

```

> #####
> ### Statistics Mistletoe Morphology ###
> #####
>
> ##Date##
> date <- "22.04.2021 by Olga Speck & Max Mylo"
>
> library(stats)
> library(ggpubr)
> library(car)
> setwd("E:/# Publikationen/2021- Mistel Morphologie/Zusätzliche Dateien")
>
>
> #define your own numeric class
> setClass('myNum')
> #define conversion
> setAs("character", "myNum", function(from) as.numeric(gsub("","\\.",gsub("\\.", "", from))))
> Mistletoe_Morphology=read.csv2("R_Mistletoe_Statistik_PK.csv", stringsAsFactors=FALSE,
+ colClasses=c("myNum", "myNum", "myNum", "myNum", "myNum", "myNum", "myNum", "myNum", "myNum", "myNum", "m
Warning messages:
1: In asMethod(object) : NAs introduced by coercion
2: In asMethod(object) : NAs introduced by coercion
>
> Mistletoe_MorphologyJuvenileFirst <- read.csv2(file= "R_Mistletoe_StatistikJuvenileFirst.csv",
+ header=TRUE, sep=";", dec=",", fill=TRUE)
> Mistletoe_MorphologyFemaleFirst <- read.csv2(file= "R_Mistletoe_StatistikFemaleFirst.csv",
+ header=TRUE, sep=";", dec=",", fill=TRUE)
>
>
> ###AGE###
> ## Shapiro-Test for normal distribution##
> ## Age [a] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$Alter)

      Shapiro-Wilk normality test

data:  Mistletoe_Morphology$Alter
W = 0.94143, p-value = 2.637e-05

>
> ## d_max mean [mm] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$d_max)

      Shapiro-Wilk normality test

data:  Mistletoe_Morphology$d_max
W = 0.97773, p-value = 0.03203

>
> ## d_acro mean [mm] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$d_acro)

      Shapiro-Wilk normality test

data:  Mistletoe_Morphology$d_acro
W = 0.96051, p-value = 0.0008921

>
> ## d_basi mean [mm] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$d_basi)

      Shapiro-Wilk normality test

```

```
data: Mistletoe_Morphology$d_basi
W = 0.9516, p-value = 0.0001936
```

```
>
> ## d_mist [mm] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$d_mist)
```

Shapiro-Wilk normality test

```
data: Mistletoe_Morphology$d_mist
W = 0.90783, p-value = 2.273e-06
```

```
>
> ## l_hyp [mm] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$l_hyp)
```

Shapiro-Wilk normality test

```
data: Mistletoe_Morphology$l_hyp
W = 0.90904, p-value = 4.889e-07
```

```
>
> ## d_max/l_hyp [mm] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$d_max.l_hyp)
```

Shapiro-Wilk normality test

```
data: Mistletoe_Morphology$d_max.l_hyp
W = 0.88099, p-value = 1.913e-08
```

```
>
> ## d_max*l_hyp [mm²] alle -->> not-normally distributed
> shapiro.test (as.numeric(Mistletoe_Morphology$d_max.l_hyp.1))
```

Shapiro-Wilk normality test

```
data: as.numeric(Mistletoe_Morphology$d_max.l_hyp.1)
W = 0.80307, p-value = 1.701e-11
```

```
>
> ## d_max/((d_basi+d_acro)/2) [/] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$d_max.d_basi.d_acro)
```

Shapiro-Wilk normality test

```
data: Mistletoe_Morphology$d_max.d_basi.d_acro
W = 0.87207, p-value = 5.508e-09
```

```
>
> ## d_max/d_basi[/] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$d_max.d_basi)
```

Shapiro-Wilk normality test

```
data: Mistletoe_Morphology$d_max.d_basi
W = 0.89925, p-value = 1.022e-07
```

```
>
> ## d_max/d_acro[/] alle -->> not-normally distributed
> shapiro.test (Mistletoe_Morphology$d_max.d_acro)
```

Shapiro-Wilk normality test

```
data: Mistletoe_Morphology$d_max.d_acro
W = 0.8737, p-value = 4.793e-09
```

```
>
>
> ###Levene Test###
> leveneTest(Mistletoe_Morphology$d_max, Mistletoe_Morphology$d_acro)
Levene's Test for Homogeneity of Variance (center = median)
      Df    F value    Pr(>F)
group 119 9.9592e+27 < 2.2e-16 ***
      8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Warning messages:
1: In leveneTest.default(Mistletoe_Morphology$d_max, Mistletoe_Morphology$d_acro) :
  Mistletoe_Morphology$d_acro coerced to factor.
2: In anova.lm(lm(resp ~ group)) :
  ANOVA F-tests on an essentially perfect fit are unreliable
> leveneTest(Mistletoe_Morphology$d_max, Mistletoe_Morphology$d_basi)
Levene's Test for Homogeneity of Variance (center = median)
      Df    F value    Pr(>F)
group 117 7.4834e+28 < 2.2e-16 ***
      8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Warning messages:
1: In leveneTest.default(Mistletoe_Morphology$d_max, Mistletoe_Morphology$d_basi) :
  Mistletoe_Morphology$d_basi coerced to factor.
2: In anova.lm(lm(resp ~ group)) :
  ANOVA F-tests on an essentially perfect fit are unreliable
> leveneTest(Mistletoe_Morphology$d_basi, Mistletoe_Morphology$d_acro)
Levene's Test for Homogeneity of Variance (center = median)
      Df    F value    Pr(>F)
group 116 2.4263e+28 < 2.2e-16 ***
      8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Warning messages:
1: In leveneTest.default(Mistletoe_Morphology$d_basi, Mistletoe_Morphology$d_acro) :
  Mistletoe_Morphology$d_acro coerced to factor.
2: In anova.lm(lm(resp ~ group)) :
  ANOVA F-tests on an essentially perfect fit are unreliable
>
> #####
> # Friedmann-Test with post-hoc#
> R_Mistletoe_Statistik <- read.csv2(file= "R_Mistletoe_Statistik.csv",header=TRUE,
+                                     sep=";", dec=".", fill=TRUE)
> matrix <- as.matrix(R_Mistletoe_Statistik)
>
> friedman.test(diameter~localisation|probe, data=matrix)
```

Friedman rank sum test

```
data: diameter and localisation and probe
Friedman chi-squared = 174.74, df = 2, p-value < 2.2e-16
```

```
> compare_means(diameter~localisation, R_Mistletoe_Statistik,
+               method="wilcox.test", alternative = "two.sided",
+               paired=TRUE, p.adjust.methods="holm")
# A tibble: 3 x 8
```

	.y. <chr>	group1 <chr>	group2 <chr>	p <dbl>	p.adj <dbl>	p.format <chr>	p.signif <chr>	method <chr>
1	diameter	d_acro	d_basi	2.69e- 2	2.7e- 2	0.027	*	Wilcoxon
2	diameter	d_acro	d_max	3.91e-22	1.2e-21	<2e-16	****	Wilcoxon
3	diameter	d_basi	d_max	1.02e-21	2 e-21	<2e-16	****	Wilcoxon

```

>
>
> #####Spearman & Pearson Correlation analyses with age#####
> ### D max ###
> Spearman_dMax = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max,
  method = "spearman")          ##### Rank correlation
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max,  :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_dMax$estimate
  rho
0.6914435
>
> Pearson_dMax = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max,
  method = "pearson")          ##### Linear Correlation
> Pearson_dMax$estimate
  cor
0.7010392
> Pearson_dMax$estimate*Pearson_dMax$estimate
  cor
0.491456
>
> ### D acro ###
> Spearman_dAcro = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_acro,
  method = "spearman")
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_acro,  :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_dAcro$estimate
  rho
0.4960559
>
> Pearson_dAcro = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_acro,
  method = "pearson")
> Pearson_dAcro$estimate
  cor
0.4663922
> Pearson_dAcro$estimate*Pearson_dAcro$estimate
  cor
0.2175217
>
> ### D basi ###
> Spearman_dBasi = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_basi,
  method = "spearman")
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_basi,  :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_dBasi$estimate
  rho
0.5039506
>
> Pearson_dBasi = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_basi,
  method = "pearson")
> Pearson_dBasi$estimate
  cor
0.4813901
> Pearson_dBasi$estimate*Pearson_dBasi$estimate

```

```

cor
0.2317364
>
> ### D mist ###
> Spearman_dMist = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_mist,
method = "spearman")
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_mist, :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_dMist$estimate
rho
0.8070118
>
> Pearson_dMist = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_mist,
method = "pearson")
> Pearson_dMist$estimate
cor
0.780944
> Pearson_dMist$estimate*Pearson_dMist$estimate
cor
0.6098735
>
> ### L hyp ###
> Spearman_LHyp = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$l_hyp,
method = "spearman")
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$l_hyp, :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_LHyp$estimate
rho
0.6633592
>
> Pearson_LHyp = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$l_hyp,
method = "pearson")
> Pearson_LHyp$estimate
cor
0.6455243
> Pearson_LHyp$estimate*Pearson_LHyp$estimate
cor
0.4167016
>
> ### D max * L hyp ###
> Spearman_DmaxLHyp = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.l_hyp.1,
method = "spearman")
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.l_hyp.1, :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_DmaxLHyp$estimate
rho
0.6984122
>
> Pearson_DmaxLHyp = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.l_hyp.1,
method = "pearson")
> Pearson_DmaxLHyp$estimate
cor
0.6353101
> Pearson_DmaxLHyp$estimate*Pearson_DmaxLHyp$estimate
cor
0.4036189
>
> ### D max / L hyp ###
> Spearman_Dmax_LHyp = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.l_hyp,

```

```

method = "spearman")
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.l_hyp, :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_Dmax_LHyp$estimate
      rho
-0.4129759
>
> Pearson_Dmax_LHyp = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.l_hyp,
  method = "pearson")
> Pearson_Dmax_LHyp$estimate
      cor
-0.4452346
> Pearson_Dmax_LHyp$estimate*Pearson_Dmax_LHyp$estimate
      cor
0.1982339
>
> ### D max / D acro ###
> Spearman_Dmax_DAcro = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.d_acro,
  method = "spearman")
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.d_acro, :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_Dmax_DAcro$estimate
      rho
0.2665412
>
> Pearson_Dmax_DAcro = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.d_acro,
  method = "pearson")
> Pearson_Dmax_DAcro$estimate
      cor
0.2405767
> Pearson_Dmax_DAcro$estimate*Pearson_Dmax_DAcro$estimate
      cor
0.05787717
>
> ### D max / D basi ###
> Spearman_Dmax_DBasi = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.d_basi,
  method = "spearman")
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.d_basi, :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_Dmax_DBasi$estimate
      rho
0.2641797
>
> Pearson_Dmax_DBasi = cor.test(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.d_basi,
  method = "pearson")
> Pearson_Dmax_DBasi$estimate
      cor
0.2327968
> Pearson_Dmax_DBasi$estimate*Pearson_Dmax_DBasi$estimate
      cor
0.05419435
>
> ### D max / ((D basi + D acro) / 2) ###
> Spearman_Dmax_DBasi_DAcro = cor.test(Mistletoe_Morphology$Alter,
Mistletoe_Morphology$d_max.d_basi.d_acro, method = "spearman")
Warning message:
In cor.test.default(Mistletoe_Morphology$Alter, Mistletoe_Morphology$d_max.d_basi.d_acro, :
  Kann exakten p-Wert bei Bindungen nicht berechnen
> Spearman_Dmax_DBasi_DAcro$estimate

```

```

      rho
0.2879521
>
> Pearson_Dmax_DBasi_DAcro = cor.test(Mistletoe_Morphology$Alter,
Mistletoe_Morphology$d_max.d_basi.d_acro, method = "pearson")
> Pearson_Dmax_DBasi_DAcro$estimate
      cor
0.2492075
> Pearson_Dmax_DBasi_DAcro$estimate*Pearson_Dmax_DBasi_DAcro$estimate
      cor
0.06210439
>
>
>
> ##### Multiple Regression #####
> ### D max ###
> MultRegVSJuvenile_DMAx <- lm(d_max ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_DMAx)

Call:
lm(formula = d_max ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)

Residuals:
    Min       1Q   Median       3Q      Max
-18.016  -6.926  -1.064   4.962  27.688

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    10.3587     2.9041   3.567 0.000513 ***
Alter           2.5863     0.3034   8.523 4.24e-14 ***
GeschlechtB (female)  5.6264     3.3399   1.685 0.094568 .
GeschlechtC (male)   6.1852     3.5843   1.726 0.086884 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.11 on 125 degrees of freedom
(1 observation deleted due to missingness)
Multiple R-squared:  0.5043, Adjusted R-squared:  0.4924
F-statistic: 42.4 on 3 and 125 DF, p-value: < 2.2e-16

>
> MultRegVSFemale_DMAx <- lm(d_max ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_DMAx)

Call:
lm(formula = d_max ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)

Residuals:
    Min       1Q   Median       3Q      Max
-18.016  -6.926  -1.064   4.962  27.688

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    15.9851     3.2417   4.931 2.55e-06 ***
Alter           2.5863     0.3034   8.523 4.24e-14 ***
GeschlechtB (male)  0.5588     2.2440   0.249  0.8037
GeschlechtC (juvenile) -5.6264     3.3399  -1.685  0.0946 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.11 on 125 degrees of freedom

```

```

(1 observation deleted due to missingness)
Multiple R-squared:  0.5043,   Adjusted R-squared:  0.4924
F-statistic:  42.4 on 3 and 125 DF,  p-value: < 2.2e-16

>
> ### D acro ###
> MultRegVSJuvenile_DAcro <- lm(d_acro ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_DAcro)

Call:
lm(formula = d_acro ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)

Residuals:
    Min       1Q   Median       3Q      Max
-18.867  -6.656  -1.245   4.667  23.791

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    12.3368    2.6476   4.660 8.04e-06 ***
Alter           1.1695    0.2771   4.221 4.66e-05 ***
GeschlechtB (female)  4.6158    3.0509   1.513  0.133
GeschlechtC (male)   1.2708    3.2676   0.389  0.698
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.211 on 124 degrees of freedom
(2 observations deleted due to missingness)
Multiple R-squared:  0.2422,   Adjusted R-squared:  0.2239
F-statistic: 13.21 on 3 and 124 DF,  p-value: 1.531e-07

>
> MultRegVSFemale_DAcro <- lm(d_acro ~ Alter + Geschlecht,
data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_DAcro)

Call:
lm(formula = d_acro ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)

Residuals:
    Min       1Q   Median       3Q      Max
-18.867  -6.656  -1.245   4.667  23.791

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    16.9526    2.9677   5.712 7.80e-08 ***
Alter           1.1695    0.2771   4.221 4.66e-05 ***
GeschlechtB (male)  -3.3450    2.0487  -1.633  0.105
GeschlechtC (juvenile) -4.6158    3.0509  -1.513  0.133
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.211 on 124 degrees of freedom
(2 observations deleted due to missingness)
Multiple R-squared:  0.2422,   Adjusted R-squared:  0.2239
F-statistic: 13.21 on 3 and 124 DF,  p-value: 1.531e-07

>
> ### D basi ###
> MultRegVSJuvenile_DBasi <- lm(d_basi ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_DBasi)

```

```
Call:
lm(formula = d_basi ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-18.500	-7.338	-1.454	5.218	25.792

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	12.050	2.840	4.243	4.31e-05 ***
Alter	1.374	0.298	4.611	9.95e-06 ***
GeschlechtB (female)	3.204	3.279	0.977	0.331
GeschlechtC (male)	1.786	3.530	0.506	0.614

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.872 on 122 degrees of freedom

(4 observations deleted due to missingness)

Multiple R-squared: 0.2388, Adjusted R-squared: 0.2201

F-statistic: 12.76 on 3 and 122 DF, p-value: 2.617e-07

```
>
> MultRegVSFemale_DBasi <- lm(d_basi ~ Alter + Geschlecht,
data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_DBasi)
```

```
Call:
lm(formula = d_basi ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-18.500	-7.338	-1.454	5.218	25.792

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	15.254	3.200	4.767	5.22e-06 ***
Alter	1.374	0.298	4.611	9.95e-06 ***
GeschlechtB (male)	-1.418	2.230	-0.636	0.526
GeschlechtC (juvenile)	-3.204	3.279	-0.977	0.331

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.872 on 122 degrees of freedom

(4 observations deleted due to missingness)

Multiple R-squared: 0.2388, Adjusted R-squared: 0.2201

F-statistic: 12.76 on 3 and 122 DF, p-value: 2.617e-07

```
>
> ### D mist ###
> MultRegVSJuvenile_DMist <- lm(d_mist ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_DMist)
```

```
Call:
lm(formula = d_mist ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-16.487	-4.219	-1.191	2.097	32.296

Coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)    -6.8974     2.4424  -2.824  0.00572 **
Alter           2.9216     0.2988   9.777 3.05e-16 ***
GeschlechtB (female) 1.7367     2.8735   0.604  0.54695
GeschlechtC (male)  -1.0803     3.0155  -0.358  0.72092
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

Residual standard error: 7.878 on 100 degrees of freedom
(26 observations deleted due to missingness)
Multiple R-squared:  0.6179, Adjusted R-squared:  0.6065
F-statistic: 53.91 on 3 and 100 DF, p-value: < 2.2e-16

```

```

>
> MultRegVSFemale_DMist <- lm(d_mist ~ Alter + Geschlecht,
data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_DMist)

```

```

Call:
lm(formula = d_mist ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)

```

```

Residuals:
    Min       1Q   Median       3Q      Max
-16.487  -4.219  -1.191   2.097  32.296

```

```

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    -5.1607     3.0954  -1.667  0.0986 .
Alter           2.9216     0.2988   9.777 3.05e-16 ***
GeschlechtB (male) -2.8170     1.9637  -1.435  0.1545
GeschlechtC (juvenile) -1.7367     2.8735  -0.604  0.5469
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

Residual standard error: 7.878 on 100 degrees of freedom
(26 observations deleted due to missingness)
Multiple R-squared:  0.6179, Adjusted R-squared:  0.6065
F-statistic: 53.91 on 3 and 100 DF, p-value: < 2.2e-16

```

```

>
> ### L hyp ###
> MultRegVSJuvenile_Lhyp <- lm(l_hyp ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_Lhyp)

```

```

Call:
lm(formula = l_hyp ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)

```

```

Residuals:
    Min       1Q   Median       3Q      Max
-12.5385  -3.6996  -0.9186   1.4673  19.2334

```

```

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    -1.1779     1.7888  -0.658  0.512
Alter           1.3240     0.1842   7.187 6.5e-11 ***
GeschlechtB (female) 2.7047     2.0564   1.315  0.191
GeschlechtC (male)  2.8971     2.2118   1.310  0.193
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

Residual standard error: 6.053 on 118 degrees of freedom

```

```
(8 observations deleted due to missingness)
Multiple R-squared:  0.426,    Adjusted R-squared:  0.4114
F-statistic:  29.2 on 3 and 118 DF,  p-value: 3.424e-14
```

```
>
> MultRegVSFemale_Lhyp <- lm(l_hyp ~ Alter + Geschlecht,
data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_Lhyp)
```

```
Call:
lm(formula = l_hyp ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)
```

```
Residuals:
    Min       1Q   Median       3Q      Max
-12.5385  -3.6996  -0.9186   1.4673  19.2334
```

```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.5268     1.9598   0.779    0.437
Alter             1.3240     0.1842   7.187 6.5e-11 ***
GeschlechtB (male)  0.1924     1.3706   0.140    0.889
GeschlechtC (juvenile) -2.7047     2.0564  -1.315    0.191
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 6.053 on 118 degrees of freedom
(8 observations deleted due to missingness)
Multiple R-squared:  0.426,    Adjusted R-squared:  0.4114
F-statistic:  29.2 on 3 and 118 DF,  p-value: 3.424e-14
```

```
>
> ### D max * L hyp ###
> MultRegVSJuvenile_DmaxLHyp <- lm(d_max.l_hyp.1 ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_DmaxLHyp)
```

```
Call:
lm(formula = d_max.l_hyp.1 ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)
```

```
Residuals:
    Min       1Q   Median       3Q      Max
-2981145 -1532589 -1088170   239630 23924090
```

```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      33362     960943   0.035    0.972
Alter             47078     98962    0.476    0.635
GeschlechtB (female) 1042011  1104653   0.943    0.347
GeschlechtC (male)   1961560  1188167   1.651    0.101
```

```
Residual standard error: 3252000 on 118 degrees of freedom
(8 observations deleted due to missingness)
Multiple R-squared:  0.03611, Adjusted R-squared:  0.0116
F-statistic: 1.473 on 3 and 118 DF,  p-value: 0.2253
```

```
>
> MultRegVSFemale_DmaxLHyp <- lm(d_max.l_hyp.1 ~ Alter + Geschlecht,
data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_DmaxLHyp)
```

```
Call:
lm(formula = d_max.l_hyp.1 ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)
```

```

Residuals:
      Min       1Q   Median       3Q      Max
-2981145 -1532589 -1088170  239630 23924090

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    1075372   1052761    1.021   0.309
Alter           47078     98962    0.476   0.635
GeschlechtB (male)  919550    736247    1.249   0.214
GeschlechtC (juvenile) -1042011  1104653   -0.943   0.347

Residual standard error: 3252000 on 118 degrees of freedom
(8 observations deleted due to missingness)
Multiple R-squared:  0.03611, Adjusted R-squared:  0.0116
F-statistic: 1.473 on 3 and 118 DF, p-value: 0.2253

>
> ### D max / L hyp ###
> MultRegVSJuvenile_Dmax_LHyp <- lm(d_max.l_hyp ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_Dmax_LHyp)

Call:
lm(formula = d_max.l_hyp ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)

Residuals:
      Min       1Q   Median       3Q      Max
-2.1544 -0.7542 -0.0776  0.4891  3.7549

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    5.73164    0.33220  17.254 < 2e-16 ***
Alter          -0.09453    0.03421  -2.763 0.006641 **
GeschlechtB (female) -1.58569    0.38188  -4.152 6.25e-05 ***
GeschlechtC (male)   -1.64996    0.41075  -4.017 0.000104 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.124 on 118 degrees of freedom
(8 observations deleted due to missingness)
Multiple R-squared:  0.3075, Adjusted R-squared:  0.2899
F-statistic: 17.47 on 3 and 118 DF, p-value: 1.89e-09

>
> MultRegVSFemale_Dmax_LHyp <- lm(d_max.l_hyp ~ Alter + Geschlecht,
data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_Dmax_LHyp)

Call:
lm(formula = d_max.l_hyp ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)

Residuals:
      Min       1Q   Median       3Q      Max
-2.1544 -0.7542 -0.0776  0.4891  3.7549

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    4.14595    0.36394  11.392 < 2e-16 ***
Alter          -0.09453    0.03421  -2.763 0.00664 **
GeschlechtB (male) -0.06427    0.25452  -0.253 0.80108
GeschlechtC (juvenile) 1.58569    0.38188   4.152 6.25e-05 ***

```

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.124 on 118 degrees of freedom
(8 observations deleted due to missingness)
Multiple R-squared:  0.3075,    Adjusted R-squared:  0.2899
F-statistic: 17.47 on 3 and 118 DF,  p-value: 1.89e-09

>
> ### D max / D acro ###
> MultRegVSJuvenile_Dmax_DAcro <- lm(d_max.d_acro ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_Dmax_DAcro)

Call:
lm(formula = d_max.d_acro ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)

Residuals:
    Min       1Q   Median       3Q      Max
-0.65365 -0.25722 -0.09331  0.16149  1.98635

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    1.17646    0.11945   9.849  <2e-16 ***
Alter          0.02338    0.01250   1.871   0.0638 .
GeschlechtB (female) 0.13998    0.13764   1.017   0.3111
GeschlechtC (male)  0.34149    0.14742   2.316   0.0222 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4155 on 124 degrees of freedom
(2 observations deleted due to missingness)
Multiple R-squared:  0.1093,    Adjusted R-squared:  0.08774
F-statistic: 5.071 on 3 and 124 DF,  p-value: 0.0024

>
> MultRegVSFemale_Dmax_DAcro <- lm(d_max.d_acro ~ Alter + Geschlecht,
data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_Dmax_DAcro)

Call:
lm(formula = d_max.d_acro ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)

Residuals:
    Min       1Q   Median       3Q      Max
-0.65365 -0.25722 -0.09331  0.16149  1.98635

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    1.31644    0.13389   9.833  <2e-16 ***
Alter          0.02338    0.01250   1.871   0.0638 .
GeschlechtB (male)  0.20150    0.09243   2.180   0.0311 *
GeschlechtC (juvenile) -0.13998    0.13764  -1.017   0.3111
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4155 on 124 degrees of freedom
(2 observations deleted due to missingness)
Multiple R-squared:  0.1093,    Adjusted R-squared:  0.08774
F-statistic: 5.071 on 3 and 124 DF,  p-value: 0.0024

>

```

```

> ### D max / D basi ###
> MultRegVSJuvenile_Dmax_DBasi <- lm(d_max.d_basi ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_Dmax_DBasi)

Call:
lm(formula = d_max.d_basi ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)

Residuals:
    Min       1Q   Median       3Q      Max
-0.61930 -0.27225 -0.07469  0.19019  1.73070

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    1.14643    0.11436  10.025  <2e-16 ***
Alter           0.01641    0.01200   1.367   0.1741
GeschlechtB (female) 0.22240    0.13206   1.684   0.0947 .
GeschlechtC (male)   0.29545    0.14215   2.079   0.0398 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3976 on 122 degrees of freedom
(4 observations deleted due to missingness)
Multiple R-squared:  0.08658, Adjusted R-squared:  0.06412
F-statistic: 3.855 on 3 and 122 DF, p-value: 0.01123

>
> MultRegVSFemale_Dmax_DBasi <- lm(d_max.d_basi ~ Alter + Geschlecht,
data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_Dmax_DBasi)

Call:
lm(formula = d_max.d_basi ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)

Residuals:
    Min       1Q   Median       3Q      Max
-0.61930 -0.27225 -0.07469  0.19019  1.73070

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    1.36883    0.12886  10.623  <2e-16 ***
Alter           0.01641    0.01200   1.367   0.1741
GeschlechtB (male) 0.07305    0.08979   0.814   0.4175
GeschlechtC (juvenile) -0.22240    0.13206  -1.684   0.0947 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3976 on 122 degrees of freedom
(4 observations deleted due to missingness)
Multiple R-squared:  0.08658, Adjusted R-squared:  0.06412
F-statistic: 3.855 on 3 and 122 DF, p-value: 0.01123

>
> ### D max / ((D basi + D acro) / 2) ###
> MultRegVSJuvenile_Dmax_DBasi_DAcro <- lm(d_max.d_basi.d_acro ~ Alter + Geschlecht,
data = Mistletoe_MorphologyJuvenileFirst)
> summary(MultRegVSJuvenile_Dmax_DBasi_DAcro)

Call:
lm(formula = d_max.d_basi.d_acro ~ Alter + Geschlecht, data = Mistletoe_MorphologyJuvenileFirst)

Residuals:

```

	Min	1Q	Median	3Q	Max
	-0.61651	-0.23747	-0.08683	0.16468	1.87349

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.16001	0.10890	10.652	<2e-16 ***
Alter	0.01968	0.01145	1.719	0.0882 .
GeschlechtB (female)	0.17003	0.12602	1.349	0.1798
GeschlechtC (male)	0.30755	0.13536	2.272	0.0248 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3784 on 121 degrees of freedom

(5 observations deleted due to missingness)

Multiple R-squared: 0.1041, Adjusted R-squared: 0.0819

F-statistic: 4.687 on 3 and 121 DF, p-value: 0.003925

>

```
> MultRegVSFemale_Dmax_DBasi_DAcro <- lm(d_max.d_basi.d_acro ~ Alter + Geschlecht,
data = Mistletoe_MorphologyFemaleFirst)
> summary(MultRegVSFemale_Dmax_DBasi_DAcro)
```

Call:

lm(formula = d_max.d_basi.d_acro ~ Alter + Geschlecht, data = Mistletoe_MorphologyFemaleFirst)

Residuals:

	Min	1Q	Median	3Q	Max
	-0.61651	-0.23747	-0.08683	0.16468	1.87349

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.33004	0.12324	10.792	<2e-16 ***
Alter	0.01968	0.01145	1.719	0.0882 .
GeschlechtB (male)	0.13752	0.08562	1.606	0.1108
GeschlechtC (juvenile)	-0.17003	0.12602	-1.349	0.1798

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3784 on 121 degrees of freedom

(5 observations deleted due to missingness)

Multiple R-squared: 0.1041, Adjusted R-squared: 0.0819

F-statistic: 4.687 on 3 and 121 DF, p-value: 0.003925

>