

Two-Way ANOVA analysis and interpretation

General Setup

Data in columns, one column for response, two columns for treatment levels.

```
library(car)
```

Fit the linear model e.g.

```
m1 <- lm(response~factor1*factor2, data=data)
```

Checking the assumptions

1. Equal variances:

```
plot(m1, which=1)
```

If spread of residual values changes along the x axis (for example a triangle of values) then consider transformation.

Check equality formally:

```
leveneTest(response~factor1*factor2, data=data)
```

2. Normality of residuals

```
plot(m1, which=2)
```

If residuals do not fall close to line then consider transformation

Check normality formally

```
shapiro.test(m1$residuals)
```

Interpreting the results

If plots and tests are OK, then proceed:

```
Anova(m1, type=3)
```

Look at significance of each line in the ANOVA table, **starting with the interaction**

Interaction (factor1:factor2)
significant ($p < 0.05$)

To visualise differences,
use Interaction plot:

```
interaction.plot(dat  
a$factor1,  
data$factor2,  
data$response,  
type="b", pch=19)
```

Use

```
TukeyHSD(aov(m1),  
which=c("factor1:fact  
or2"))
```


to look at mean for each
combination of treatments

Examine output to determine
where significant differences
lie between all combinations,
but really only need to
interpret those which are
biologically interesting

For figure, use boxplot or
beeswarm for all combinations
of factor levels e.g.

```
boxplot(response~factor1*  
factor2, data=data)
```

Interaction not significant ($p > 0.05$), but
one or more main effects significant

One main effect
significant

To visualise differences, use
boxplot or beeswarm
(

```
response~factor,  
data=data
```

). Factor is the main
effect that is significant

Use

```
TukeyHSD(aov(m1),  
which=c(factor)), specify  
the factor that is significant
```

Examine output to determine
where significant differences
lie between levels of
significant factor

For figure, use boxplot or
beeswarm for the significant
factor
e.g.

```
boxplot(response~factor1,  
data=data)
```

Both main effects
significant

To visualise differences, use Interaction
plot:

```
interaction.plot(data$factor1,  
data$factor2, data$response,  
type="b", pch=19)
```

Use

```
TukeyHSD(aov(m1),  
which=c(factor1,  
factor2))
```


to look at both factors

Examine output to determine where
significant differences lie between
levels of each factor **separately**

For figure, use boxplot or beeswarm for both
of the significant factors e.g.

```
boxplot(response~factor1*factor2,  
data=data)
```

No significant results (all effects
 $p > 0.05$)

Stop