

Photobiology-ANOVA and mixed effects model

Code ▼

Or Ben-Zvi

load packages

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```
library(car)
library(ggplot2)
library(lme4)
library(lmerTest)
library(MASS)
library(cowplot)
library(dplyr)
library(doBy)
```

read data

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```
data_pamin <- read.csv(file.choose())
```

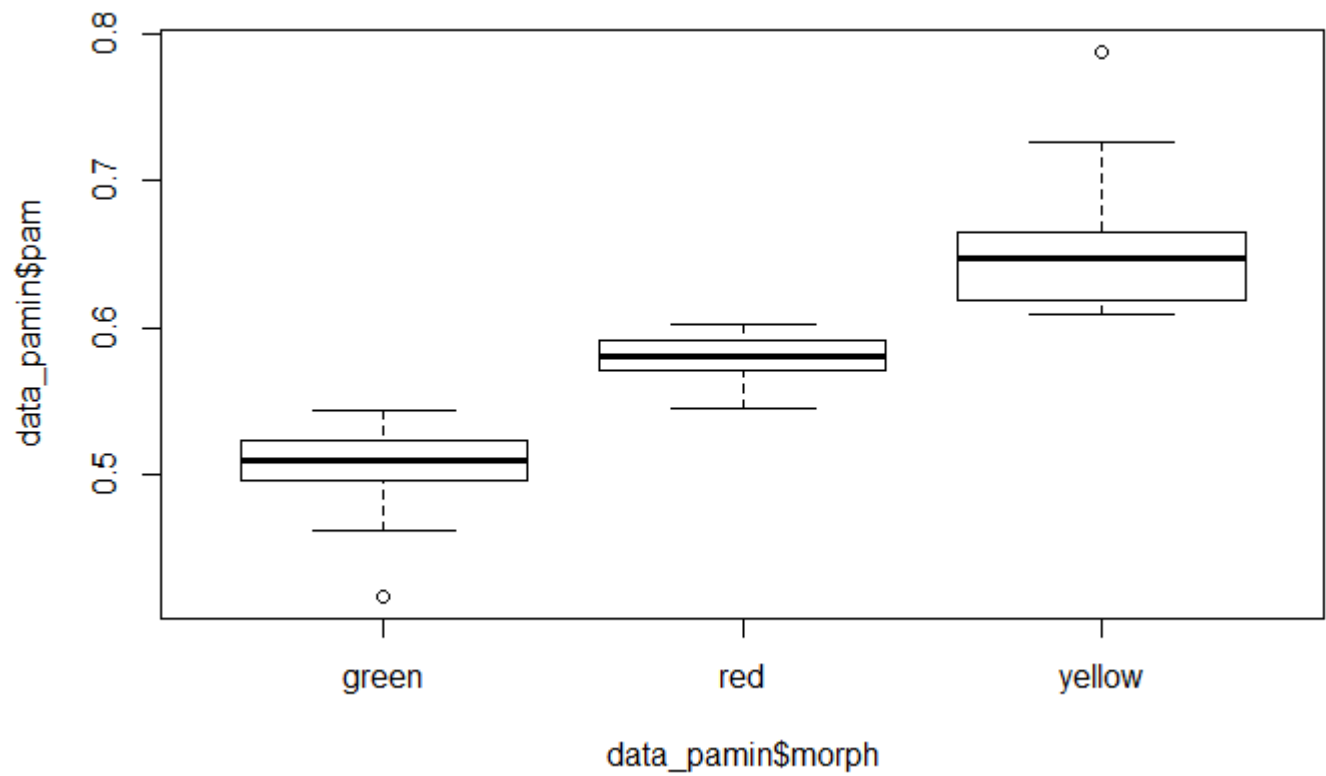
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```
str(data_pamin)
```

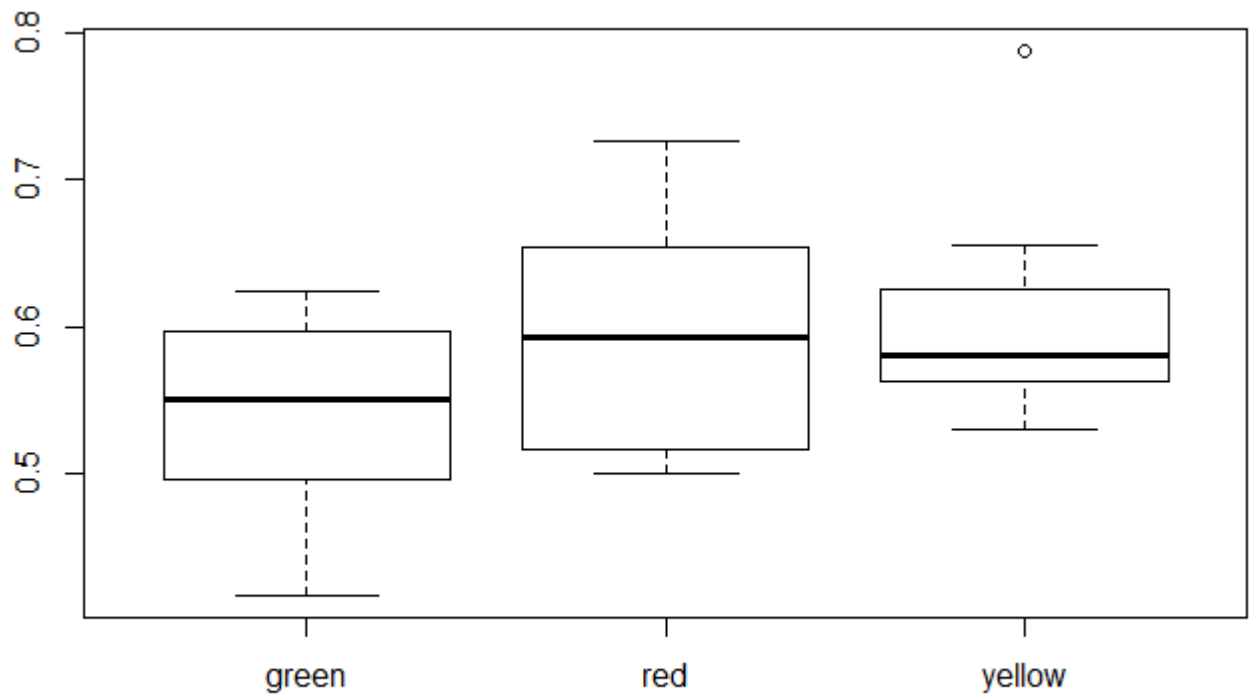
```
'data.frame':  36 obs. of  3 variables:
 $ no   : int  1 2 3 4 5 6 7 8 9 10 ...
 $ morph: Factor w/ 3 levels "green","red",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ pam  : num  0.573 0.592 0.613 0.529 0.491 0.463 0.591 0.501 0.602 0.625 ...
```

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```
qqplot(data_pamin$morph,data_pamin$pam)
```

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```
plot(data_pamin$morph,data_pamin$pam)
```

[Hide](#)

```
data_pam <- read.csv(file.choose())
```

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```
str(data_pam)
```

```
'data.frame': 79 obs. of 9 variables:
 $ id      : Factor w/ 79 levels "GA1","GA2","GA3",...: 1 2 3 4 5 6 7 8 9 10 ...
 $ treatment: Factor w/ 2 levels "par","paruv": 1 1 1 2 2 2 1 1 1 2 ...
 $ morph    : Factor w/ 3 levels "green","red",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ colony   : Factor w/ 14 levels "a","b","c","d",...: 1 1 1 1 1 1 2 2 2 2 ...
 $ tank     : int  1 2 3 4 5 6 1 2 3 4 ...
 $ pamt0    : Factor w/ 56 levels "0.593","0.594",...: 30 39 7 41 46 34 22 5 24 22 ...
 $ pamt1    : num  0.207 0.17 0.087 0.319 0.175 0.308 0.289 0.118 0.09 0.283 ...
 $ dpam     : Factor w/ 67 levels "-0.195","-0.247",...: 47 58 60 25 59 24 25 56 65 28 ...
 $ ppam     : Factor w/ 79 levels "-26.97095436",...: 56 66 77 21 65 26 33 73 78 36 ...
```

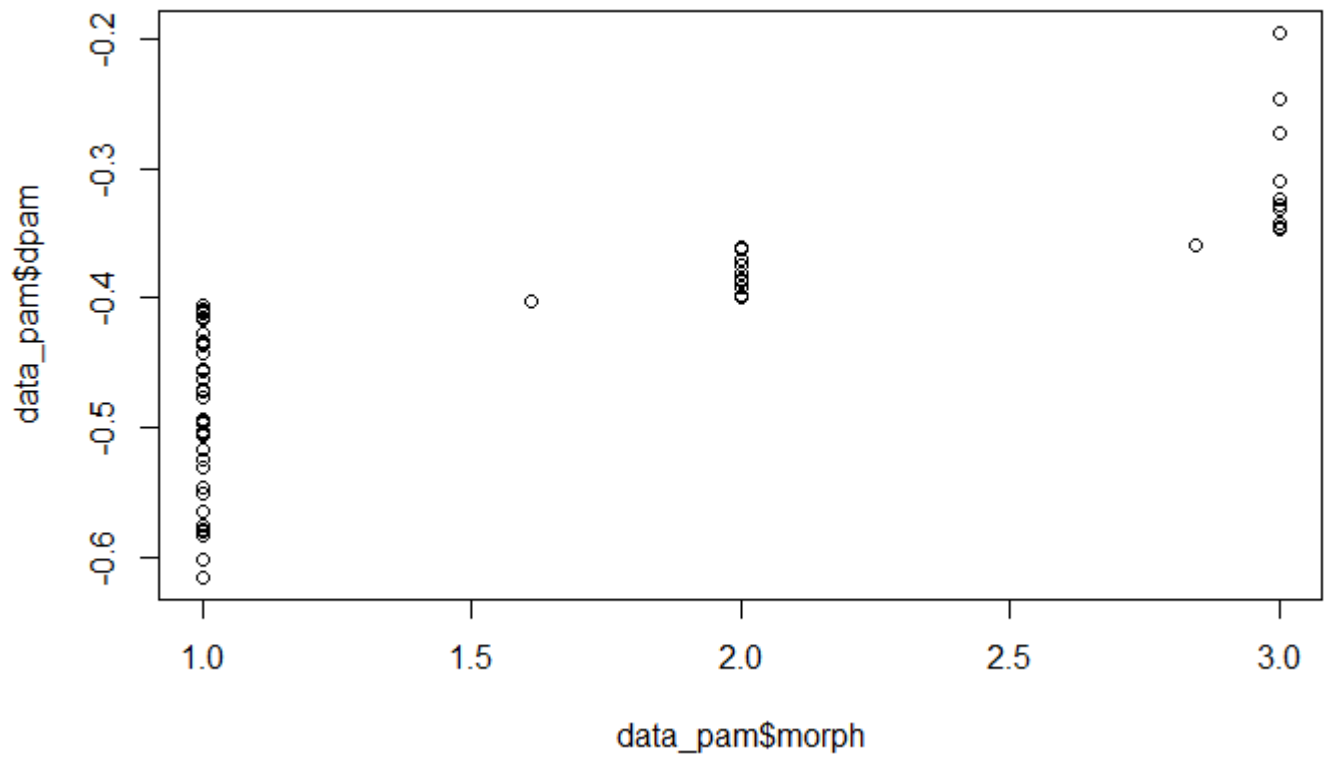
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```
data_pam$pamt0 <- as.numeric(as.character(data_pam$pamt0))
data_pam$dpam <- as.numeric(as.character(data_pam$dpam))
data_pam$ppam <- as.numeric(as.character(data_pam$ppam))
data_pam$tank <- as.factor(data_pam$tank)
str(data_pam)
```

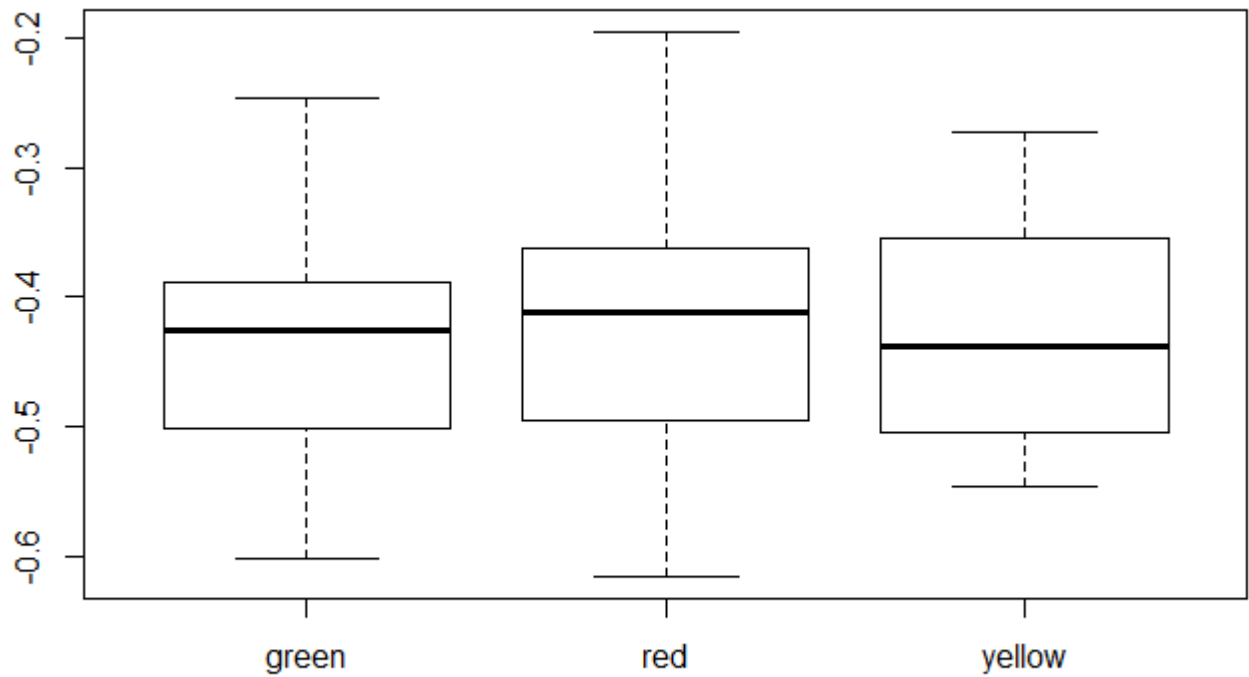
```
'data.frame': 79 obs. of 9 variables:
 $ id      : Factor w/ 79 levels "GA1","GA2","GA3",...: 1 2 3 4 5 6 7 8 9 10 ...
 $ treatment: Factor w/ 2 levels "par","paruv": 1 1 1 2 2 2 1 1 1 2 ...
 $ morph    : Factor w/ 3 levels "green","red",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ colony   : Factor w/ 14 levels "a","b","c","d",...: 1 1 1 1 1 1 2 2 2 2 ...
 $ tank     : Factor w/ 6 levels "1","2","3","4",...: 1 2 3 4 5 6 1 2 3 4 ...
 $ pamt0    : num  0.7 0.716 0.652 0.719 0.726 0.707 0.689 0.643 0.691 0.689 ...
 $ pamt1    : num  0.207 0.17 0.087 0.319 0.175 0.308 0.289 0.118 0.09 0.283 ...
 $ dpam     : num  -0.493 -0.546 -0.565 -0.4 -0.551 -0.399 -0.4 -0.525 -0.601 -0.406 ...
 $ ppam     : num  -70.4 -76.3 -86.7 -55.6 -75.9 ...
```

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```
qqplot(data_pam$morph,data_pam$dpam)
```

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```
plot(data_pam$morph,data_pam$dpm)
```

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```
data_zoox <- read.csv(file.choose())
```

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```
str(data_zoox)
```

```
'data.frame': 79 obs. of 13 variables:
 $ id      : Factor w/ 79 levels "GA1","GA2","GA3",...: 1 2 3 4 5 6 7 8 9 10 ...
 $ treatment: Factor w/ 2 levels "par","paruv": 1 1 1 2 2 2 1 1 1 2 ...
 $ morph    : Factor w/ 3 levels "green","red",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ colony   : Factor w/ 14 levels "a","b","c","d",...: 1 1 1 1 1 1 1 2 2 2 ...
 $ tank     : int 1 2 3 4 5 6 1 2 3 4 ...
 $ zooxt0   : Factor w/ 77 levels "#DIV/0!","1004.955947",...: 38 39 44 12 75 10 54 59 71 29 ...
 $ zooxt1   : Factor w/ 76 levels "#DIV/0!","1036.946002",...: 40 25 44 29 22 9 36 17 10 57 ...
 $ dzoox    : Factor w/ 75 levels "-1021.435311",...: 15 25 19 1 52 2 30 38 54 68 ...
 $ pzoox    : Factor w/ 74 levels "-11.97741366",...: 14 24 13 49 47 60 23 37 53 72 ...
 $ chlt0    : Factor w/ 78 levels "#DIV/0!","102.0633083",...: 17 27 10 44 67 48 22 38 30 24 ...
 $ chlt1    : Factor w/ 76 levels "#DIV/0!","121.2534694",...: 66 26 72 67 2 13 32 19 18 50 ...
 $ dchl     : Factor w/ 74 levels "-11.63029507",...: 2 8 21 63 72 34 49 22 20 71 ...
 $ pchl     : Factor w/ 74 levels "-12.02408654",...: 46 13 11 63 72 40 57 30 27 73 ...
```

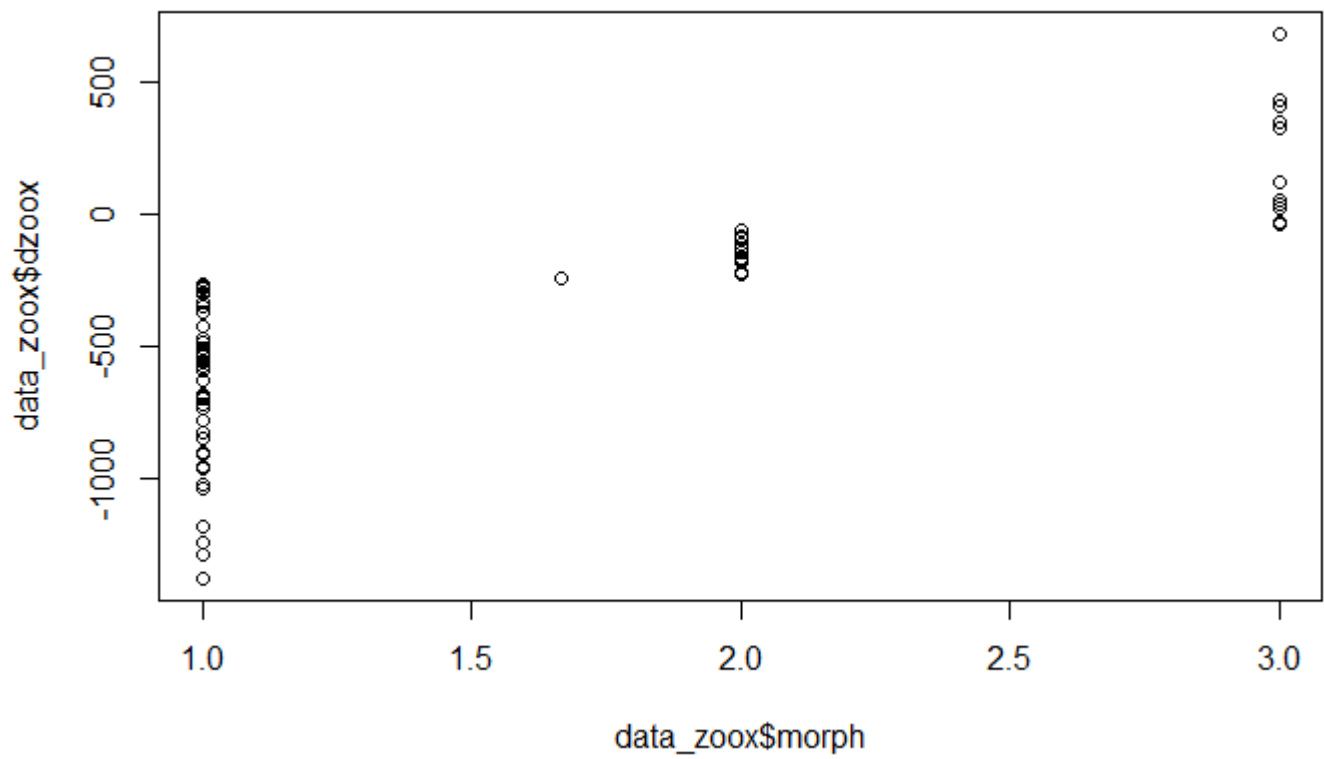
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```
data_zoox$zooxt0 <- as.numeric(as.character(data_zoox$zooxt0))
data_zoox$zooxt1 <- as.numeric(as.character(data_zoox$zooxt1))
data_zoox$dzoox <- as.numeric(as.character(data_zoox$dzoox))
data_zoox$pzoox <- as.numeric(as.character(data_zoox$pzoox))
data_zoox$chlt0 <- as.numeric(as.character(data_zoox$chlt0))
data_zoox$chlt1 <- as.numeric(as.character(data_zoox$chlt1))
data_zoox$dchl <- as.numeric(as.character(data_zoox$dchl))
data_zoox$pch1 <- as.numeric(as.character(data_zoox$pch1))
data_zoox$tank <- as.factor(data_zoox$tank)
str(data_zoox)
```

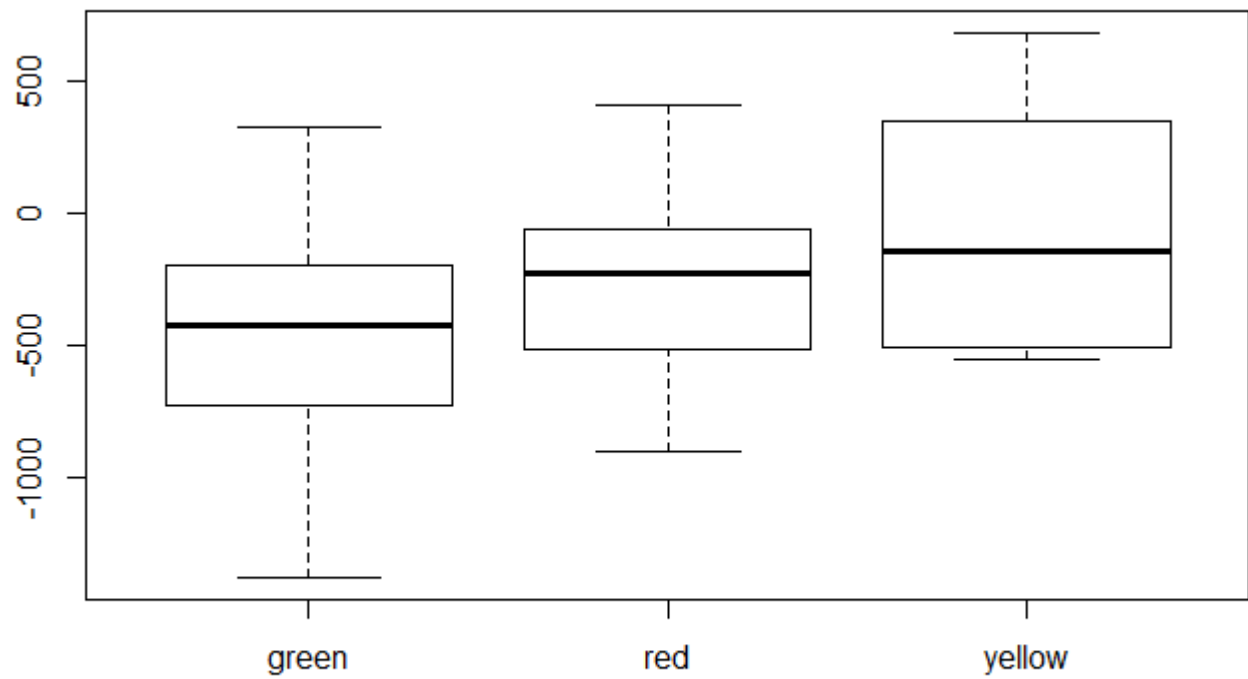
```
'data.frame': 79 obs. of 13 variables:
 $ id      : Factor w/ 79 levels "GA1","GA2","GA3",...: 1 2 3 4 5 6 7 8 9 10 ...
 $ treatment: Factor w/ 2 levels "par","paruv": 1 1 1 2 2 2 1 1 1 2 ...
 $ morph    : Factor w/ 3 levels "green","red",...: 1 1 1 1 1 1 1 1 1 1 ...
 $ colony   : Factor w/ 14 levels "a","b","c","d",...: 1 1 1 1 1 1 1 2 2 2 ...
 $ tank     : Factor w/ 6 levels "1","2","3","4",...: 1 2 3 4 5 6 1 2 3 4 ...
 $ zooxt0   : num 566 567 598 1329 977 ...
 $ zooxt1   : num 349 273 374 307 259 ...
 $ dzoox    : num -217 -294 -224 -1021 -718 ...
 $ pzoox    : num -38.3 -51.9 -37.5 -76.9 -73.5 ...
 $ chlt0    : num 181.6 61 111.8 70.8 86.2 ...
 $ chlt1    : num 70.4 46.4 85.7 71.1 121.3 ...
 $ dchl     : num -111.251 -14.568 -26.07 0.264 35.072 ...
 $ pchl     : num -61.25 -23.876 -23.319 0.372 40.696 ...
```

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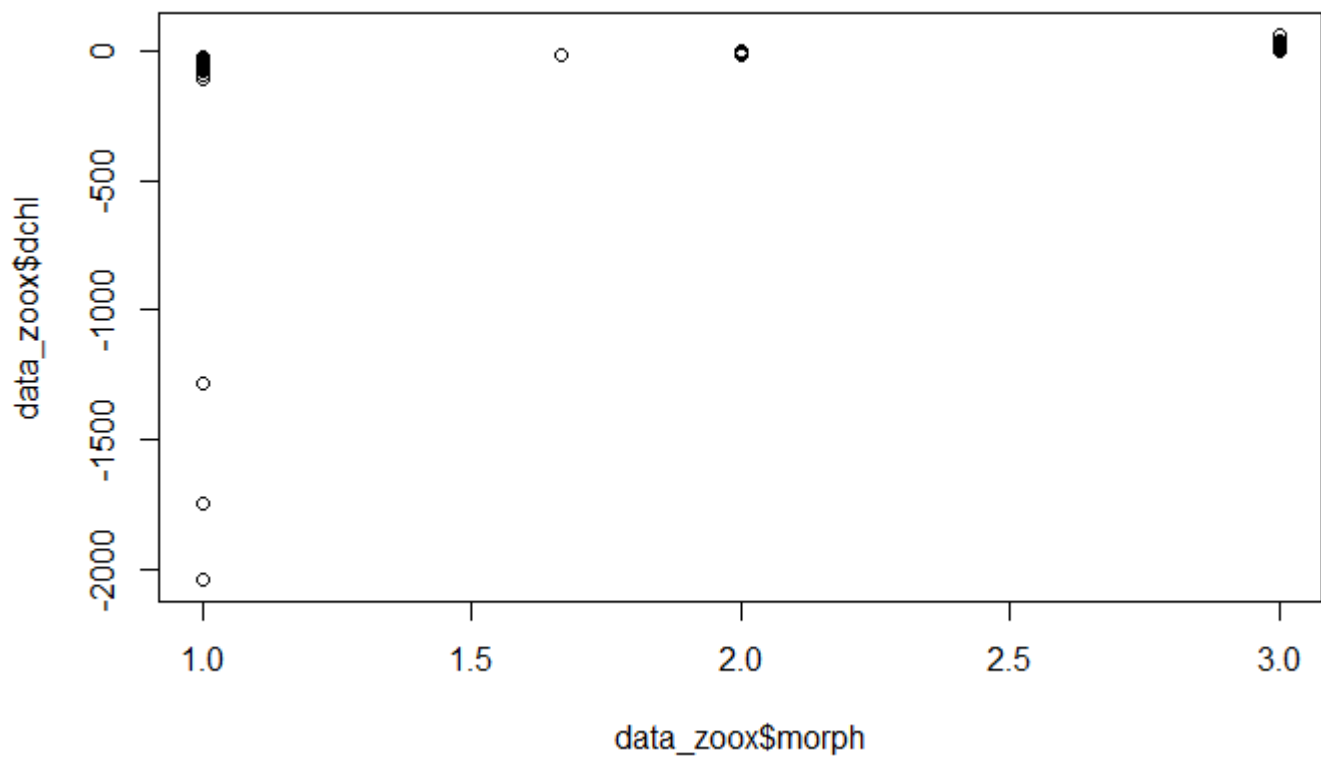
```
qqplot(data_zoos$morph,data_zoos$dzoos)
```

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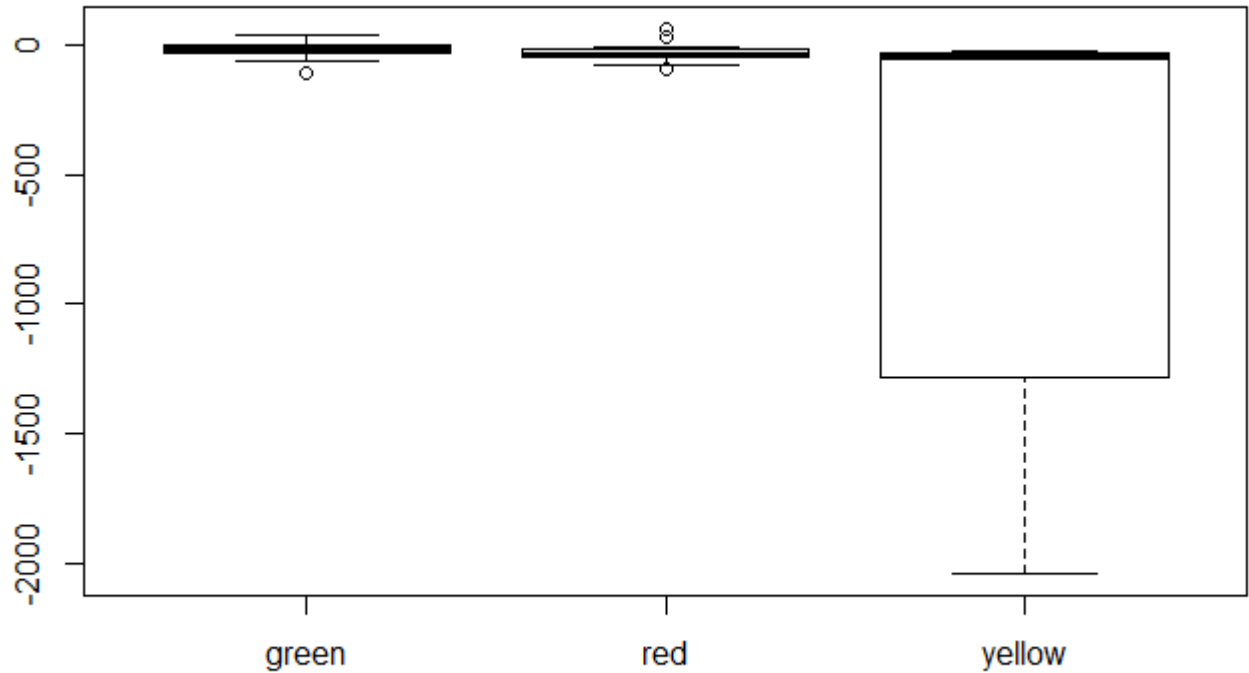
```
plot(data_zoos$morph,data_zoos$dzoos)
```

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```
qqplot(data_zoos$morph,data_zoos$dchl1)
```

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```
plot(data_zoox$morph,data_zoox$dchl)
```



Test with one-way ANOVA or mixed effect model

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```
model_pamin <- aov(data=data_pamin, pam ~ morph)
summary(model_pamin)
```

```
      Df Sum Sq Mean Sq F value Pr(>F)
morph    2  0.02533   0.012666    2.538  0.0944 .
Residuals 33  0.16471   0.004991
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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```
model_pam <- lmer(dpam ~ treatment*morph + (1|morph/colony) + (1|treatment/tank) ,
                  data=data_pam, REML=FALSE)
summary(model_pam)
```


Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method ['lmerModLmerT
est']

Formula: dpam ~ treatment * morph + (1 | morph/colony) + (1 | treatment/tank)

Data: data_pam

AIC	BIC	logLik	deviance	df.resid
-163.3	-137.3	92.6	-185.3	67

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.09766	-0.69686	-0.06277	0.66340	2.62477

Random effects:

Groups	Name	Variance	Std.Dev.
colony:morph	(Intercept)	1.889e-04	0.013745
tank:treatment	(Intercept)	4.683e-05	0.006843
morph	(Intercept)	0.000e+00	0.000000
treatment	(Intercept)	0.000e+00	0.000000
Residual		5.227e-03	0.072296

Number of obs: 78, groups: colony:morph, 14; tank:treatment, 6; morph, 3; treatment, 2

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.484792	0.016031	12.529449	-30.240	4.34e-13 ***
treatmentparuv	0.087667	0.021605	14.784746	4.058	0.00106 **
morphred	0.033458	0.029751	38.508224	1.125	0.26771
morphyellow	0.001404	0.034458	49.944242	0.041	0.96766
treatmentparuv:morphred	-0.034000	0.039963	58.490474	-0.851	0.39836
treatmentparuv:morphyellow	0.028601	0.046717	60.611072	0.612	0.54268

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

Correlation of Fixed Effects:

	(Intr)	trtmnt mrphrd	mrphyl	trtmntprv:mrphr
treatmntprv	-0.674			
morphred	-0.506	0.339		
morphyellow	-0.437	0.293	0.235	
trtmntprv:mrphr	0.340	-0.504	-0.672	-0.158
trtmntprv:mrphy	0.291	-0.432	-0.157	-0.678
			0.233	

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anova(model_pam)

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
treatment	0.095681	0.095681	1	10.897	18.3061	0.00133 **
morph	0.004000	0.002000	2	15.895	0.3826	0.68818
treatment:morph	0.007416	0.003708	2	59.640	0.7095	0.49601

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

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```
model_pam1 <- lmer(dpam ~ treatment + (1|morph/colony) + (1|treatment/tank) ,
  data=data_pam, REML=FALSE)
model_pam2 <- lmer(dpam ~ morph + (1|morph/colony) + (1|treatment/tank) ,
  data=data_pam, REML=FALSE)
anova(model_pam, model_pam1)
```

Data: data_pam

Models:

```
model_pam1: dpam ~ treatment + (1 | morph/colony) + (1 | treatment/tank)
model_pam: dpam ~ treatment * morph + (1 | morph/colony) + (1 | treatment/tank)
      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
model_pam1  7 -169.13 -152.63 91.564 -183.13
model_pam  11 -163.25 -137.33 92.626 -185.25 2.1244      4      0.7129
```

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```
anova(model_pam, model_pam2)
```

Data: data_pam

Models:

```
model_pam2: dpam ~ morph + (1 | morph/colony) + (1 | treatment/tank)
model_pam: dpam ~ treatment * morph + (1 | morph/colony) + (1 | treatment/tank)
      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
model_pam2  8 -161.28 -142.43 88.642 -177.28
model_pam  11 -163.25 -137.33 92.626 -185.25 7.9693      3      0.04665 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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```
model_zoox <- lmer(dzoox ~ treatment*morph + (1|morph/colony) + (1|treatment/tank) ,
  data=data_zoox, REML=FALSE)
summary(model_zoox)
```

Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: dzoox ~ treatment * morph + (1 | morph/colony) + (1 | treatment/tank)

Data: data_zoox

AIC	BIC	logLik	deviance	df.resid
1096.7	1121.9	-537.4	1074.7	62

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.06794	-0.61375	0.07522	0.65401	1.81945

Random effects:

Groups	Name	Variance	Std.Dev.
colony:morph	(Intercept)	12798	113.1
tank:treatment	(Intercept)	0	0.0
morph	(Intercept)	0	0.0
treatment	(Intercept)	0	0.0
Residual		134358	366.5

Number of obs: 73, groups: colony:morph, 14; tank:treatment, 6; morph, 3; treatment, 2

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-443.733	84.841	29.291	-5.230	1.3e-05 ***
treatmentparuv	-122.588	105.948	60.115	-1.157	0.25183
morphred	207.222	168.371	32.354	1.231	0.22729
morphyellow	558.056	185.631	38.830	3.006	0.00462 **
treatmentparuv:morphred	5.647	212.339	61.126	0.027	0.97887
treatmentparuv:morphyellow	-396.640	281.080	61.874	-1.411	0.16322

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

Correlation of Fixed Effects:

	(Intr)	trtmnt	mrphrd	mrphyl	trtmntprv:mrphr
treatmentprv	-0.623				
morphred	-0.504	0.314			
morphyellow	-0.457	0.285	0.230		
trtmntprv:mrphr	0.311	-0.499	-0.630	-0.142	
trtmntprv:mrphy	0.235	-0.377	-0.118	-0.525	0.188

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anova(model_zoox)

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
treatment	685324	685324	1	61.749	5.1007	0.02746 *
morph	835318	417659	2	16.802	3.1085	0.07102 .
treatment:morph	279420	139710	2	61.551	1.0398	0.35964

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

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```
model_zoos1 <- lmer(dzoox ~ treatment + (1|morph/colony) + (1|treatment/tank) ,
  data=data_zoos, REML=FALSE)
model_zoos2 <- lmer(dzoox ~ morph + (1|morph/colony) + (1|treatment/tank) ,
  data=data_zoos, REML=FALSE)
anova(model_zoos, model_zoos1)
```

Data: data_zoos

Models:

```
model_zoos1: dzoox ~ treatment + (1 | morph/colony) + (1 | treatment/tank)
model_zoos: dzoox ~ treatment * morph + (1 | morph/colony) + (1 | treatment/tank)
      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
model_zoos1  7 1096.7 1112.7 -541.34  1082.7
model_zoos  11 1096.7 1121.9 -537.37  1074.7 7.942    4    0.09372 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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```
anova(model_zoos, model_zoos2)
```

Data: data_zoos

Models:

```
model_zoos2: dzoox ~ morph + (1 | morph/colony) + (1 | treatment/tank)
model_zoos: dzoox ~ treatment * morph + (1 | morph/colony) + (1 | treatment/tank)
      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
model_zoos2  8 1095.8 1114.1 -539.88  1079.8
model_zoos  11 1096.7 1121.9 -537.37  1074.7 5.0065    3    0.1713
```

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```
model_ch1 <- lmer(dchl ~ treatment*morph + (1|morph/colony) + (1|treatment/tank) ,
  data=data_zoos, REML=FALSE)
summary(model_ch1)
```

Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: dchl ~ treatment * morph + (1 | morph/colony) + (1 | treatment/tank)

Data: data_zoox

AIC	BIC	logLik	deviance	df.resid
910.5	935.7	-444.3	888.5	62

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.5090	-0.2745	-0.0177	0.2933	4.0930

Random effects:

Groups	Name	Variance	Std.Dev.
colony:morph	(Intercept)	123420	351.31
tank:treatment	(Intercept)	0	0.00
morph	(Intercept)	0	0.00
treatment	(Intercept)	0	0.00
Residual		4371	66.12

Number of obs: 73, groups: colony:morph, 14; tank:treatment, 6; morph, 3; treatment, 2

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-20.980	124.975	14.011	-0.168	0.869084
treatmentparuv	2.726	19.467	58.888	0.140	0.889117
morphred	-3.401	239.404	14.033	-0.014	0.988866
morphyellow	-647.206	239.941	14.159	-2.697	0.017211 *
treatmentparuv:morphred	-17.754	38.725	58.894	-0.458	0.648306
treatmentparuv:morphyellow	179.754	47.176	58.897	3.810	0.000334 ***

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

Correlation of Fixed Effects:

	(Intr)	trtmnt mrphrd	mrphyl	trtmntprv:mrphr
treatmntprv	-0.079			
morphred	-0.522	0.041		
morphyellow	-0.521	0.041	0.272	
trtmntprv:mrphr	0.040	-0.503	-0.081	-0.021
trtmntprv:mrphy	0.033	-0.413	-0.017	-0.084
				0.207

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anova(model_ch1)

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
treatment	37832	37832	1	58.896	8.6546	0.0046586 **
morph	25349	12675	2	13.912	2.8995	0.0885955 .
treatment:morph	70587	35293	2	58.895	8.0739	0.0007965 ***

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

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```
model_chl1 <- lmer(dchl ~ treatment + (1|morph/colony) + (1|treatment/tank) ,
                  data=data_zoos, REML=FALSE)
model_chl2 <- lmer(dchl ~ morph + (1|morph/colony) + (1|treatment/tank) ,
                  data=data_zoos, REML=FALSE)
anova(model_chl, model_chl1)
```

Data: data_zoos

Models:

```
model_chl1: dchl ~ treatment + (1 | morph/colony) + (1 | treatment/tank)
model_chl: dchl ~ treatment * morph + (1 | morph/colony) + (1 | treatment/tank)
      Df    AIC    BIC loglik deviance  Chisq Chi Df Pr(>Chisq)
model_chl1  7 921.78 937.81 -453.89   907.78
model_chl  11 910.55 935.74 -444.27   888.55 19.232      4 0.0007078 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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```
anova(model_chl, model_chl2)
```

Data: data_zoos

Models:

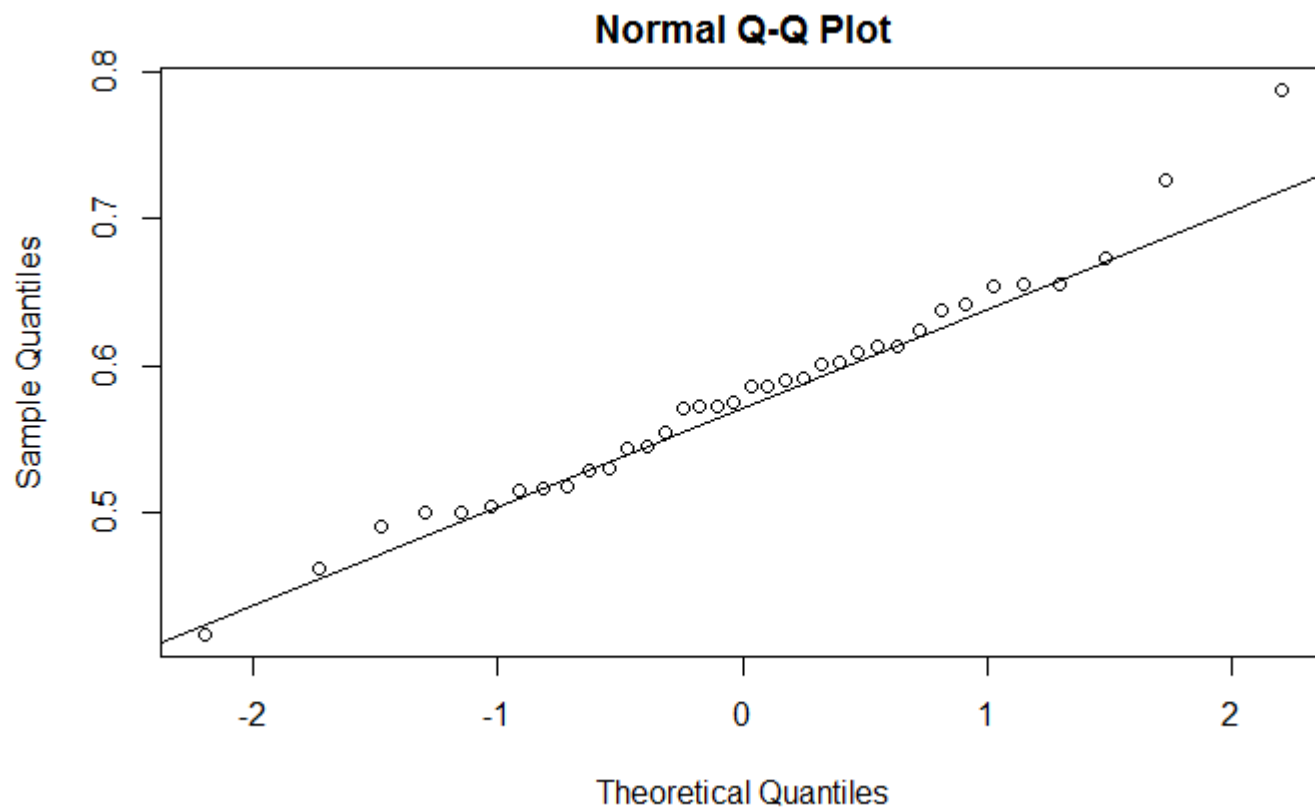
```
model_chl2: dchl ~ morph + (1 | morph/colony) + (1 | treatment/tank)
model_chl: dchl ~ treatment * morph + (1 | morph/colony) + (1 | treatment/tank)
      Df    AIC    BIC loglik deviance  Chisq Chi Df Pr(>Chisq)
model_chl2  8 920.39 938.71 -452.19   904.39
model_chl  11 910.55 935.74 -444.27   888.55 15.844      3 0.001221 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Check the ANOVA and LMM assumptions

Check the normality of data or model residuals

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```
qqnorm(data_pamin$pam)
qqline(data_pamin$pam)
```

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```
shapiro.test(data_pamin$pam)
```

Shapiro-Wilk normality test

data: data_pamin\$pam

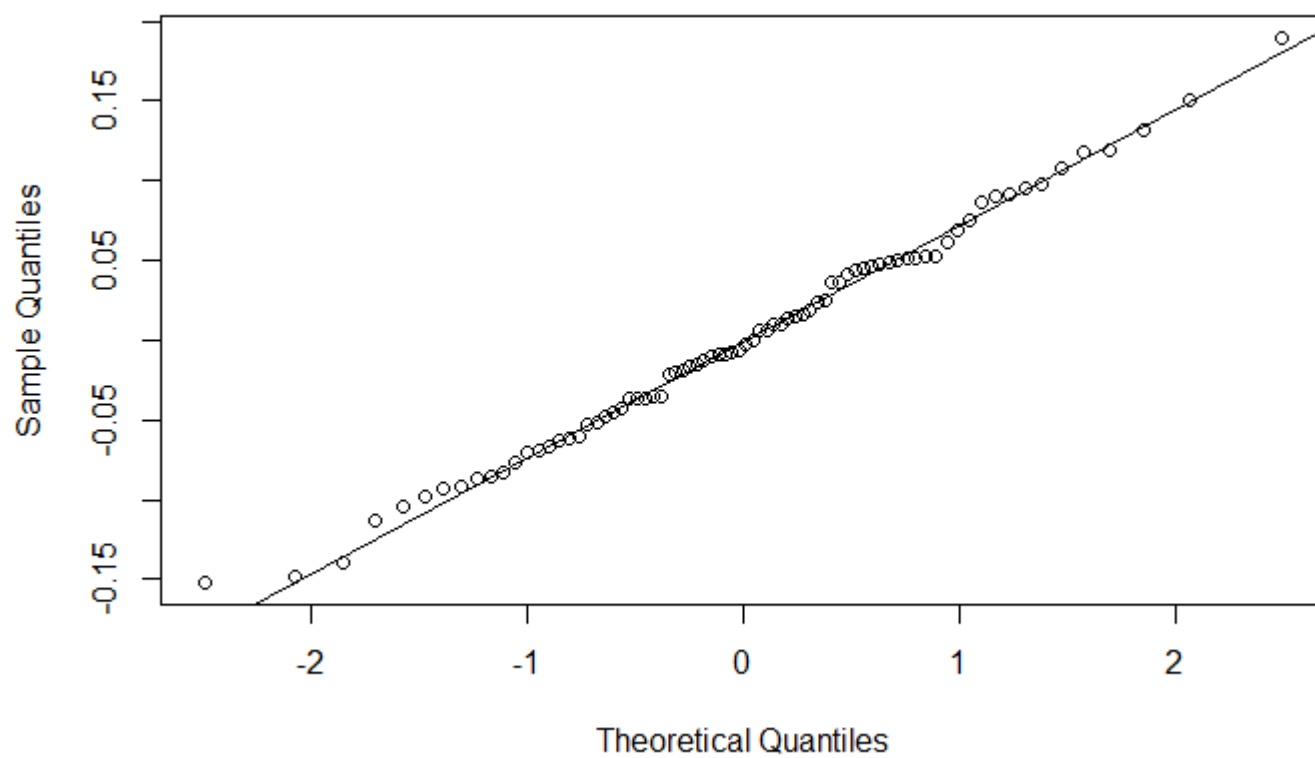
W = 0.9802, p-value = 0.752

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```
qqnorm(resid(model_pam))
```

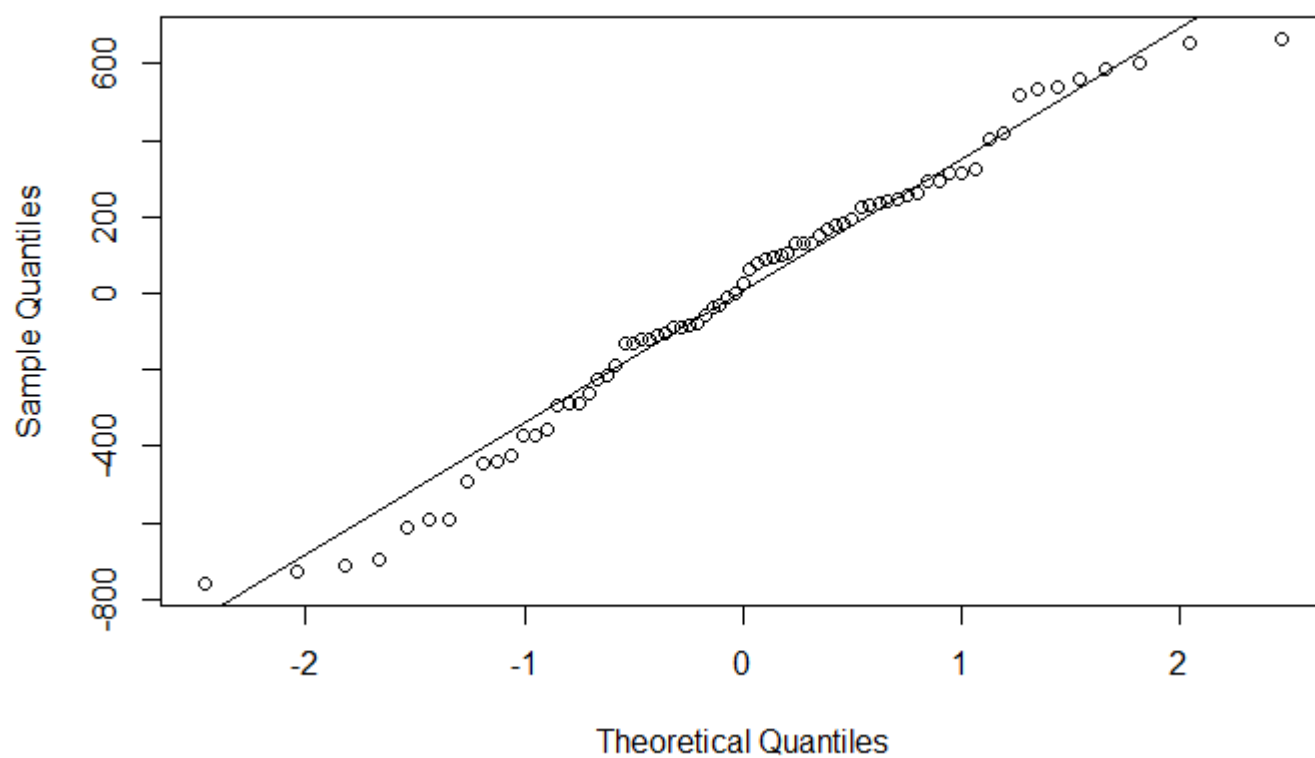
```
qqline(resid(model_pam))
```

Normal Q-Q Plot

[Hide](#)

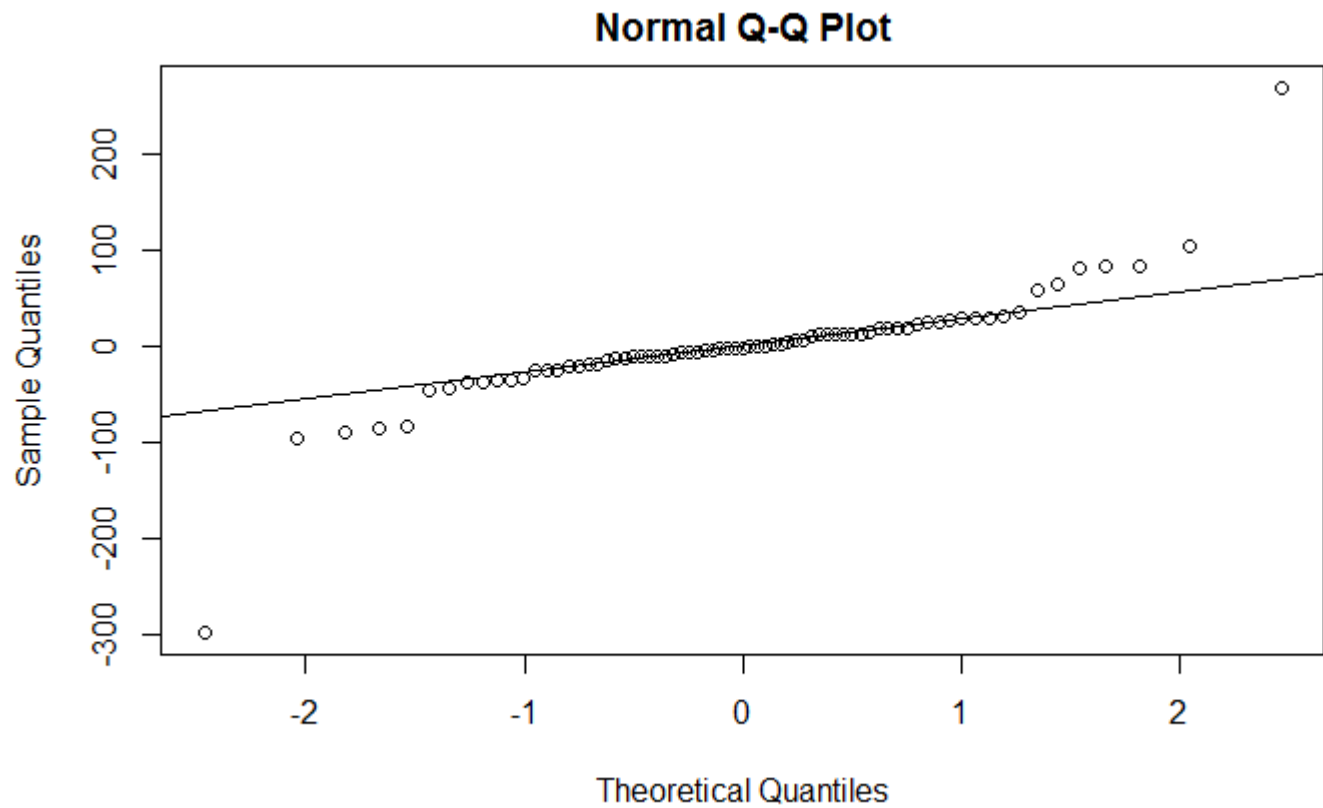
```
qqnorm(resid(model_zoox))  
qqline(resid(model_zoox))
```

Normal Q-Q Plot



[Hide](#)

```
qqnorm(resid(model_ch1))  
qqline(resid(model_ch1))
```

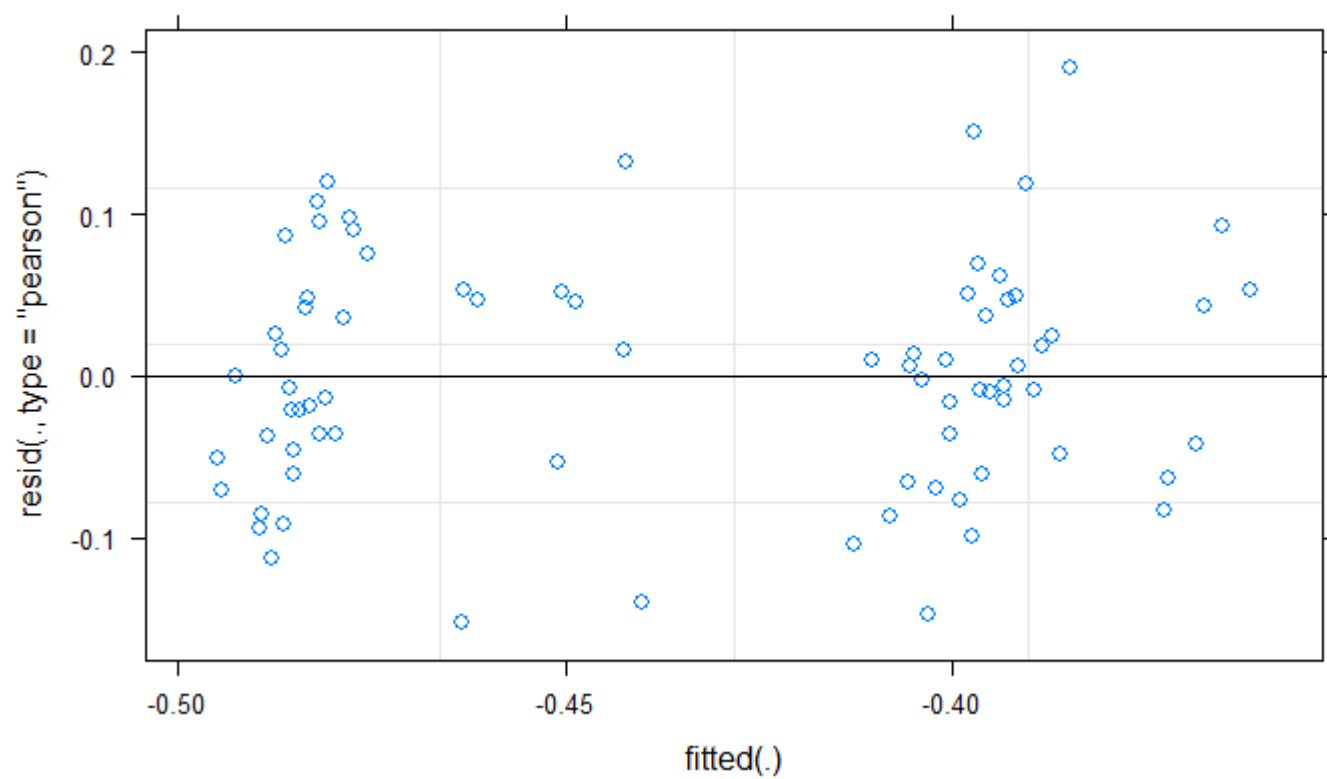
[Hide](#)

```
leveneTest(pam ~ morph, data=data_pamin)
```

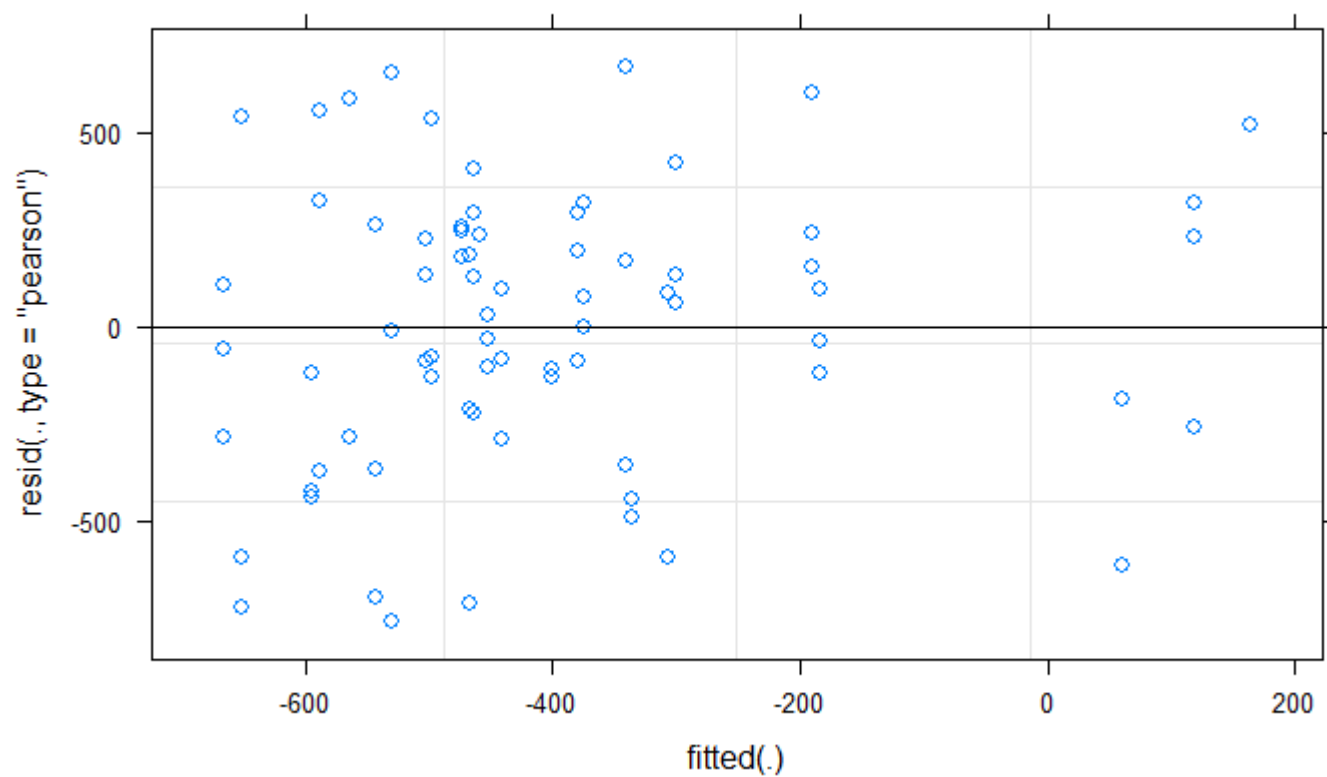
```
Levene's Test for Homogeneity of Variance (center = median)  
      Df F value Pr(>F)  
group  2  0.6616 0.5227  
      33
```

[Hide](#)

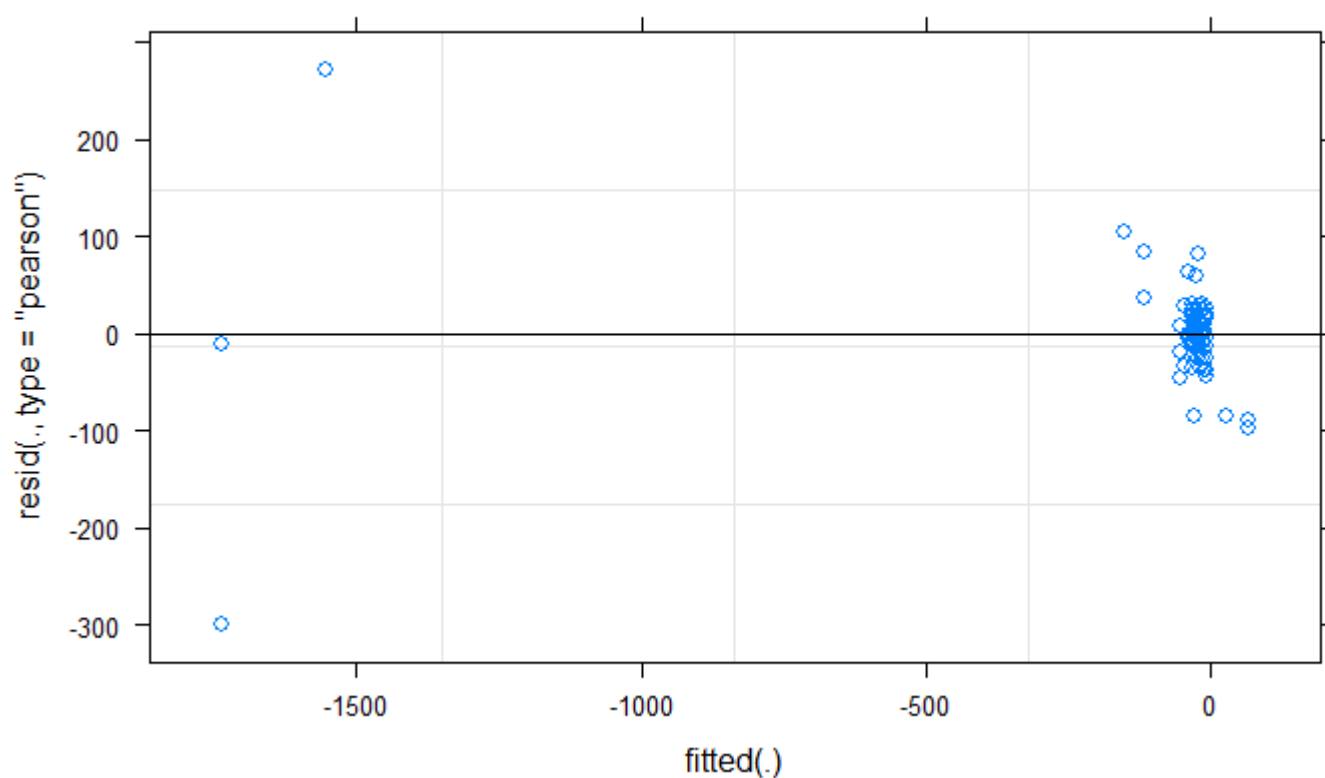
```
plot(model_pam)
```

[Hide](#)

```
plot(model_zoox)
```

[Hide](#)

```
plot(model_ch1)
```



Obtain mean and SD

[Hide](#)

```
sumfun <- function(x, ...){
  c(mean=mean(x, na.rm=TRUE, ...), sd=sd(x, na.rm=TRUE, ...), l=length(x))
}
mean(data_pamin$pam, na.rm = TRUE)
```

```
[1] 0.5799444
```

[Hide](#)

```
sd(data_pamin$pam, na.rm = TRUE)
```

```
[1] 0.07368696
```

[Hide](#)

```
summaryBy(pam~morph, data=data_pamin, FUN=sumfun)
```

morph
<fctr>

pam.mean
<dbl>

pam.sd
<dbl>

pam.l
<dbl>

morph <fctr>	pam.mean <dbl>	pam.sd <dbl>	pam.l <dbl>
1 green	0.5428333	0.06614562	12
2 red	0.5937500	0.07636054	12
3 yellow	0.6032500	0.06904692	12
3 rows			

Hide

```
mean(data_pam$pamt0, na.rm = TRUE)
```

```
[1] 0.6965513
```

Hide

```
sd(data_pam$pamt0, na.rm = TRUE)
```

```
[1] 0.03221706
```

Hide

```
summaryBy(pamt0 ~morph, data=data_pam, FUN=sumfun)
```

morph <fctr>	pamt0.mean <dbl>	pamt0.sd <dbl>	pamt0.l <dbl>
1 green	0.6961042	0.03182882	48
2 red	0.7091111	0.02055663	18
3 yellow	0.6795000	0.04132466	13
3 rows			

Hide

```
summaryBy(pamt0 ~morph * treatment, data=data_pam, FUN=sumfun)
```

morph <fctr>	treatment <fctr>	pamt0.mean <dbl>	pamt0.sd <dbl>	pamt0.l <dbl>
1 green	par	0.6755417	0.03011569	24
2 green	paruv	0.7166667	0.01675830	24
3 red	par	0.7012222	0.02474761	9
4 red	paruv	0.7170000	0.01206234	9
5 yellow	par	0.6788333	0.04727966	7

morph <fctr>	treatment <fctr>	pamt0.mean <dbl>	pamt0.sd <dbl>	pamt0.l <dbl>
6 yellow	paruv	0.6801667	0.03899444	6

6 rows

Hide

```
mean(data_pam$pamt1, na.rm = TRUE)
```

```
[1] 0.2631392
```

Hide

```
sd(data_pam$pamt1, na.rm = TRUE)
```

```
[1] 0.09081155
```

Hide

```
summaryBy(pamt1 ~morph * treatment, data=data_pam, FUN=sumfun)
```

morph <fctr>	treatment <fctr>	pamt1.mean <dbl>	pamt1.sd <dbl>	pamt1.l <dbl>
1 green	par	0.1907500	0.07048543	24
2 green	paruv	0.3195417	0.05983236	24
3 red	par	0.2498889	0.07984742	9
4 red	paruv	0.3193333	0.09890147	9
5 yellow	par	0.2205714	0.07776430	7
6 yellow	paruv	0.3123333	0.06599899	6

6 rows

Hide

```
summaryBy(pamt1 ~morph, data=data_pam, FUN=sumfun)
```

morph <fctr>	pamt1.mean <dbl>	pamt1.sd <dbl>	pamt1.l <dbl>
1 green	0.2551458	0.09175058	48
2 red	0.2846111	0.09423321	18
3 yellow	0.2629231	0.08429458	13

3 rows

[Hide](#)

```
summaryBy(pamt1 ~treatment, data=data_pam, FUN=sumfun)
```

treatment <fctr>	pamt1.mean <dbl>	pamt1.sd <dbl>	pamt1.l <dbl>
1 par	0.2092750	0.07604519	40
2 paruv	0.3183846	0.06932555	39
2 rows			

[Hide](#)

```
summaryBy(ppam ~morph * treatment, data=data_pam, FUN=sumfun)
```

morph <fctr>	treatment <fctr>	ppam.mean <dbl>	ppam.sd <dbl>	ppam.l <dbl>
1 green	par	-71.75833	10.318092	24
2 green	paruv	-55.32584	8.743633	24
3 red	par	-64.10850	12.080702	9
4 red	paruv	-55.47203	13.637559	9
5 yellow	par	-71.09991	6.631839	7
6 yellow	paruv	-53.98160	10.081318	6
6 rows				

[Hide](#)

```
summaryBy(ppam ~morph, data=data_pam, FUN=sumfun)
```

morph <fctr>	ppam.mean <dbl>	ppam.sd <dbl>	ppam.l <dbl>
1 green	-63.54209	12.58786	48
2 red	-59.79027	13.26442	18
3 yellow	-62.54076	12.08749	13
3 rows			

[Hide](#)

```
summaryBy(ppam ~treatment, data=data_pam, FUN=sumfun)
```

treatment <fctr>	ppam.mean <dbl>	ppam.sd <dbl>	ppam.l <dbl>
----------------------------	---------------------------	-------------------------	------------------------

treatment <fctr>	ppam.mean <dbl>	ppam.sd <dbl>	ppam.l <dbl>
1 par	-69.89169	10.549998	40
2 paruv	-55.15277	9.952877	39
2 rows			

Hide

summaryBy(zooxt0 ~morph, data=data_zoox, FUN=sumfun)

morph <fctr>	zooxt0.mean <dbl>	zooxt0.sd <dbl>	zooxt0.l <dbl>
1 green	877.2043	366.9444	48
2 red	700.0046	287.2100	18
3 yellow	561.7729	174.1258	13
3 rows			

Hide

summaryBy(zooxt0 ~morph * treatment, data=data_zoox, FUN=sumfun)

morph <fctr>	treatment <fctr>	zooxt0.mean <dbl>	zooxt0.sd <dbl>	zooxt0.l <dbl>
1 green	par	852.5480	360.2724	24
2 green	paruv	900.8332	379.4112	24
3 red	par	673.7593	249.7771	9
4 red	paruv	729.5306	339.6533	9
5 yellow	par	545.4056	198.4607	7
6 yellow	paruv	590.4156	143.4357	6
6 rows				

Hide

summaryBy(zooxt1 ~morph, data=data_zoox, FUN=sumfun)

morph <fctr>	zooxt1.mean <dbl>	zooxt1.sd <dbl>	zooxt1.l <dbl>
1 green	356.0033	205.3376	48
2 red	417.0104	146.5229	18

morph <fctr>	zooxt1.mean <dbl>	zooxt1.sd <dbl>	zooxt1.l <dbl>
3 yellow	476.1941	294.2763	13

3 rows

Hide

```
summaryBy(zooxt1 ~treatment, data=data_zoox, FUN=sumfun)
```

treatment <fctr>	zooxt1.mean <dbl>	zooxt1.sd <dbl>	zooxt1.l <dbl>
1 par	431.3732	204.2094	40
2 paruv	339.1106	207.0245	39

2 rows

Hide

```
summaryBy(zooxt1 ~morph * treatment, data=data_zoox, FUN=sumfun)
```

morph <fctr>	treatment <fctr>	zooxt1.mean <dbl>	zooxt1.sd <dbl>	zooxt1.l <dbl>
1 green	par	373.2927	161.0556	24
2 green	paruv	338.7138	244.1261	24
3 red	par	463.9263	171.8080	9
4 red	paruv	375.3074	113.8070	9
5 yellow	par	620.2913	295.3492	7
6 yellow	paruv	260.0483	102.9092	6

6 rows

Hide

```
summaryBy(pzoox ~morph, data=data_zoox, FUN=sumfun)
```

morph <fctr>	pzoox.mean <dbl>	pzoox.sd <dbl>	pzoox.l <dbl>
1 green	-53.144234	30.53565	48
2 red	-26.543193	54.10201	18
3 yellow	9.355533	96.53849	13

3 rows

[Hide](#)

```
summaryBy(pzoox ~treatment, data=data_zoox, FUN=sumfun)
```

treatment <fctr>	pzoox.mean <dbl>	pzoox.sd <dbl>	pzoox.l <dbl>
1 par	-26.11650	62.97242	40
2 paruv	-53.48456	33.44919	39
2 rows			

[Hide](#)

```
summaryBy(pzoox ~morph * treatment, data=data_zoox, FUN=sumfun)
```

morph <fctr>	treatment <fctr>	pzoox.mean <dbl>	pzoox.sd <dbl>	pzoox.l <dbl>
1 green	par	-49.25933	27.81767	24
2 green	paruv	-56.86726	33.09255	24
3 red	par	-13.44898	66.81140	9
4 red	paruv	-39.63741	37.63687	9
5 yellow	par	45.70764	99.93391	7
6 yellow	paruv	-63.34869	20.45646	6
6 rows				

[Hide](#)

```
summaryBy(chlt0 ~morph, data=data_zoox, FUN=sumfun)
```

morph <fctr>	chlt0.mean <dbl>	chlt0.sd <dbl>	chlt0.l <dbl>
1 green	80.87664	21.94802	48
2 red	84.60205	20.75916	18
3 yellow	472.72747	740.88358	13
3 rows			

[Hide](#)

```
summaryBy(chlt0 ~morph * treatment, data=data_zoox, FUN=sumfun)
```

morph <fctr>	treatment <fctr>	chlt0.mean <dbl>	chlt0.sd <dbl>	chlt0.l <dbl>
------------------------	----------------------------	----------------------------	--------------------------	-------------------------

morph <fctr>	treatment <fctr>	chl10.mean <dbl>	chl10.sd <dbl>	chl10.I <dbl>
1 green	par	80.23823	27.70785	24
2 green	paruv	81.48845	15.10918	24
3 red	par	79.29656	14.13213	9
4 red	paruv	90.57072	26.07411	9
5 yellow	par	614.19179	911.39154	7
6 yellow	paruv	307.68576	509.81898	6
6 rows				

Hide

```
summaryBy(chl1 ~morph, data=data_zoox, FUN=sumfun)
```

morph <fctr>	chl1.mean <dbl>	chl1.sd <dbl>	chl1.I <dbl>
1 green	61.14871	16.84027	48
2 red	51.42898	30.47010	18
3 yellow	49.39895	11.34627	13
3 rows			

Hide

```
summaryBy(chl1 ~treatment, data=data_zoox, FUN=sumfun)
```

treatment <fctr>	chl1.mean <dbl>	chl1.sd <dbl>	chl1.I <dbl>
1 par	55.42346	17.18178	40
2 paruv	59.38727	23.59716	39
2 rows			

Hide

```
summaryBy(chl1 ~morph * treatment, data=data_zoox, FUN=sumfun)
```

morph <fctr>	treatment <fctr>	chl1.mean <dbl>	chl1.sd <dbl>	chl1.I <dbl>
1 green	par	58.81527	15.227555	24
2 green	paruv	63.48216	18.337870	24

morph <fctr>	treatment <fctr>	chl1.mean <dbl>	chl1.sd <dbl>	chl1.l <dbl>
3 red	par	53.60451	23.614794	9
4 red	paruv	49.49518	36.877666	9
5 yellow	par	44.28149	11.301842	7
6 yellow	paruv	57.07516	6.510371	6
6 rows				

Hide

```
summaryBy(pchl ~morph, data=data_zoox, FUN=sumfun)
```

morph <fctr>	pchl.mean <dbl>	pchl.sd <dbl>	pchl.l <dbl>
1 green	-20.60309	26.15835	48
2 red	-35.10809	41.29988	18
3 yellow	-61.41762	27.63443	13
3 rows			

Hide

```
summaryBy(pchl ~treatment, data=data_zoox, FUN=sumfun)
```

treatment <fctr>	pchl.mean <dbl>	pchl.sd <dbl>	pchl.l <dbl>
1 par	-32.30350	29.23262	40
2 paruv	-26.36171	36.62002	39
2 rows			

Hide

```
summaryBy(pchl ~morph * treatment, data=data_zoox, FUN=sumfun)
```

morph <fctr>	treatment <fctr>	pchl.mean <dbl>	pchl.sd <dbl>	pchl.l <dbl>
1 green	par	-22.95787	21.96706	24
2 green	paruv	-18.34642	29.93474	24
3 red	par	-32.73554	32.17263	9
4 red	paruv	-37.48064	51.05963	9

morph <fctr>	treatment <fctr>	pchl.mean <dbl>	pchl.sd <dbl>	pchl.l <dbl>
5 yellow	par	-67.55234	26.21738	7
6 yellow	paruv	-52.21554	30.93908	6
6 rows				

Hide

```
mean(data_zoox$pchl, na.rm = TRUE)
```

```
[1] -29.3733
```

Hide

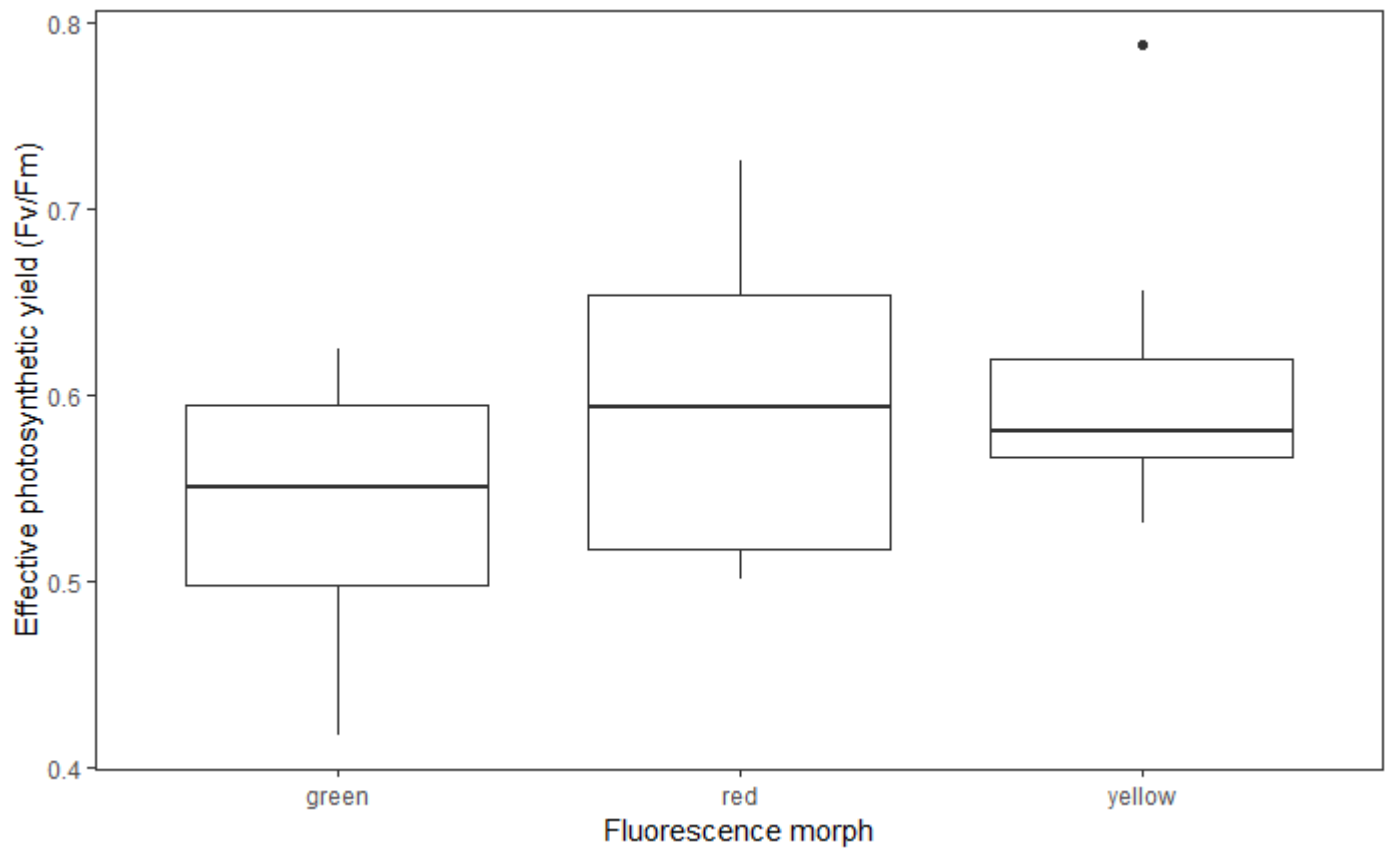
```
sd(data_zoox$pchl, na.rm = TRUE)
```

```
[1] 32.98648
```

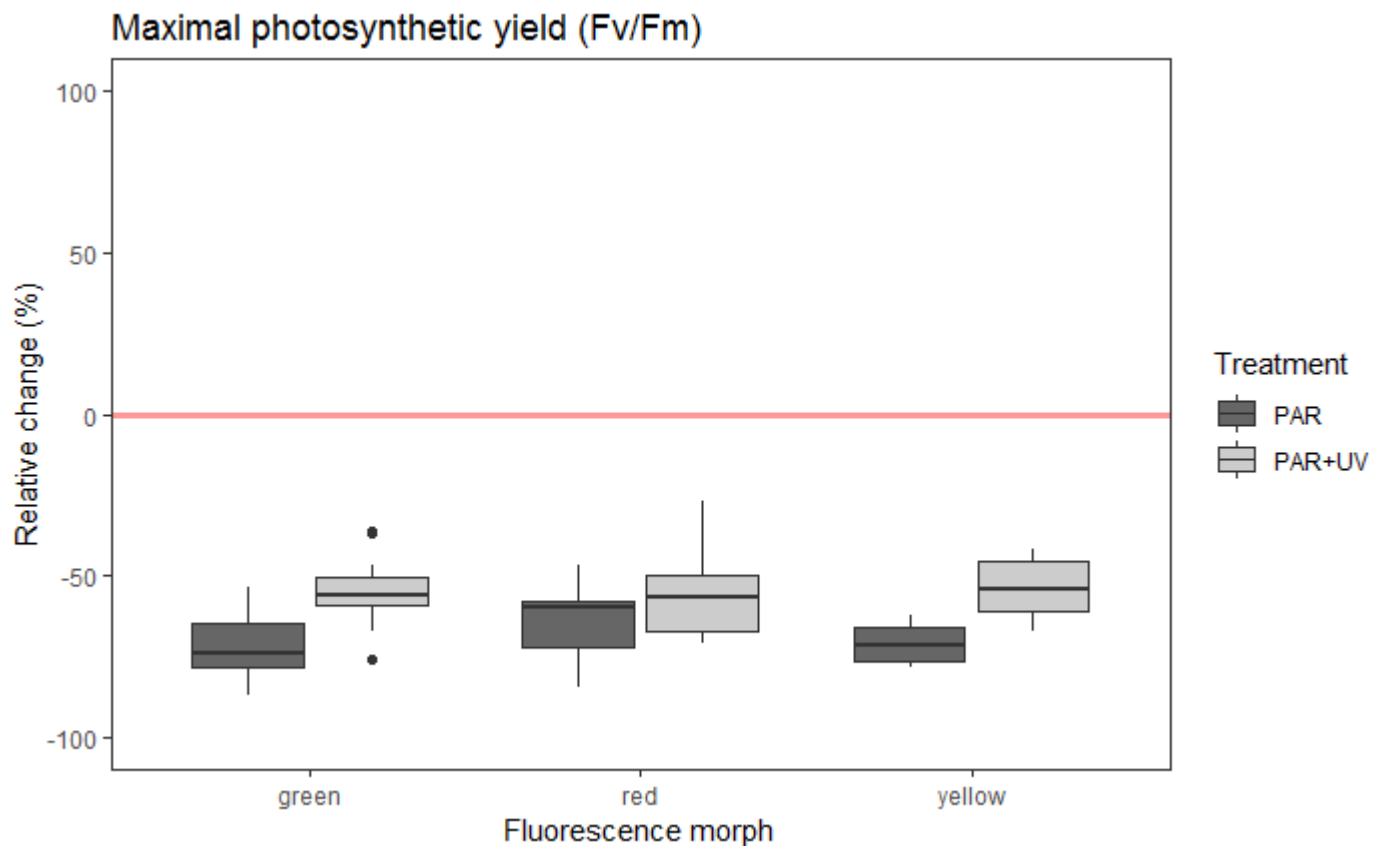
Visualize the data as a box plot

Hide

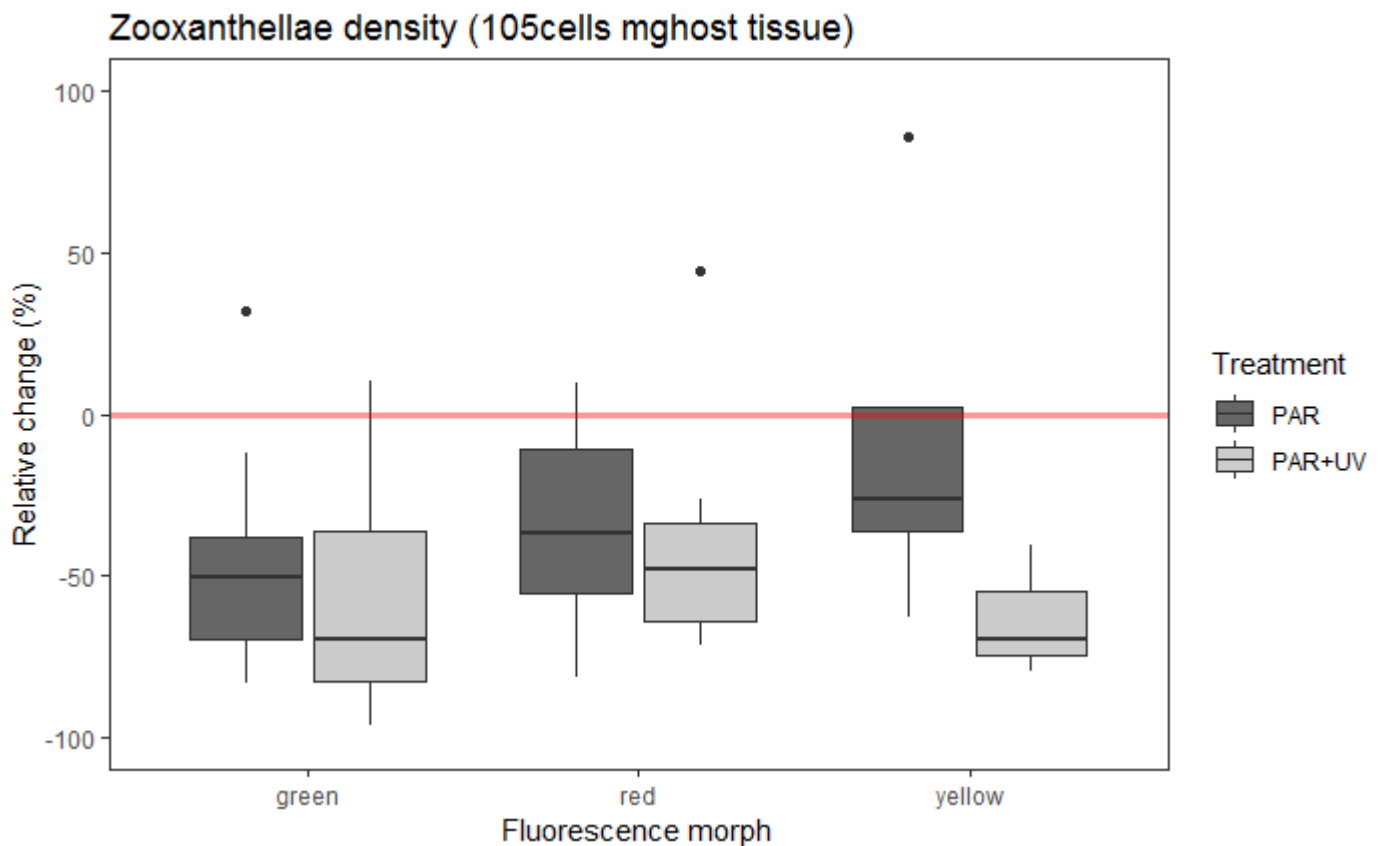
```
pamin_plot <- ggplot(data = data_pamin, aes(x=morph, y=pam)) +
  geom_boxplot() +
  labs(x="Fluorescence morph", y="Effective photosynthetic yield (Fv/Fm)") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank()) +
  theme(legend.position = "none")
pamin_plot
```


[Hide](#)

```
pam_plot <- ggplot(data = data_pam, aes(x=morph, y=ppam)) +
  geom_boxplot(aes(fill=treatment)) +
  labs(title= "Maximal photosynthetic yield (Fv/Fm)", x="Fluorescence morph", y="Relative change (%)") +
  ylim(-100, 100) +
  geom_hline(yintercept=0, color= "red", size = 1.25, alpha = 0.4) +
  scale_fill_grey(start = 0.4, end = 0.8, name="Treatment", breaks=c("par", "paruv"), labels=c("PAR", "PAR+UV")) +
  theme_bw() +
  theme(legend.position="right")+
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
pam_plot
```


[Hide](#)

```
zoox_plot <- ggplot(data = data_zoox, aes(x=morph, y=pzoox)) +
  geom_boxplot(aes(fill=treatment)) +
  labs(title = "Zooxanthellae density (105cells mghost tissue)", x="Fluorescence morph", y="Relative change (%)") +
  ylim(-100, 100) +
  geom_hline(yintercept=0, color= "red", size = 1.25, alpha = 0.4) +
  scale_fill_grey(start = 0.4, end = 0.8, name="Treatment", breaks=c("par", "paruv"), labels=c("PAR", "PAR+UV")) +
  theme_bw() +
  theme(legend.position="right")+
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
zoox_plot
```


[Hide](#)

```
chl_plot <- ggplot(data = data_zoos, aes(x=morph, y=pchl)) +
  geom_boxplot(aes(fill=treatment)) +
  labs(title = "Chlorophyll a concentration (pgchlorophyll a cell-1)", x="Fluorescence morph",
  y="Relative change (%)") +
  ylim(-100, 100) +
  geom_hline(yintercept=0, color= "red", size = 1.25, alpha = 0.4) +
  scale_fill_grey(start = 0.4, end = 0.8, name="Treatment", breaks=c("par", "paruv"), labels=c("P
AR", "PAR+UV")) +
  theme_bw() +
  theme(legend.position="right")+
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
chl_plot
```

