.
- $Z_{\alpha/2}$ denotes the critical value of the normal distribution at the desired significance level (α). For example, for a 95% confidence level ($\alpha = 0.05$, $Z_{\alpha/2} = 1.96$).
- Z_{β} is the Z-score corresponding to the desired power of the test ($1 - \beta$). For 80% power ($\beta = 0.2$), you would use the Z-score that corresponds to 80% in the normal distribution table.
- SD_1 and SD_2 are the standard deviations of the two groups being compared.
- δ is the minimum difference in means between the two groups that the study is designed to detect, also known as the effect size.

Sample size and power

Sample size & Power

In a nut shell...

High Power: If a test has high power (close to 1), it means that the probability of committing a Type II error is low. This indicates that the test is very likely to detect an effect or difference when one exists.

Low Power: Conversely, if a test has low power, the probability of committing a Type II error is high. This means the test is less likely to detect an effect or difference, even if one exists.

Sample size: Generally power increases as sample size increases, but so does time and costs!

The t-distribution and degrees of freedom?

The T-distribution has the following properties:

- It is bell-shaped, symmetrical about the mean, median and mode, which are all of equal value. [It is a little flatter than the normal distribution.]
- The area under the curve = 1, as is the case for all continuous probability distributions.
- The probability density function is defined by three parameters, the mean μ , the standard deviation σ and the sample size n .
- The exact shape of the t distribution depends on the quantity called degrees of freedom, df. The $df = n - 1$ for any t distribution.

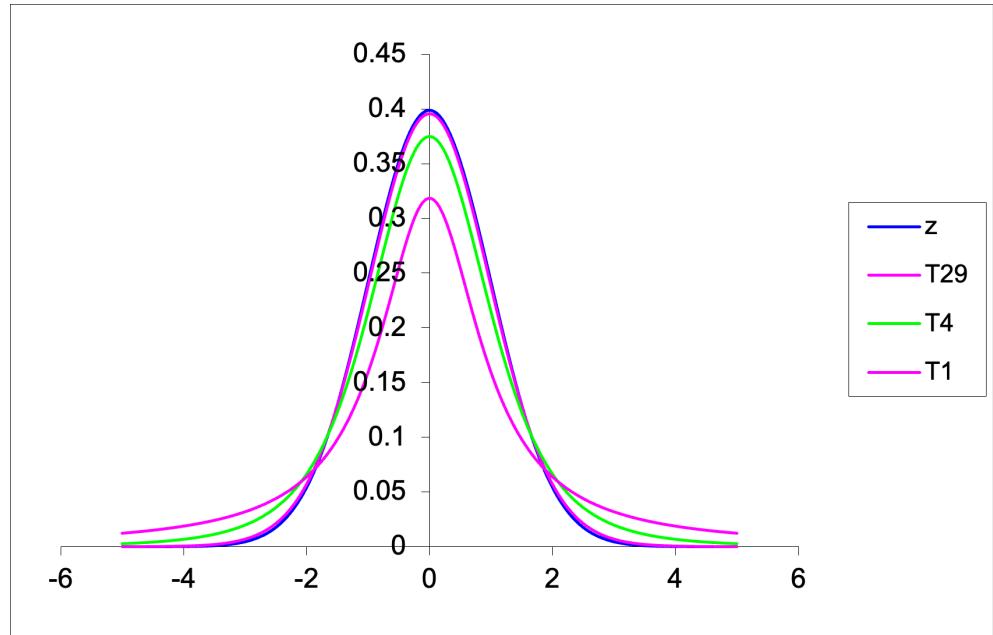


Figure 3: Comparing the shapes of the Student's T and the Z (normal) curve

Example 1: One sample t-test



Figure 4: Generated using DALL.E 3

Hypothesis

Say our hippie friend here has seen the light after a helping of mung beans and wishes to test whether ENVX1002 student average heart rates differ from the global average of 70 bpm (beats per minute).

State the Null and Alternate hypothesis!

- $H_0 = 70$ bpm (Null hypothesis)
- $H_1 \neq 70$ bpm (Alternate hypothesis)

Example 1: One sample t-test

Assumptions

- This time we are testing a data set where the **variance is unknown**.
- A key assumption for the one-sample t-test is that the sample is “reasonably” normally distributed.
- Why do we need to test the assumption of normality?
- Think about if our distribution is right skewed, then our *mean* may not reflect the central tendency of our sample population.

Example 1: One sample t-test

Assumptions

Small Samples: With small samples (typically $n < 30$), even slight deviations from normality can significantly impact the t-test's validity because the t-test relies heavily on the assumption of normality in this scenario. However, if the data are symmetrically distributed and don't have outliers, the t-test can be robust to mild violations of normality. Note that the t-test adjusts for the sample size, so the larger the sample, the less important the normality assumption becomes.

Large Samples: For larger samples ($n > 30$), the Central Limit Theorem (CLT) suggests that the distribution of the sample means tends to be normal, regardless of the population distribution. This means that for sufficiently large samples, the t-test can be robust to violations of normality. *However, extreme skewness, heavy tails, or outliers can still affect the test's performance.*

Example 1: One sample t-test

```
library(ggplot2)

# Assuming 'skewed_sample' is your skewed data.
# For this example, let's simulate it
set.seed(0) # For reproducibility
skewed_sample ← rlnorm(100, meanlog = 0, sdlog = 1) - exp(0.5) # Skewed data, centered around 0

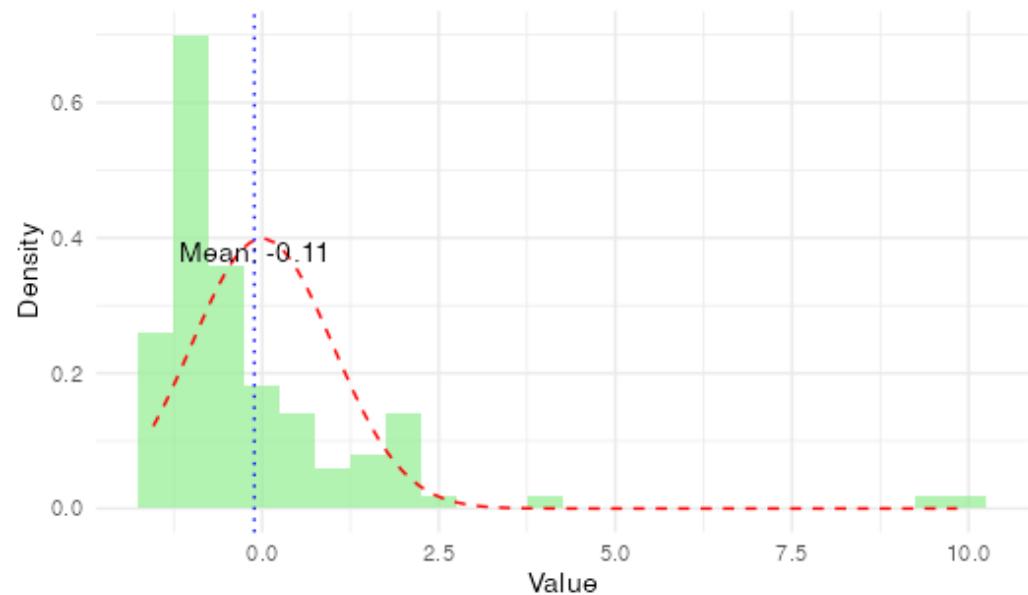
# Create a data frame for ggplot
data ← data.frame(value = skewed_sample)

# Plot
p ← ggplot(data, aes(x = value)) +
  geom_histogram(aes(y = ..density..), binwidth = 0.5, fill = "lightgreen", alpha = 0.7) +
  stat_function(fun = dnorm, args = list(mean = 0, sd = 1), color = "red", linetype = "dashed") +
  labs(title = "Skewed Distributed Sample", x = "Value", y = "Density") +
  theme_minimal() +
  geom_vline(aes(xintercept = mean(value)), color = "blue", linetype = "dotted") +
  annotate("text", x = mean(skewed_sample), y =
```

```
print(p)
```

Warning: The dot-dot notation (`..density..`)
was deprecated in ggplot2 3.4.0.
i Please use `after_stat(density)` instead.

Skewed Distributed Sample



Example 1: One sample t-test

Assumptions

- Let's help out our hippie friend: We have asked students to measure their heart rate and randomly selected heart rates from 21 students (a *completely randomised design*) in our hippie friends ENVX1002 class. Note we will do this exercise in class!!

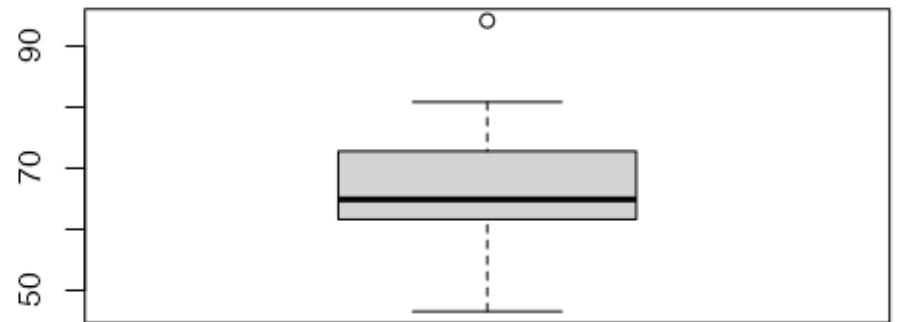
```
set.seed(1234)  
heart_rate ← rnorm(21, mean = 70, sd = 10)
```

- We have a small sample size so often we use a *stem plot* `boxplot(heart_rate)`
symmetrical!

```
stem(heart_rate)
```

The decimal point is 1 digit(s) to the right
of the |

4	7
5	8
6	01122445559
7	11345
8	01
9	4



Example 1: One sample t-test

Assumptions

- We can also look at the 6 number summary and the histogram. The histogram looks quite symmetrical and the 6 number summary is quite symmetrical.

```
summary(heart_rate)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
46.54	61.63	64.89	67.68	72.77	94.16

- We can see that the mean and the median are quite similar. This is a good sign that the data is symmetrical and perhaps normally distributed.
- We can also start to think how our student heart rate compares to the national average of 70 bpm.

Example: One sample t-test

R base graphics

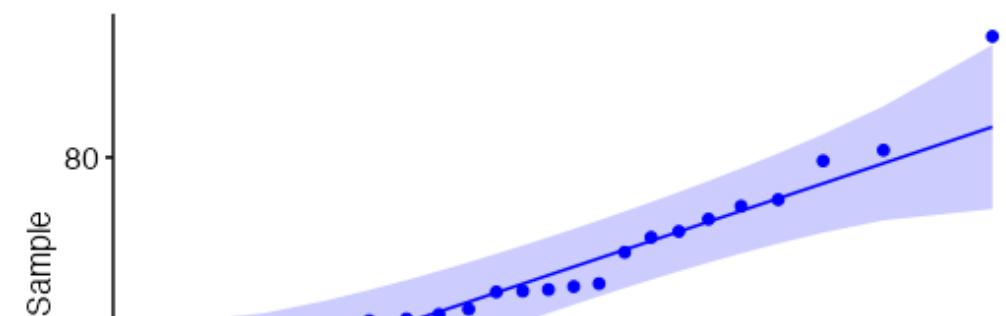
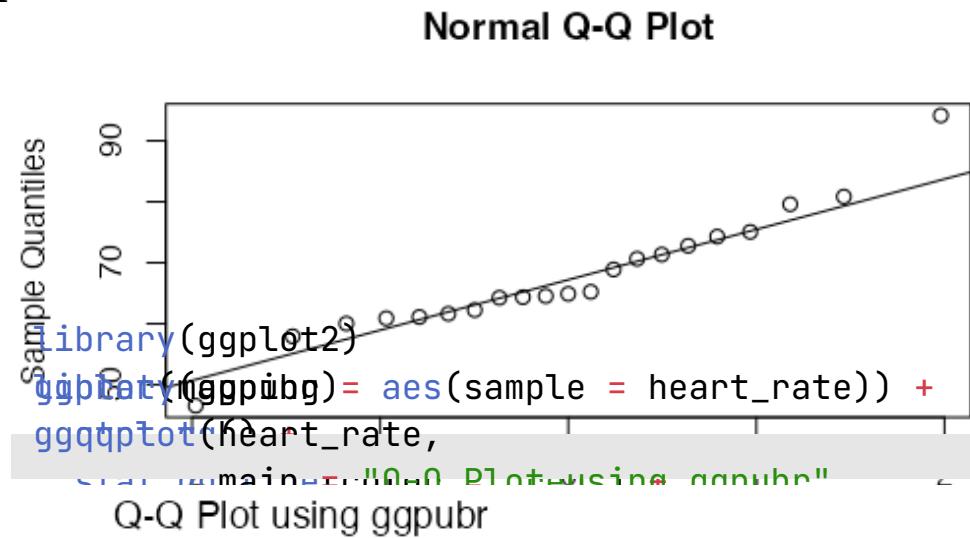
- We can also use a hypothesis test called the *Shapiro Test* and
- We can see that the p-value of the shapiro test > 0.05 - no strong evidence that the distribution is not normal.
- We can see that the points on the Q-Q plot are

Assumption:
`qqnorm(heart_rate)`
`qqline(heart_rate)`

```
shapiro.test(heart_rate)
```

Shapiro-Wilk normality test

```
data: heart_rate  
W = 0.94441, p-value = 0.266
```



Example 1: One sample t-test

Test statistic

t-test

- The formula is the same as the z-test but we use the t-distribution instead of the normal distribution and we use the sample standard deviation instead of the population standard deviation.

$$t = \frac{\bar{y} - \mu}{s/\sqrt{n}} \text{ population variance unknown (estimate } s^2\text{)}$$

- \bar{y} is the sample mean
- μ is the population mean
- s is the sample standard deviation
- n is the sample size

Example 1: One sample t-test

CI & T-Statistic & P-value

Luckily for us we have a function in RStudio that does all of
the above in one function!

```
t.test(heart_rate,  
       mu = 70,  
       alternative = "two.sided",  
       conf.level = 0.95  
)
```

```
One Sample t-test  
  
data: heart_rate  
t = -1.0736, df = 20, p-value = 0.2958  
alternative hypothesis: true mean is not equal  
to 70  
95 percent confidence interval:  
 63.16242 72.19073  
sample estimates:  
mean of x  
67.67657
```

We can see the following output:

- the t-statistic = -1.0736
- the degrees of freedom = 20 ($n - 1$)
- the p-value = 0.2958
- the 95% confidence interval = (63.16242 72.19073)
- the sample mean = 67.67657

Example 1: One sample t-test



usion

Let's revisit our hippie friend's hypothesis

- $H_0 = 70 \text{ bpm}$ (Null hypothesis)
- $H_1 \neq 70 \text{ bpm}$ (Alternate hypothesis)
- The p-value is 0.2958 which is not less than 0.05. We retain null hypothesis.
- There is no strong evidence to indicate that the mean heart rate of ENVX1002 students is different to the global mean of 70 bpm. We can be 95% confident that the true mean heart rate of 63 and 72 (0 d.p.) beats per minute. Our global mean lies within this interval. Therefore we are pretty confident that the class average heart rate is similar to the global average.

Figure 5: Generated using DALL-E 2

Confidence intervals

- A confidence interval is a range of values, derived from a sample, that is likely to contain the value of an unknown population parameter.
- Confidence are important and many people prefer them to formal hypothesis tests because they give a range of values rather than a single value.
- There are two types we are going to look at:
 - Confidence interval where we **know** the population variance
 - Confidence interval where we **do not know** the population variance

Confidence intervals - known variance

- Assuming our sample comes from a normal population, we can calculate the confidence interval for the mean of a population when the population **variance is known**. An example may be in manufacturing where we know the variance of a process.
- The formula for the confidence interval is:

$$CI = \bar{y} \pm Z_{\alpha/2} \cdot \frac{\sigma}{\sqrt{n}}$$

for the 95% confidence interval, $\alpha = 0.05$ and $Z_{\alpha/2} = 1.96$ i.e. 2 standard errors from the mean.

Confidence intervals - known variance

- \bar{y} is a random variable with a sampling distribution.
- Because there is an infinite number of values of \bar{y} , there is an infinite number of intervals of the form $CI = \bar{y} \pm 1.96 \cdot \frac{\sigma}{\sqrt{n}}$.
- The probability statement says that 95% of these intervals will actually include μ between the limits.
- For any one interval, $CI = \bar{y} \pm 1.96 \cdot \frac{\sigma}{\sqrt{n}}$, we say that we are 95% confident that μ lies between these limits.

Confidence intervals - known variance

Example

Say we have measured the weights of 6 chocolate bars from Florry's chocolate factory. The readings were:

48 43 45 51 49 40

The mean for these six values is $\bar{y} = 46$ g. Let's assume that the bar weights follow a normal distribution and that $\sigma = 1$ g
These assumptions allow us to calculate a 95% z-based confidence interval:

So the 95% CI for the current example is

$$CI = 46 \pm 1.96 \cdot \frac{1}{\sqrt{6}} \text{ or } CI = 46 \pm 0.80 \text{ or } CI = (45.20, 46.80)$$

So we are 95% confident that the true mean weight of the chocolate bars is between 45.20 and 46.80g.

- We will calculate confidence intervals with **unknown variance** in later on.

Confidence intervals - Unknown variance

- We can also calculate a confidence interval when we do not know the population variance.

- The formula for the confidence interval is:

$$CI = \bar{y} \pm t_{\alpha/2} \cdot \frac{s}{\sqrt{n}}$$

- For the 95% confidence interval, $\alpha = 0.05$ and $t_{\alpha/2} = 2.093$ (for 20 degrees of freedom)

- The degrees of freedom is $n - 1$

```
qt(0.975, df = 20)
```

```
[1] 2.085963
```

Confidence intervals - Unknown variance

- Another interesting result to contemplate can be demonstrated through the following simulation of 100 studies, each containing $n = 6$ observations of a fictitious toxic substance concentration ($\mu\text{g/l}$) assumed to be $\sim N(0.3, 0.12)$. For each sample the 95% confidence interval calculated:

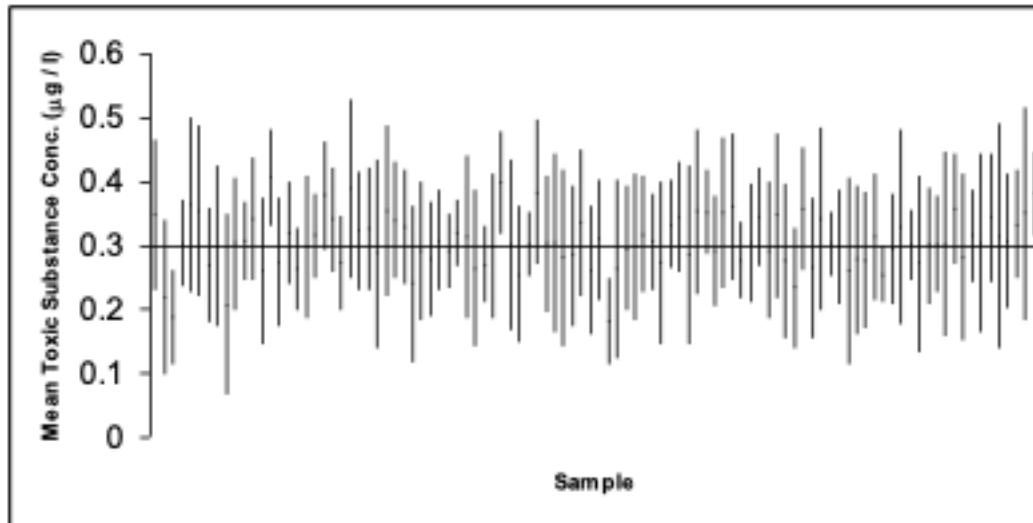


Figure 6: Depiction of confidence intervals from each of 100 simulated samples

Confidence intervals - Unknown variance

- Approximately 95% of these simulated samples have a confidence interval that includes the true value of 0.3 ($\mu\text{g/l}$). In the graph above, a confidence interval includes the true mean value of 0.3 if the vertical line (representing the width of the CI) crosses the horizontal line.
- We have to accept that 5% of the time we will not capture the true mean.
- We can widen the confidence interval to 99% so we are more confident but this can increase the chance of a type II error.

Example 2: One sample test

What happens when the assumptions are not met?

1. We can try and transform the data to make it more normal (and equal variance for later)
2. We can use a non-parametric test (later)

Example 2: Data transformations

My data is not normal :(what can I do? - Sometimes we can transform our data to make it more normal. - Let's look at an example: - Total nitrogen (TN) levels @ Wallacia in western Sydney on the Nepean River - According to the ANZECC guidelines, the maximum acceptable level of TN in an lowland river is $500 \mu\text{g/L}$ and for an upland river = $250 \mu\text{g/l}$. (see Table 3.3.2 in Australian and New Zealand Guidelines for Fresh and Marine Water Quality)

```
TN ← read.csv("data/TN_Wallacia.csv")
str(TN)
```

```
'data.frame': 29 obs. of 1 variable:
 $ TN: int 1020 1120 1170 920 920 1010 850 910 800 710 ...
```

```
mean(TN$TN, na.rm = TRUE) # na.rm=TRUE if we have missing values
```

```
[1] 855.8621
```

```
median(TN$TN, na.rm = TRUE)
```

```
[1] 800
```

Example 2: State Hypothesis

- $H_0 : \mu = 500 \mu g/l$ (Null hypothesis)
- $H_1 : \mu \neq 500 \mu g/l$ (Alternate hypothesis)

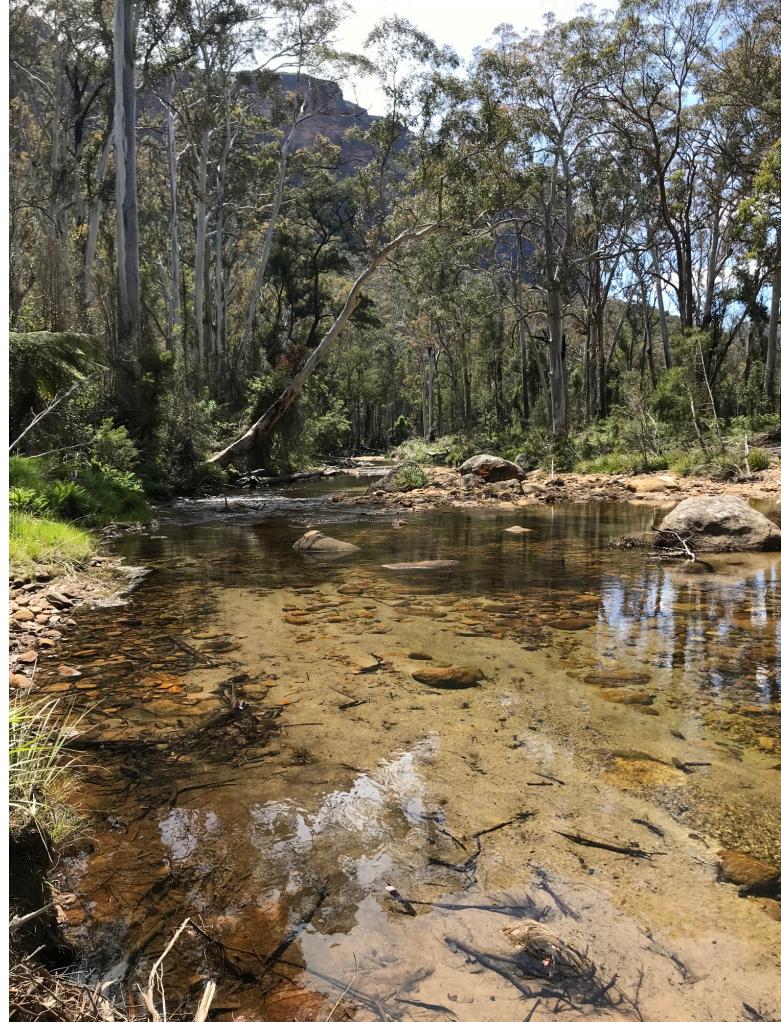


Figure 7: Grose River - Floris van Ogtrop

Example 2: Check assumptions

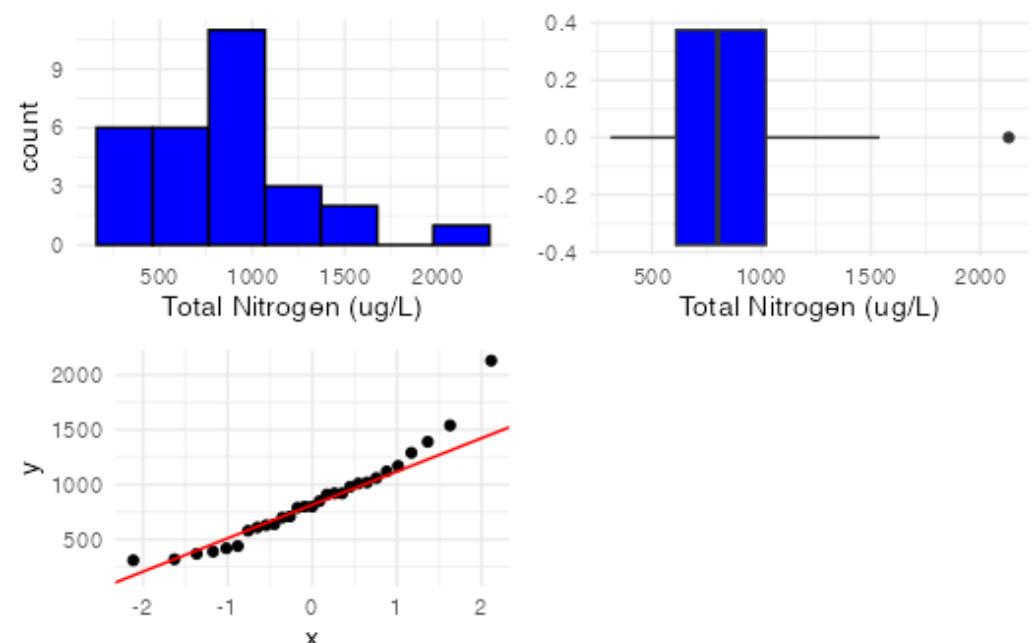
```
library(ggplot2)
library(gridExtra)

# Histogram
p1 ← ggplot(TN, aes(x = TN)) +
  geom_histogram(
    fill = "blue", color = "black",
    bins = 7
  ) +
  xlab("Total Nitrogen (ug/L)") +
  theme_minimal()

# Boxplot
p2 ← ggplot(TN, aes(x = TN)) +
  geom_boxplot(fill = "blue") +
  xlab("Total Nitrogen (ug/L)") +
  theme_minimal()

# Q-Q plot
p3 ← ggplot(TN, aes(sample = TN)) +
  stat_qq() +
  stat_qq_line(col = "red") +
  theme_minimal()
```

```
# Arrange the plots in a 2x2 layout
grid.arrange(p1, p2, p3, ncol = 2)
```



Example 2: Check assumptions

Shapiro-Wilk normality test

- For smaller sample sizes, use the Shapiro-Wilk test (say < 50)

```
shapiro.test(TN$TN)
```

```
Shapiro-Wilk normality test
```

```
data: TN$TN
W = 0.92582, p-value = 0.04293
```

- We see P<0.05 so we **reject** the null hypothesis that the data is normally distributed.
- For really large samples (>>30) the central limit theorem suggests that the distribution of the sample means tends to be normal, regardless of the population distribution. This means that for sufficiently large samples, the t-test can be robust to violations of normality. However, extreme skewness, heavy tails, or outliers can still affect the test's performance.

Example 2: Transformations

For right (positive) skewed data, we can use a

- $1/x$ inverse transformation for highly skewed data.
- \log_{10} or \log_e transformation for very skewed data.
- \sqrt{x} square root transformation for moderately skewed data.

For left (negative) skewed data (which is rare to find), we can “try” a

- x^2 or x^3 transformation.

Example 2: Transformations & Recheck assumptions

```
# Let's try a log10 transformation  
# We start by creating a new column in our data frame called log10_TN  
# We then take the log10 of the TN column and store it in the new column  
TN$log10_TN ← log10(TN$TN)
```

Geometric mean

Note that now we are looking at the geometric mean as opposed the the arithmetic mean which was 855.86 in our case

```
10^mean(TN$log10_TN)
```

```
[1] 770.0666
```

Example 2: Recheck assumptions

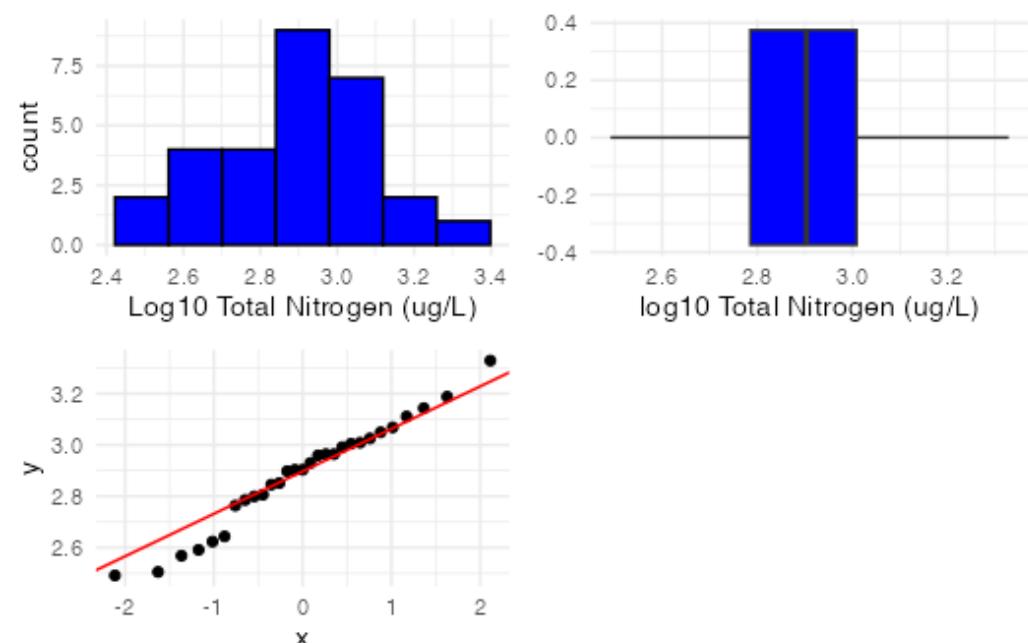
```
library(ggplot2)
library(gridExtra)

# Histogram
p1 ← ggplot(TN, aes(x = log10_TN)) +
  geom_histogram(
    fill = "blue", color = "black",
    bins = 7
  ) +
  xlab("Log10 Total Nitrogen (ug/L)") +
  theme_minimal()

# Boxplot
p2 ← ggplot(TN, aes(x = log10_TN)) +
  geom_boxplot(fill = "blue") +
  xlab("log10 Total Nitrogen (ug/L)") +
  theme_minimal()

# Q-Q plot
p3 ← ggplot(TN, aes(sample = log10_TN)) +
  stat_qq() +
  stat_qq_line(col = "red") +
  theme_minimal()
```

```
# Arrange the plots in a 2x2 layout
grid.arrange(p1, p2, p3, ncol = 2)
```



Example 2: Recheck assumptions

Shapiro-Wilk normality test

```
shapiro.test(TN$log10_TN)
```

```
Shapiro-Wilk normality test
```

```
data: TN$log10_TN  
W = 0.97279, p-value = 0.6375
```

- From our previous slide, our data seems to be quite symmetrical
- Now P>0.05 so we **fail to reject** the null hypothesis that the data is normally distributed.
- We can now proceed with our t-test using the log transformed data.
- **NOTE:** *We will also need to transform the hypothesised mean of 500 to the log10 scale.*

Example 2: T-test & P-Value

```
t.test(TN$log10_TN,  
       mu = log10(500),  
       alternative = "two.sided",  
       conf.level = 0.95  
)
```

One Sample t-test

```
data: TN$log10_TN  
t = 4.8768, df = 28, p-value = 3.884e-05  
alternative hypothesis: true mean is not equal to 2.69897  
95 percent confidence interval:  
 2.807748 2.965309  
sample estimates:  
mean of x  
2.886528
```

- The p-value is <0.001 (3.d.p.) which is less than 0.05. Therefore, we reject the null hypothesis.
- There is strong evidence that the mean value of TN in Nepean River is different to 500 ug/L.
 - Can we say something about the direction??

Example 2: Confidence intervals

- We need to back transform the confidence interval to the original scale.
- To back-transform the confidence interval we can use the following:

$$10^{CI_{low}} \text{ and } 10^{CI_{high}}$$

```
10^(2.81)
```

```
[1] 645.6542
```

```
10^(2.97)
```

```
[1] 933.2543
```

- This means that we are 95% confident that the geometric mean (back-transformed mean) of the sample is between approximately 646 and 933 ug/l. This is higher than the hypothesised mean.

Example 2: Conclusion

1. The data was log10 transformed to meet the assumptions of the t-test.
2. We have strong evidence that the mean value of Total Nitrogen in Nepean River is different to 500 ug/L.
3. We are 95% confident that the geometric mean (back-transformed mean) of the sample is between approximately 646 and 933 ug/l.
4. Looking at the confidence interval, we can say that the mean value of TN in Nepean River is significantly greater than 500 ug/L.

Example 3: One tailed test

- We can also use a one tailed test if we are specifically interested in whether the observed value is greater or less than the expected value.
- In this case we only want to know if the TN concentration is greater than the ANZECC guidelines of $500 \mu g/l$.
- $H_0 : \mu = 500 \mu g/l$ (Null hypothesis)
- $H_1 : \mu > 500 \mu g/l$ (Alternate hypothesis)

Example 3: One tailed test

```
t.test(TN$log10_TN,  
       mu = log10(500),  
       alternative = "greater",  
       conf.level = 0.95  
)
```

One Sample t-test

```
data: TN$log10_TN  
t = 4.8768, df = 28, p-value = 1.942e-05  
alternative hypothesis: true mean is greater than 2.69897  
95 percent confidence interval:  
 2.821104      Inf  
sample estimates:  
mean of x  
2.886528
```

- $P < 0.001$ (3.d.p.) so we reject the null hypothesis.
- Because we are doing a one tailed test we can now conclude that the mean value of TN in Nepean River is greater than 500 mg/L . What do you notice when comparing to the two tailed test?

Example 3: One tailed test

Ruxton and Neuhäuser 2010

Methods in Ecology and Evolution



Methods in Ecology and Evolution 2010, **1**, 114–117

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When should we use one-tailed hypothesis testing?

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Thanks!

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