SIMPLE PARAMETRIC TESTS

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Introduction

Parametric test are those statistical approaches which rely on **assumptions** about the parameters which define a population.

Prominent parametric tests include:

- Pearson correlation (Seminar 9 - Correlation Tests)
- **t-Test**
- **An**alysis **O**f **Va**riance (ANOVA)
- Linear regression
- Multivariate extensions of parametric methods
- ...

Terminology

A reminder about the distinction of parametric and non-parametric tests (taken from Seminar 6):

Non-Parametric Tests

- Less *restrictive*
- Make *little to no assumptions*
- Often a **black box**
- Require *more data*

Parametric Tests

- More *restrictive*
- Make *strict assumptions*
- **Easy to interpret**
- Require *less data*

$\rightarrow$ Parametric tests are **numerous**!

Purpose And Assumptions

t-Test (unpaired)

t.test(..., paired = FALSE) in base R

Purpose:
To identify whether groups of variable values are different from one another.

H_0
There is no difference in characteristics of the response variable values in dependence of the classes of the predictor variable.

Assumptions:
- Predictor variable is binary
- Response variable is metric and **normal distributed** within their groups
- Variable values are **independent** (not paired)

$\rightarrow$ Test whether variance of response variable values in groups are equal (var.test()) and adjust t.test() argument var.equal accordingly.

Minimal Working Example

Let's feed data to our `t.test(..., paired = FALSE)` function that holds two groups with clearly differing means:

```
data <- c(rnorm(10, 5, 1), rnorm(10, 10, 1))
factors <- as.factor(rep(c("A", "B"), each = 10))
t.test(data ~ factors, paired = FALSE)
```

```
##
##   Welch Two Sample t-test
##
## data:  data by factors
## t = -12, df = 14, p-value = 1e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -6.4 -4.4
## sample estimates:
## mean in group A mean in group B
##             4.4             9.8
```

The output above tells us that the means of our two groups are significantly different.

Purpose And Assumptions

t-Test (paired)

t.test(..., paired = TRUE) in base R

Purpose:
To identify whether groups of variable values are different from one another.

H_0
There is no difference in characteristics of the response variable values in dependence of the classes of the predictor variable.

Assumptions:

- Predictor variable is binary
- Response variable is metric
- *Difference of response variable pairs* is **normal distributed**
- Variable values are **dependent** (paired)

$\rightarrow$ Test whether variance of response variable values in groups are equal (var.test()) and adjust t.test() argument var.equal accordingly.

Minimal Working Example

Let's feed data to our `t.test(..., paired = TRUE)` function that holds two
connected groups with clearly differing means:

```
data <- c(rnorm(10, 5, 1), rnorm(10, 10, 1))
factors <- as.factor(rep(c("A", "B"), each = 10))
t.test(data ~ factors, paired = TRUE)

##
##  Paired t-test
##
## data:  data by factors
## t = -10, df = 9, p-value = 3e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -5.7 -3.7
## sample estimates:
## mean of the differences
##                    -4.7
```

The output above tells us that the means of our two connected groups are significantly
different.

Introduction to ANOVA

ANOVAs are used to test whether there is a difference between groups of variable values.

There are **multiple versions of ANOVAs**:

- One-way ANOVA (one predictor variable)
- Two-Way ANOVA (multiple predictor variables)
- MANOVA (multivariate ANOVA/multiple response variables)
- ANCOVA (categorical and continuous predictor variables)
- MANCOVA (multivariate ANCOVA)

Data for ANOVA

We will use the `crabs` data set from the `MASS` package

```r
library(MASS)
data(crabs)
head(crabs)
```

```
##   sp sex index   FL  RW CL CW  BD
## 1  B   M     1  8.1 6.7 16 19 7.0
## 2  B   M     2  8.8 7.7 18 21 7.4
## 3  B   M     3  9.2 7.8 19 22 7.7
## 4  B   M     4  9.6 7.9 20 23 8.2
## 5  B   M     5  9.8 8.0 20 23 8.2
## 6  B   M     6 10.8 9.0 23 26 9.8
```

Purpose And Assumptions

One-Way ANOVA

anova() in base R

Purpose: To explain the variance of a continuous response variable in relation to one predictor variables.

H_0 *Variance of response variable values is equal between levels of predictor variable.*

Assumptions:

- Predictor variable is categorical
- Response variable is metric
- *Response variable residuals* are **normal distributed**
- Variance of populations/samples are equal (**homogeneity**)
- Variable values are **independent** (not paired)

$\rightarrow$ Test whether residuals are normal distributed with shapiro.test() in base R, test for homogeneity with leveneTest() in the car package.

Minimal Working Example - Assumptions

Let's test whether body depth (BD) of crabs are varying when grouped by sex:

```
OneWay <- with(crabs, lm(BD ~ sex)) # MODEL
```
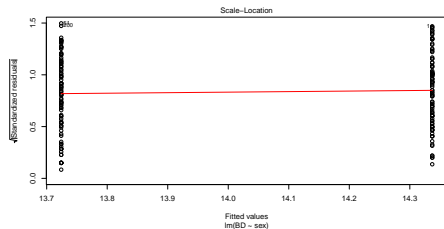
```
plot(OneWay, 2) # Normality
```



```
plot(OneWay, 3) # Homogeneity
```
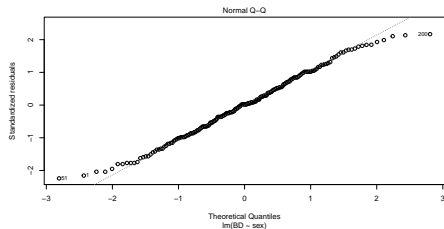


```
shapiro.test(residuals(OneWay))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(OneWay)
## W = 1, p-value = 0.2
```

```
library("car")
leveneTest(BD ~ sex, data = crabs)
```

```
## Levene's Test for Homogeneity of Variance (center = media
##        Df F value Pr(>F)
## group   1    0.36   0.55
##       198
```

All good on the assumption check!

Minimal Working Example - Analysis

Now let's run the analysis:

```
anova(OneWay)
```

```
## Analysis of Variance Table
##
## Response: BD
##            Df Sum Sq Mean Sq F value Pr(>F)
## sex         1     19    18.8    1.61   0.21
## Residuals 198   2315    11.7
```

As we can see, sex does not make for a statistically significant predictor of crab body depth.

Minimal Working Example - Interpretation

Let's interpret the result anyways:

```
summary(OneWay)
```

```
##
## Call:
## lm(formula = BD ~ sex)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -7.624 -2.449  0.076  2.463  7.376
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   13.724      0.342   40.13   <2e-16 ***
## sexM           0.613      0.484    1.27     0.21
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.4 on 198 degrees of freedom
## Multiple R-squared:  0.00805,    Adjusted R-squared:  0.00304
## F-statistic: 1.61 on 1 and 198 DF,  p-value: 0.206
```

- Female crabs are estimated to have a body depth of 13.72cm (**Intercept**) with males being 0.61cm bigger, on average.
- While we can be certain of the female estimate, we cannot say the same about the different to males.

Purpose And Assumptions

Two-Way ANOVA

anova() in base R

Purpose: To explain the variance of a continuous response variable in relation to multiple predictor variables.

H_0 *Variance of response variable values is equal between levels of predictor variables.*

Assumptions:

- Predictor variables are categorical
- Response variable is metric
- *Response variable residuals* are **normal distributed**
- Variance of populations/samples are equal (**homogeneity**)
- Variable values are **independent** (not paired)

$\rightarrow$ Test whether residuals are normal distributed with shapiro.test() in base R, test for homogeneity with leveneTest() in the car package.

Minimal Working Example - Assumptions

Let's test whether body depth (BD) of crabs are varying when grouped by sex and species as well as their interaction:

```
TwoWay <- with(crabs, lm(BD ~ sex * sp))
```
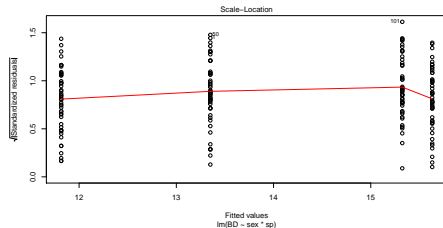
```
plot(TwoWay, 2) # Normality
```



```
plot(TwoWay, 3) # Homogeneity
```
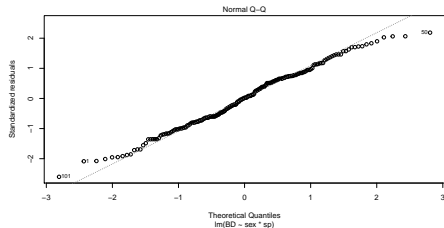


```
shapiro.test(residuals(TwoWay))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals(TwoWay)
## W = 1, p-value = 0.2
```

```
library("car")
leveneTest(BD ~ sex*sp, data = crabs)
```

```
## Levene's Test for Homogeneity of Variance (center = media
##        Df F value Pr(>F)
## group   3    2.02   0.11
##       196
```

All good on the assumption check!

Minimal Working Example - Analysis

Now let's run the analysis:
```
anova(TwoWay)
```
```
## Analysis of Variance Table
##
## Response: BD
##             Df Sum Sq Mean Sq F value  Pr(>F)
## sex          1     19      19    1.99   0.160
## sp           1    419     419   44.31 2.8e-10 ***
## sex:sp       1     42      42    4.48   0.035 *
## Residuals  196   1854       9
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The output above tells us that species and the interaction effect of sex and species are meaningful for understanding body depth of crabs.

Minimal Working Example - Interpretation

```
summary(TwoWay)
```

```
##
## Call:
## lm(formula = BD ~ sex * sp)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -7.924 -2.224  0.059  2.250  6.650
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   11.816      0.435   27.17  < 2e-16 ***
## sexM           1.534      0.615    2.49    0.013 *
## spO            3.816      0.615    6.20  3.2e-09 ***
## sexM:spO      -1.842      0.870   -2.12    0.035 *
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.1 on 196 degrees of freedom
## Multiple R-squared:  0.206,  Adjusted R-squared:  0.194
## F-statistic: 16.9 on 3 and 196 DF,  p-value: 8.13e-10
```

- Female crabs of species B are estimated to have a body depth of 11.82cm (**Intercept**) with males of species B being 1.53cm bigger, on average.
- Female crabs of species O are estimated to have a body depth of 3.82cm bigger than their female species B counterparts.
- The difference in sex- vs. species-dependant change in body depth is -1.84cm.
- All estimates are statistically significant.

Purpose And Assumptions

ANCOVA

anova() in base R

Purpose:

To explain the variance of a continuous response variable in relation to mixed (continuous and categorical) predictor variables.

H_0

Adjusted variance and means of response variable values is equal between levels of predictor variables.

Assumptions:

- Predictor variables are categorical or continuous
- Response variable is metric
- *Response variable residuals* are **normal distributed**
- Variance of populations/samples are equal (**homogeneity**)
- Variable values are **independent** (not paired)
- Relationship between the response and covariate is linear.

$\rightarrow$ Test whether residuals are normal distributed with shapiro.test() in base R, test for homogeneity with leveneTest() in the car package.

Minimal Working Example - Assumptions

Let's test whether carapace length (CL) of crabs are varying when grouped by species and the carapace width as a covariate:

```
Ancova <- with(crabs, lm(CL ~ sp * CW))
```
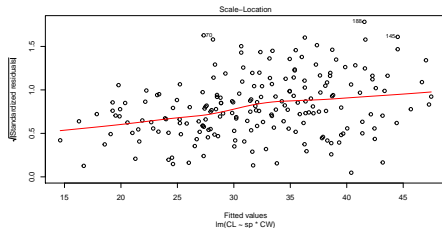
```
plot(Ancova, 2) # Normality
```

```
plot(Ancova, 3) # Homogeneity
```
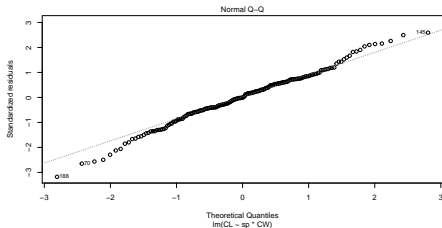


```
shapiro.test(residuals(Ancova))
```

```
## 
##  Shapiro-Wilk normality test
## 
## data:  residuals(Ancova)
## W = 1, p-value = 0.2
```

```
library("car")
leveneTest(CL ~ sp, data = crabs)
```

```
## Levene's Test for Homogeneity of Variance (center = media
##        Df F value Pr(>F)
## group   1     0.1   0.75
##       198
```

Assumptions are met!

Minimal Working Example - Analysis

Now let's run the analysis:

```
anova(Ancova)
```

```
## Analysis of Variance Table
##
## Response: CL
##             Df Sum Sq Mean Sq  F value  Pr(>F)
## sp           1    838     838  3868.20  <2e-16 ***
## CW           1   9203    9203 42460.12  <2e-16 ***
## sp:CW        1      1       1     4.29    0.04 *
## Residuals  196     42       0
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The output above tells us that all of our model coefficients are significant.

Minimal Working Example - Interpretation

```
summary(Ancova)
```

```
##
## Call:
## lm(formula = CL ~ sp * CW)
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -1.4634 -0.2611 -0.0041  0.2907  1.1861
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.36442    0.21170   -1.72    0.087 .
## spO          0.44111    0.32079    1.38    0.171
## CW           0.87630    0.00595  147.31   <2e-16 ***
## spO:CW       0.01781    0.00860    2.07    0.040 *
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.47 on 196 degrees of freedom
## Multiple R-squared:  0.996,  Adjusted R-squared:  0.996
## F-statistic: 1.54e+04 on 3 and 196 DF,  p-value: <2e-16
```

- Crabs of species B have an estimated carapace length of -0.36cm when their carpace width would be 0cm (**Intercept**) with members of species B being 0.44cm bigger, on average at 0cm carapace width.
- For each additional cm in carapace width, carapacae length in species B increases by 0.88cm.
- For each additional cm in carapace width, carapacae length in species O increases by 0.88cm more than in species B.
- All estimates except for the species-difference are statistically significant.

Variables We Can Use

Response variables (metric)

- Weight
- Height
- Wing Chord
- Nesting Height
- Number of Eggs
- Egg Weight

Predictor variables (categorical)

- Sex (binary)
- Climate (binary)
- Climate (3 levels - Continental, Semi-Coastal, Coastal)
- Home Range (3 levels - Small, Medium, Large)
- Site Index (11 levels)
- Predator Presence/Type (3 levels - Avian vs. Non-Avian vs. None)

Research Questions And Hypotheses

So which of our major research questions (seminar 6) can we answer?

unpaired t-Test
- *Climate Warming/Extremes:* Does sparrow morphology change depend on climate?
- *Sexual Dimorphism:* Does sparrow morphology change depend on Sex?

Use the `1 - Sparrow_Data_READY.rds` data set for these analyses.

paired t-Test (suppose a resettling program)
- *Climate Warming/Extremes:* Does sparrow morphology change depend on climate?

Use the `2b - Sparrow_ResettledSIUK_READY.rds` data set for these analyses.

One-Way ANOVA
- *Climate Warming/Extremes:* Does sparrow morphology depend on climate?
- *Predation:* Does nesting height depend on predator characteristics?

Two-Way ANOVA
- *Sexual Dimorphism:* Does sparrow morphology depend on population status and sex?

ANCOVA
- *Climate Warming/Extremes:* Do sparrow characteristics depend on climate and latitude?

Use the `1 - Sparrow_Data_READY.rds` data set for these analyses.

Remember to diligently **check assumptions**!