

ANOVA, ANCOVA & Factorial ANOVA Materials

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Introduction to ANOVA

Running ANOVA

```
library(car)
library(psych)
library(multcomp)
library(effects)
library(tidyverse)
library(sjstats)
```

```
data <- dplyr::starwars
```

```

data <- data %>%
  dplyr::select(height, mass, hair_color, species, sex) %>%
  na.omit() %>%
  filter(species == "Gungan" | species == "Human" | species == "Wookiee")

height_species_aov <- aov(height ~ species, data = data)
summary(height_species_aov)

# Post Hoc Test (Tukey)
TukeyHSD(height_species_aov)
# Bonferroni Adjustment vs Tukey
pairwise.t.test(data$height, data$species, p.adjust.method = "bonferroni")

```

Line 14

Here we are using the `filter()` function to filter for “Gungan”, “Human” and “Wookiee”

Line 16

This is the `aov()` function. Here we are specifying the ANOVA formula.

Line 17

The `summary()` function will give you the output of the ANOVA

Line 20

Because the species variable has more than 2 conditions, we might want to figure out which comparisons are statistically different from each other. The `TukeyHSD()` function allows us to perform a post hoc Tukey test

Line 22

Maybe Tukey isn’t your favorite correction. Another route might be to use a pairwise t test that corrects for multiple comparisons using a Bonferroni correction. You can do that with the `pairwise.t.test()` function.

```

              Df Sum Sq Mean Sq F value    Pr(>F)
species        2   5841   2920.6    21.11 9.43e-06 ***
Residuals     21   2906    138.4
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Tukey multiple comparisons of means
 95% family-wise confidence level

Fit: aov(formula = height ~ species, data = data)

$species
      diff      lwr      upr    p adj
Human-Gungan -29.75 -51.738704 -7.761296 0.0071194
Wookiee-Gungan 21.00  -8.649562 50.649562 0.1987756

```

```
Wookiee-Human    50.75   28.761296  72.738704  0.0000258
```

Pairwise comparisons using t tests with pooled SD

```
data: data$height and data$species
```

```
      Gungan Human  
Human  0.0079  -  
Wookiee 0.2660 2.7e-05
```

```
P value adjustment method: bonferroni
```

Assumptions of ANOVA

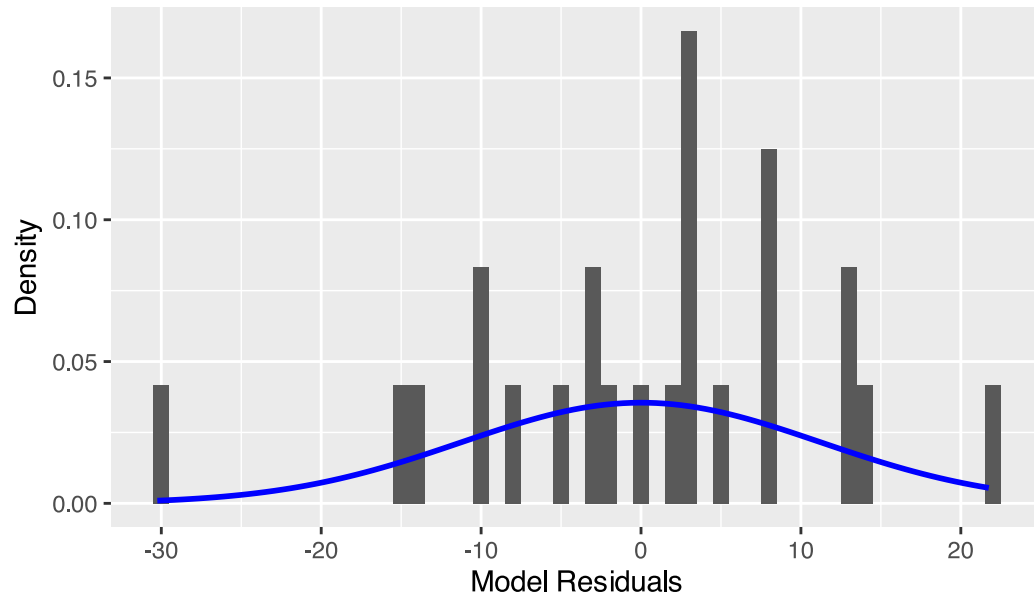
As ANOVA is just a special case of linear regression, the same assumptions exist for ANOVA that exist for linear regression. We will test each assumption below. The code will look awfully similar to the code used for linear regression previously

Model Normality

Graphical

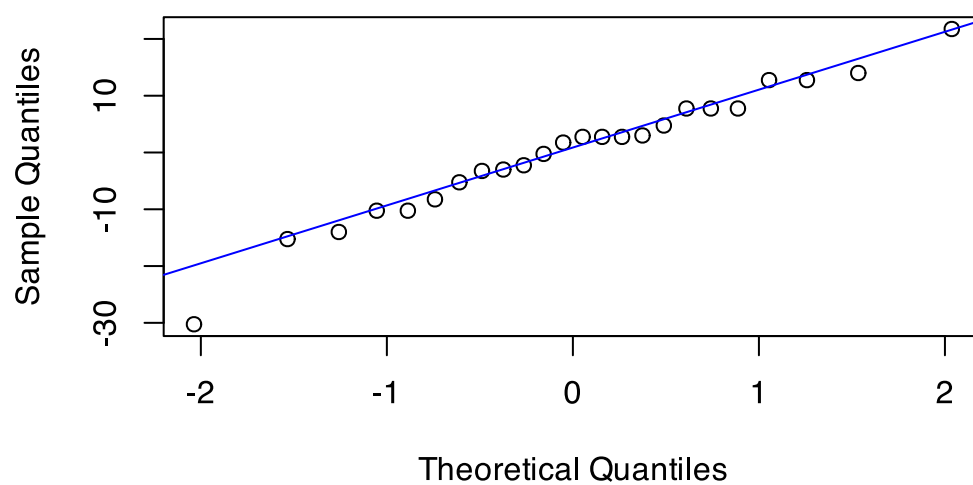
```
density_plot <- data %>% ggplot(aes(x = height_species_aov$residuals)) +  
  geom_histogram(aes(y= after_stat(density)),binwidth = 1) +  
  stat_function(fun = dnorm,  
               args = list(mean = mean(height_species_aov$residuals),  
                           sd = sd(height_species_aov$residuals)),  
               col = "blue",  
               linewidth = 1) +  
  labs(title = "Figure 1. Histogram of Model Residual Scores",  
       x = "Model Residuals",  
       y = "Density")  
  
density_plot
```

Figure 1. Histogram of Model Residual Scores



```
# OR  
  
qqnorm(height_species_aov$residuals)  
qqline(height_species_aov$residuals, col = "blue")
```

Normal Q-Q Plot



1. When running the `qqnorm()` and `qqline()` functions at the same time, you will get a qq-plot which will graphically assess the normality of the argument given (in this case the model residuals). The `col` argument simply tells R which color to make the reference line.

Statistical

```
psych::describe(height_species_aov$residuals)
shapiro.test(height_species_aov$residuals)
```

Line 1

Another way to assess normality is to look at the skew and kurtosis of the data. Typically skew and kurtosis between -1 and 1 are acceptable. We can see this using the `describe()` function within the `psych` package.

```
vars  n mean    sd median trimmed  mad   min   max range  skew kurtosis
X1    1 24    0 11.24   2.25   0.49 8.15 -30.25 21.75   52 -0.53    0.35
      se
X1 2.29

Shapiro-Wilk normality test

data:  height_species_aov$residuals
W = 0.97026, p-value = 0.6734
```

Homogeneity of Variance

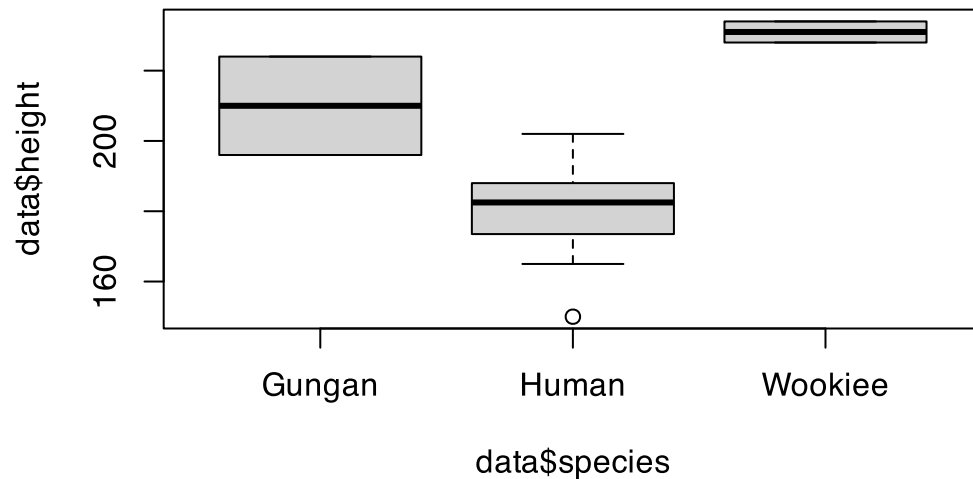
As with regression, homogeneity of variance is also important for ANOVA. We will graphically and statistically assess this assumption below.

Graphical

```
boxplot(data$height ~ data$species)
```

Line 1

The `boxplot()` function will give us a visual representation of the DV at each level of the IV. We are looking for boxplots that are roughly the same height across each group.



Statistical

Statistically, we can assess homogeneity of variance using Levene's Test. Here we want the results to not be statistically significant.

```
leveneTest(data$height ~ data$species)
```

Line 1

The `leveneTest()` function from the `car` package takes a DV and IV as arguments.

```
Levene's Test for Homogeneity of Variance (center = median)
  Df F value Pr(>F)
group 2  1.0572 0.3652
  21
```

Introduction to ANCOVA

Running ANCOVA

ANCOVA refers to any ANOVA model with 2 or more parameters. These models require similar assumptions to ANOVA with a couple of additional ones. Below we will see how to run an ANCOVA and then test its assumptions.

```
data <- data %>% mutate(species = as.factor(species))
# Type I SS
ancova <- aov(height ~ species + mass, data = data)
```

```

summary(ancova)
# Reversed Order
ancova2 <- aov(height ~ mass + species, data = data)
summary(ancova2)

car::Anova(ancova2, type = "III")

# Std Means
summary_data <- data %>%
  dplyr::group_by(species) %>%
  dplyr::summarise(n = n(),
                  mean = mean(height))

# Adjust means for covariate effect
adjustedMeans<- effect("species", ancova, se=TRUE)
summary(adjustedMeans)
adjustedMeans$se

# Post Hoc Tests

posthoc <- multcomp::glht(ancova, linfct = multcomp::mcp(species = "Tukey"))
summary(posthoc)
confint(posthoc)

# Effect size
sjstats::anova_stats(car::Anova(ancova,type = "III"))

```

Line 4

This displays our ANCOVA output with species and then mass.

Line 7

This displays our ANCOVA output with mass and then species. We can see that 1 and 2 are different. This is because R by default does a sequential ANCOVA so order matters.

Line 9

To get around this, we can use the `Anova()` function in the `car` package to specify that we want Type III sums of squares. This will then generate an ANCOVA where the order of predictors doesn't matter

Line 18

When having covariates, one might wish to report adjusted means. We can do that using the `effect()` function from the `effects` package.

Line 24

To run a post hoc analysis, we need to use the `glht()` function from the `multcomp` package. There are additional corrections you can do outside of Tukey. To investigate, please see the documentation.

Line 29

To get basic ANOVA effect size statistics, we can use the `anova_stats()` function from the `sjstats` package.

```
      Df Sum Sq Mean Sq F value    Pr(>F)
species    2   5841   2920.6   28.662 1.34e-06 ***
mass       1    868    867.8    8.516 0.0085 **
Residuals 20   2038    101.9
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

      Df Sum Sq Mean Sq F value    Pr(>F)
mass       1   3231    3231   31.70 1.64e-05 ***
species    2   3478    1739   17.07 4.74e-05 ***
Residuals 20   2038     102
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Anova Table (Type III tests)

Response: height
      Sum Sq Df F value    Pr(>F)
(Intercept) 27816.3 1 272.9827 3.998e-13 ***
mass         867.8 1   8.5164 0.0085 **
species     3478.5 2  17.0684 4.736e-05 ***
Residuals   2038.0 20
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

species effect
species
  Gungan   Human  Wookiee
213.4855 181.2518 217.4968

Lower 95 Percent Confidence Limits
species
  Gungan   Human  Wookiee
198.3892 176.4892 199.7528

Upper 95 Percent Confidence Limits
species
  Gungan   Human  Wookiee
228.5818 186.0143 235.2409
[1] 7.237078 2.283137 8.506395
```

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


```
Fit: aov(formula = height ~ species + mass, data = data)

Linear Hypotheses:
              Estimate Std. Error t value Pr(>|t|)
Human - Gungan == 0    -32.234      7.534  -4.278 < 0.001 ***
Wookiee - Gungan == 0     4.011     11.653   0.344  0.93377
Wookiee - Human == 0     36.245      8.986   4.034  0.00164 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

Simultaneous Confidence Intervals

Multiple Comparisons of Means: Tukey Contrasts

```
Fit: aov(formula = height ~ species + mass, data = data)
```

Quantile = 2.5032
95% family-wise confidence level

Linear Hypotheses:

	Estimate	lwr	upr
Human - Gungan == 0	-32.2337	-51.0940	-13.3735
Wookiee - Gungan == 0	4.0113	-25.1579	33.1806
Wookiee - Human == 0	36.2451	13.7513	58.7389

etasq	partial.etasq	omegasq	partial.omegasq	epsilon _{sq}	cohens.f	
term	sumsq	df	meansq	statistic	p.value	power
0.545	0.631	0.505	0.572	0.513	1.306	
species	3478.457	2	1739.228	17.068	< .001	1.000
0.136	0.299	0.118	0.238	0.120	0.653	
mass	867.799	1	867.799	8.516	0.008	0.829
Residuals	2037.951	20	101.898			

Assumptions of ANCOVA

ANCOVA requires the same assumptions as ANOVA with two additional assumptions: 1) That the predictor and covariate are independent 2) The regression slopes are homogeneous

We will test each of the traditional parametric tests as well as the two additional assumptions below.

Predictor x Covariate Independence

Statistical

```
predictor_assumption <- aov(mass ~ species, data = data)
summary(predictor_assumption)
```

Line 1

To assess this statistically, one needs to run an ANOVA looking at each predictor with each additional parameter. We do not want these to be statistically significant.

```
              Df Sum Sq Mean Sq F value Pr(>F)
species        2   3543   1771.6    4.949  0.0173 *
Residuals     21   7517    357.9
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Tip

Here the statistical test for this assumption is statistically significant (which is bad). It actually means we can't do this (unless we have random assignment)

Homogeneity of Regression Slopes

Statistical

```
regression_slope_assumption <- aov(height ~ species*mass, data = data)
car::Anova(regression_slope_assumption, type = "III")
```

Line 2

To test this assumption, one just needs to test the interaction effects within the model. The code for this is shown here.

Anova Table (Type III tests)

```
Response: height
              Sum Sq Df F value  Pr(>F)
(Intercept)  149.72  1   1.5160  0.23407
species       164.06  2   0.8306  0.45183
mass          392.00  1   3.9692  0.06173 .
species:mass   260.25  2   1.3176  0.29241
Residuals    1777.70 18
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



Tip

For the above example, the interaction is NOT significant so assumption is met

Residual Normality (DV ~ IV)

Residual normality is an assumption shared with standard regression. We can assess it the same way we did previously when looking at simple ANOVA. The same is true for the homogeneity of variance assumption.

Statistical

```
height_mass_resid <- scale(residuals(aov(height ~ mass, data = data)))
psych::describe(height_mass_resid)
shapiro.test(height_mass_resid)
```

Line 1

The `scale()` function will scale the residuals of the ANOVA. The `residuals()` function pulls out the residuals within the ANOVA

Line 2

Statistical summary of the residuals using the `describe()` function in the `psych` package

Line 3

Statistical test (Shapiro Wilks) of the residuals using the `shapiro.test()` function

```
vars  n mean sd median trimmed  mad   min  max range skew kurtosis  se
X1    1 24   0  1  -0.07  -0.06 0.93 -1.83 2.47   4.3  0.6   -0.15 0.2

Shapiro-Wilk normality test

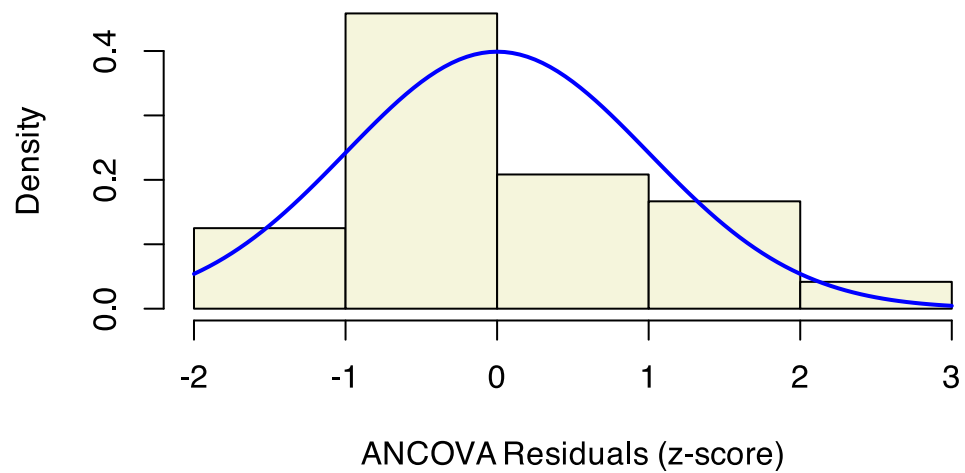
data:  height_mass_resid
W = 0.9563, p-value = 0.3686
```

Graphical

```
hist(height_mass_resid, col = 'beige',
      main="", xlab = "ANCOVA Residuals (z-score)",
      probability = TRUE)
curve(dnorm(x, mean = mean(height_mass_resid),
            sd = sd(height_mass_resid)),
      add = TRUE, lwd = 2, col = 'blue')
```

Lines 1-6

A graphical histogram (with normal distribution overlay) of the model residuals



Homogeneity of Variance

Statistical

```
# Levene's Test to Assess Equal Variance for Species
car::leveneTest(data$height ~ data$species)
```

Line 2

A statistical test (Levene's test) of the homogeneity assumption using the `leveneTest()` function in the `car` package.

```
Levene's Test for Homogeneity of Variance (center = median)
      Df F value Pr(>F)
group  2  1.0572 0.3652
      21
```

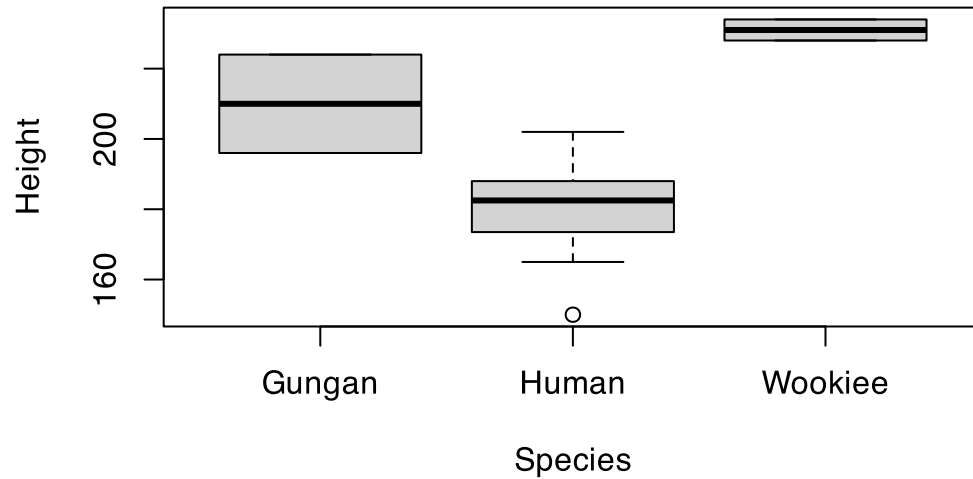
Graphical

```
# Boxplot Height by Species
boxplot(height ~ species, data=data, main="Height Variance by Species ",
        xlab="Species", ylab="Height")
```

Lines 2-3

A visual representation of the homogeneity of variance assumption using a boxplot

Height Variance by Species



Linearity of CV & DV

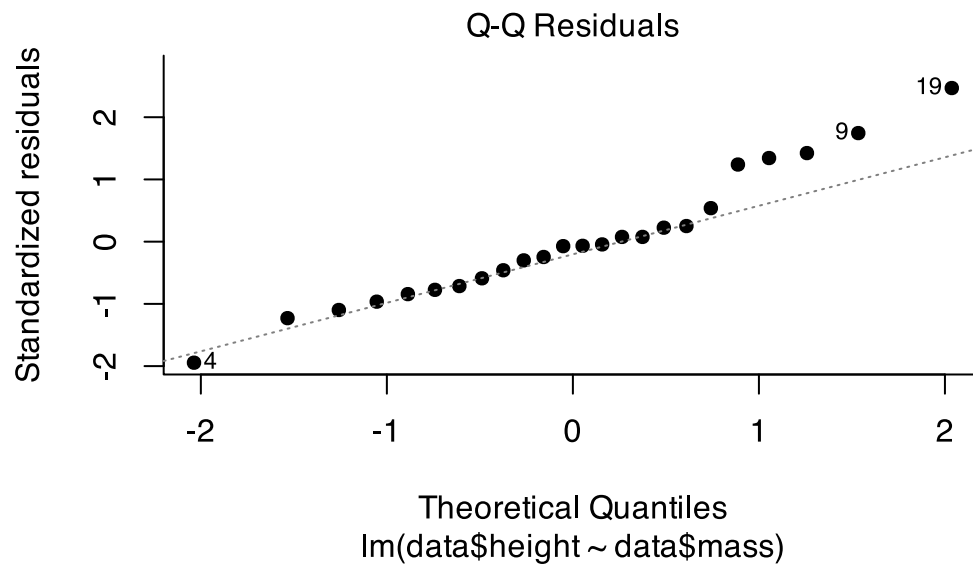
The last assumption is that the CV and DV are linearly related. We can test this using the code below graphically.

Graphical

```
plot(lm(data$height ~ data$mass, data = data),  
     pch = 16, bty = 'l', 2)
```

Lines 1-2

Visual representation of the CV to DV linearity assumption



Introduction to Factorial ANOVA

Running Factorial ANOVA

```
library(tidyverse)
factorial_data <- starwars %>%
  select(mass, homeworld, species) %>%
  mutate(homeworld = as.factor(homeworld),
         species = as.factor(species)) %>%
  filter(homeworld == "Tatooine" | homeworld == "Naboo") %>%
  filter(species == "Human" | species == "Droid") %>% na.omit()
# Modeling As Factorial ANOVA
aov_factorial <- aov(mass ~ species*homeworld, data = factorial_data)
Anova(aov_factorial, type = "III")

# Modeling As A Regression (For SS Analyses)
reg_fanova <- lm(mass ~ homeworld*species, data = factorial_data)
summary(reg_fanova)
```

Line 2

Start with the starwars data set

Line 3

Use the select() function to pull out mass, homeworld and species variables

Line 4

Call the mutate() function to format the homeworld variable using the as.factor() function.

Line 5

Format the species variables as a factor using the `as.factor()` function.

Line 6

Use the `filter()` function to filter for observations with `homeworld = "Tatooine" OR "Naboo"`

Line 7

Use the `filter()` function to filter for observations with `species = "Human" OR "Droid"`

Line 9

Create an ANOVA object using the `aov()` function

Line 10

Use the `Anova()` function from the `car()` package to specify Type III Sums of Squares

Line 13

Create an Regression object using the `lm()` function

Line 14

Show output of the regression object using the `summary()` function.

Anova Table (Type III tests)

Response: mass

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	1024.0	1	1.5447	0.2539
species	522.7	1	0.7884	0.4041
homeworld	308.2	1	0.4649	0.5173
species:homeworld	97.0	1	0.1464	0.7134
Residuals	4640.5	7		

Call:

```
lm(formula = mass ~ homeworld * species, data = factorial_data)
```

Residuals:

Min	1Q	Median	3Q	Max
-21.50	-17.00	-12.00	18.25	40.00

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	32.00	25.75	1.243	0.254
homeworldTatooine	21.50	31.53	0.682	0.517
speciesHuman	28.00	31.53	0.888	0.404
homeworldTatooine:speciesHuman	14.50	37.90	0.383	0.713

Residual standard error: 25.75 on 7 degrees of freedom

Multiple R-squared: 0.5581, Adjusted R-squared: 0.3687

F-statistic: 2.947 on 3 and 7 DF, p-value: 0.108

Assumptions of Factorial ANOVA

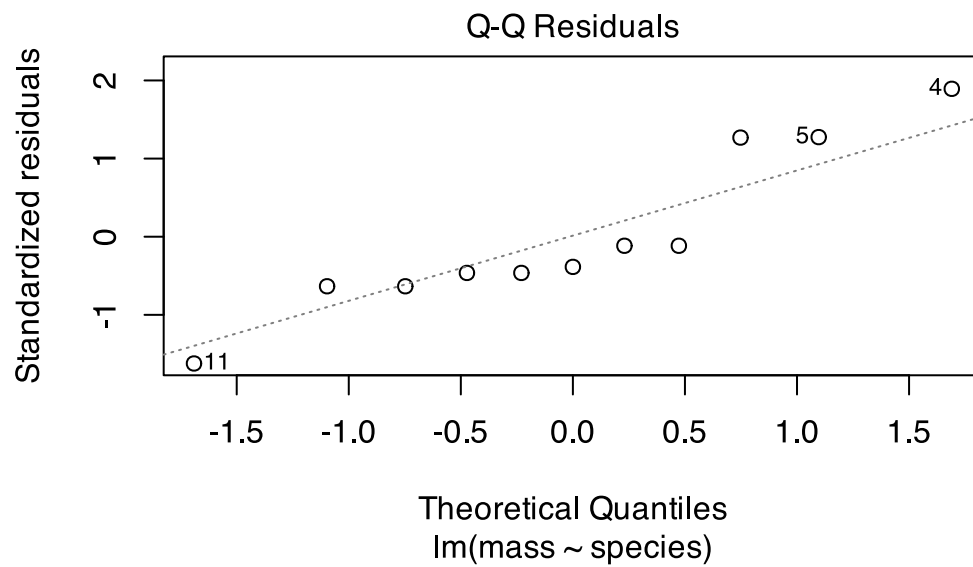
Linearity of IV to DV (Regression)

Graphical

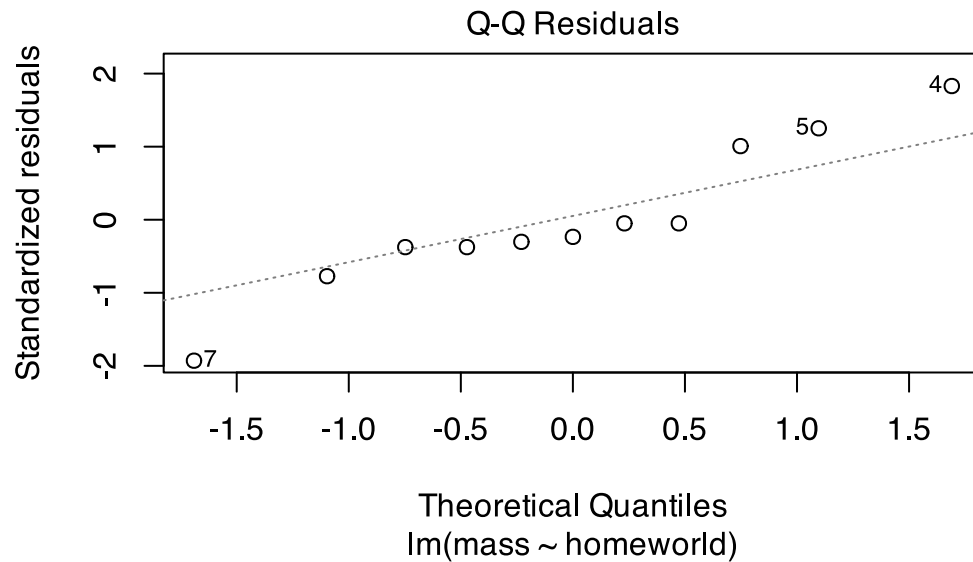
```
plot(lm(mass ~ species, data = factorial_data), 2)
```

Line 1

Plot the residuals of the model using the `plot()` and `lm()` functions for mass on homeworld



```
plot(lm(mass ~ homeworld, data = factorial_data), 2)
```

Statistical

```
psych::describe(resid(aov_factorial))
shapiro.test(resid(aov_factorial))
```

Line 1

Statistical summary of the model residuals using the `describe()` function in the `psych` package

Line 2

Statistical test (Shapiro Wilk) of the residuals using the `resid()` and `shapiro.test()` functions

	vars	n	mean	sd	median	trimmed	mad	min	max	range	skew	kurtosis	se
X1	1	11	0	21.54	-12	-2.06	14.08	-21.5	40	61.5	0.53	-1.4	6.5

Shapiro-Wilk normality test

```
data: resid(aov_factorial)
W = 0.87299, p-value = 0.08468
```

Homogeneity of Variance (Regression)

Graphical

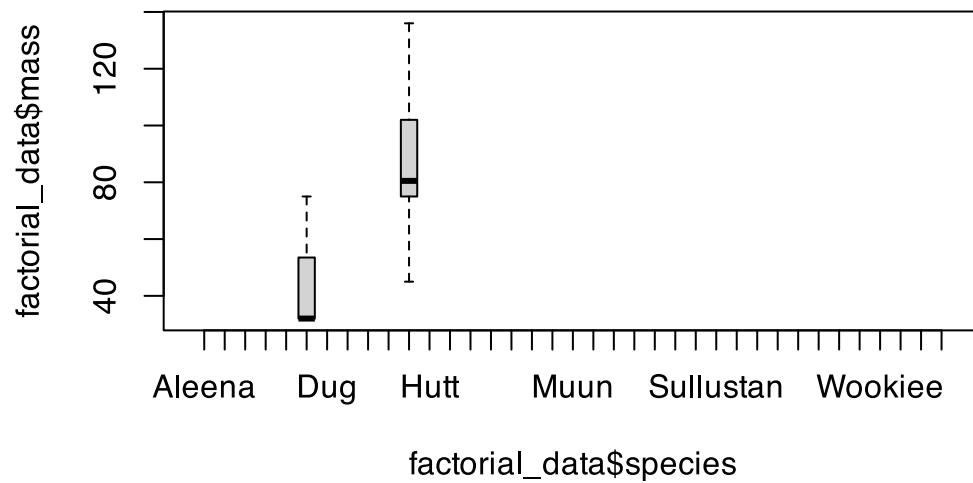
```
boxplot(factorial_data$mass ~ factorial_data$species)
```

Lines 2-3

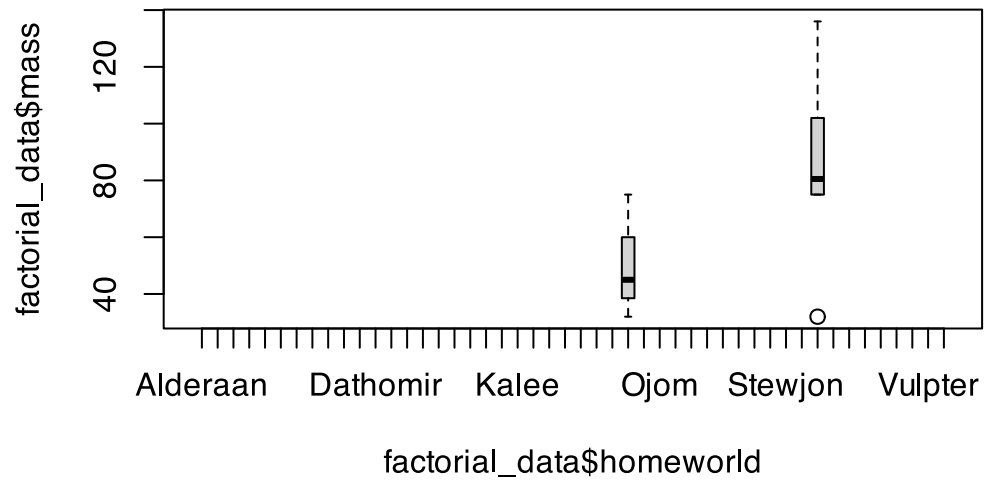
Fitted object of the ANCOVA

Line 5

Plot of the residual x fitted data using the `plot()` function

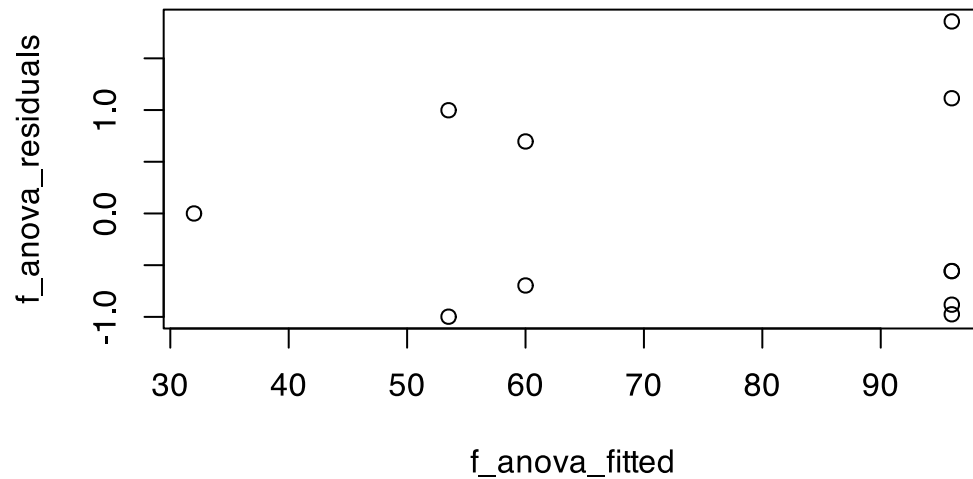


```
boxplot(factorial_data$mass ~ factorial_data$homeworld)
```



```
# Residuals
f_anova_residuals <- scale(residuals(lm(mass ~ species*homeworld, data =
factorial_data)))
f_anova_fitted <- fitted(lm(mass ~ species*homeworld, data = factorial_data))

plot(f_anova_residuals ~ f_anova_fitted)
```



Statistical

```

leveneTest(factorial_data$mass ~ factorial_data$species)

leveneTest(factorial_data$mass ~ factorial_data$homeworld)

leveneTest(factorial_data$mass
interaction(factorial_data$homeworld, factorial_data$species))

```

Line 1

Levene test of mass x species using leveneTest() function

Line 3

Levene test of mass x homeworld using leveneTest() function

Line 5

Levene test of mass x species/homeworld interaction using leveneTest() function

```

Levene's Test for Homogeneity of Variance (center = median)
  Df F value Pr(>F)
group 1  0.0985 0.7608
  9

Levene's Test for Homogeneity of Variance (center = median)
  Df F value Pr(>F)
group 1  0.1878 0.675
  9

```

```
Levene's Test for Homogeneity of Variance (center = median)
  Df F value Pr(>F)
group 3  0.3299 0.8043
      7
```

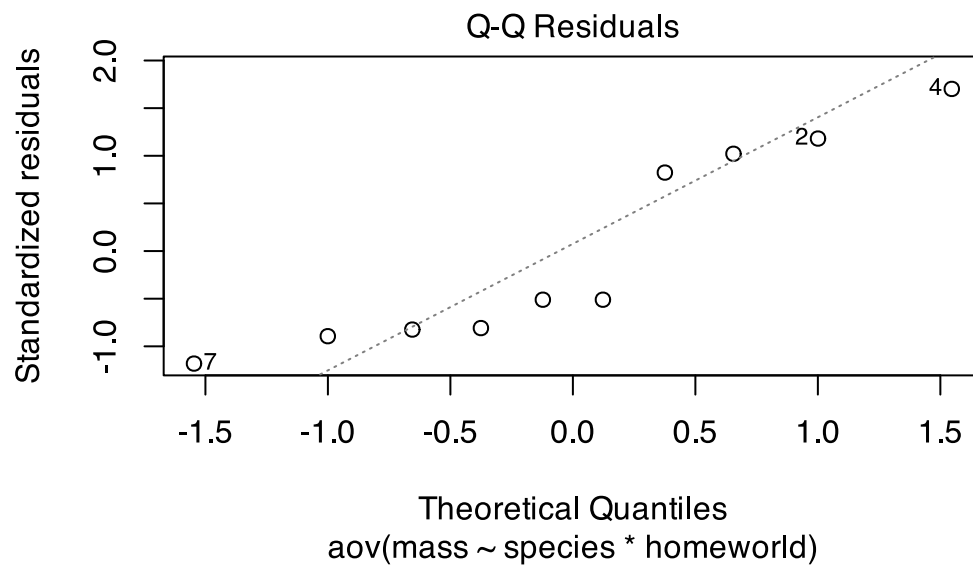
Normality of Residuals

Graphical

```
plot(aov_factorial, 2)
```

Line 1

Plot ANOVA residuals using `plot()` function



Statistical

```
fanova_residuals <- aov_factorial$residuals
shapiro.test(fanova_residuals)
psych::describe(fanova_residuals)
```

Line 1

Create residual data set

Line 3

Statistical test of residual normality using `shapiro.test()` function

Line 5

Descriptive statistics of residuals using `describe()` function in the `psych` package

```
Shapiro-Wilk normality test

data:  fanova_residuals
W = 0.87299, p-value = 0.08468

  vars  n mean    sd median trimmed   mad   min max range skew kurtosis   se
X1    1 11   0 21.54   -12   -2.06 14.08 -21.5  40  61.5 0.53    -1.4 6.5
```