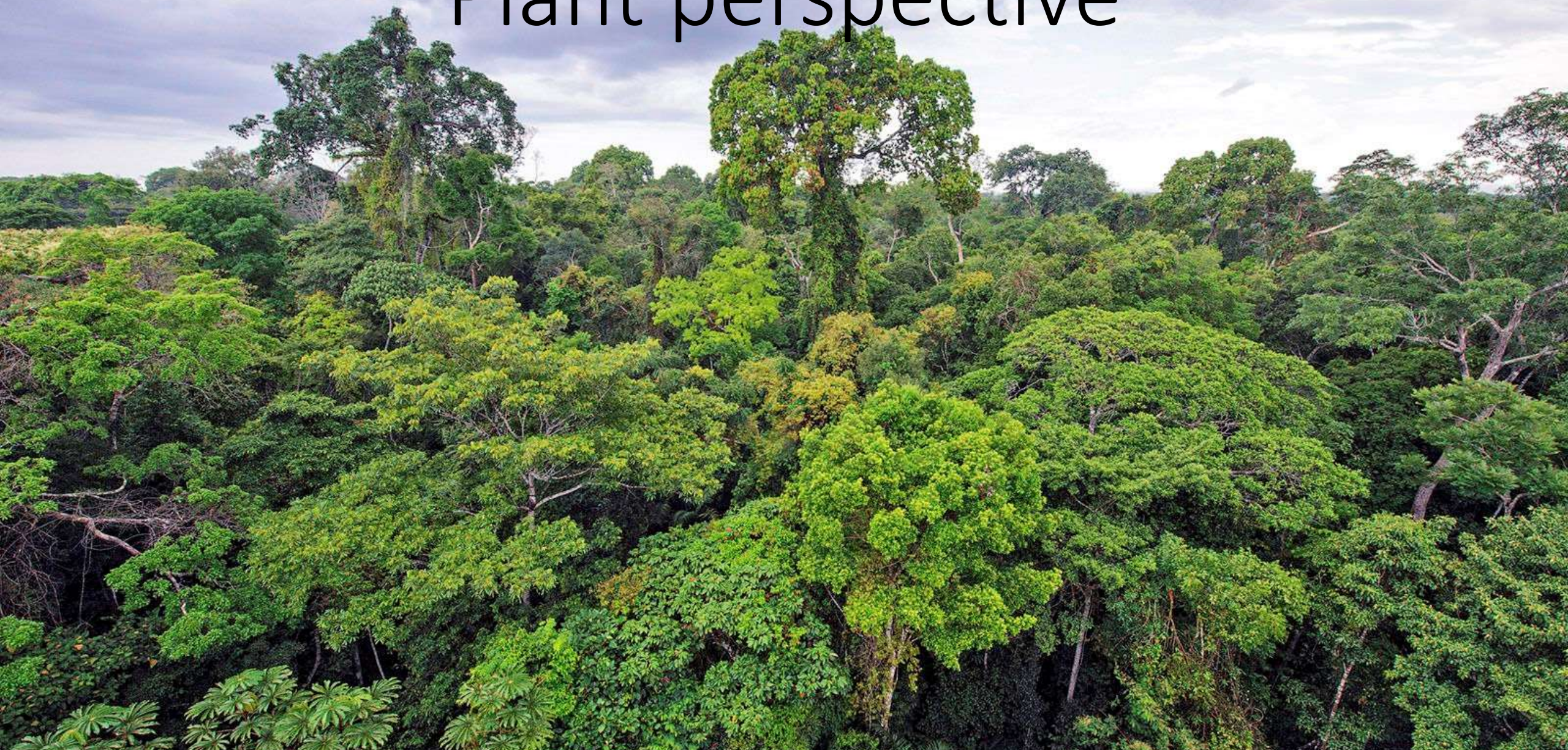


# Plant perspective





# Plant perspective

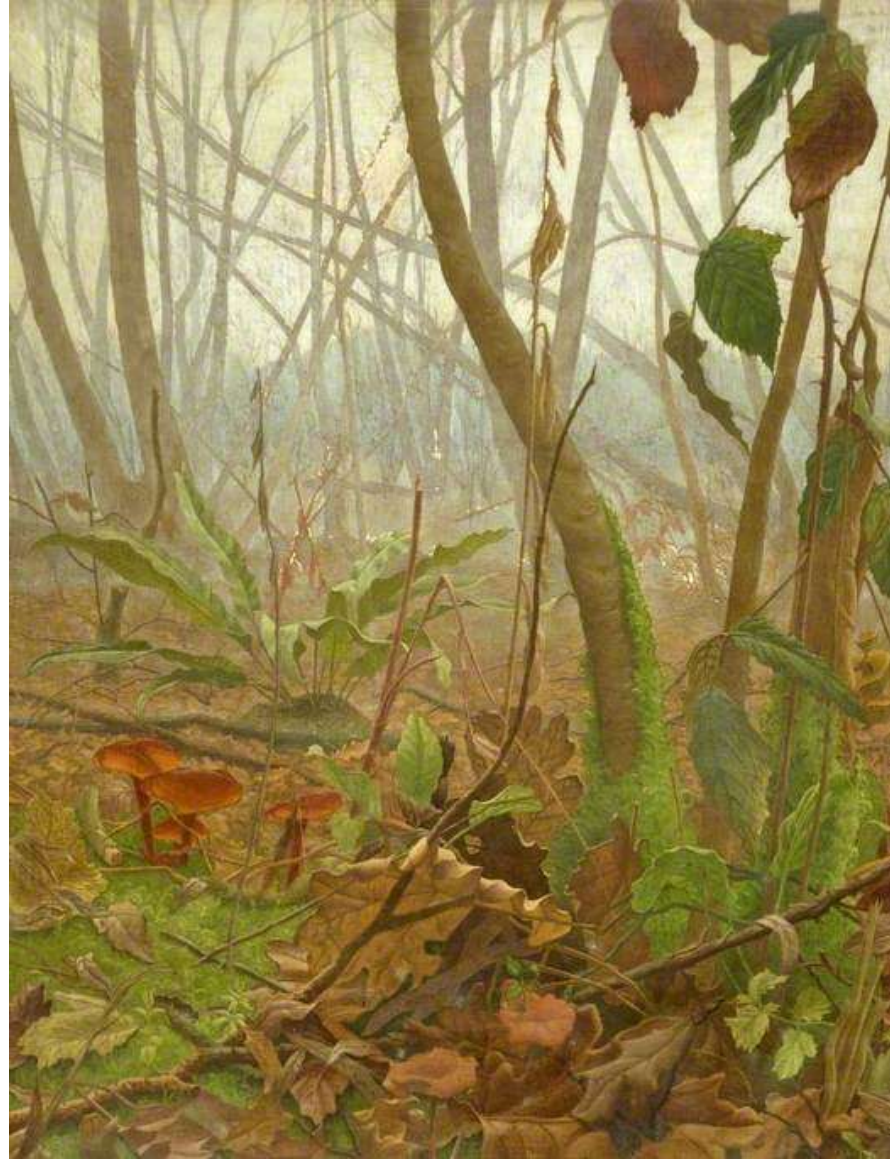
Think about the basics of statistics

Go through the analysis of a greenhouse experiment

Understand linear models and interpret results

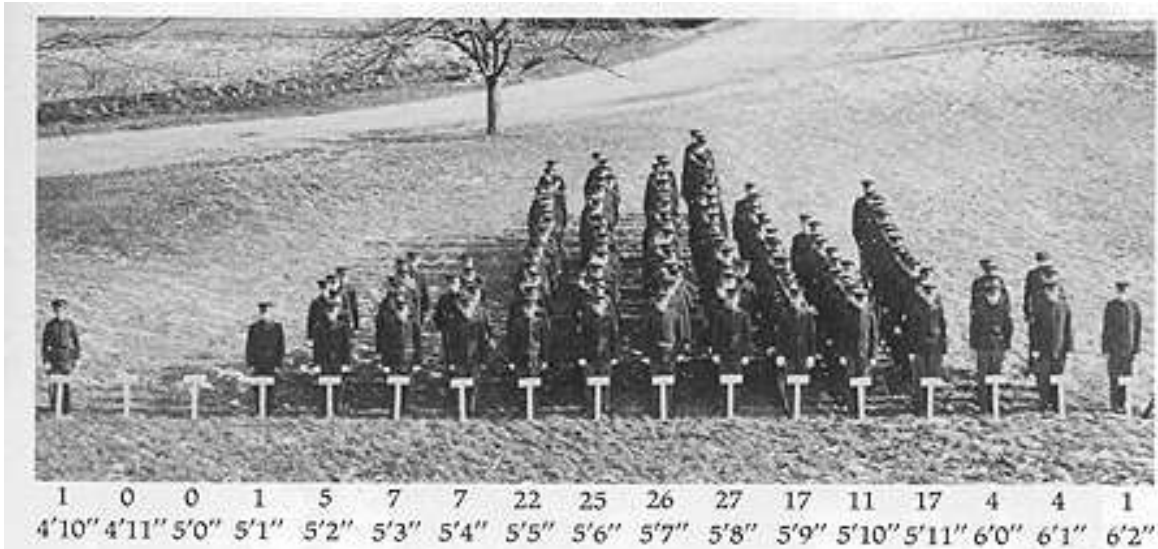


# Plant perspective



Eliot Hodgkin

# Everything varies

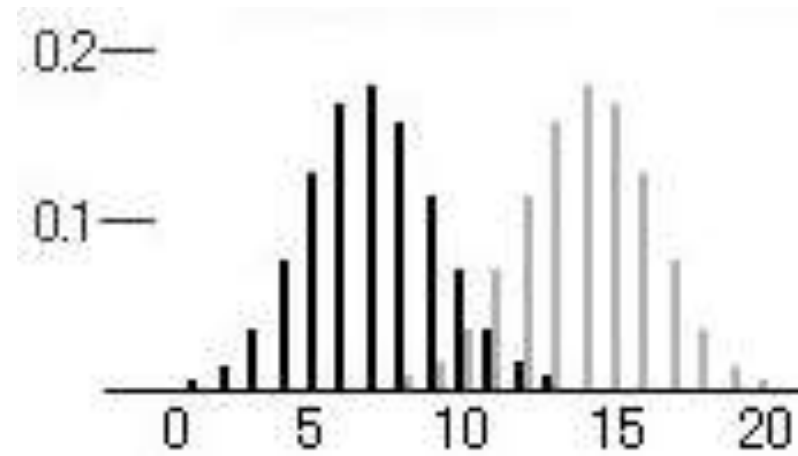


**Figure 1.5**  
*Differences in height in the same population: heights of conscripts over 60 years ago. (From A. Blakeslee, *Journal of Heredity*, vol. 5, 1914.)*

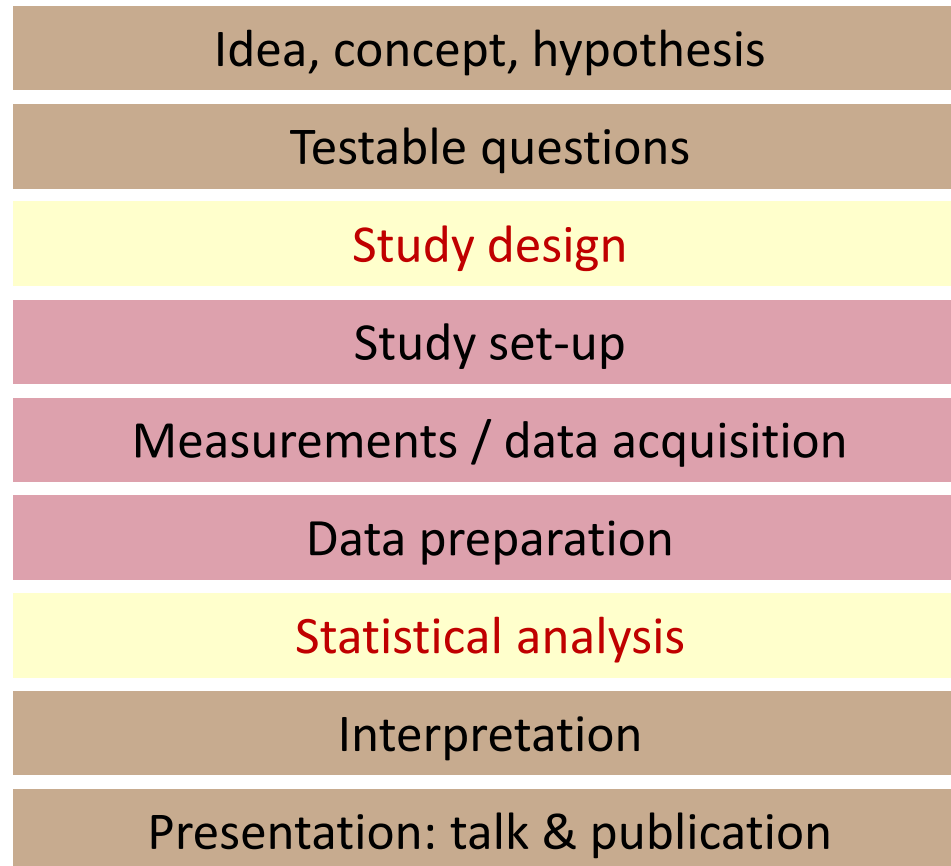


# Statistics

# Statistics: the grammar of empirical thinking



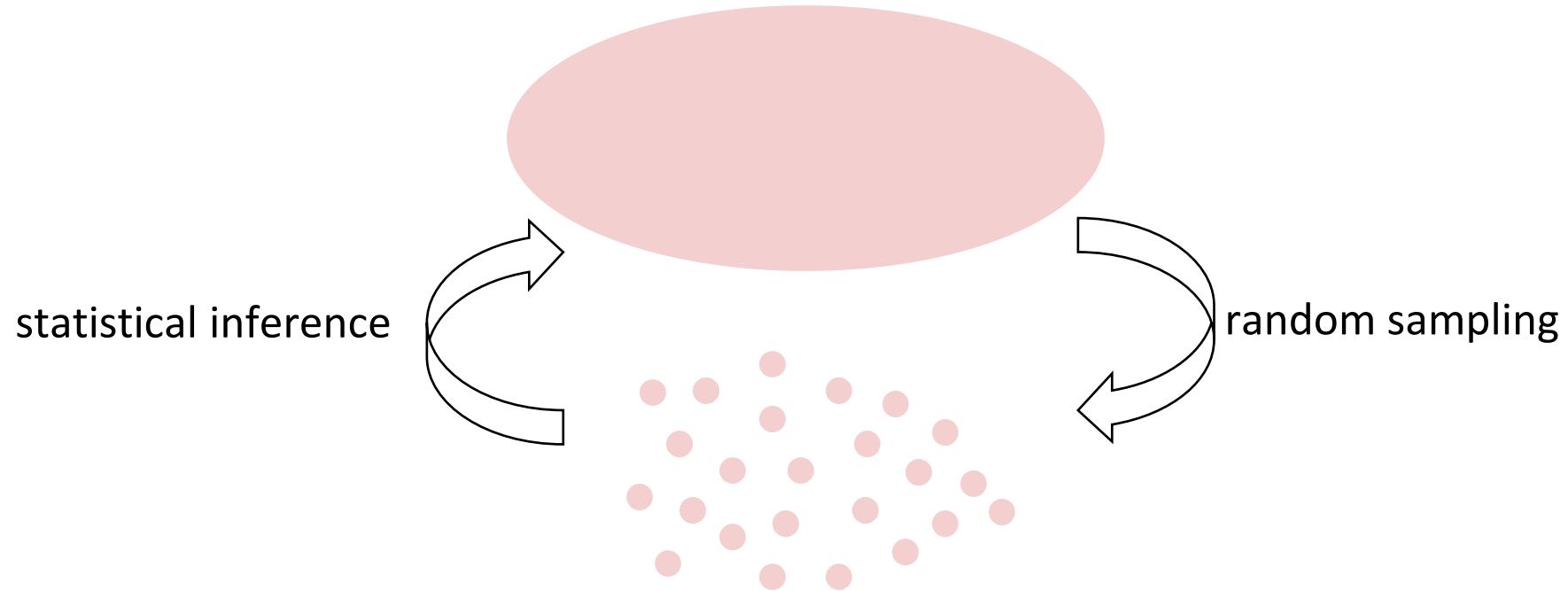
# The long way of a scientific investigation



**being understood by others**

# Economics

The basic population is the collection of all individuals of which we make a scientific statement



The sample population is a subset of these individuals which we actually measure



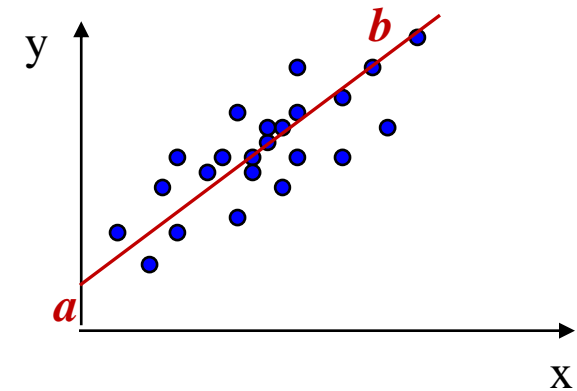
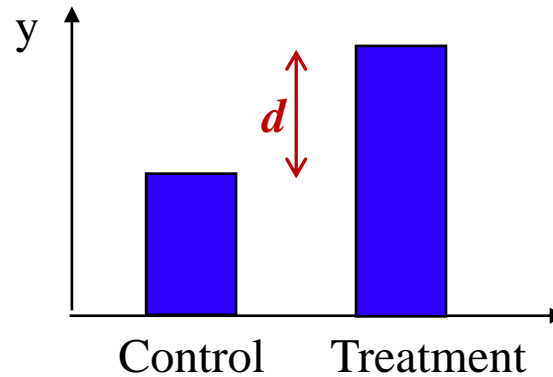
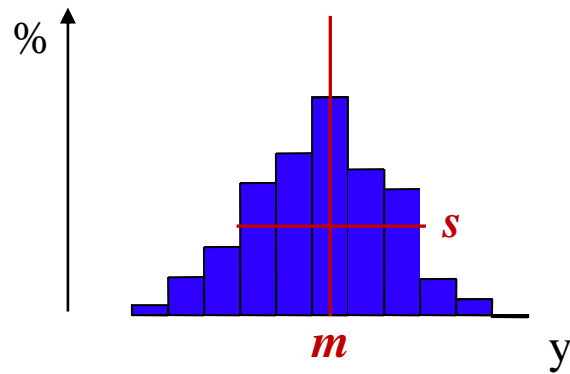
# Types of data

Types	Mathematics	Examples
<b>Categorical</b>		
Nominal	$=, \neq$ , mode	<ul style="list-style-type: none"><li>• names of species, places</li><li>• control vs. treatment</li></ul>
Ordinal	$<, >$ , median	<ul style="list-style-type: none"><li>• ranks</li><li>• XS, S, M, L, XL</li><li>• Braun-Blanquet scale</li></ul>
<b>Numeric (<math>\approx</math> continuous)</b>		
with negative values	$+, -$ arithmetic mean, standard deviation	<ul style="list-style-type: none"><li>• degree Celsius</li><li>• growth rate</li><li>• relative measures</li></ul>
without negative values	$\div, \times, \%$ geometric and harmonic mean	<ul style="list-style-type: none"><li>• degree Kelvin</li><li>• biomass</li></ul>
Integer		<ul style="list-style-type: none"><li>• number of offspring</li></ul>

# Parameter estimates

Parameters: quantities that describe data

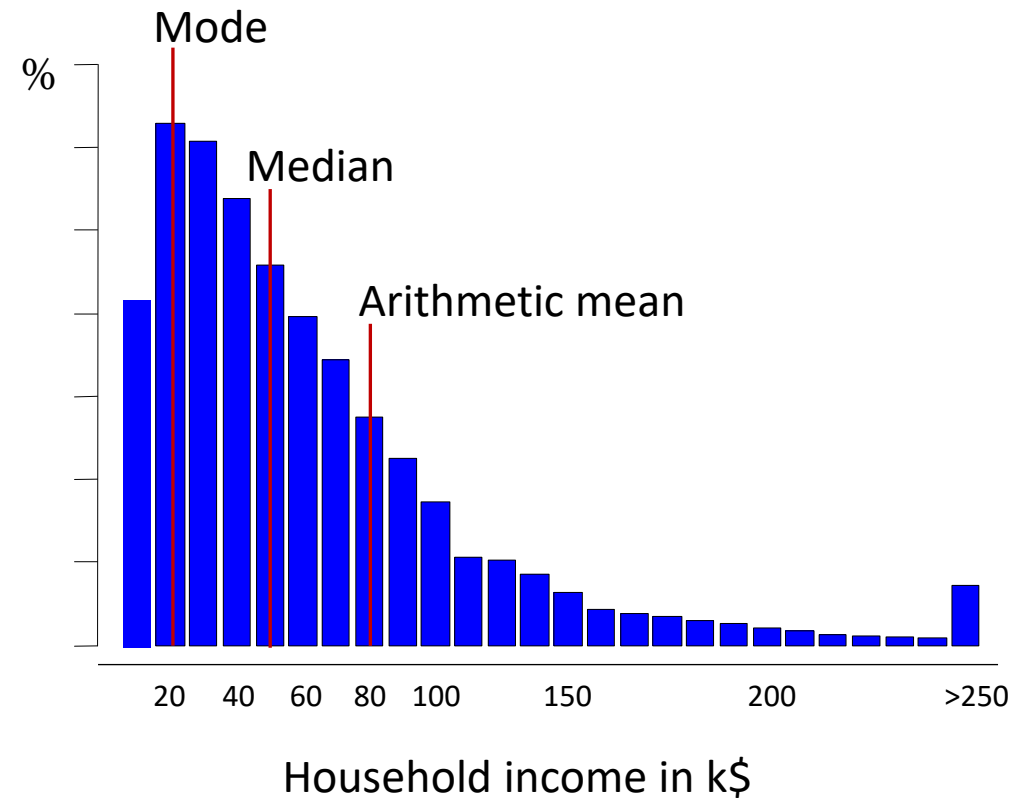
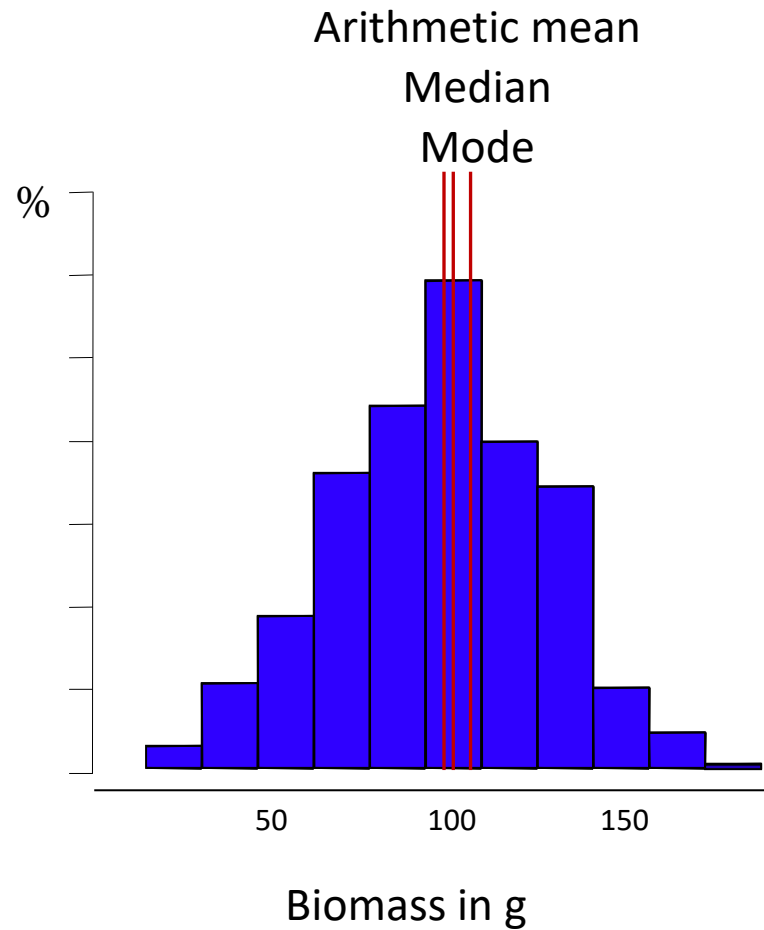
- averages of data  $m$
- variability around the average  $s$
- effect sizes  $d$
- intercept & slopes  $a, b$





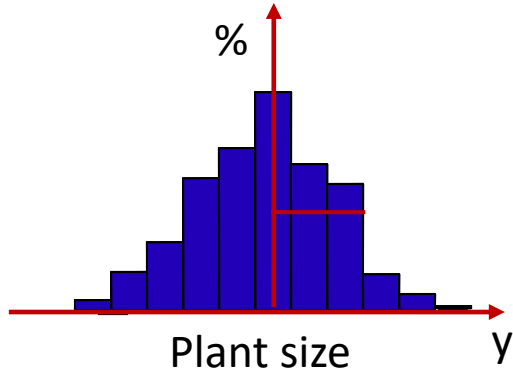
# Parameter estimates

The choice of the parameter depends on the data distribution

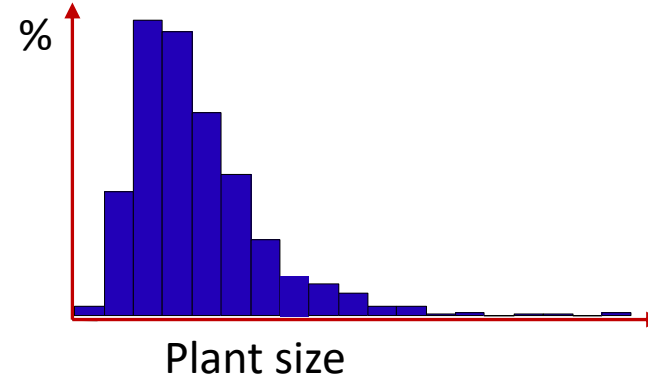


# Types of distributions

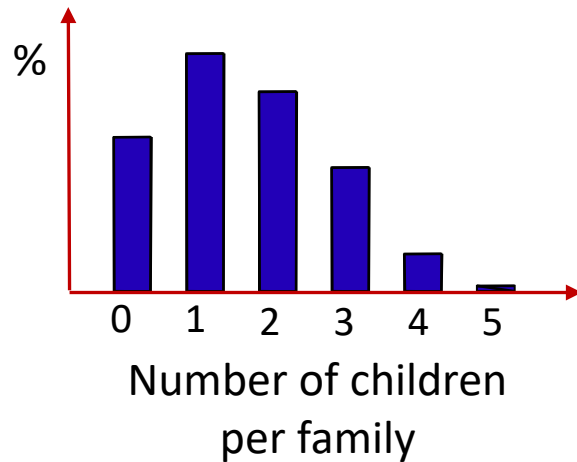
Normal distribution



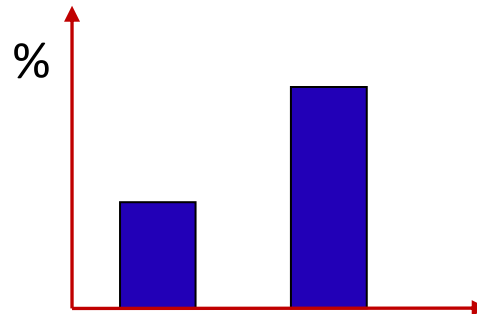
Log-Normal distribution



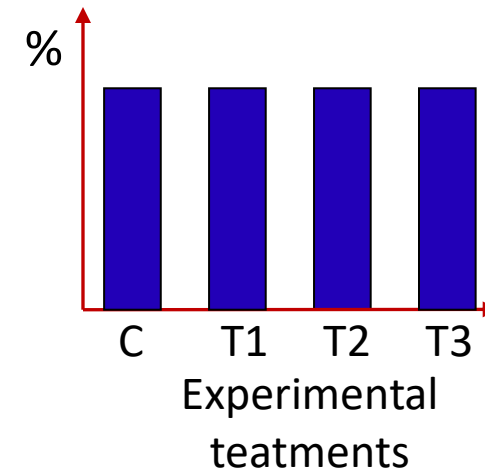
Poisson distribution



Binomial distribution



Uniform distribution

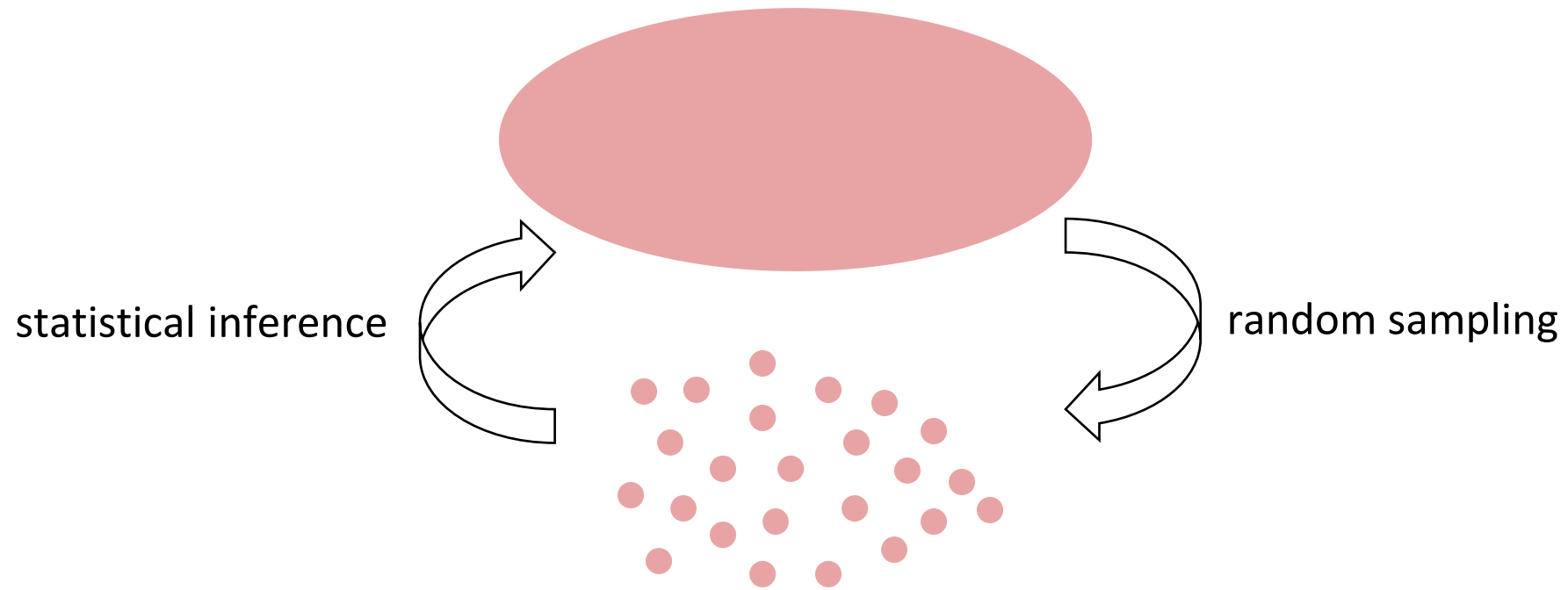




# Parameter estimation

We calculate parameters in the sample...

...to get an estimate for the basic population

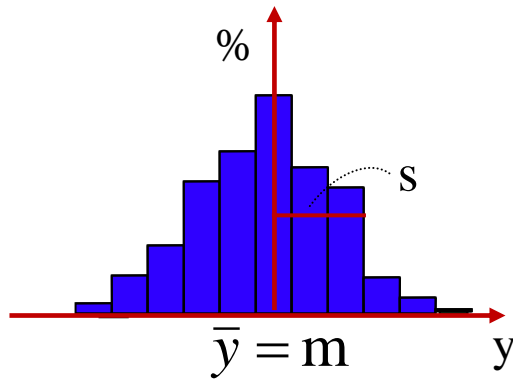


# Types of distributions

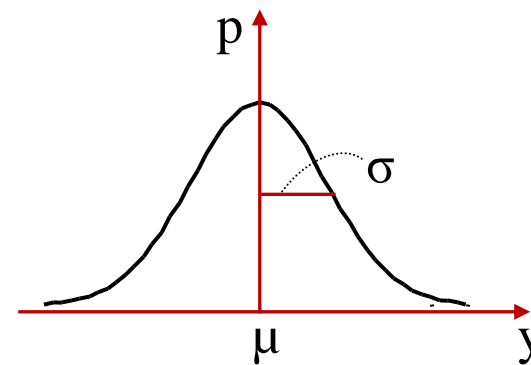
Sample data have frequency distributions which describe how often particular states occur

Frequency distributions approach probability distributions as the sample size increases and approaches the basic population

Frequency distribution

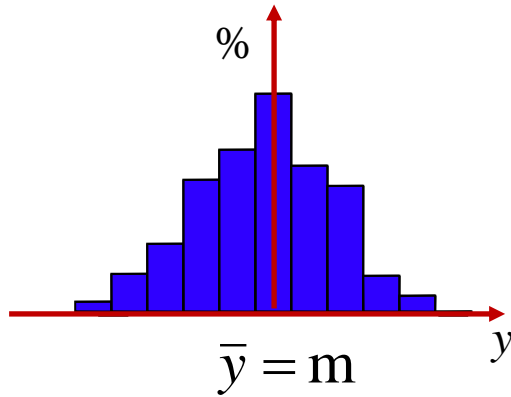


Probability distribution





# Measures of variability



## Standard deviation

$$s = \text{SD} = \sqrt{\frac{\sum_{i=1}^n (y_i - \bar{y})^2}{n-1}}$$

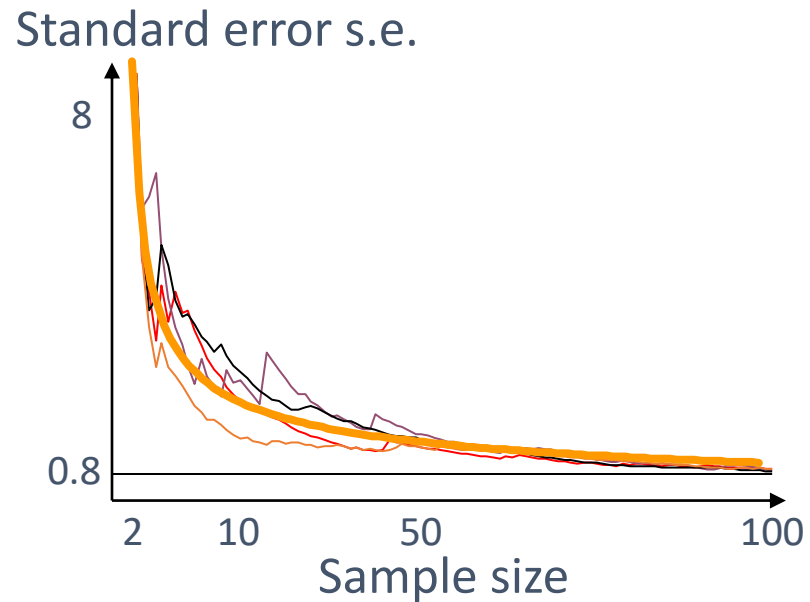
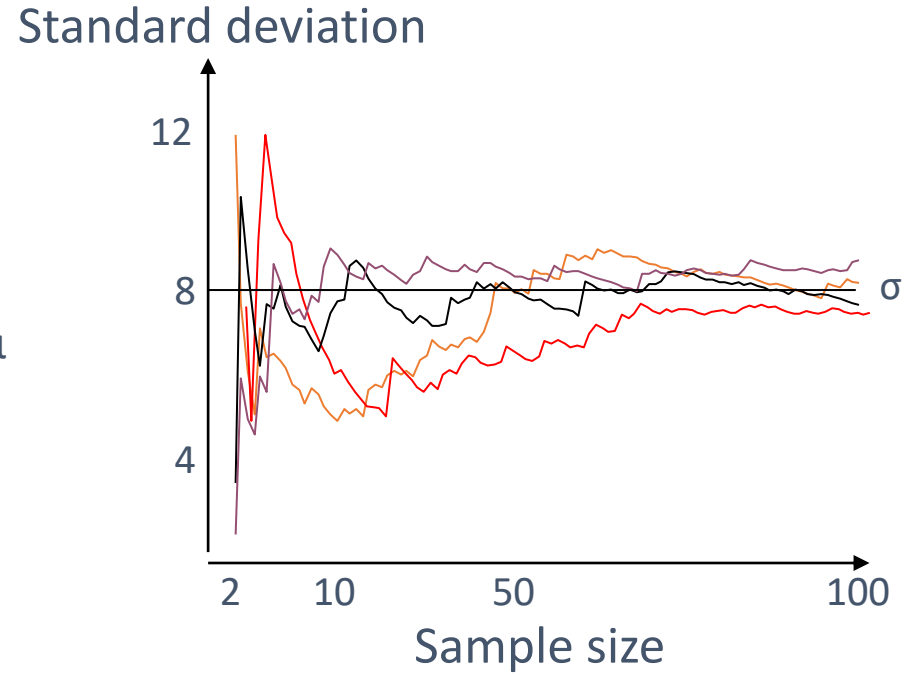
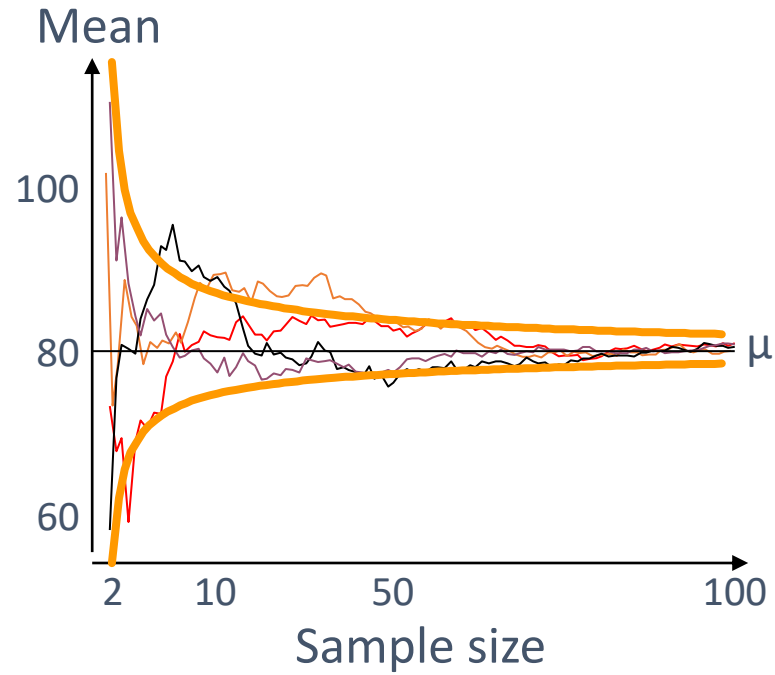
## Variance

$$s^2 = \text{var}(y) = \frac{\sum (y_i - \bar{y})^2}{n-1} = \frac{\text{Sum of squares}}{\text{degree of freedom}}$$

## Coefficient of variation

$$CV = s / \bar{y}$$

# Mean, standard deviation & standard error



$$SE_{\bar{x}} = \frac{s}{\sqrt{n}}$$



# Related, but completely different!

## Standard deviation

and variance, coefficient of variation

- measures of **variability of the data**
- How variable are the data?
- becomes more **accurate** with increasing sample size
- used to describe the data

## Standard error

and confidence intervals

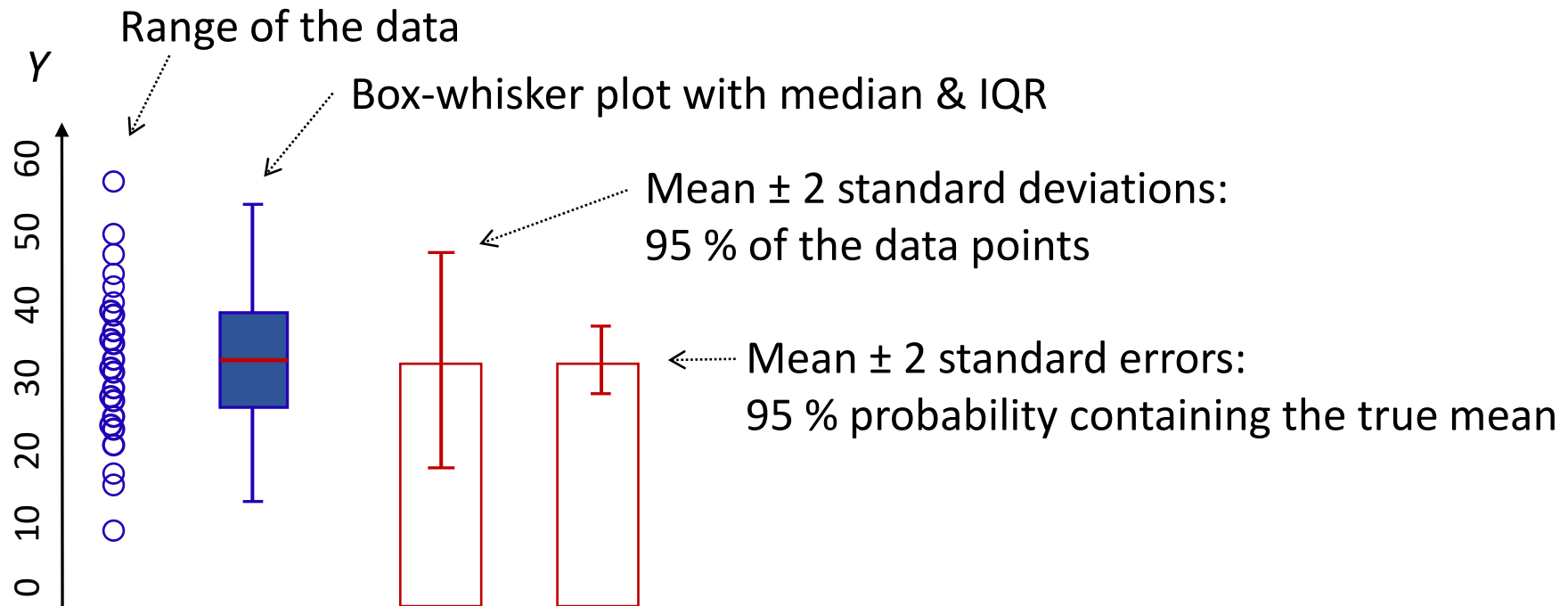
- measures of the **accuracy of the mean**
  - How good is the mean estimated ?
- becomes **smaller** with increasing sample size
  - used for statistical testing

# Confidence interval

The 95% confidence interval  $CI = \text{mean} \pm 2 \text{ standard errors}$

- gives the interval within the true mean lies within 95 % probability

The confidence interval depends on the specified probability level (99% CI > 95% CI) and the sample size (CI decreases with the sample size)





There are two types of errors made when we measure data

## 1. Measuring errors

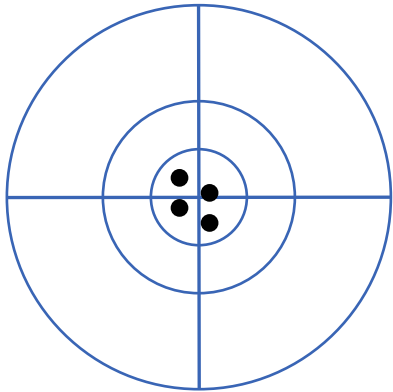
There are always measuring errors. The important distinction is between *precision* and *accuracy*

## 2. Sampling errors

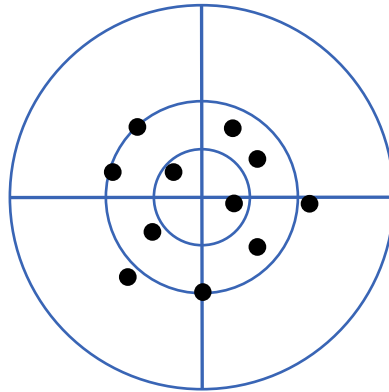
We measure samples to estimate parameters of the basic population. To what degree would we get other estimates, if we had chosen a different sample?

Both errors are inevitable!

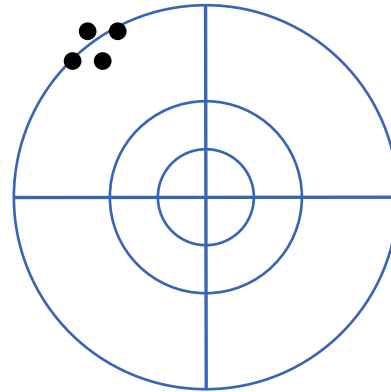
# Precision & accuracy



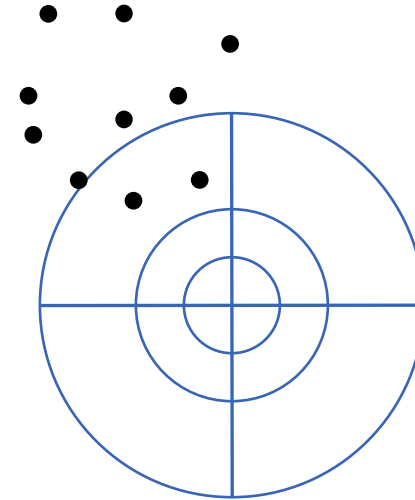
accurate  
and precise



accurate  
but not precise



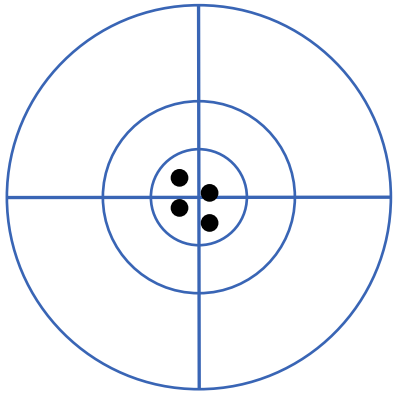
not accurate  
but precise



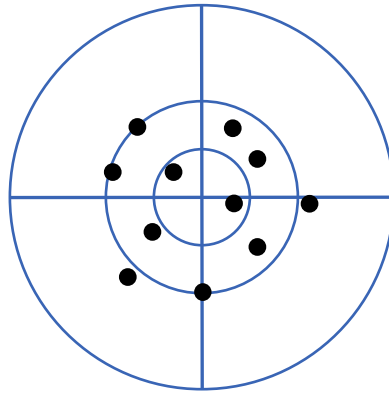
neither accurate  
nor precise



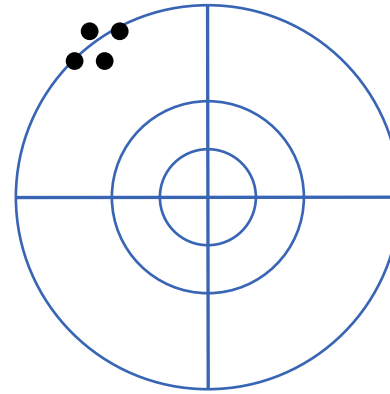
# Precision & accuracy



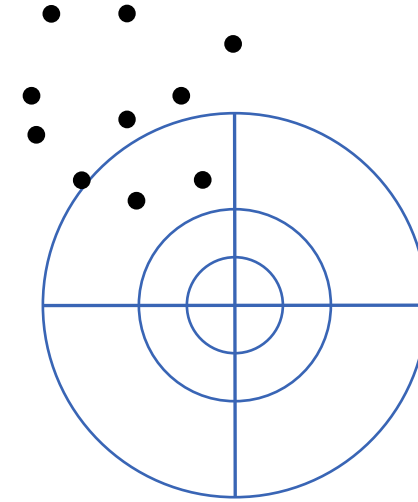
accurate  
and precise



accurate  
but not precise



not accurate  
but precise



neither accurate  
nor precise



# Hypothesis testing

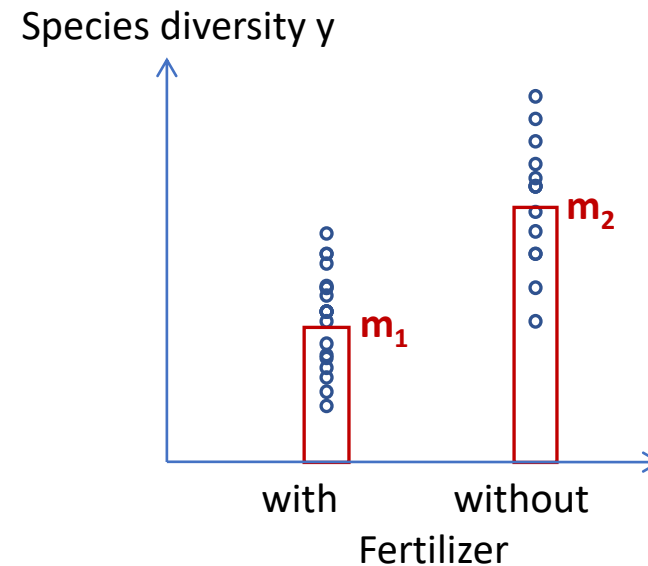
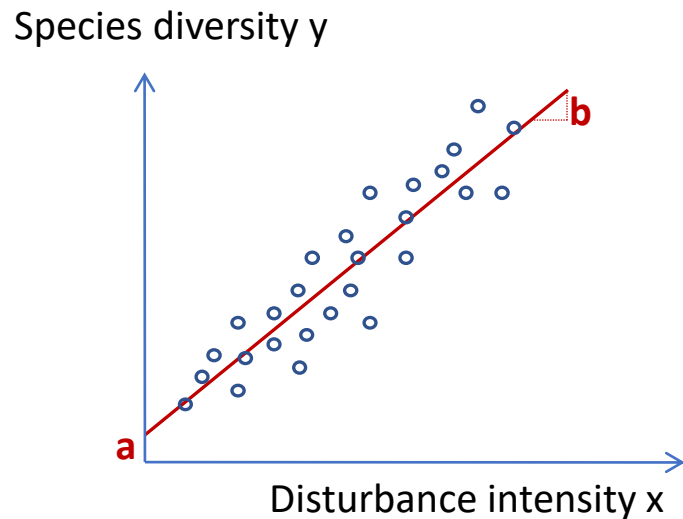
# Degrees of freedom

The goal is to describe the data with a limited set of parameters

The total number of observations ( $N$ ) are called *degrees of freedom*

The parameters of the model are called *degrees of freedom of the model*  
(2 df in the examples below)

The rest is called the *residual degrees of freedom*



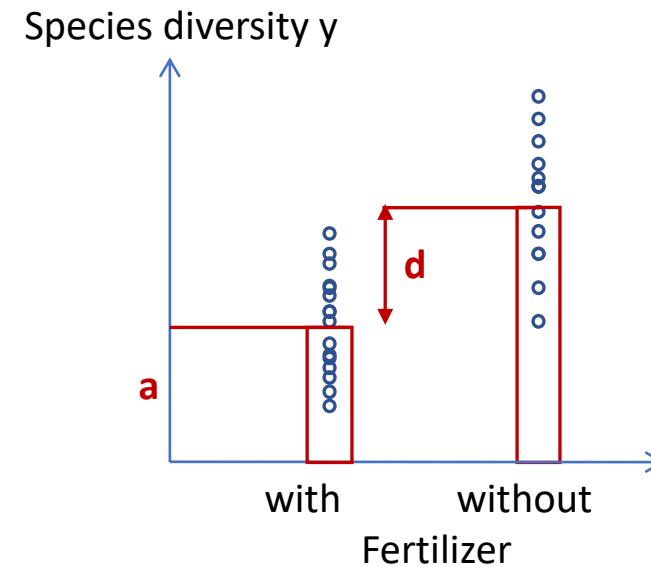
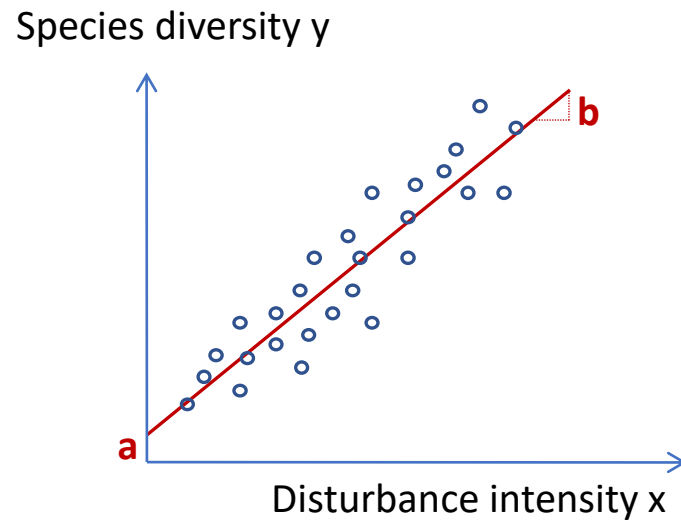


# Degrees of freedom

24

The goal is to describe the data with a limited set of parameters

Intercept & a slope, or an intercept & a difference



# Model fitting

$$y = a + b * x$$

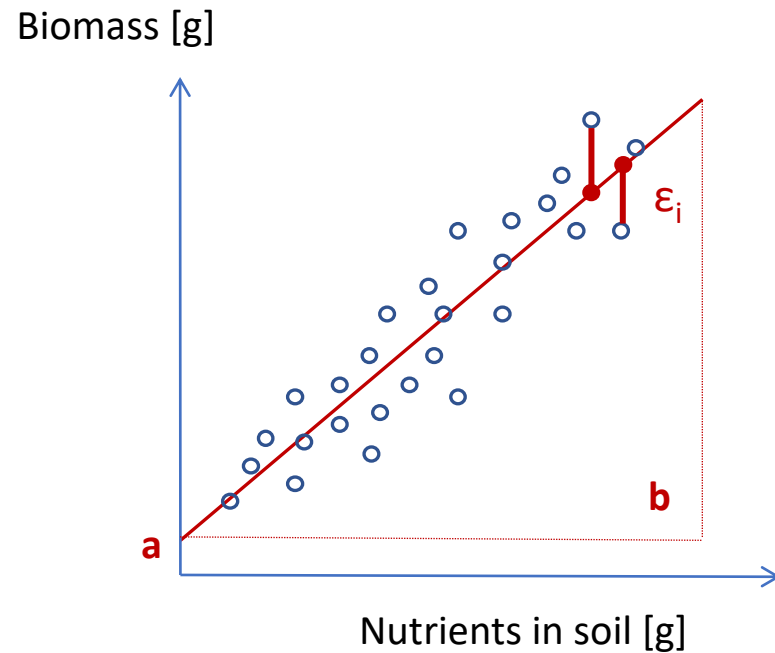
$$Y_i = a + b * X_i + \varepsilon_i$$

$\varepsilon_i$  ...error (residual)

$\varepsilon_i$  are called the **residuals**

$\hat{Y}$  are the **predicted or fitted values**

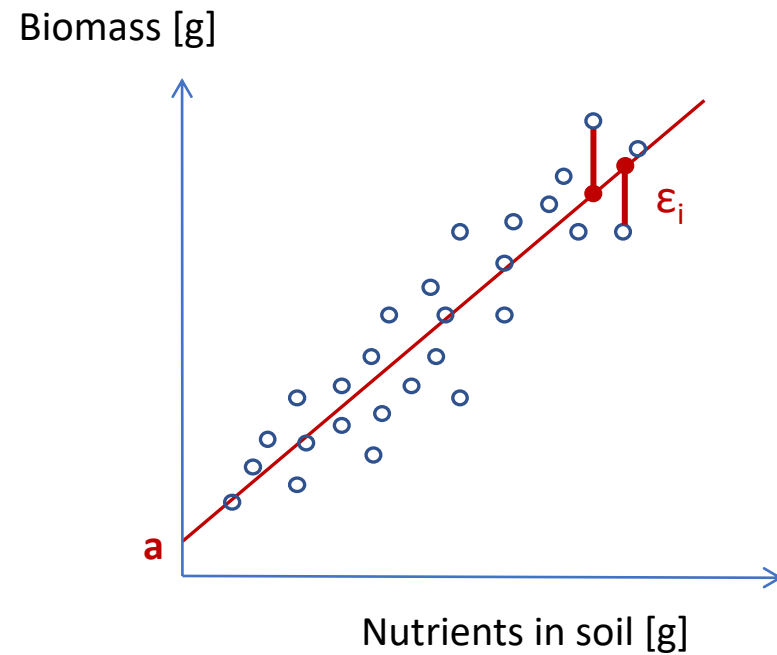
The residuals  $\varepsilon_i$  are the difference between the observed ( $\circ$ ) and predicted ( $\bullet$ ) values



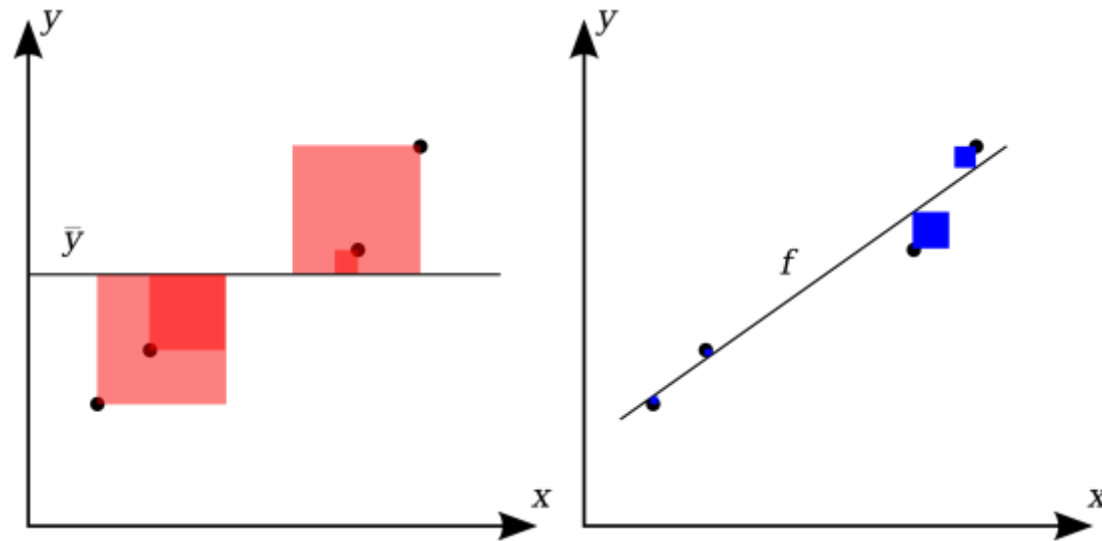
Criteria for parameter estimates: **Least square approach**

The sum of squared residuals is minimal:  $\text{Min } \sum \varepsilon_i^2$

Assumes normally distributed residuals





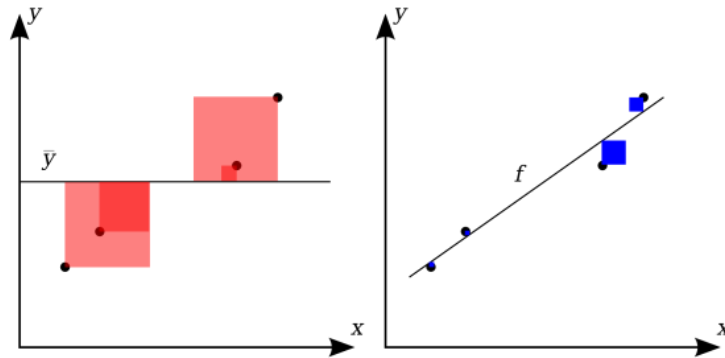


$$\text{Total variation} - \text{Residual variation} = \text{Explained variation}$$

Variance is expressed in sum of squares (SS).

# What is an F test?

$$F = \frac{\text{explained variance}}{\text{unexplained variance}},$$



# The F distribution

		Degrees of freedom in the nominator													
		1	2	3	4	5	6	7	8	9	10	20	30	50	100
Degrees of freedom in the denominator	1	161	200	216	225	230	234	237	239	241	242	248	250	252	253
	2	18.5	19.0	19.2	19.2	19.3	19.3	19.4	19.4	19.4	19.4	19.4	19.4	19.5	19.5
	3	10.1	9.55	9.28	9.12	9.01	8.94	8.89	8.85	8.81	8.79	8.66	8.62	8.58	8.55
	4	7.71	6.94	6.59	6.39	6.26	6.16	6.09	6.04	6.00	5.96	5.80	5.75	5.70	5.66
	5	6.61	5.79	5.41	5.19	5.05	4.95	4.88	4.82	4.77	4.74	4.56	4.50	4.44	4.41
	6	5.99	5.14	4.76	4.53	4.39	4.28	4.21	4.15	4.10	4.06	3.87	3.81	3.75	3.71
	7	5.59	4.74	4.35	4.12	3.97	3.87	3.79	3.73	3.68	3.64	3.44	3.38	3.32	3.27
	8	5.32	4.46	4.07	3.84	3.69	3.58	3.50	3.44	3.39	3.35	3.15	3.08	3.02	2.97
	9	5.12	4.26	3.86	3.63	3.48	3.37	3.29	3.23	3.18	3.14	2.94	2.86	2.80	2.76
	10	4.96	4.10	3.71	3.48	3.32	3.22	3.14	3.07	3.02	2.98	2.77	2.70	2.64	2.59
	20	4.35	3.49	3.10	2.87	2.71	2.60	2.51	2.45	2.39	2.35	2.12	2.04	1.97	1.91
	30	4.17	3.32	2.92	2.69	2.53	2.42	2.33	2.27	2.21	2.16	1.93	1.84	1.76	1.69
	50	4.03	3.18	2.79	2.56	2.40	2.29	2.20	2.13	2.07	2.03	1.78	1.69	1.60	1.52
	100	3.94	3.09	2.70	2.46	2.31	2.19	2.10	2.03	1.97	1.93	1.68	1.57	1.48	1.39

# Statistical significance $\alpha$

Probability  $F \leq F_{\text{critical}}$

Levels of significance: some people prefer „exact“ error probabilities, some only different levels

ns     $p > 0.1$        non significant

.      $p < 0.1$        marginally significant

\*      $p < 0.05$        significant

**	$p < 0.01$	} highly significant
***	$p < 0.001$	



# Hypothesis testing

## Null Hypothesis $H_0$

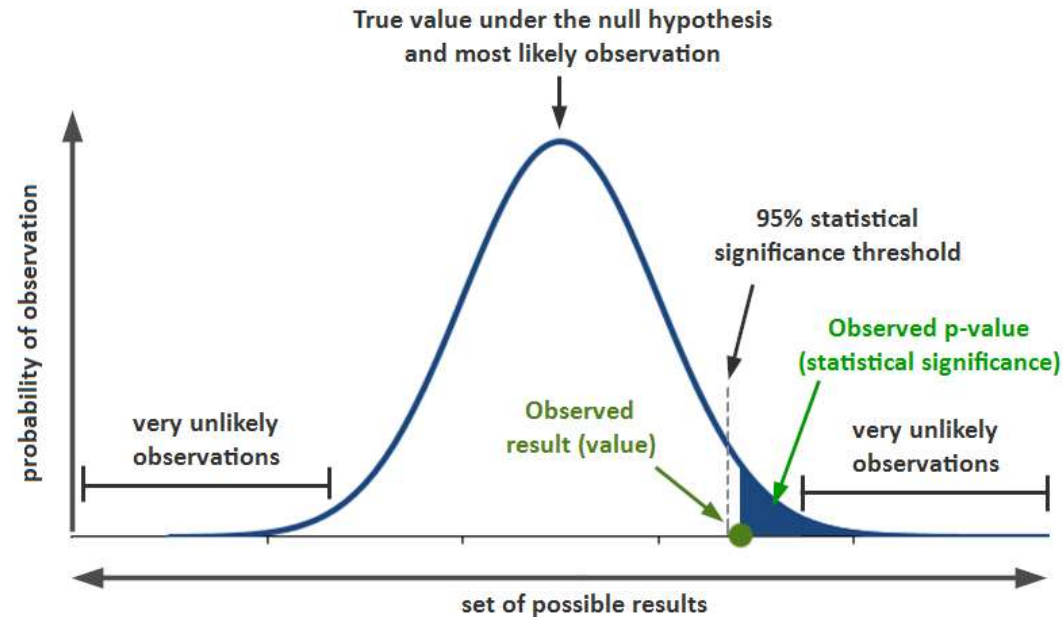
Examples of  $H_0$ :

- Mean of a population is 3.0
- In a genetic association study, there is no association between disease state and the genotypes of a particular SNP

## Alternative Hypothesis $H_1$

• Examples of  $H_1$ :

- Mean of population  $> 3.0$
- There is an association between disease and genotype



# Hypothesis testing

Null-hypothesis	Reality	
	true	false
accept	correct	type II
reject	type I	correct

Type I error: To reject the Null-hypothesis, although it is true (False positive)

Type II error: To accept the Null-hypothesis, although it is wrong (False negative)

# Hypothesis testing

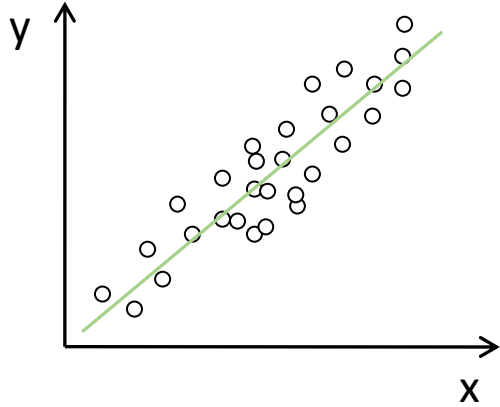
Null-hypothesis	Reality	
	true	false
accept	correct	type II
reject	type I	correct

Type I error: To reject the Null-hypothesis, although it is true (False negative)

Type II error: To accept the Null-hypothesis, although it is wrong (False positive)

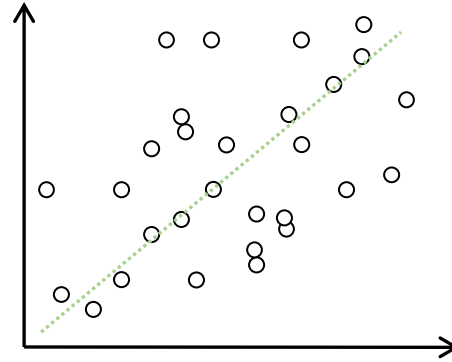
## Which one is worse?

# Absence of evidence is not evidence for the absence



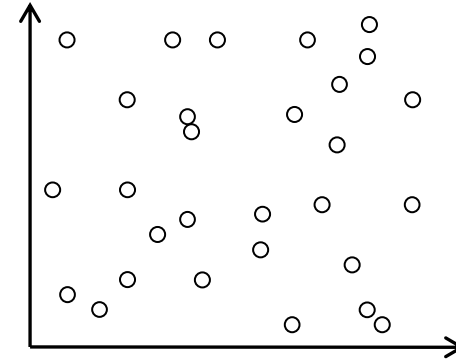
$$p_{\alpha} < 0.05$$

There is a relationship  
between x and y...



$$p_{\alpha} > 0.05$$

Nothing I can say for sure



$$p_{\alpha} > 0.05$$



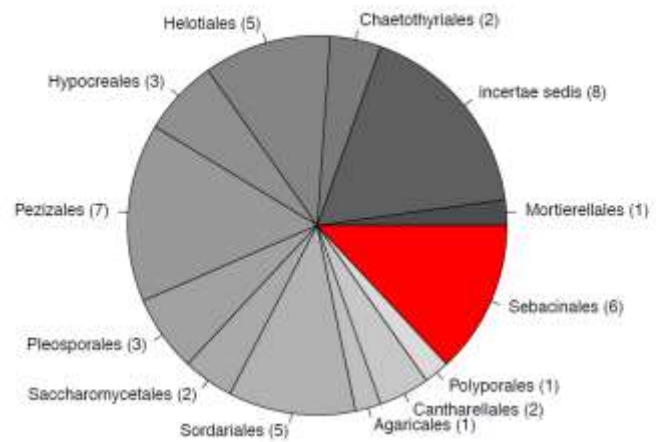
A photograph of a narrow river or stream flowing through a dense forest. The water is calm and reflects the surrounding greenery. The banks are heavily overgrown with various types of green plants and trees. A yellow rectangular text box is superimposed over the upper middle part of the image.

focus <- a bad invader

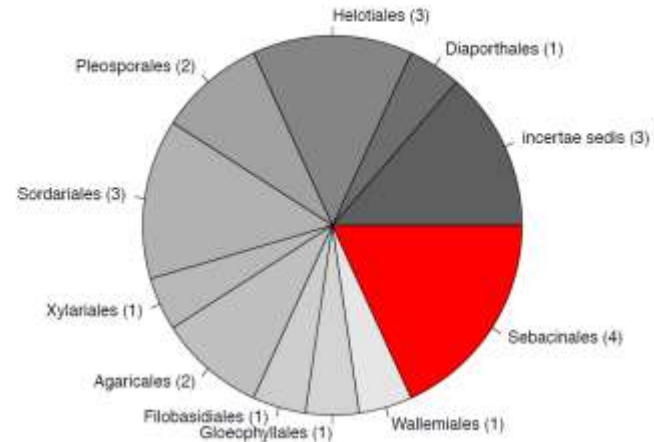




**Riverside habitats**

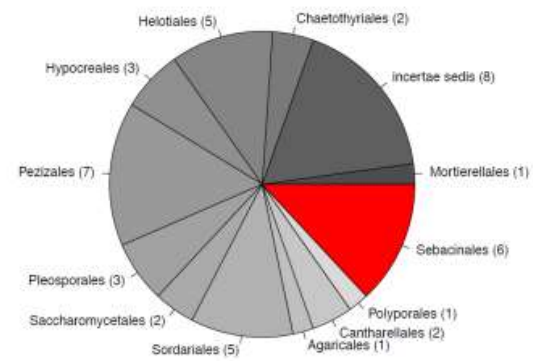


**Ruderal habitats**

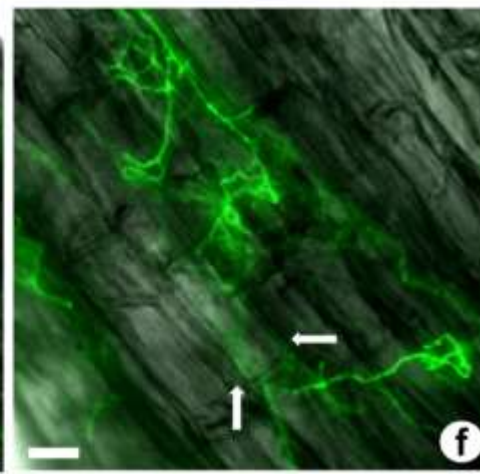
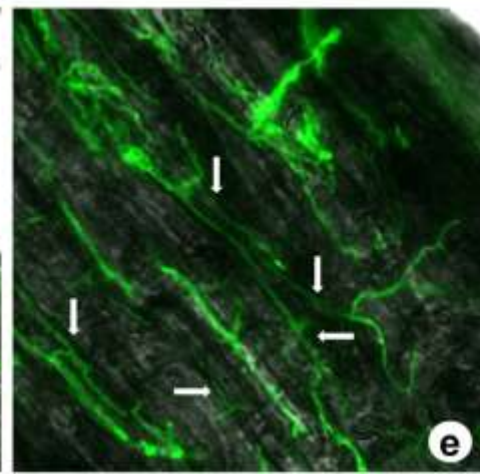
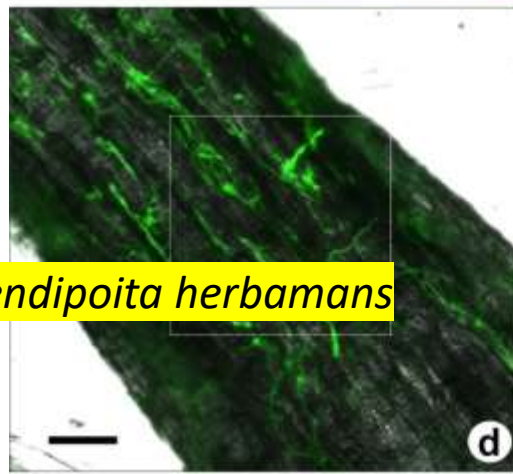
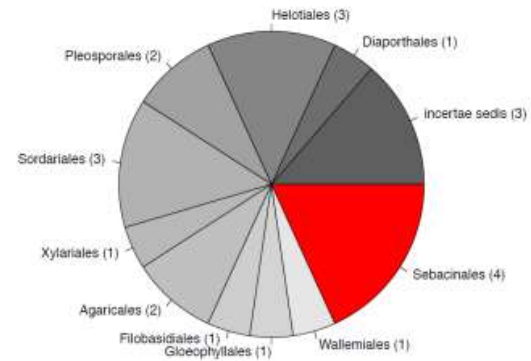




**Riverside habitats**



**Ruderal habitats**



*Serendipita herbamans*

# A greenhouse experiment

Sterilized  
rhizomes



Without  
fungi (-F)



With  
fungi (+F)

*Serendipita herbamans*







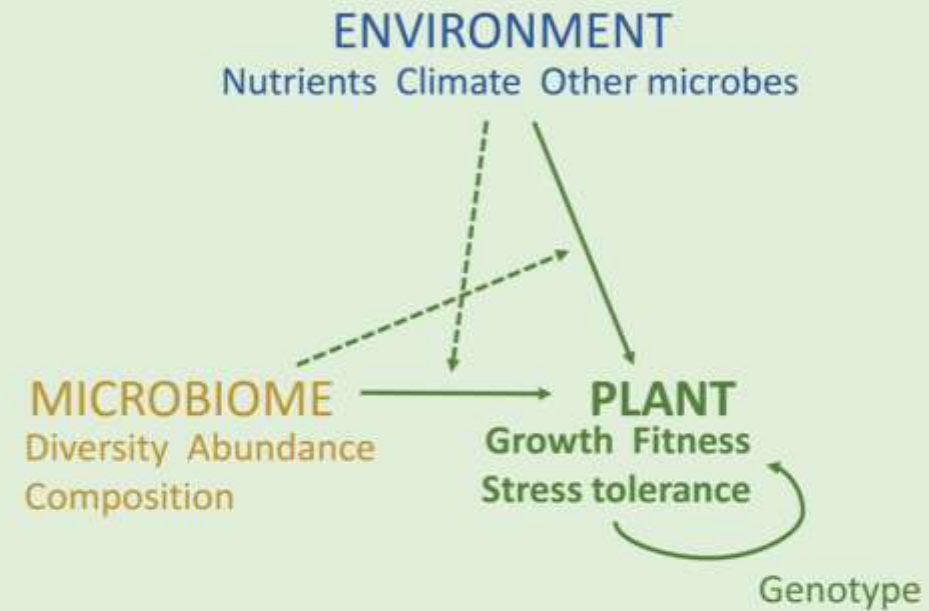


Without  
fungi (-F)



With  
fungi (+F)

## Plant perspective



## Load the data

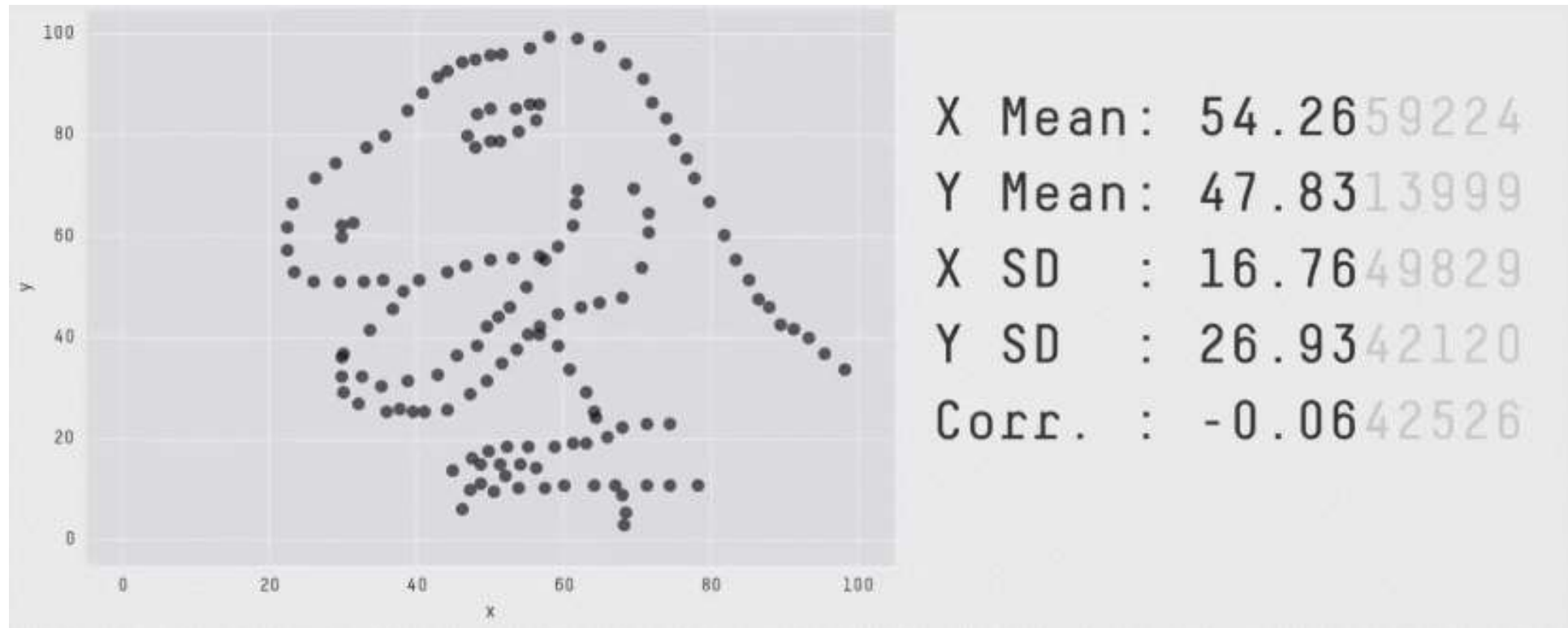
```
install.packages("readxl")  
require(readxl)
```

```
data_file<-"/Users/..."  
dt<-read_excel(data_file)  
dim(dt)  
str(dt)
```

Visualize and understand the data

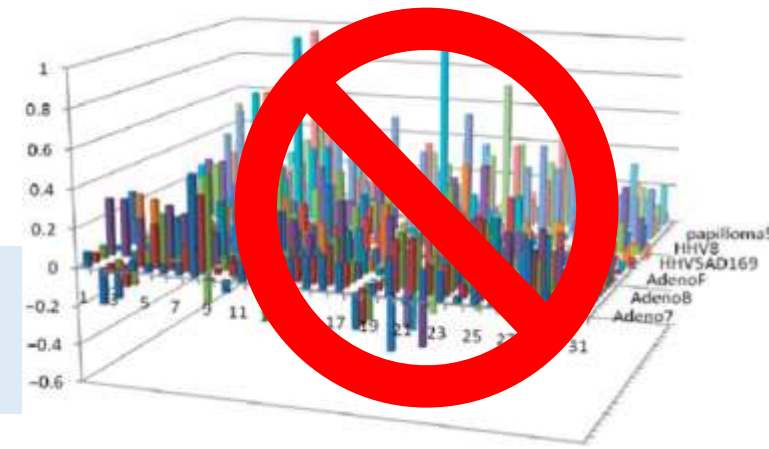
```
X Mean: 54.26  
Y Mean: 47.83  
X SD   : 16.76  
Y SD   : 26.93  
Corr.  : -0.06
```

# Visualize



# Visualize

```
> install.packages("ggplot2")  
> require(ggplot2)
```



## Statistics and Computing

Leland Wilkinson

## The Grammar of Graphics



## The Visual Display of Quantitative Information

EDWARD R. TUFTE



Use R!

Hadley Wickham

## ggplot2

Elegant Graphics for Data Analysis

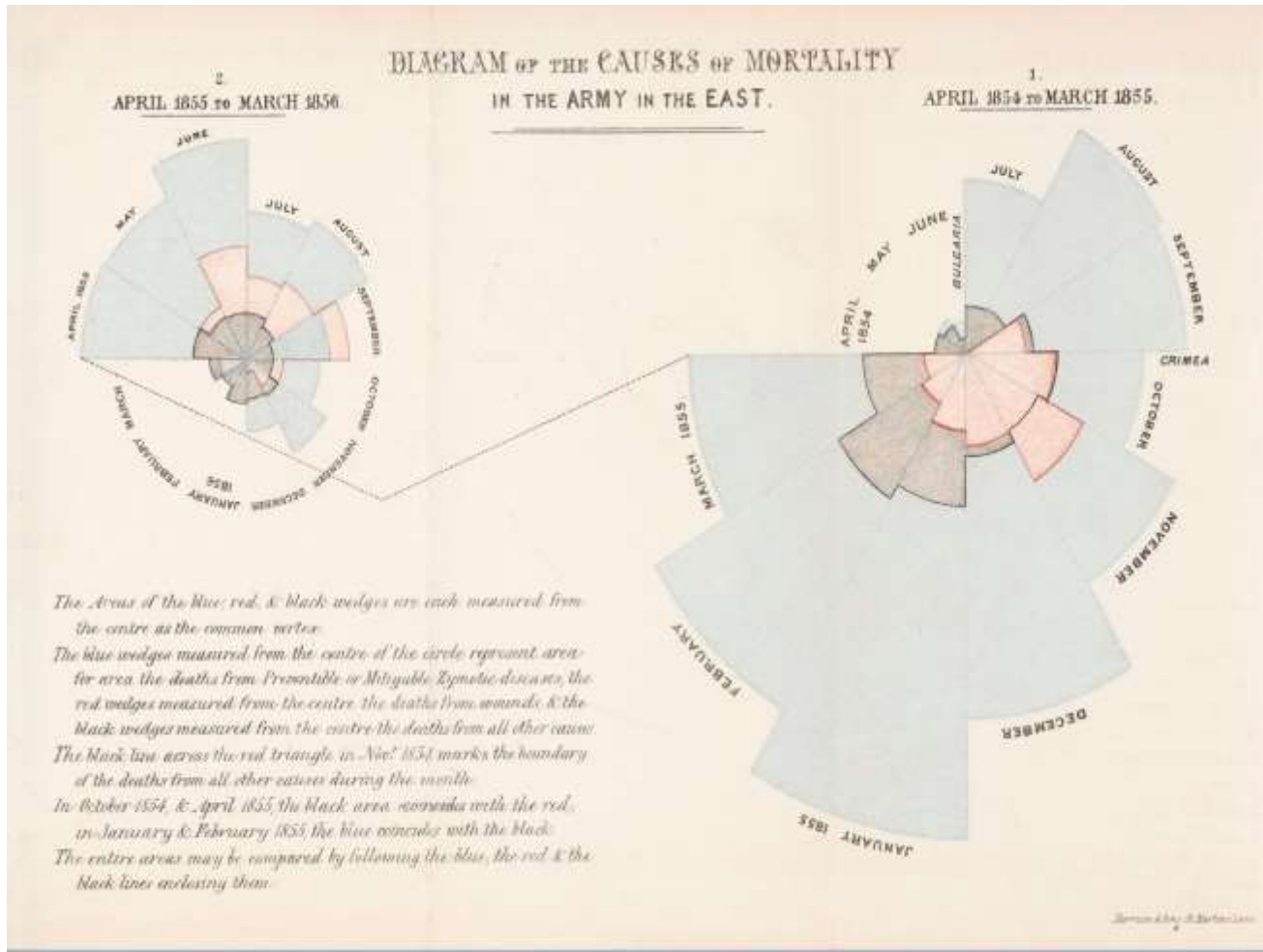
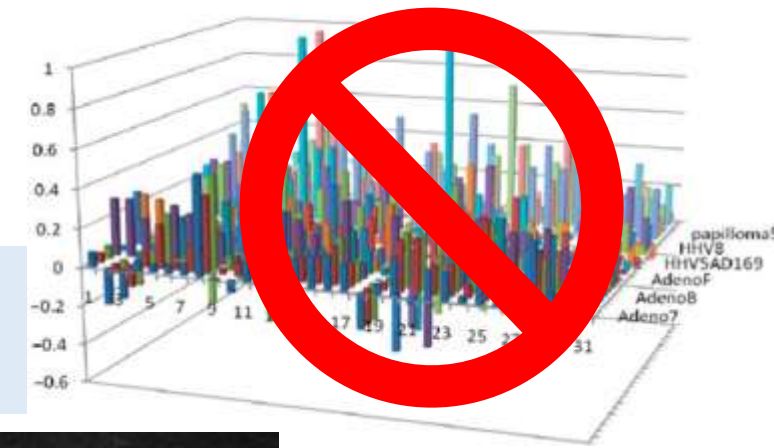
Springer





# Visualize

```
install.packages("ggplot2")  
require(ggplot2)
```



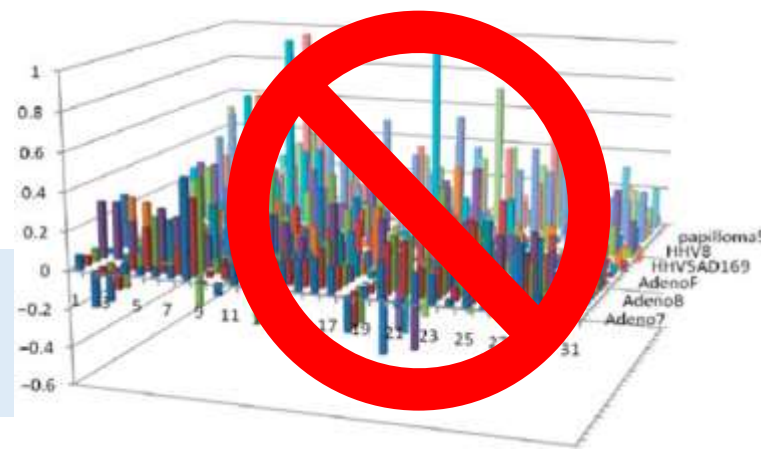
Florence Nightingale

# Visualize

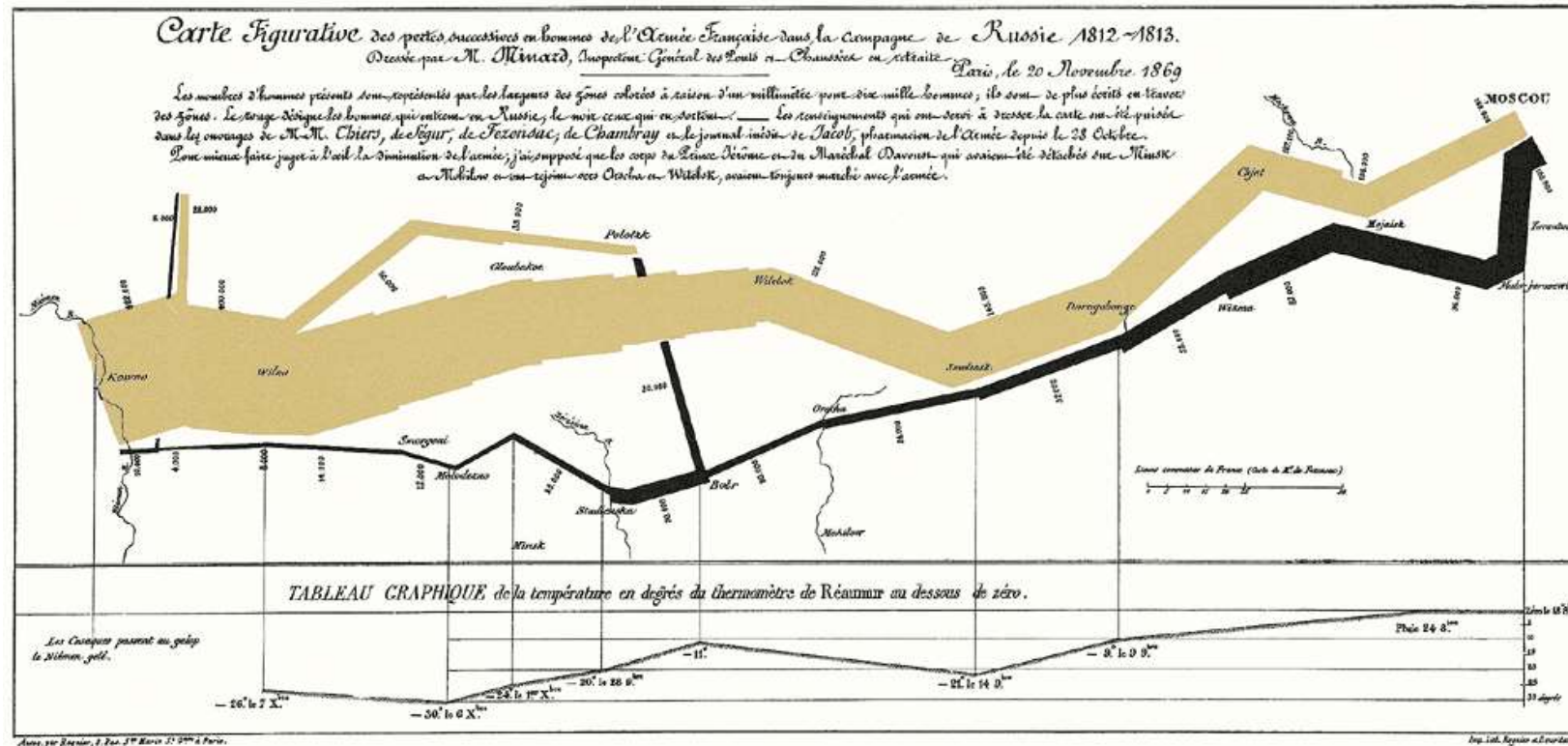
Without  
fungi (-F)



With  
fungi (+F)



```
> install.packages("ggplot2")
> require(ggplot2)
```



**Without  
fungi (-F)**



**With  
fungi (+F)**

## Fungus effect

```
g1<- ggplot(data=dt, aes(x=Fungus, y=ABm)) +  
      geom_boxplot()  
g1
```

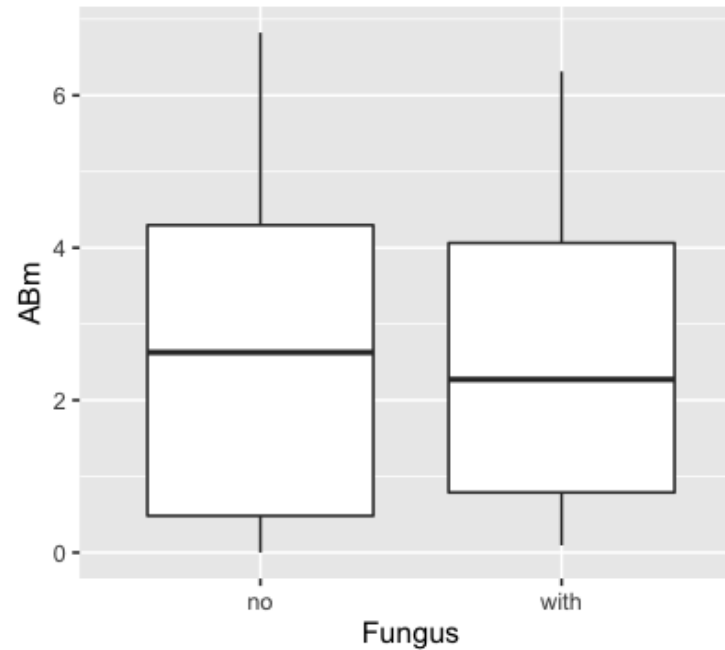
## Fungus effect

Without  
fungi (-F)



With  
fungi (+F)

```
g1<- ggplot(data=dt, aes(x=Fungus, y=ABm)) +  
  geom_boxplot()  
g1
```



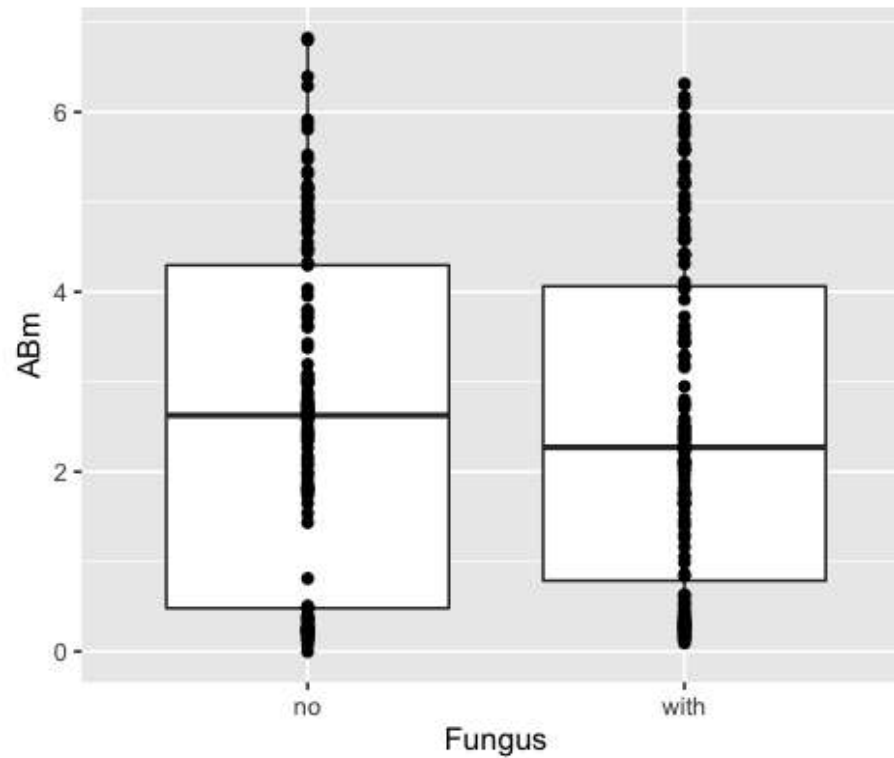
## Fungus effect

Without  
fungi (-F)



With  
fungi (+F)

```
g1<- ggplot(data=dt, aes(x=Fungus, y=ABm))+  
  geom_boxplot()+  
  geom_point()  
g1
```



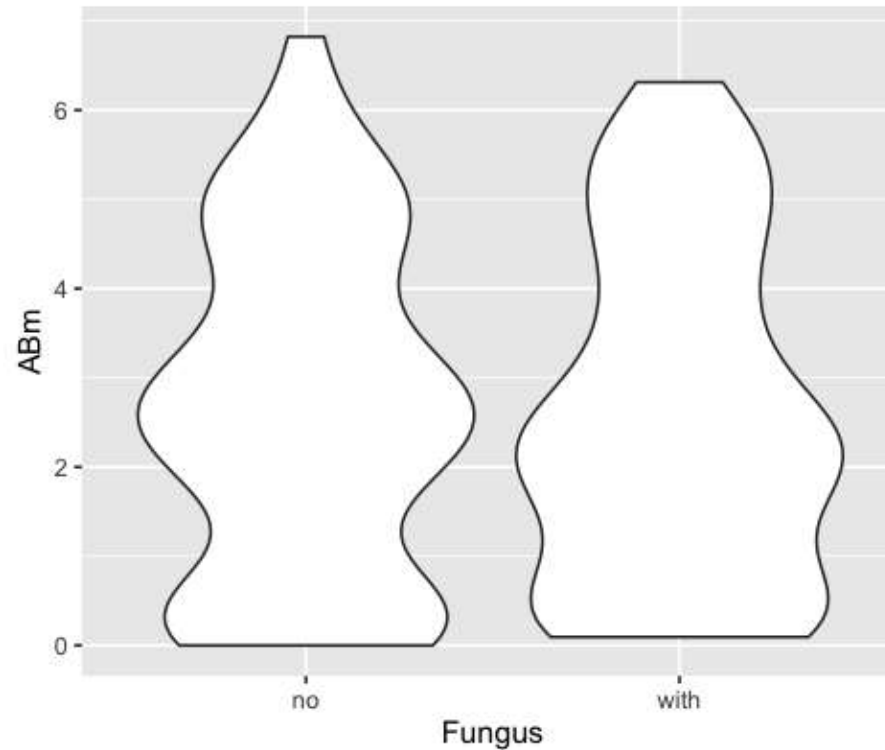
## Fungus effect

Without  
fungi (-F)



With  
fungi (+F)

```
g1<- ggplot(data=dt, aes(x=Fungus, y=ABm))+  
  geom_violin()  
g1
```





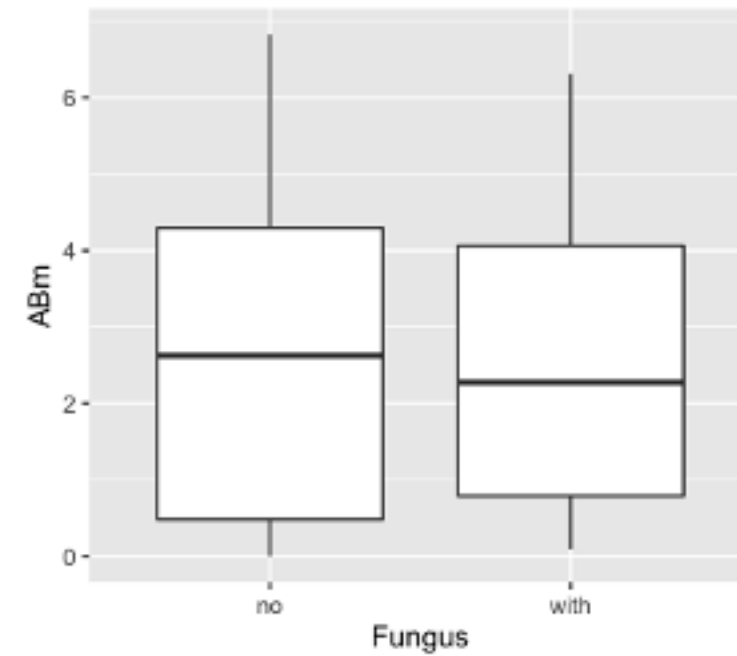
## Test fungus effect

Without  
fungi (-F)



With  
fungi (+F)

```
model1<- lm (ABm ~ Fungus, data = dt)  
summary(model1)
```



# Test fungus effect

Without  
fungi (-F)



With  
fungi (+F)

```
model1<- lm (ABm ~ Fungus, data = dt)
summary(model1)
```

Call:

```
lm(formula = ABm ~ Fungus, data = dt)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-2.6267	-1.7854	-0.1903	1.5192	4.1968

Coefficients:

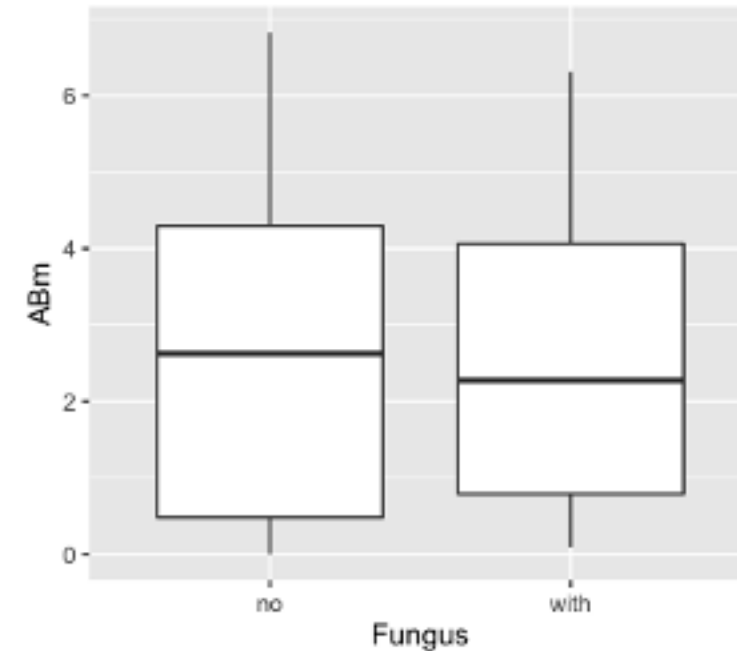
	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.62671	0.15503	16.943	<2e-16 ***
Funguswith	-0.03393	0.21811	-0.156	0.876

---

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

Residual standard error: 1.841 on 283 degrees of freedom  
Multiple R-squared: 8.551e-05, Adjusted R-squared: -0.003448

F-statistic: 0.0242 on 1 and 283 DF, p-value: 0.8765



## Test fungus effect

**Without  
fungi (-F)**



**With  
fungi (+F)**

```
modell1<- lm (ABm ~ Fungus, data = dt)
summary(modell1)
anova(modell1)
```

Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Fungus	1	0.08	0.0820	0.0242	0.8765
Residuals	283	959.10	3.3891		

# Test fungus effect

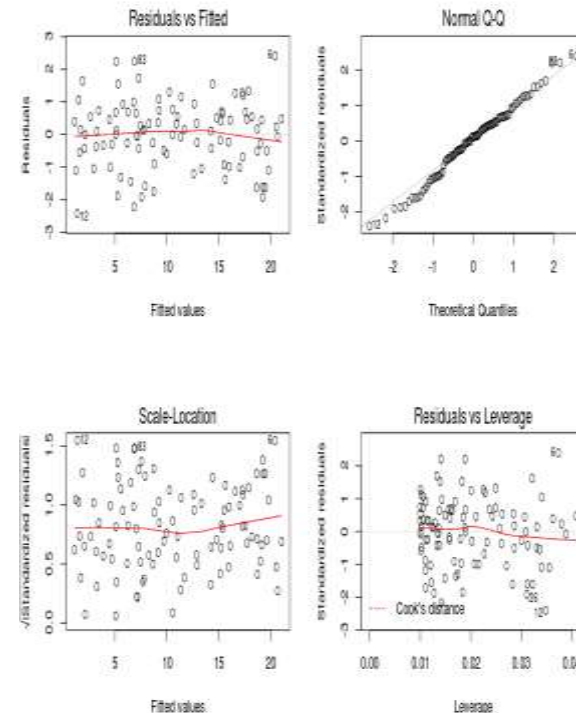
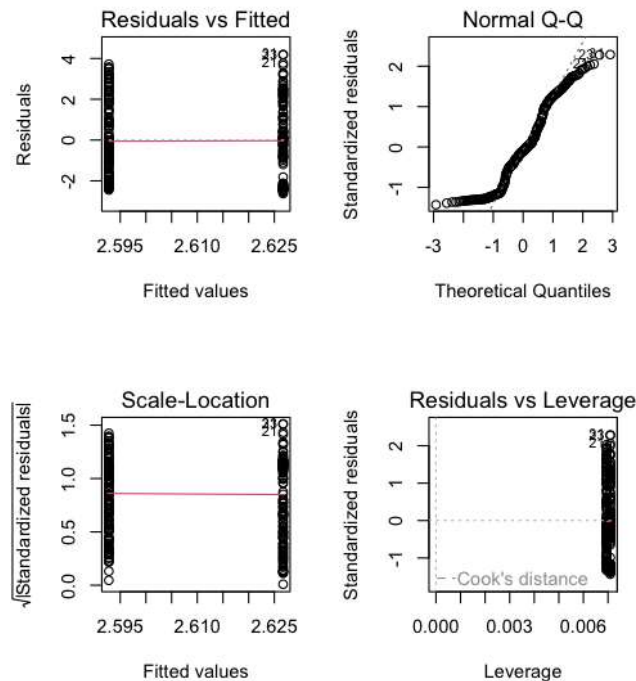
Without  
fungi (-F)



With  
fungi (+F)

```
model1 <- lm (ABm ~ Fungus, data = dt)
summary(model1)
anova(model1)

par(mfrow=c(2,2))
plot(model1)
```



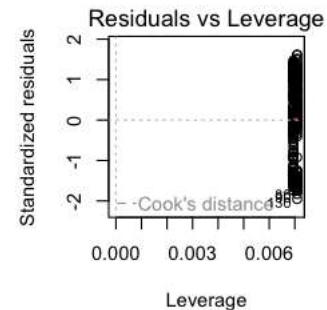
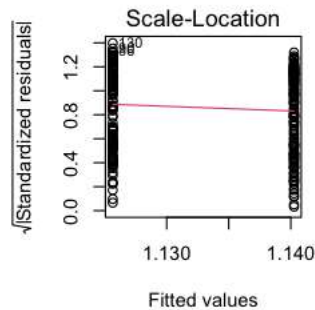
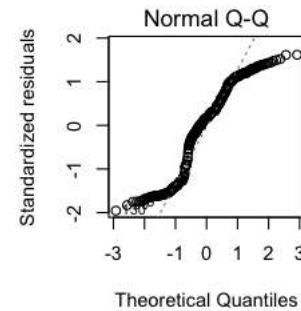
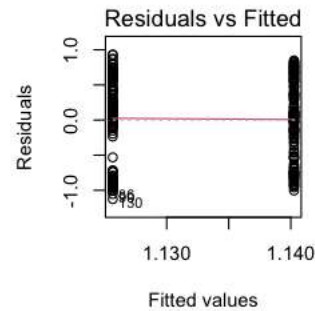
## Try a transformation

Without  
fungi (-F)



With  
fungi (+F)

```
model1<- lm (log(ABm+1) ~ Fungus, data = dt)
summary(model1)
anova(model1)
plot(model1)
```



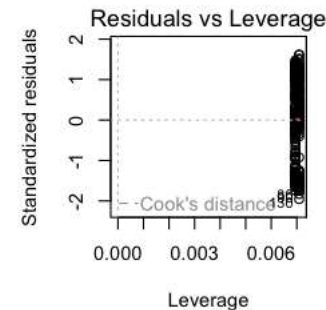
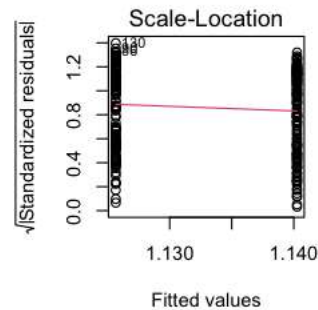
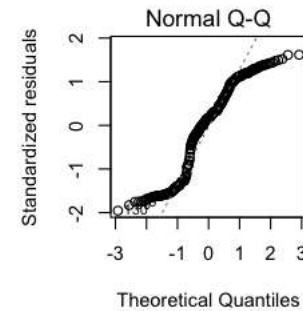
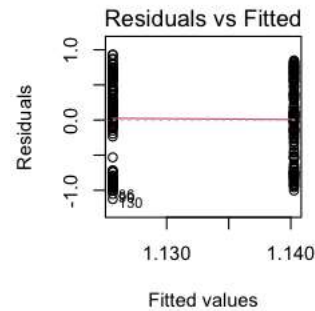
## Try a transformation

Without  
fungi (-F)



With  
fungi (+F)

```
model1<- lm (log(ABm+1) ~ Fungus, data = dt)
summary(model1)
anova(model1)
plot(model1)
```





# Account for initial size

Without  
fungi (-F)



With  
fungi (+F)



```
model1<- lm (ABm~ IR_W + Fungus, data = dt)
summary(model1)
anova(model1)
plot(model1)
```

Call:  
lm(formula = ABm ~ IR\_W + Fungus, data = dt)

Residuals:

	Min	1Q	Median	3Q	Max
	-2.8110	-1.9251	-0.1995	1.5384	3.8607

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.1910	0.2196	9.976	< 2e-16 ***
IR_W	0.4121	0.1488	2.769	0.00599 **
Funguswith	-0.0881	0.2165	-0.407	0.68432

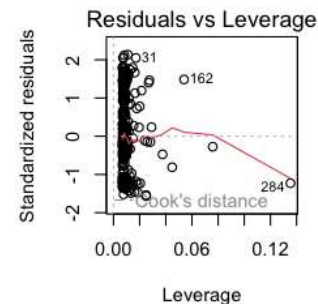
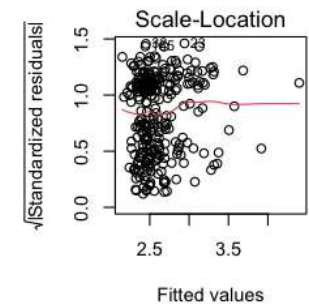
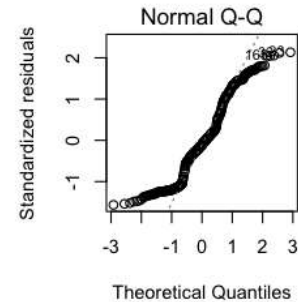
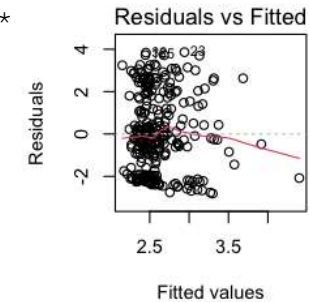
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.82 on 282 degrees of freedom  
Multiple R-squared: 0.02656, Adjusted R-squared: 0.01966  
F-statistic: 3.847 on 2 and 282 DF, p-value: 0.02247

Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.9276	7.5287	0.006462 **
Fungus	1	0.55	0.5484	0.1656	0.684322
Residuals	282	933.71	3.3110		



# Account for initial size

Without  
fungi (-F)



With  
fungi (+F)



```
model1<- lm (ABm~ IR_W + Fungus, data = dt)
summary(model1)
anova(model1)
plot(model1)
```

Call:  
lm(formula = ABm ~ IR\_W + Fungus, data = dt)

Residuals:

	Min	1Q	Median	3Q	Max
	-2.8110	-1.9251	-0.1995	1.5384	3.8607

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.1910	0.2196	9.976	< 2e-16 ***
IR_W	0.4121	0.1488	2.769	0.006462 **
Funguswith	-0.0881	0.2165	-0.407	0.684322

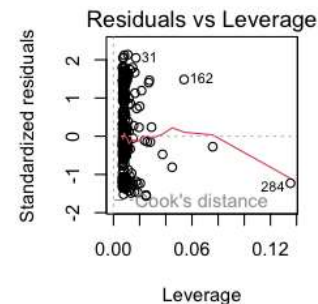
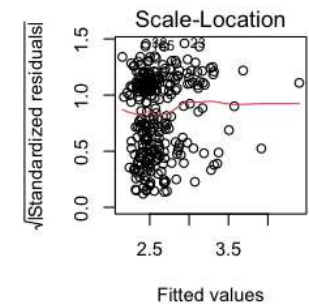
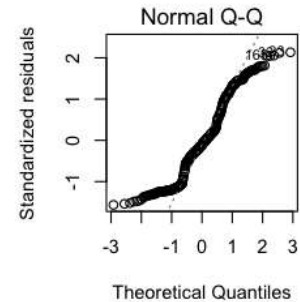
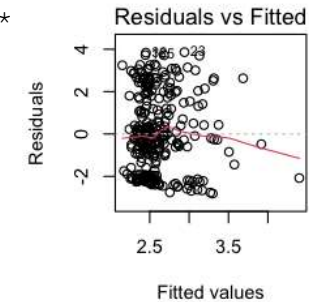
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.82 on 282 degrees of freedom  
Multiple R-squared: 0.02656, Adjusted R-squared: 0.01856  
F-statistic: 3.847 on 2 and 282 DF, p-value: 0.02656

Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.9276	7.5287	0.006462 **
Fungus	1	0.55	0.5484	0.1656	0.684322
Residuals	282	933.71	3.3110		



# Visualise the effect of rhizome weight

Without  
fungi (-F)



With  
fungi (+F)

```
g1<- ggplot(data=dt, aes(x=IR_W, y=ABm)) +  
  geom_point() +  
  geom_smooth(method="lm")  
g1
```

Sterilized  
rhizomes



Call:  
lm(formula = ABm ~ IR\_W + Fungus, data = dt)

Residuals:

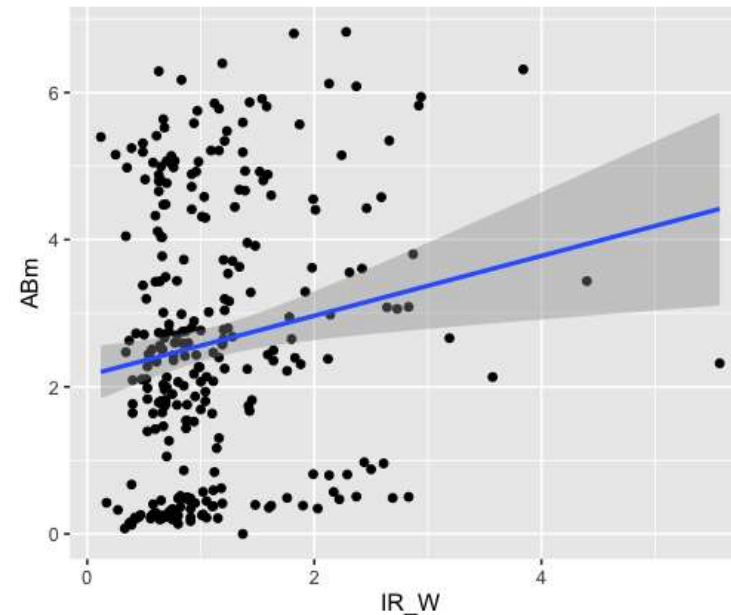
	Min	1Q	Median	3Q	Max
	-2.8658	-2.0120	-0.1843	1.5428	3.8642

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.1960	0.2221	9.885	< 2e-16 ***
IR_W	0.4074	0.1505	2.707	0.00721 **
Funguswith	-0.1236	0.2190	-0.564	0.57289

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

Residual standard error: 1.841 on 282 degrees of freedom  
Multiple R-squared: 0.02567, Adjusted R-squared: 0.01876  
F-statistic: 3.715 on 2 and 282 DF, p-value: 0.02557



# Visualise the effect of rhizome weight

Without  
fungi (-F)



With  
fungi (+F)



```
g1<- ggplot(data=dt, aes(x=IR_W, y=ABm)) +
  geom_point() +
  geom_smooth(method="lm")
g1
```

Call:  
lm(formula = ABm ~ IR\_W + Fungus, data = dt)

Residuals:

Min	1Q	Median	3Q	Max
-2.8658	-2.0120	-0.1843	1.5428	3.8642

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.1960	0.2221	9.885	< 2e-16 ***
IR_W	0.4074	0.1505	2.707	0.00721 **
Funguswith	-0.1236	0.2190	-0.564	0.57289

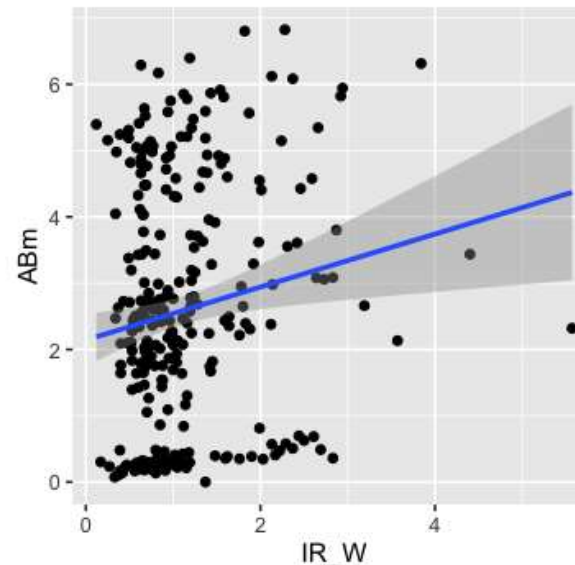
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.841 on 282 degrees of freedom  
Multiple R-squared: 0.02567, Adjusted R-squared: 0.01876  
F-statistic: 3.715 on 2 and 282 DF, p-value: 0.02557

Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.9276	7.5287	0.006462 **
Fungus	1	0.55	0.5484	0.1656	0.684322
Residuals	282	933.71	3.3110		











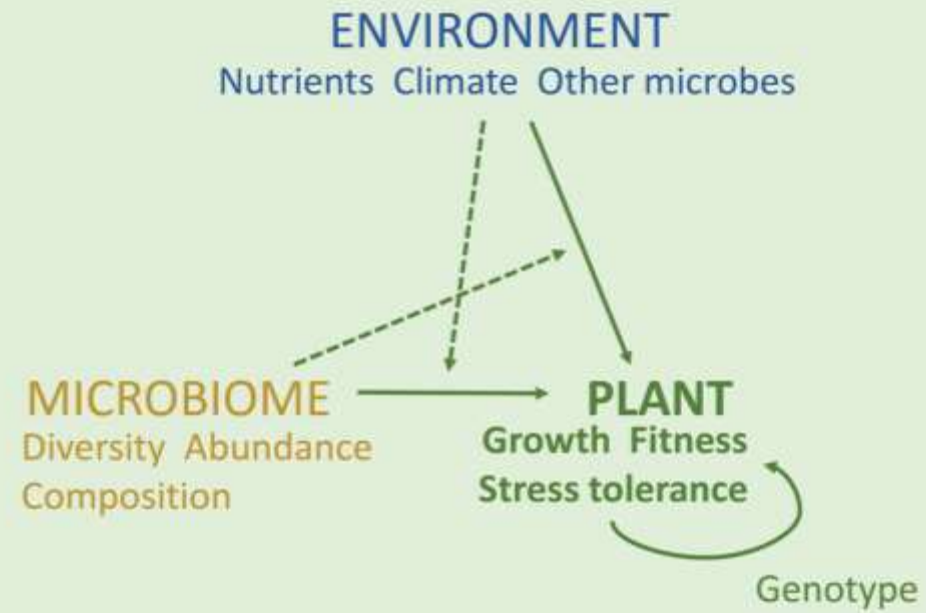


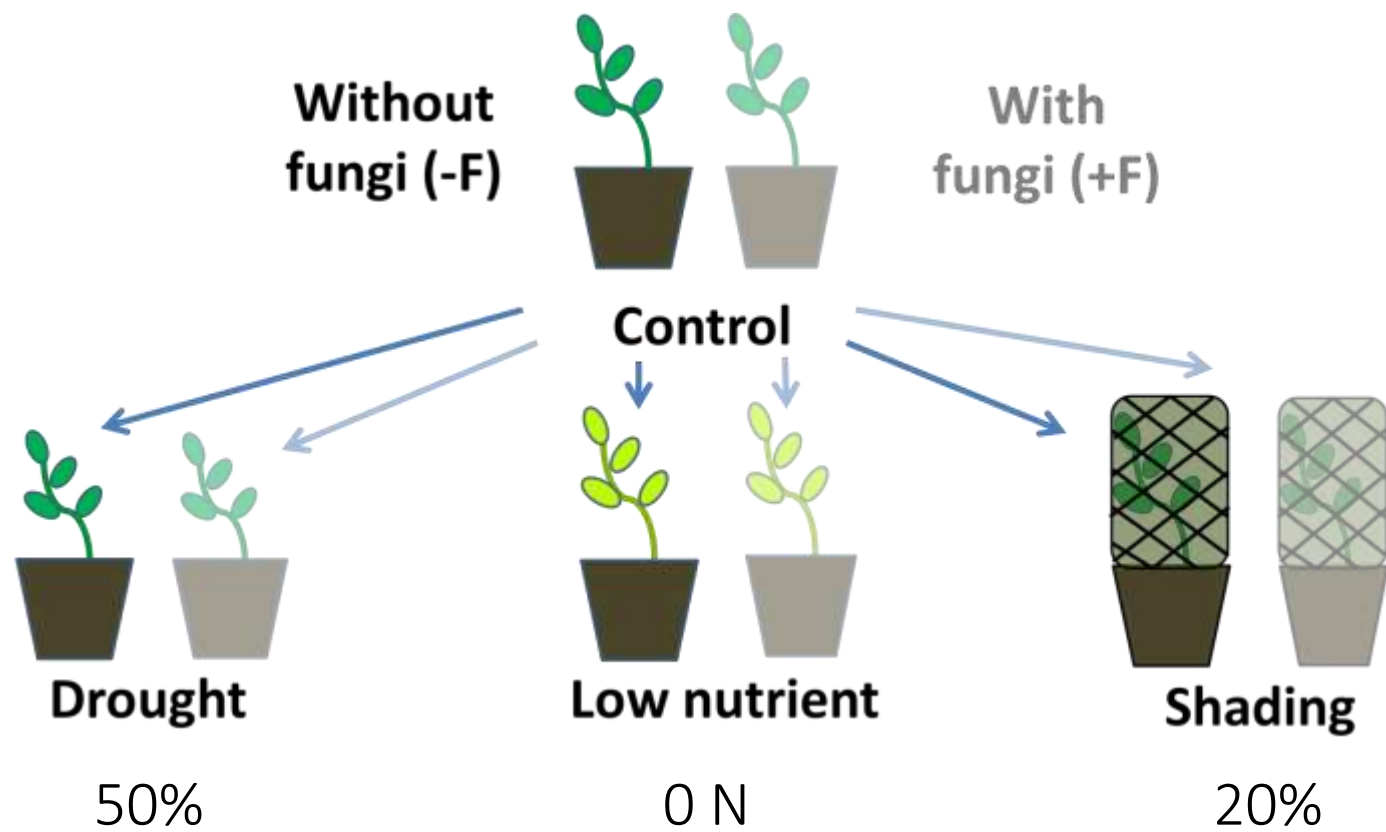


Stress treatments!



# Plant perspective





# Include stress treatments in the model

```

modell1<- lm (ABm~ IR_W + Fungus + Treatment, data = dt)
summary(modell1)
anova(modell1)

```

Call:  
lm(formula = ABm ~ IR\_W + Fungus + Treatment, data = dt)

Residuals:

	Min	1Q	Median	3Q	Max
	-2.05453	-0.27590	-0.02415	0.30265	1.50164

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	4.85116	0.08648	56.096	< 2e-16 ***
IR_W	0.27546	0.04443	6.200	2.02e-09 ***
Funguswith	-0.06280	0.06442	-0.975	0.33
TreatmentDrought	-2.25585	0.09075	-24.858	< 2e-16 ***
TreatmentLowN	-4.72484	0.08984	-52.593	< 2e-16 ***
TreatmentShading	-3.17401	0.09029	-35.154	< 2e-16 ***

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

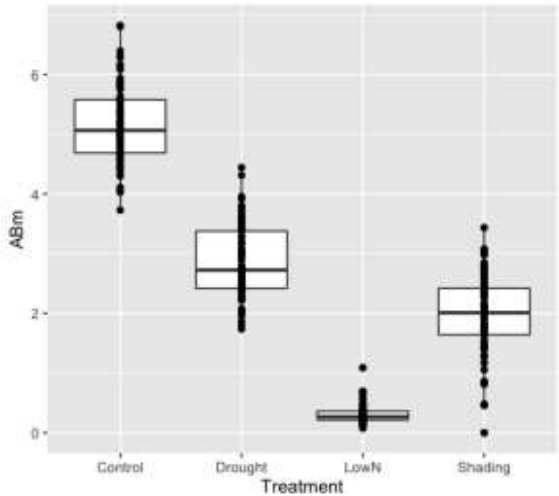
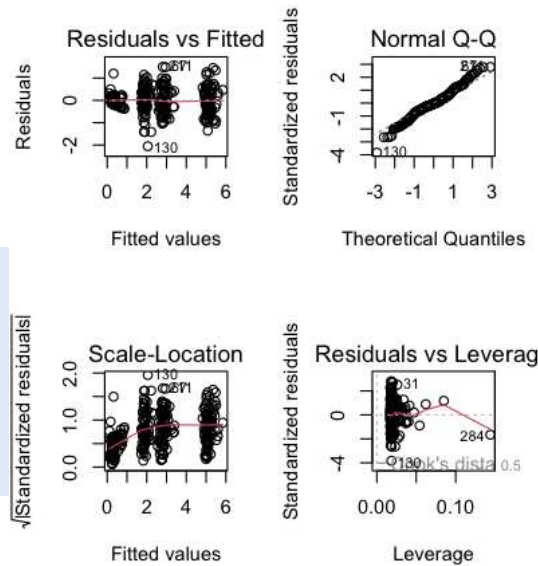
Residual standard error: 0.5415 on 279 degrees of freedom  
Multiple R-squared: 0.9147, Adjusted R-squared: 0.9132  
F-statistic: 598.5 on 5 and 279 DF, p-value: < 2.2e-16

Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.928	85.0194	<2e-16 ***
Fungus	1	0.55	0.548	1.8706	0.1725
Treatment	3	851.91	283.968	968.5187	<2e-16 ***
Residuals	279	81.80	0.293		

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





# Include stress treatments in the model

```
model1<- lm (ABm~ IR_W + Fungus + Treatment, data = dt)
summary(model1)
anova(model1)
```

Call:  
lm(formula = ABm ~ IR\_W + Fungus + Treatment, data = dt)

Residuals:

	Min	1Q	Median	3Q	Max
	-2.05453	-0.27590	-0.02415	0.30265	1.50164

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	4.85116	0.08648	56.096	< 2e-16 ***
IR_W	0.27546	0.04443	6.200	2.02e-09 ***
Funguswith	-0.06280	0.06442	-0.975	0.33
TreatmentDrought	-2.25585	0.09075	-24.858	< 2e-16 ***
TreatmentLowN	-4.72484	0.08984	-52.593	< 2e-16 ***
TreatmentShading	-3.17401	0.09029	-35.154	< 2e-16 ***

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

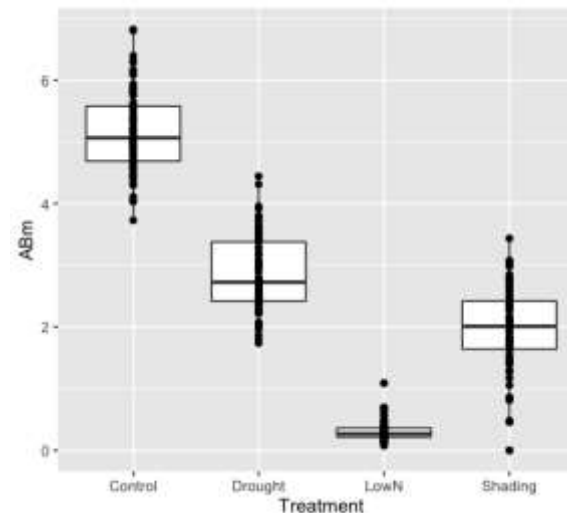
Residual standard error: 0.5415 on 279 degrees of freedom  
Multiple R-squared: 0.9147, Adjusted R-squared: 0.9132  
F-statistic: 598.5 on 5 and 279 DF, p-value: < 2.2e-16

## Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.928	85.0194	<2e-16 ***
Fungus	1	0.55	0.548	1.8706	0.1725
Treatment	3	851.91	283.968	968.5187	<2e-16 ***
Residuals	279	81.80	0.293		

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



# Include stress treatments in the model

```
model1<- lm (ABm~ IR_W + Fungus + Treatment, data = dt)
summary(model1)
anova(model1)
```

Call:  
lm(formula = ABm ~ IR\_W + Fungus + Treatment, data = dt)

Residuals:

	Min	1Q	Median	3Q	Max
	-2.05453	-0.27590	-0.02415	0.30265	1.50164

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	4.85116	0.08648	56.096	< 2e-16 ***
IR_W	0.27546	0.04443	6.200	2.02e-09 ***
Funguswith	-0.06280	0.06442	-0.975	0.33
TreatmentDrought	-2.25585	0.09075	-24.858	< 2e-16 ***
TreatmentLowN	-4.72484	0.08984	-52.593	< 2e-16 ***
TreatmentShading	-3.17401	0.09029	-35.154	< 2e-16 ***

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

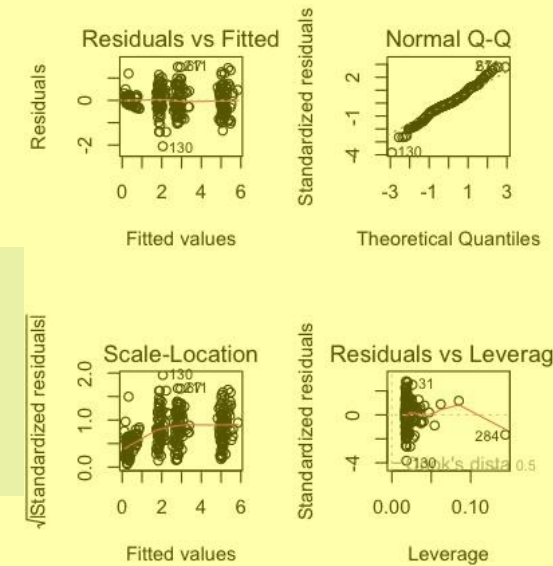
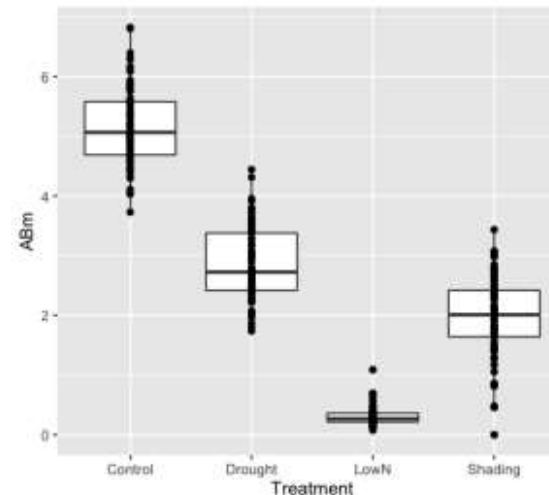
Residual standard error: 0.5415 on 279 degrees of freedom  
Multiple R-squared: 0.9147, Adjusted R-squared: 0.9132  
F-statistic: 598.5 on 5 and 279 DF, p-value: < 2.2e-16

## Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.928	85.0194	<2e-16 ***
Fungus	1	0.55	0.548	1.8706	0.1725
Treatment	3	851.91	283.968	968.5187	<2e-16 ***
Residuals	279	81.80	0.293		

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





# Include stress treatments in the model

```
model1<- lm (ABm~ IR_W + Fungus + Treatment, data = dt)
summary(model1)
anova(model1)
```

Call:  
lm(formula = ABm ~ IR\_W + Fungus + Treatment, data = dt)

Residuals:

	Min	1Q	Median	3Q	Max
	-2.05453	-0.27590	-0.02415	0.30265	1.50164

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	4.85116	0.08648	56.096	< 2e-16 ***
IR_W	0.27546	0.04443	6.200	2.02e-09 ***
Funguswith	-0.06280	0.06442	-0.975	0.33
TreatmentDrought	-2.25585	0.09075	-24.858	< 2e-16 ***
TreatmentLowN	-4.72484	0.08984	-52.593	< 2e-16 ***
TreatmentShading	-3.17401	0.09029	-35.154	< 2e-16 ***

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

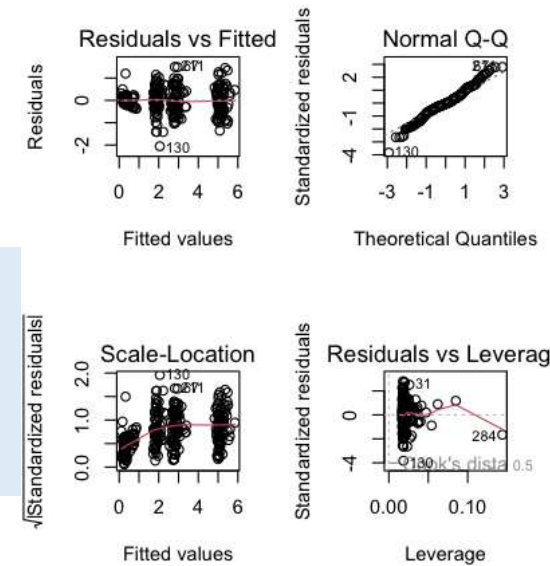
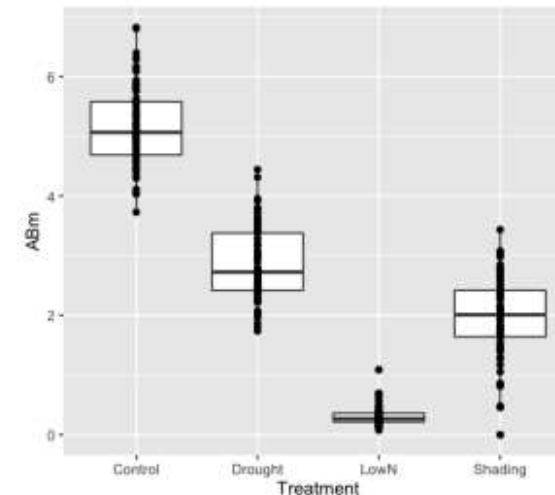
Residual standard error: 0.5415 on 279 degrees of freedom  
Multiple R-squared: 0.9147, Adjusted R-squared: 0.9132  
F-statistic: 598.5 on 5 and 279 DF, p-value: < 2.2e-16

## Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.928	85.0194	<2e-16 ***
Fungus	1	0.55	0.548	1.8706	0.1725
Treatment	3	851.91	283.968	968.5187	<2e-16 ***
Residuals	279	81.80	0.293		

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



# Include stress treatments in the model

```
model1<- lm (ABm~ IR_W + Fungus + Treatment, data = dt)
summary(model1)
anova(model1)
```

Call:  
lm(formula = ABm ~ IR\_W + Fungus + Treatment, data = dt)

Residuals:

	Min	1Q	Median	3Q	Max
	-2.05453	-0.27590	-0.02415	0.30265	1.50164

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	4.85116	0.08648	56.096	< 2e-16 ***
IR_W	0.27546	0.04443	6.200	2.02e-09 ***
Funguswith	-0.06280	0.06442	-0.975	0.33
TreatmentDrought	-2.25585	0.09075	-24.858	< 2e-16 ***
TreatmentLowN	-4.72484	0.08984	-52.593	< 2e-16 ***
TreatmentShading	-3.17401	0.09029	-35.154	< 2e-16 ***

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

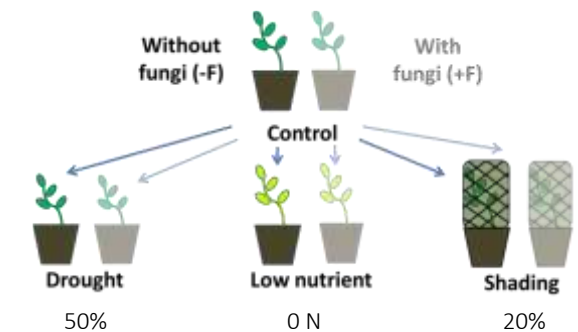
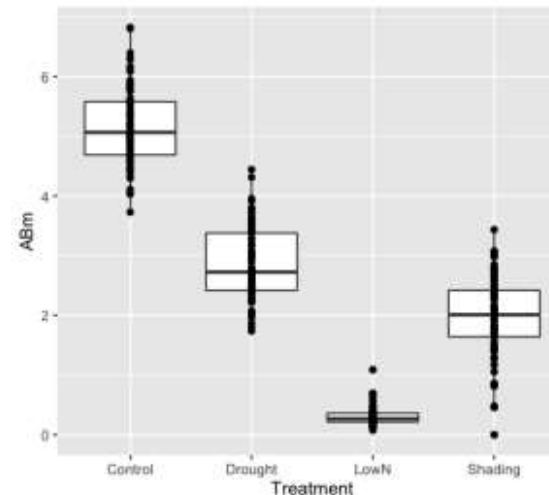
Residual standard error: 0.5415 on 279 degrees of freedom  
Multiple R-squared: 0.9147, Adjusted R-squared: 0.9132  
F-statistic: 598.5 on 5 and 279 DF, p-value: < 2.2e-16

## Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.928	85.0194	<2e-16 ***
Fungus	1	0.55	0.548	1.8706	0.1725
Treatment	3	851.91	283.968	968.5187	<2e-16 ***
Residuals	279	81.80	0.293		

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



# Include stress treatments and interactions

```
modell1<- lm (ABm ~ IR_W + Fungus*Treatment, data = dt)
summary(modell1)
anova(modell1)
plot(modell1)
```

```
Call:
lm(formula = ABm ~ IR_W + Fungus * Treatment, data = dt)
```

Residuals:

Min	1Q	Median	3Q	Max
-2.23453	-0.24639	-0.00762	0.30436	1.50611

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	4.832850	0.098688	48.971	< 2e-16	***
IR_W	0.274791	0.043829	6.270	1.39e-09	***
Funguswith	-0.024597	0.124512	-0.198	0.8435	
TreatmentDrought	-2.252505	0.126542	-17.800	< 2e-16	***
TreatmentLowN	-4.841690	0.124696	-38.828	< 2e-16	***
TreatmentShading	-2.974785	0.126568	-23.504	< 2e-16	***
Funguswith:TreatmentDrought	-0.007285	0.178798	-0.041	0.9675	
Funguswith:TreatmentLowN	0.233512	0.176499	1.323	0.1869	
Funguswith:TreatmentShading	-0.388466	0.177821	-2.185	0.0298	*

---

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

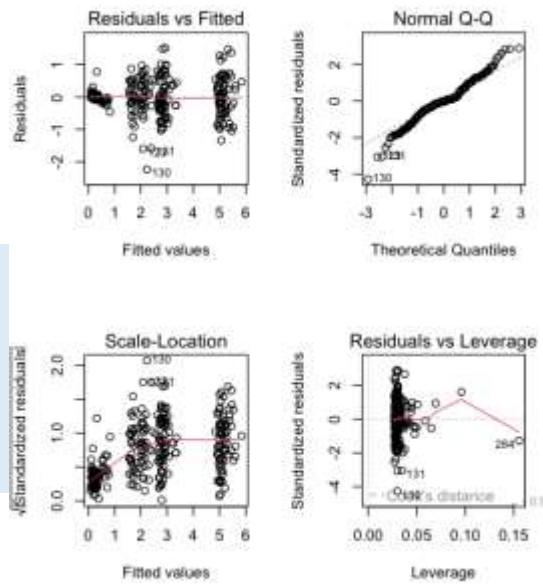
Residual standard error: 0.5326 on 276 degrees of freedom

Multiple R-squared: 0.9184, Adjusted R-squared: 0.916

F-statistic: 388.2 on 8 and 276 DF, p-value: < 2.2e-16

# Include stress treatments and interactions

```
modell1<- lm (ABm ~ IR_W + Fungus*Treatment, data = dt)
summary(modell1)
anova(modell1)
plot(modell1)
```



Call:  
lm(formula = ABm ~ IR\_W + Fungus \* Treatment, data = dt)

Residuals:

	Min	1Q	Median	3Q	Max
	-2.23453	-0.24639	-0.00762	0.30436	1.50611

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	4.832850	0.098688	48.971	< 2e-16 ***
IR_W	0.274791	0.043829	6.270	1.39e-09 ***
Funguswith	-0.024597	0.124512	-0.198	0.8435
TreatmentDrought	-2.252505	0.126542	-17.800	< 2e-16 ***
TreatmentLowN	-4.841690	0.124696	-38.828	< 2e-16 ***
TreatmentShading	-2.974785	0.126568	-23.504	< 2e-16 ***
Funguswith:TreatmentDrought	-0.007285	0.178798	-0.041	0.9675
Funguswith:TreatmentLowN	0.233512	0.176499	1.323	0.1869
Funguswith:TreatmentShading	-0.388466	0.177821	-2.185	0.0298 *

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

Analysis of Variance Table

Response: ABm

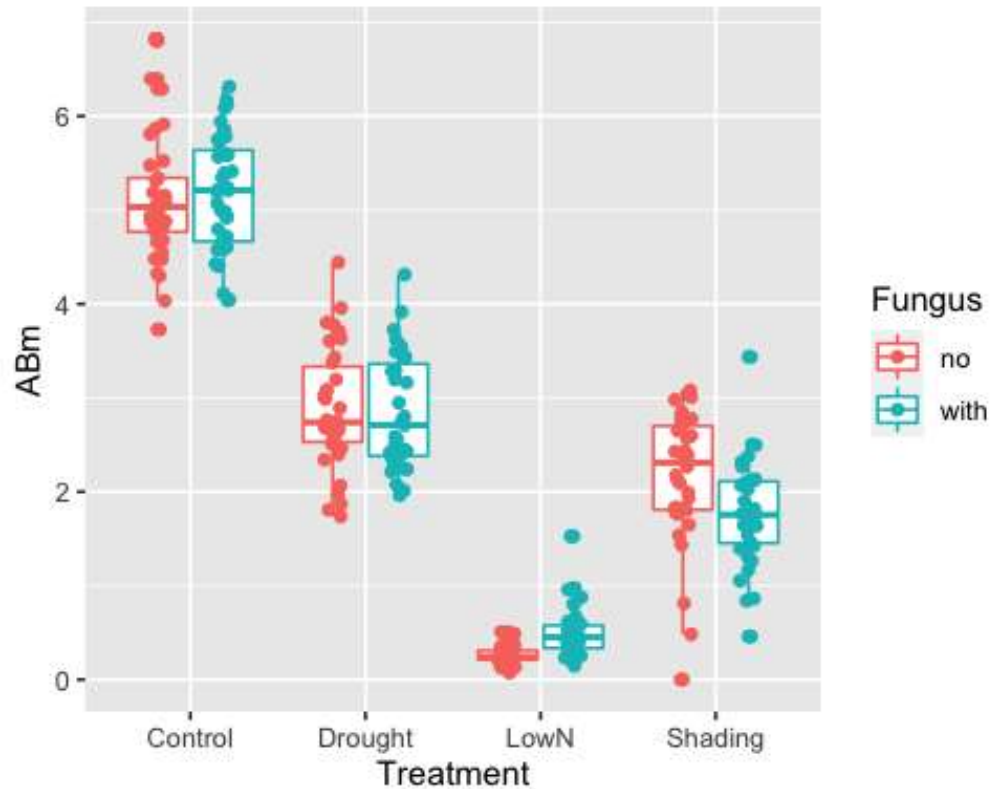
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.928	87.8843	< 2.2e-16 ***
Fungus	1	0.55	0.548	1.9336	0.165485
Treatment	3	851.91	283.968	1001.1549	< 2.2e-16 ***
Fungus:Treatment	3	3.52	1.173	4.1338	0.006878 **
Residuals	276	78.28	0.284		

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

Residual standard error: 0.5326 on 276 degrees of freedom  
Multiple R-squared: 0.9184, Adjusted R-squared: 0.916  
F-statistic: 388.2 on 8 and 276 DF, p-value: < 2.2e-16

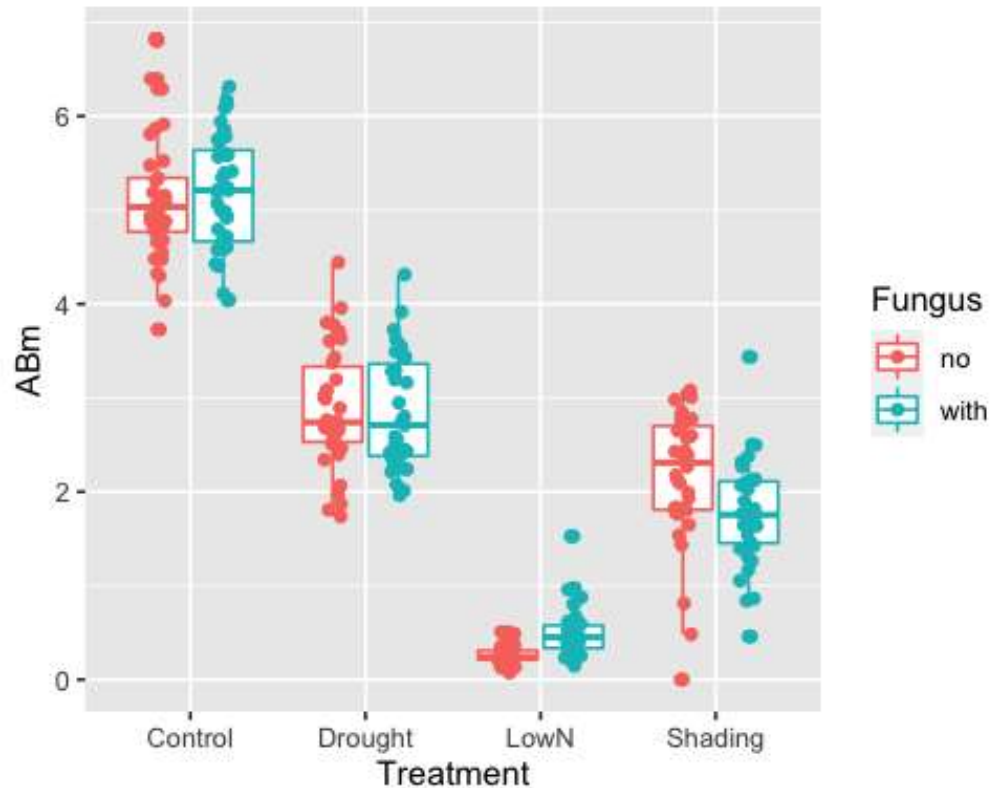
# Visualize interactions

```
g1<- ggplot(data=dt, aes(x=Treatment, y=ABm, colour=Fungus))+  
  geom_boxplot()+  
  geom_point(position=position_jitterdodge(0.1))  
g1
```

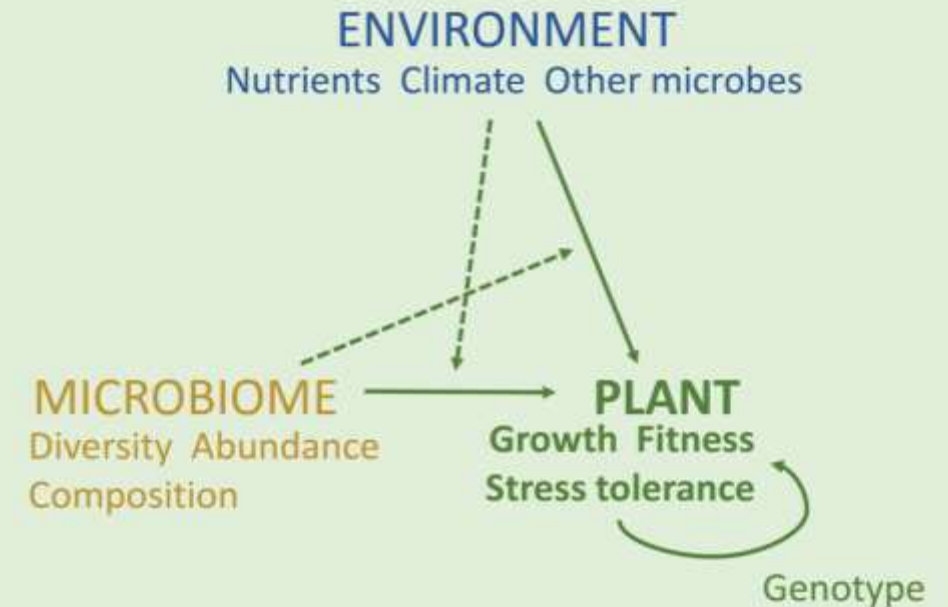


# Visualize interactions

```
g1<- ggplot(data=dt, aes(x=Treatment, y=ABm, colour=Fungus))+  
  geom_boxplot()+  
  geom_point(position=position_jitterdodge(0.1))  
g1
```

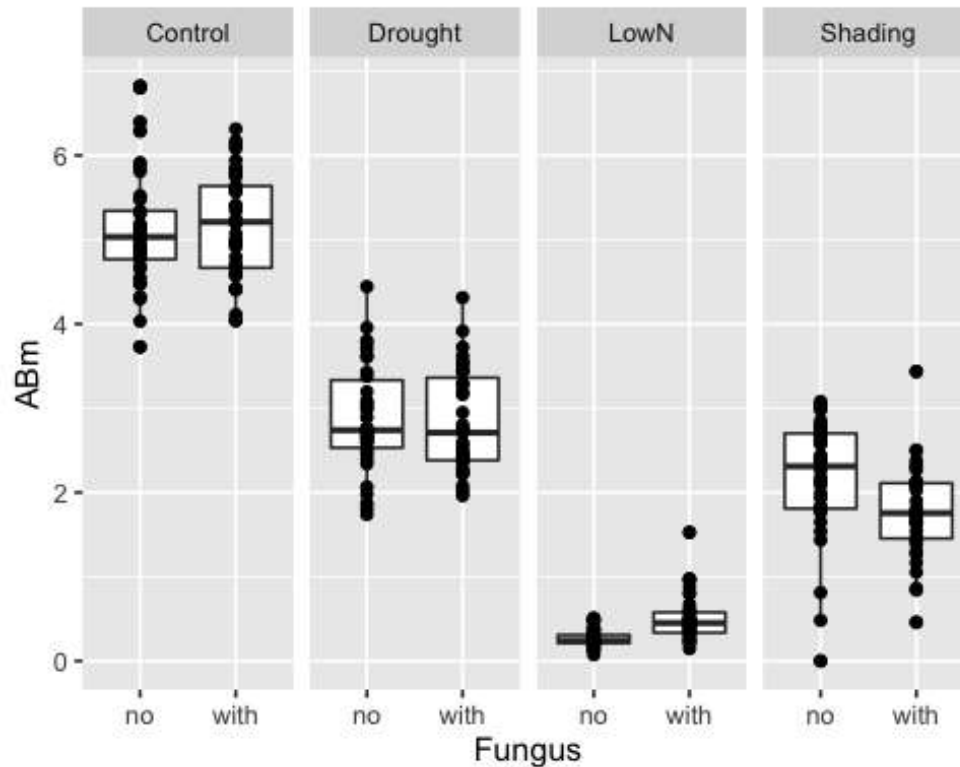


## Plant perspective



# Visualize interactions

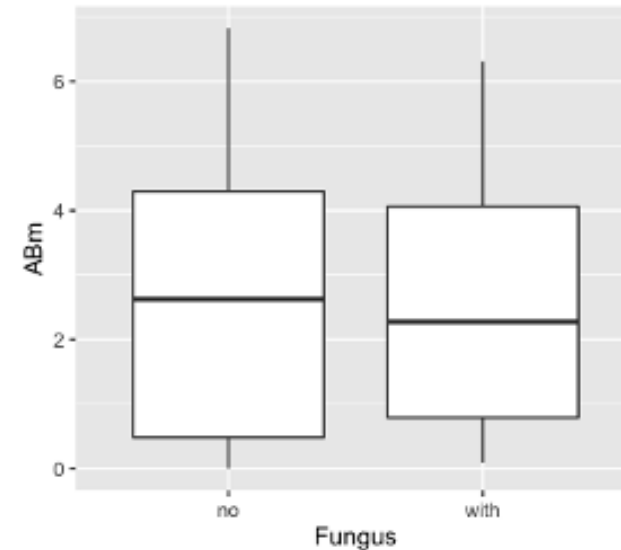
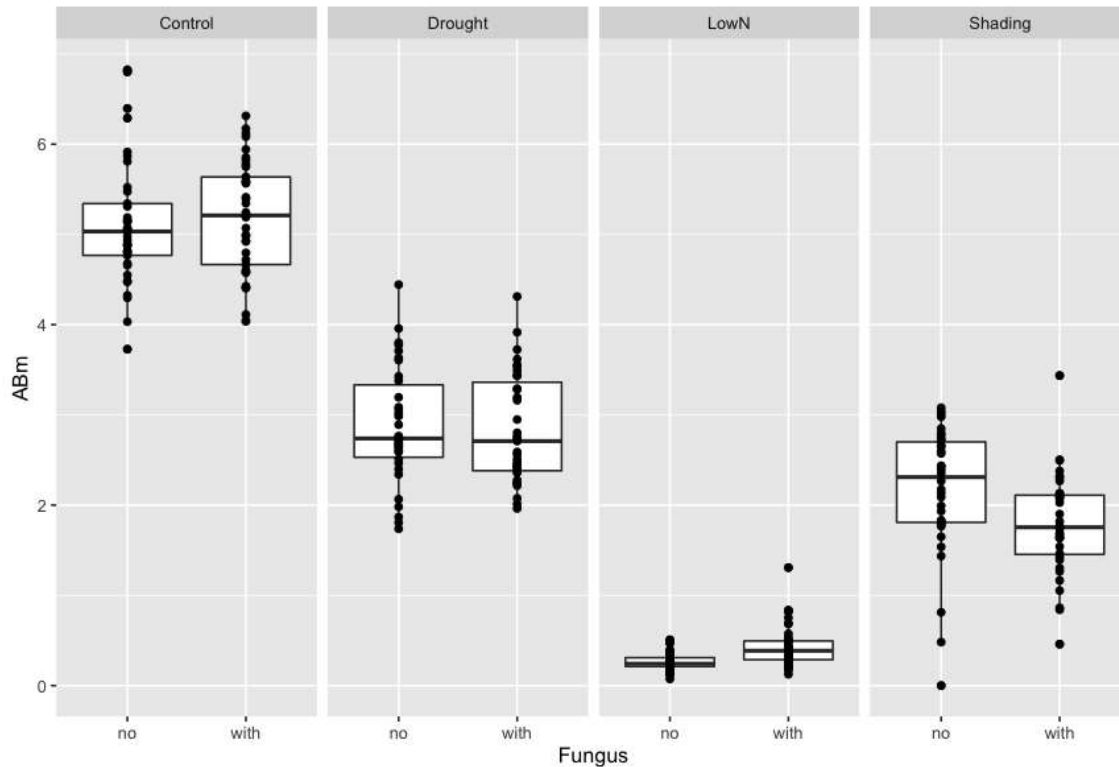
```
g1<- ggplot(data=dt, aes(x=Fungus, y=ABm)) +  
  geom_boxplot()+  
  geom_point()+  
  facet_grid(.~Treatment)  
g1
```





# Visualize interactions

```
g1<- ggplot(data=dt, aes(x=Fungus, y=ABm)) +  
  geom_boxplot() +  
  geom_point() +  
  facet_grid(.~Treatment)  
g1
```



Under which stress is the fungus effect significant?

## Post-hoc tests

```
install.packages("emmeans")
library(emmeans)

a1<-aov(ABm ~ IR_W + Fungus*Treatment, data = dt)
m2<- emmeans(a1, "Fungus", by="Treatment")
m2

pairs(m2)
```

```
Treatment = Control:
  contrast estimate      SE   df t.ratio p.value
no - with    0.0246 0.125 276    0.198  0.8435
```

```
Treatment = Drought:
  contrast estimate      SE   df t.ratio p.value
no - with    0.0319 0.128 276    0.249  0.8039
```

```
Treatment = LowN:
  contrast estimate      SE   df t.ratio p.value
no - with   -0.2089 0.126 276   -1.663  0.0975
```

```
Treatment = Shading:
  contrast estimate      SE   df t.ratio p.value
no - with    0.4131 0.127 276    3.241  0.0013
```

# Plot parameter estimates from the model

```
install.packages("effects")
require(effects)

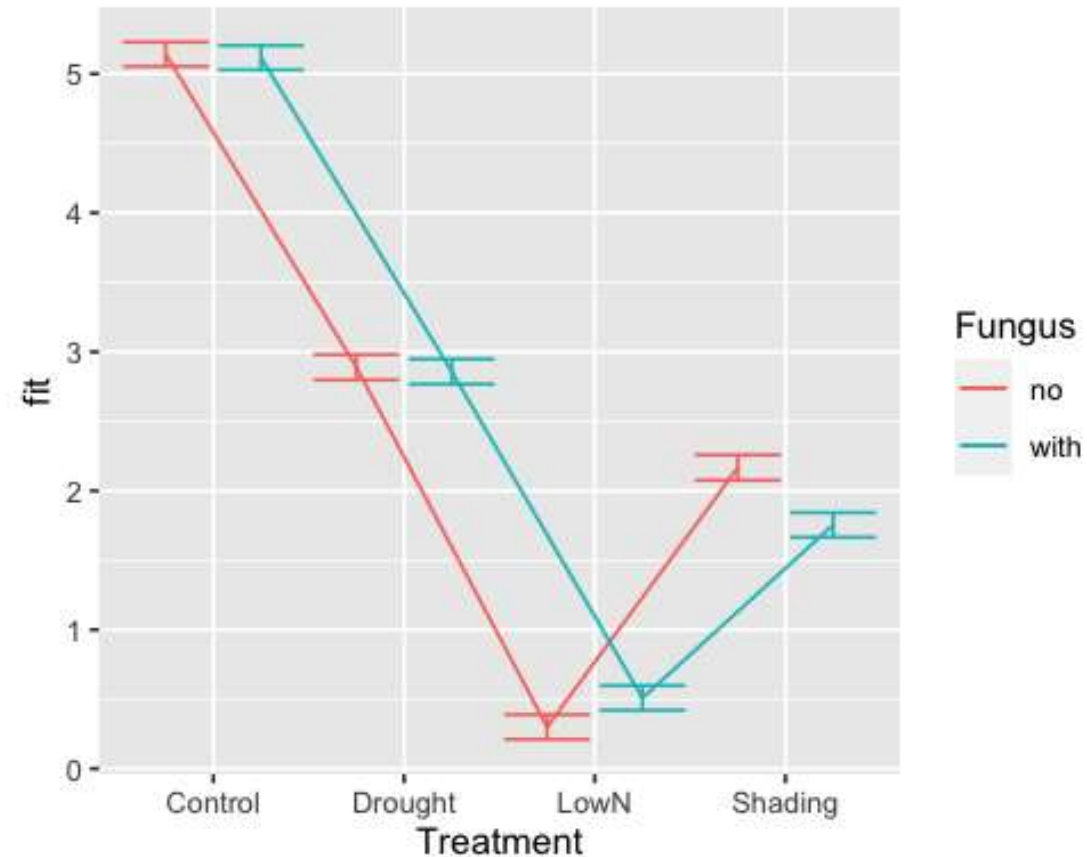
efbm <- effect("Fungus:Treatment",model1)
efbm <- as.data.frame(efbm)
efbm
```

	Fungus	Treatment	fit	se	lower	upper
1	no	Control	5.1416190	0.08763424	4.9691025	5.3141354
2	with	Control	5.1170218	0.08805609	4.9436749	5.2903687
3	no	Drought	2.8891140	0.09135003	2.7092827	3.0689453
4	with	Drought	2.8572317	0.09005113	2.6799574	3.0345061
5	no	LowN	0.2999285	0.08894838	0.1248251	0.4750320
6	with	LowN	0.5088437	0.08876480	0.3341016	0.6835857
7	no	Shading	2.1668338	0.09133746	1.9870272	2.3466404
8	with	Shading	1.7537708	0.08887739	1.5788071	1.9287344

# Plot parameter estimates from the model

```
g2<- ggplot(data=efbm, aes(x=Treatment, y=fit, colour=Fungus, group=Fungus))+  
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se), position=position_dodge(width=1))+  
  geom_line(position=position_dodge(width=1))
```

g2



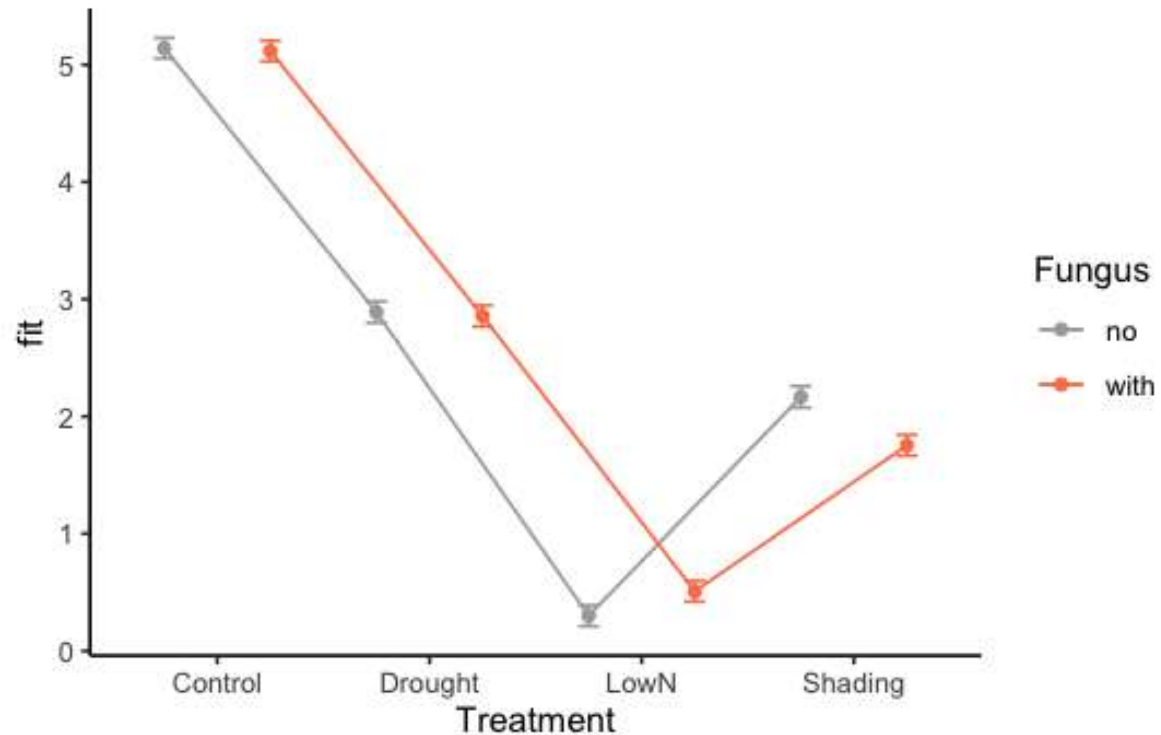


## Beautify the plot

```
g2<- ggplot(data=efbm, aes(x=Treatment, y=fit, colour=Fungus, group=Fungus))+  
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1), position=position_dodge(width=1))+  
  geom_line(position=position_dodge(width=1))+  
  geom_point(position=position_dodge(width=1))+  
  scale_color_manual(values = c("darkgrey", "coral"))+  
  theme_classic()  
g2
```

# Beautify the plot

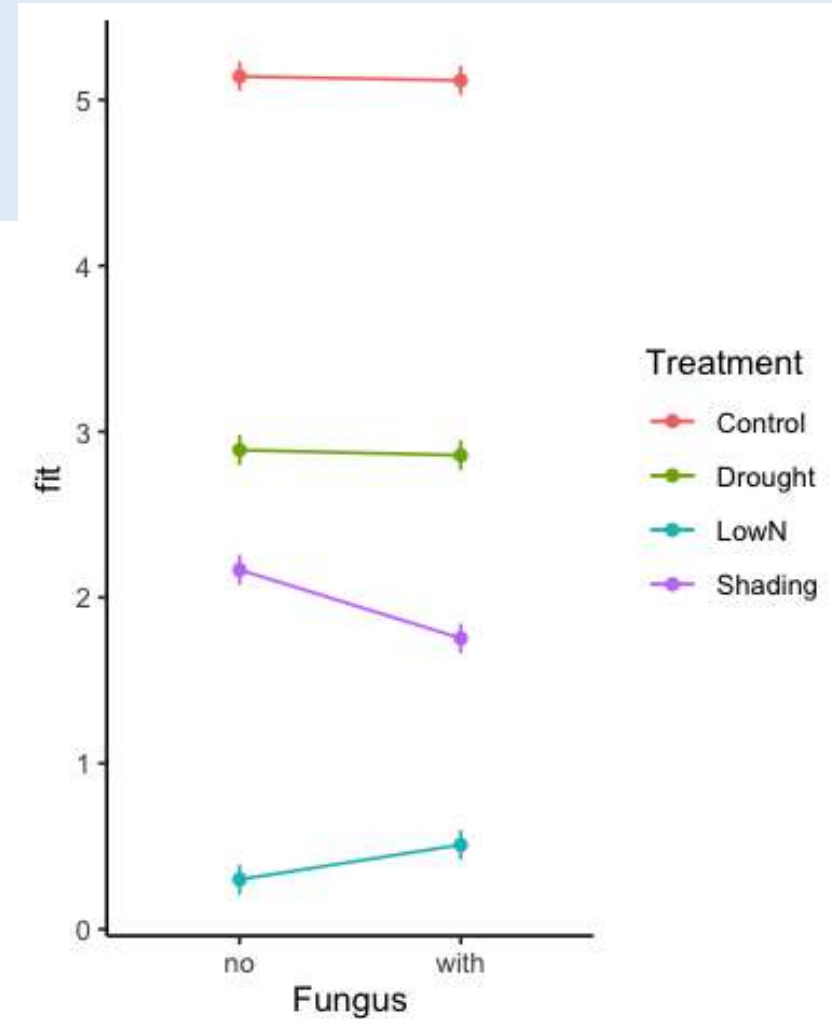
```
g2<- ggplot(data=efbm, aes(x=Treatment, y=fit, colour=Fungus, group=Fungus))+  
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1), position=position_dodge(width=1))+  
  geom_line(position=position_dodge(width=1))+  
  geom_point(position=position_dodge(width=1))+  
  scale_color_manual(values = c("darkgrey", "coral"))+  
  theme_classic()  
g2
```



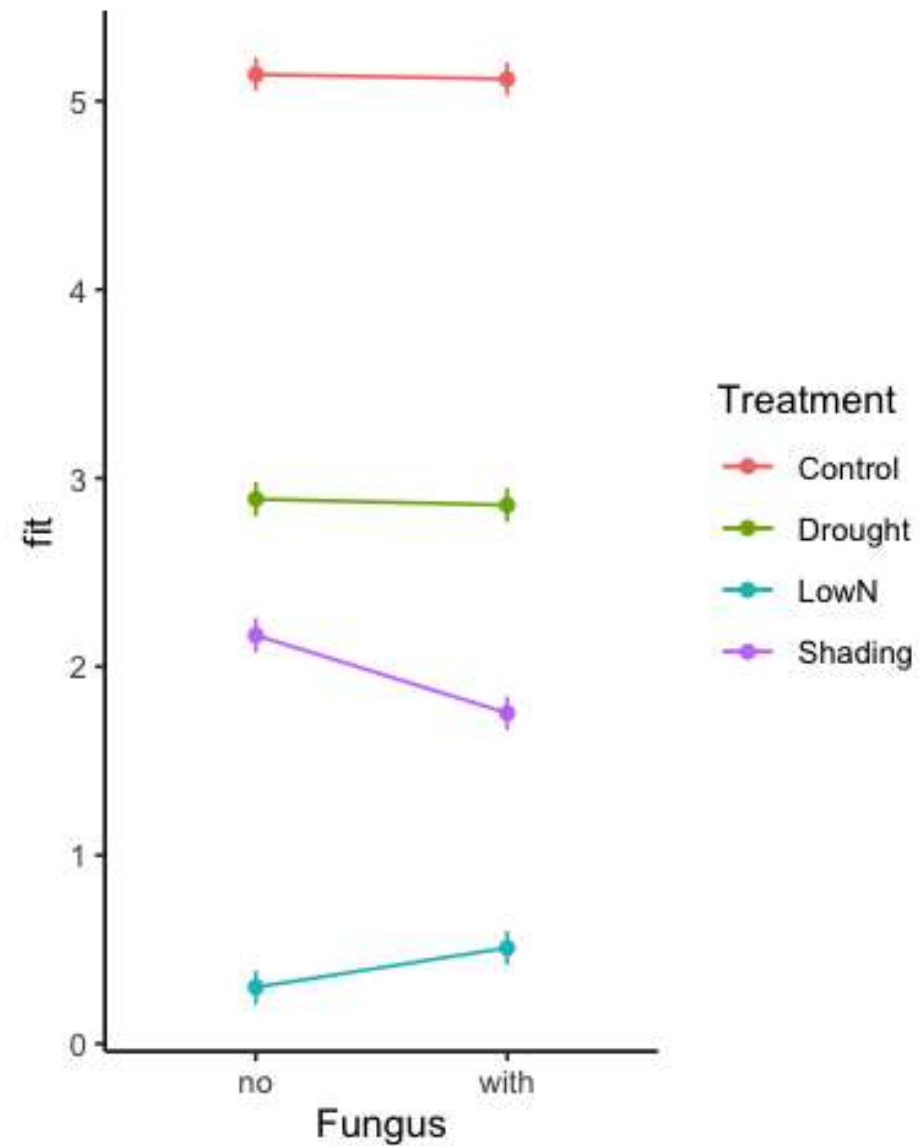
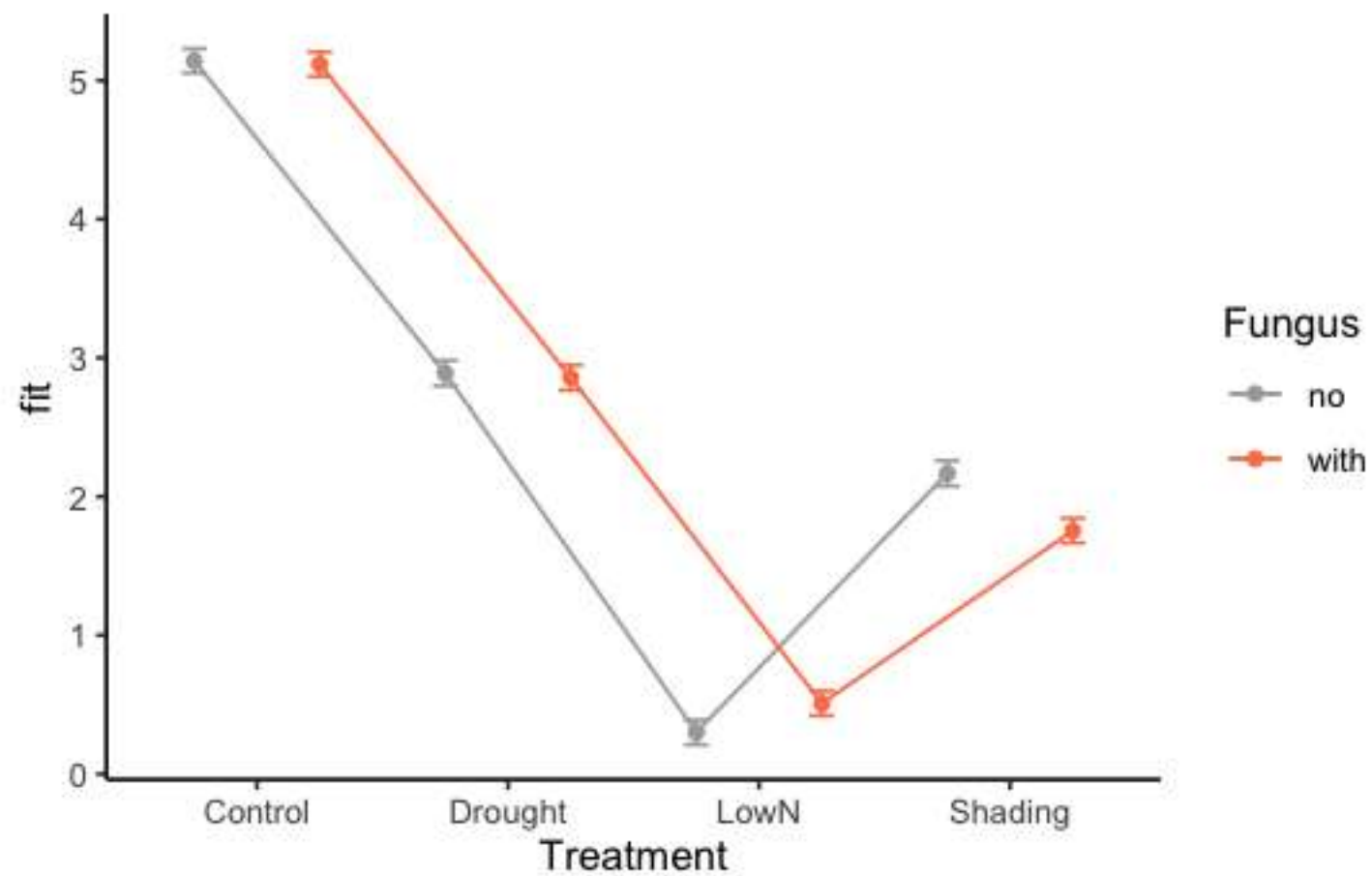
## Beautify the plot – take 2

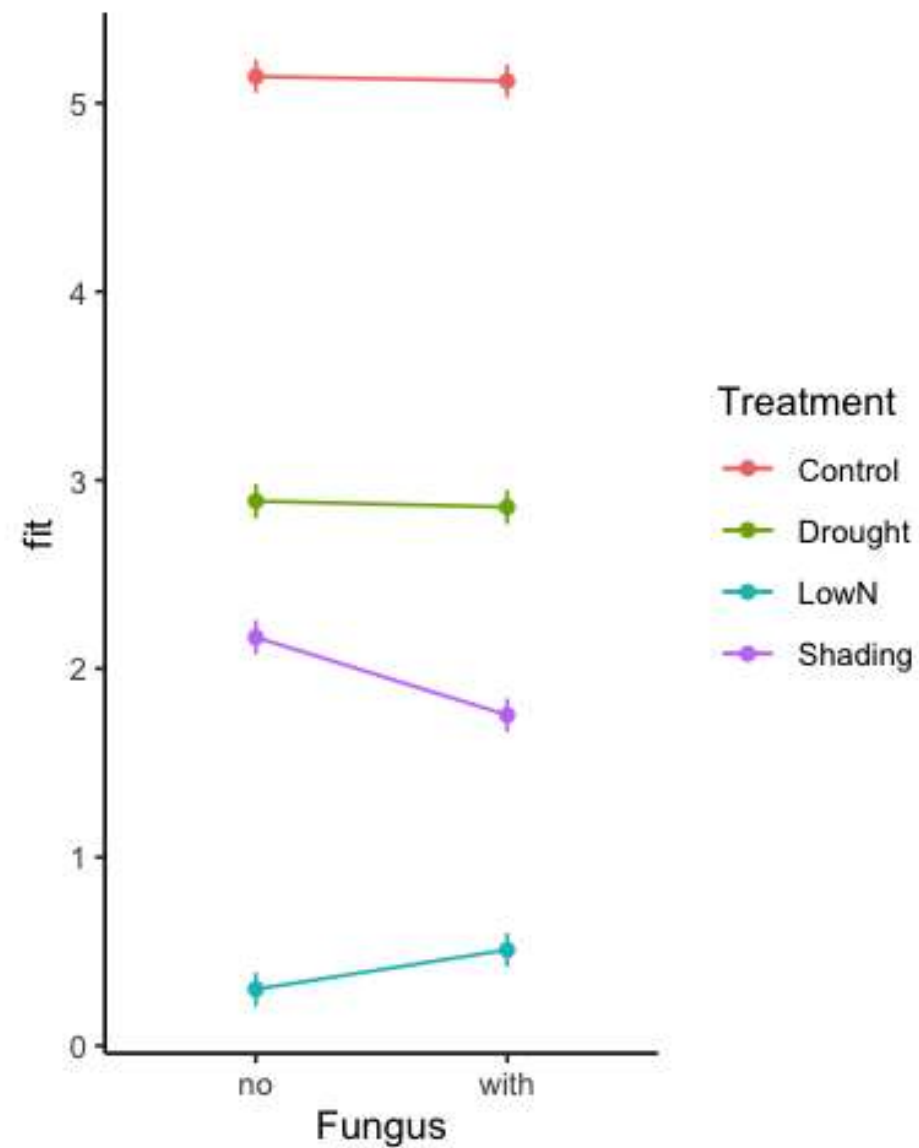
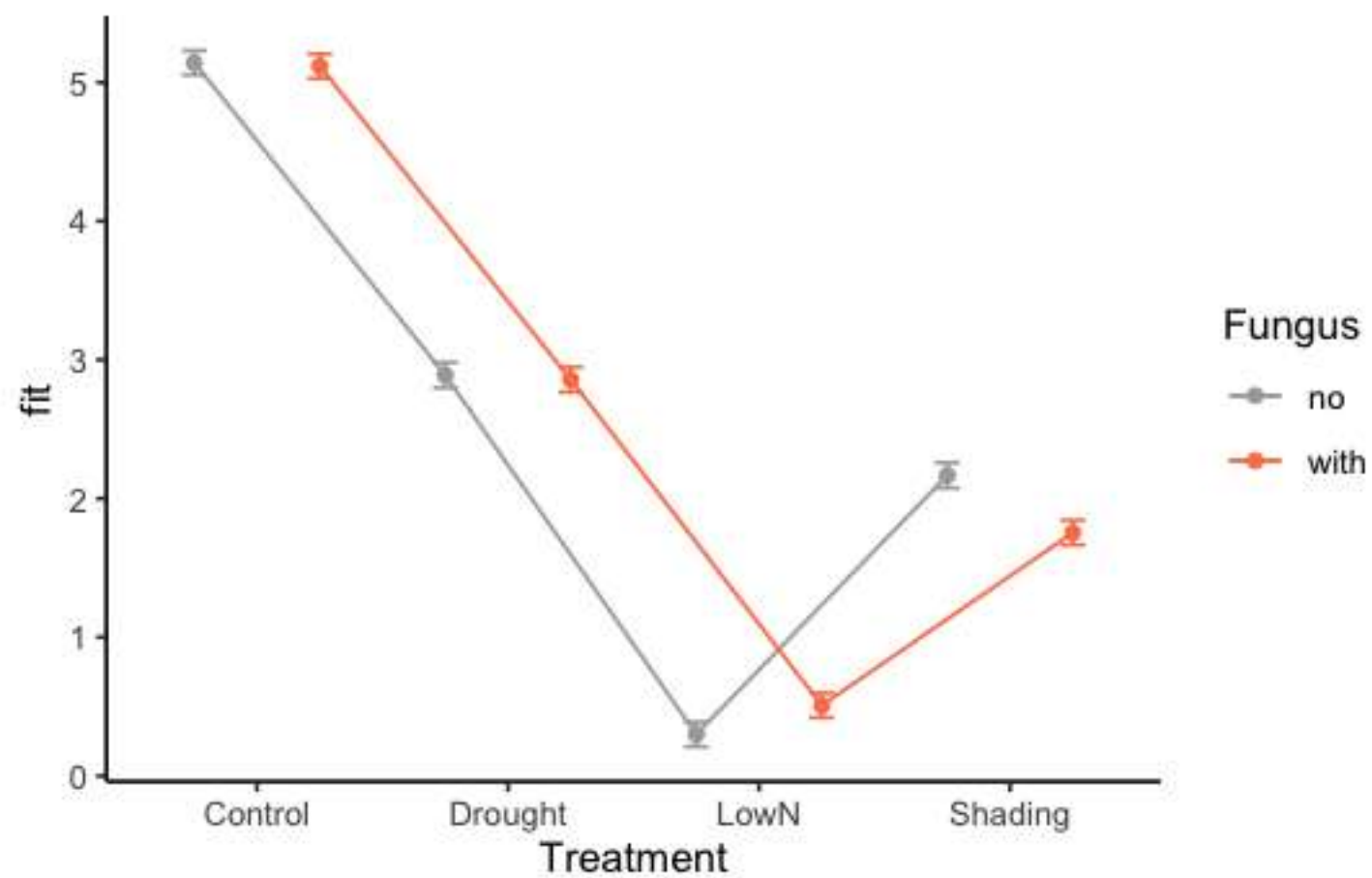
```
g2<- ggplot(data=efbm, aes(x=Fungus, y=fit, colour=Treatment, group=Treatment))+  
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0))+  
  geom_line()+  
  geom_point()+  
  theme_classic()
```

g2



```
model1<- lm (ABm ~ IR_W + Fungus*Treatment, data = dt)
```

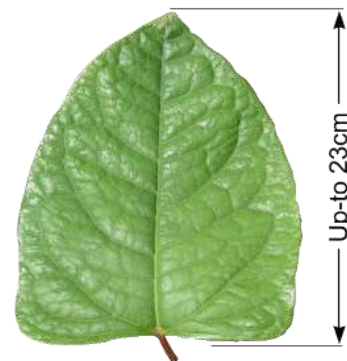
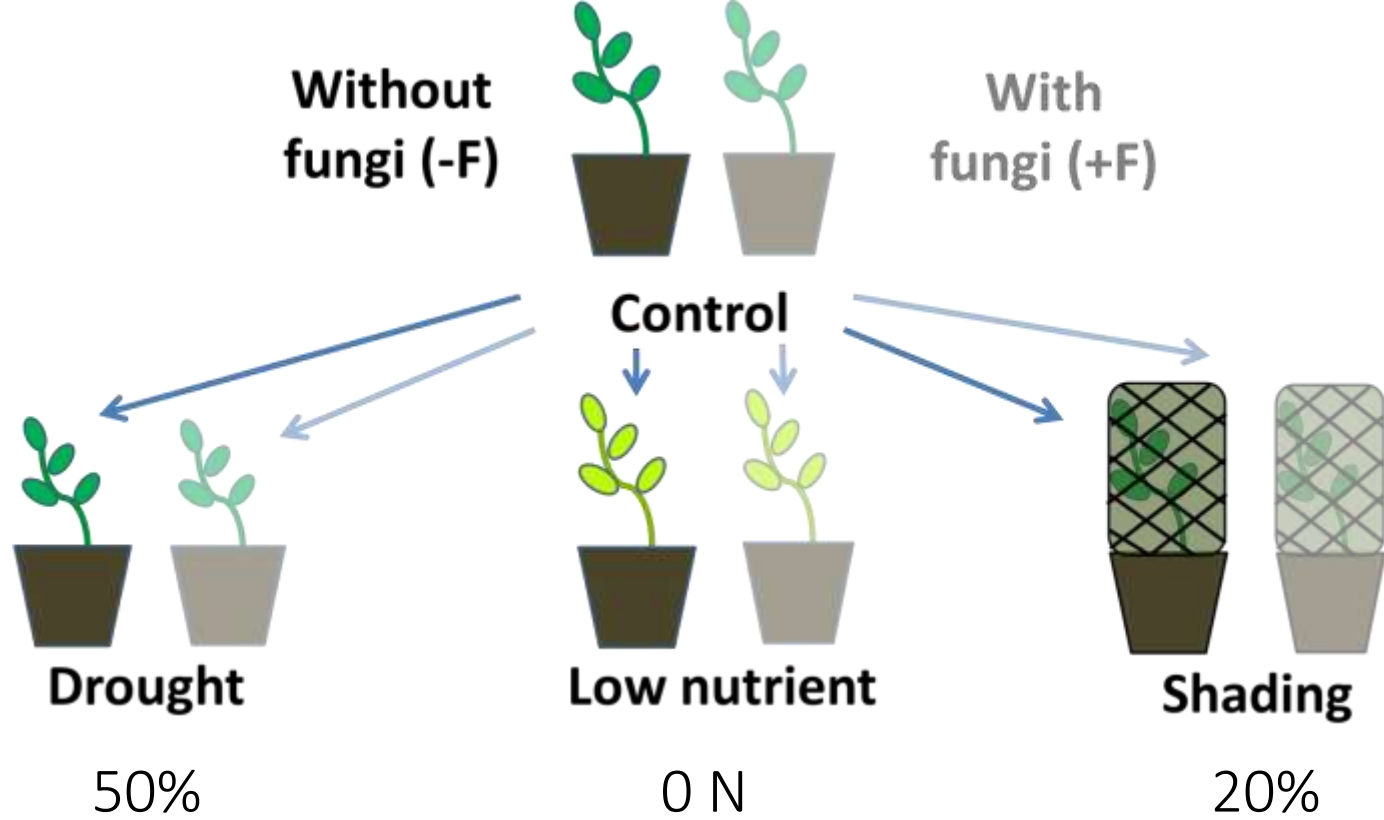






G X E

Effect of plant species



Bohemian knotweed  
(*Fallopia × bohemica*)



Japanese knotweed  
(*Fallopia japonica*)

# Include **species** in the model

```
model2<- lm (ABm ~ IR_W + Species*Fungus*Treatment, data = dt)
summary(model2)
anova(model2)
plot(model2)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	1.78498	0.04194	42.562	< 2e-16	***
IR_W	0.05214	0.01468	3.553	0.00045	***
SpeciesRJ	-0.06277	0.05116	-1.227	0.22090	
Funguswith	-0.01767	0.05333	-0.331	0.74063	
TreatmentDrought	-0.40192	0.05439	-7.389	1.89e-12	***
TreatmentLowN	-1.57873	0.05341	-29.558	< 2e-16	***
TreatmentShading	-0.70945	0.05444	-13.031	< 2e-16	***
SpeciesRJ:Funguswith	0.02288	0.07200	0.318	0.75088	
SpeciesRJ:TreatmentDrought	-0.11231	0.07332	-1.532	0.12678	
SpeciesRJ:TreatmentLowN	0.01454	0.07216	0.202	0.84043	
SpeciesRJ:TreatmentShading	0.03274	0.07337	0.446	0.65582	
Funguswith:TreatmentDrought	0.02163	0.07710	0.281	0.77925	
Funguswith:TreatmentLowN	0.23851	0.07589	3.143	0.00186	**
Funguswith:TreatmentShading	-0.06635	0.07647	-0.868	0.38639	
SpeciesRJ:Funguswith:TreatmentDrought	-0.04747	0.10392	-0.457	0.64817	
SpeciesRJ:Funguswith:TreatmentLowN	-0.13605	0.10240	-1.329	0.18508	
SpeciesRJ:Funguswith:TreatmentShading	-0.08857	0.10305	-0.859	0.39088	

---

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

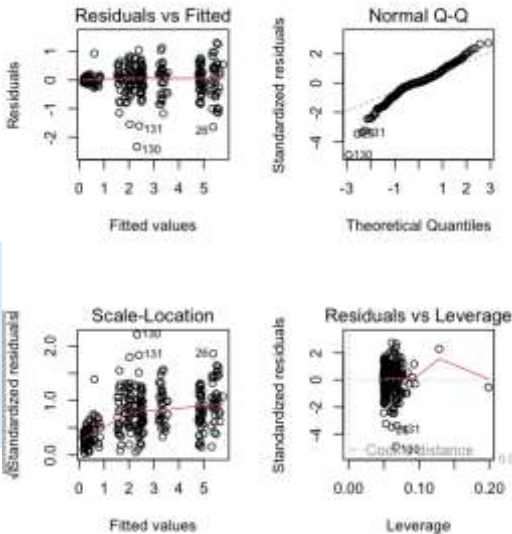
Residual standard error: 0.1533 on 268 degrees of freedom

Multiple R-squared: 0.9333, Adjusted R-squared: 0.9294

F-statistic: 234.5 on 16 and 268 DF, p-value: < 2.2e-16

# Include species in the model

```
model2<- lm (ABm ~ IR_W + Species*Fungus*Treatment, data = dt)
summary(model2)
anova(model2)
plot(model2)
```



Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	1.78498	0.04194	42.562	< 2e-16 ***
IR_W	0.05214	0.01468	3.553	0.00045 ***
SpeciesRJ	-0.06277	0.05116	-1.227	0.22090
Funguswith	-0.01767	0.05333	-0.331	0.74063
TreatmentDrought	-0.40192	0.05439	-7.389	1.89e-12 ***
TreatmentLowN	-1.57873	0.05341	-29.558	< 2e-16 ***
TreatmentShading	-0.70945	0.05444	-13.031	< 2e-16 ***
SpeciesRJ:Funguswith	0.02288	0.07200	0.318	0.75088
SpeciesRJ:TreatmentDrought	-0.11231	0.07332	-1.532	0.12678
SpeciesRJ:TreatmentLowN	0.01454	0.07216	0.202	0.84043
SpeciesRJ:TreatmentShading	0.03274	0.07337	0.446	0.65582
Funguswith:TreatmentDrought	0.02163	0.07710	0.281	0.77925
Funguswith:TreatmentLowN	0.23851	0.07589	3.143	0.00186 **
Funguswith:TreatmentShading	-0.06635	0.07647	-0.868	0.38639
SpeciesRJ:Funguswith:TreatmentDrought	-0.04747	0.10392	-0.457	0.64817
SpeciesRJ:Funguswith:TreatmentLowN	-0.13605	0.10240	-1.329	0.18508
SpeciesRJ:Funguswith:TreatmentShading	-0.08857	0.10305	-0.859	0.39088

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

Residual standard error: 0.1533 on 268 degrees of freedom  
 Multiple R-squared: 0.9333, Adjusted R-squared: 0.9294  
 F-statistic: 234.5 on 16 and 268 DF, p-value: < 2.2e-16

## Analysis of Variance Table

Response: ABm

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	24.93	24.928	103.2296	< 2.2e-16 ***
Species	1	6.18	6.178	25.5837	7.868e-07 ***
Fungus	1	0.40	0.395	1.6368	0.2018735
Treatment	3	854.81	284.936	1179.9714	< 2.2e-16 ***
Species:Fungus	1	0.09	0.091	0.3750	0.5408182
Species:Treatment	3	4.33	1.443	5.9777	0.0005873 ***
Fungus:Treatment	3	3.56	1.188	4.9200	0.0024144 **
Species:Fungus:Treatment	3	0.17	0.058	0.2401	0.8683332
Residuals	268	64.72	0.241		

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

# Include species in the model + transform

```
model2<- lm (ABm ~ IR_W + Species*Fungus*Treatment, data = dt)
summary(model2)
anova(model2)
plot(model2)
```

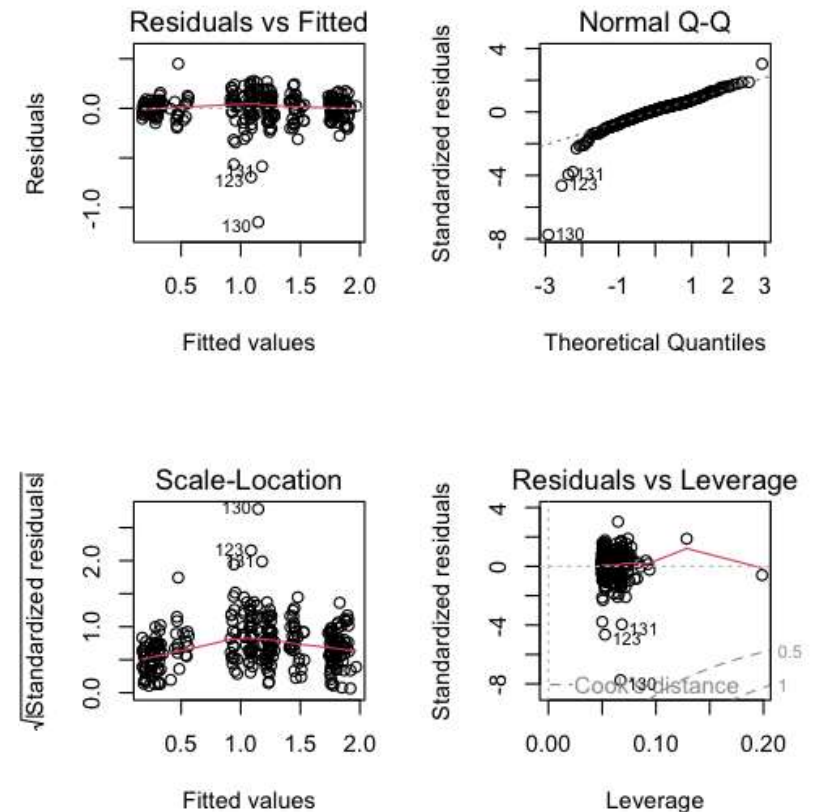
Analysis of Variance Table

Response: log(ABm + 1)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
IR_W	1	2.413	2.4132	102.6285	< 2.2e-16	***
Species	1	0.327	0.3273	13.9183	0.0002331	***
Fungus	1	0.000	0.0001	0.0033	0.9545677	
Treatment	3	84.504	28.1680	1197.9351	< 2.2e-16	***
Species:Fungus	1	0.036	0.0358	1.5217	0.2184474	
Species:Treatment	3	0.195	0.0650	2.7641	0.0424000	*
Fungus:Treatment	3	0.703	0.2342	9.9611	3.017e-06	***
Species:Fungus:Treatment	3	0.045	0.0151	0.6414	0.5890131	
Residuals	268	6.302	0.0235			

---

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





# Visualize species x treatment

```
efbm <- effect("Fungus:Treatment",model2)
efbm <- as.data.frame(efbm)
efbm
```

Species	Treatment	fit	se	lower	upper
1	RB	Control	1.8346435	0.02730202	1.7808897 1.8883972
2	RJ	Control	1.7834315	0.02464907	1.7349011 1.8319620
3	RB	Drought	1.4436541	0.02786205	1.3887977 1.4985104
4	RJ	Drought	1.2561426	0.02528754	1.2063551 1.3059301
5	RB	LowN	0.3764250	0.02738373	0.3225104 0.4303396
6	RJ	LowN	0.2710122	0.02475035	0.2222824 0.3197421
7	RB	Shading	1.0916706	0.02858240	1.0353960 1.1479452
8	RJ	Shading	1.0284448	0.02502341	0.9791773 1.0777122

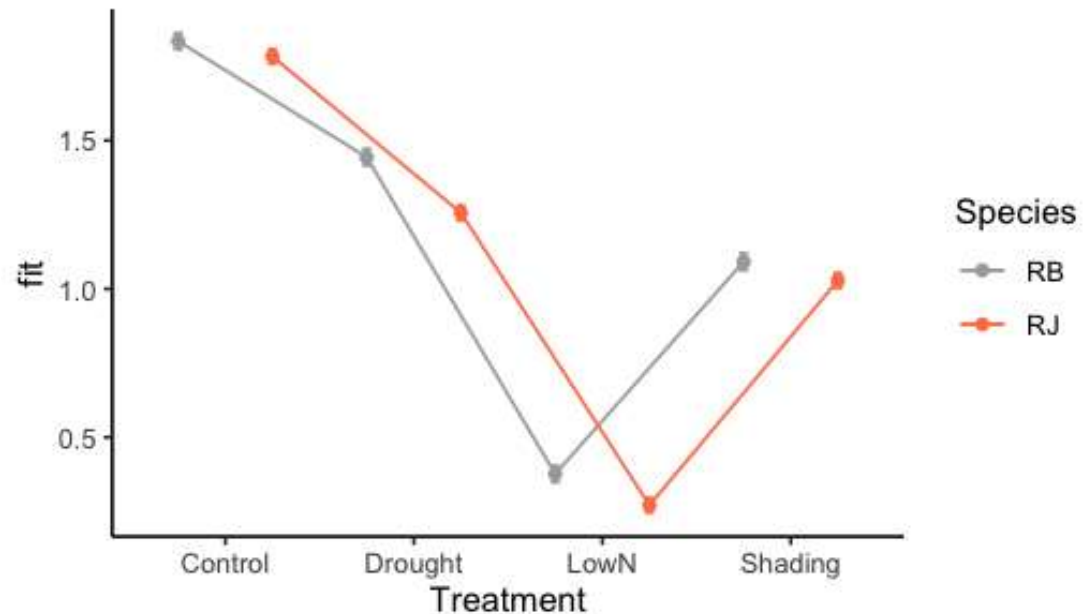
>

## Visualize species x treatment

```
g4<- ggplot(data=efsp, aes(x=Treatment, y=fit, colour=Species, group=Species))+  
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1), position=position_dodge(width=1))+  
  geom_line(position=position_dodge(width=1))+  
  geom_point(position=position_dodge(width=1))+  
  scale_color_manual(values = c("darkgrey", "coral"))+  
  theme_classic()  
g4
```

# Visualize species x treatment

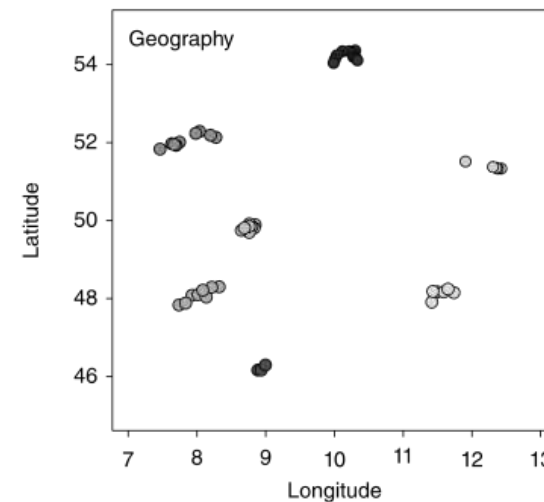
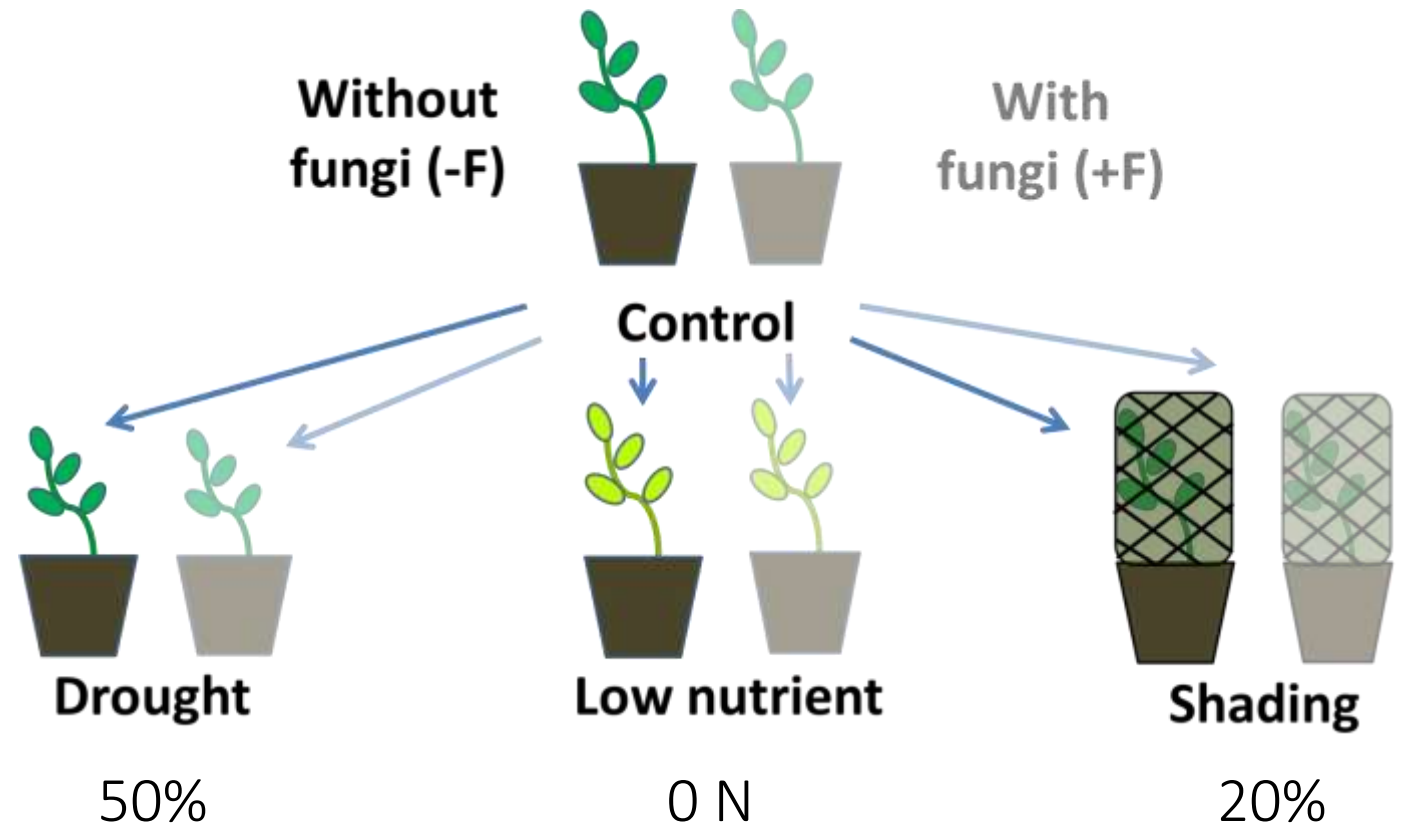
```
g4<- ggplot(data=efsp, aes(x=Treatment, y=fit, colour=Species, group=Species))+  
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1), position=position_dodge(width=1))+  
  geom_line(position=position_dodge(width=1))+  
  geom_point(position=position_dodge(width=1))+  
  scale_color_manual(values = c("darkgrey", "coral"))+  
  theme_classic()  
g4
```



G X E

Effect of plant origin

Include **region** in the model





# Include **region** in the model

```
model3<- lm (log(ABm+1) ~ IR_W + Region*Fungus*Treatment, data = dt)
summary(model3)
anova(model3)
plot(model3)
```

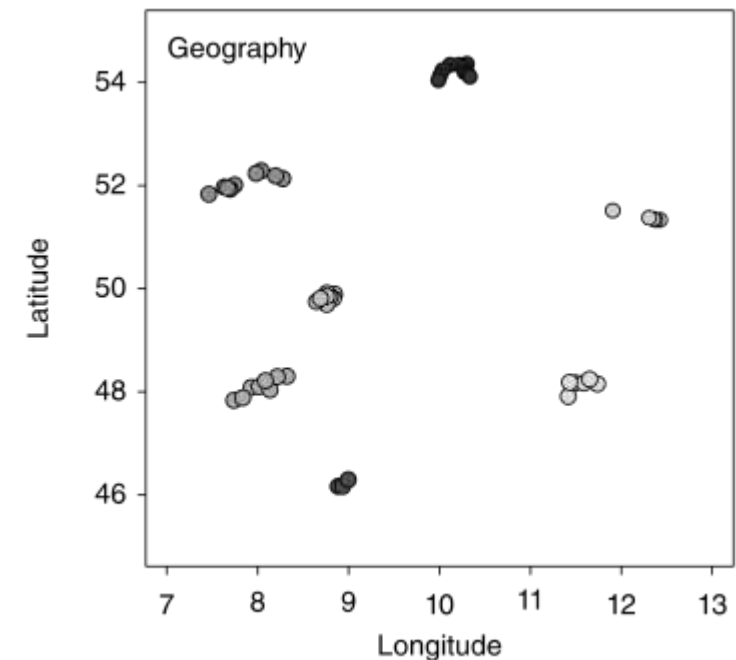
Analysis of Variance Table

Response: log(ABm + 1)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
IR_W	1	2.413	2.4132	105.4790	< 2.2e-16	***
Region	5	0.632	0.1264	5.5269	7.814e-05	***
Fungus	1	0.000	0.0003	0.0143	0.90486	
Treatment	3	84.519	28.1729	1231.4245	< 2.2e-16	***
Region:Fungus	5	0.029	0.0057	0.2492	0.93994	
Region:Treatment	15	0.701	0.0468	2.0439	0.01343	*
Fungus:Treatment	3	0.686	0.2285	9.9884	3.189e-06	***
Region:Fungus:Treatment	15	0.146	0.0097	0.4241	0.97118	
Residuals	236	5.399	0.0229			

---

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



# Include **region** in the model

```
model3<- lm (log(ABm+1) ~ IR_W + Region*Fungus*Treatment, data = dt)
summary(model3)
anova(model3)
plot(model3)
```

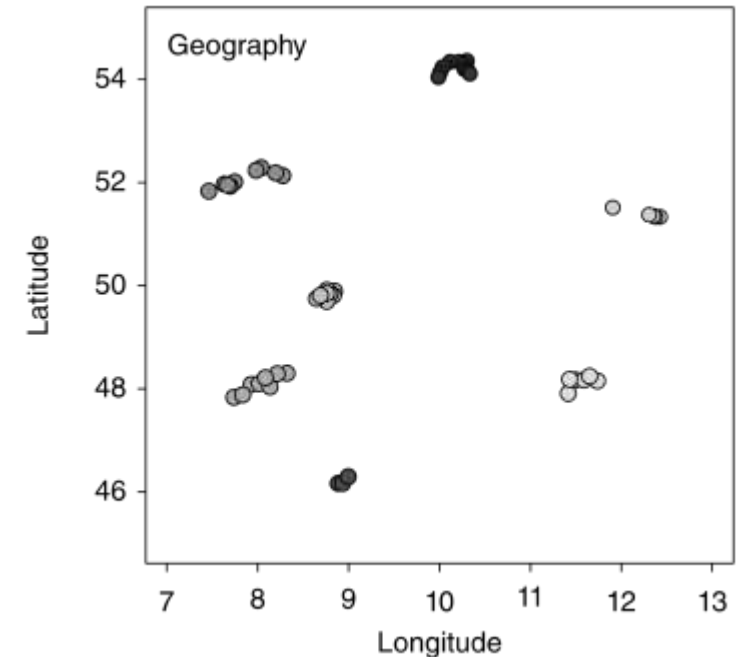
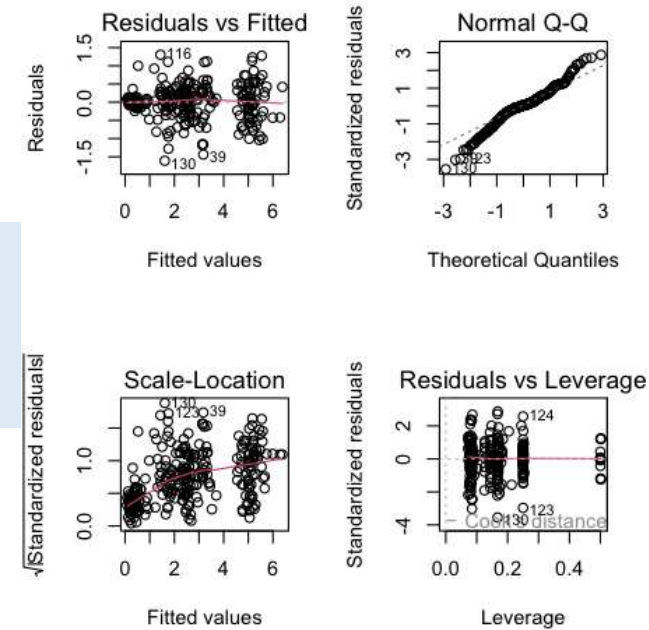
Analysis of Variance Table

Response: log(ABm + 1)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
IR_W	1	2.413	2.4132	105.4790	< 2.2e-16 ***
Region	5	0.632	0.1264	5.5269	7.814e-05 ***
Fungus	1	0.000	0.0003	0.0143	0.90486
Treatment	3	84.519	28.1729	1231.4245	< 2.2e-16 ***
Region:Fungus	5	0.029	0.0057	0.2492	0.93994
Region:Treatment	15	0.701	0.0468	2.0439	0.01343 *
Fungus:Treatment	3	0.686	0.2285	9.9884	3.189e-06 ***
Region:Fungus:Treatment	15	0.146	0.0097	0.4241	0.97118
Residuals	236	5.399	0.0229		

---

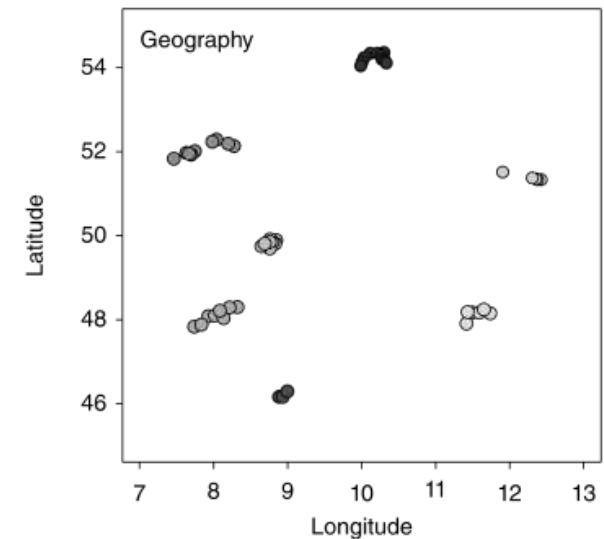
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1



# Plot region effect

```
efreg <- effect("Region:Treatment",model3)
efreg <- as.data.frame(efreg)
efreg
```

```
g5<- ggplot(data=efreg, aes(x=Treatment, y=fit, colour=Region, group=Region))+
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1), position=position_dodge(width=1))+
  geom_line(position=position_dodge(width=1))+
  geom_point(position=position_dodge(width=1))+
  theme_classic()
g5
```

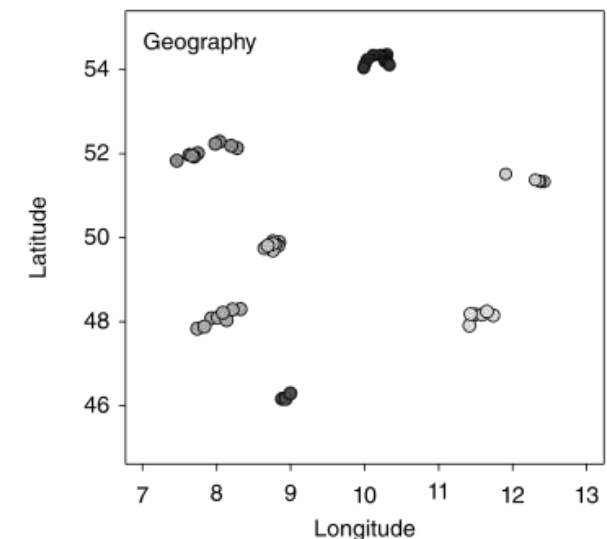
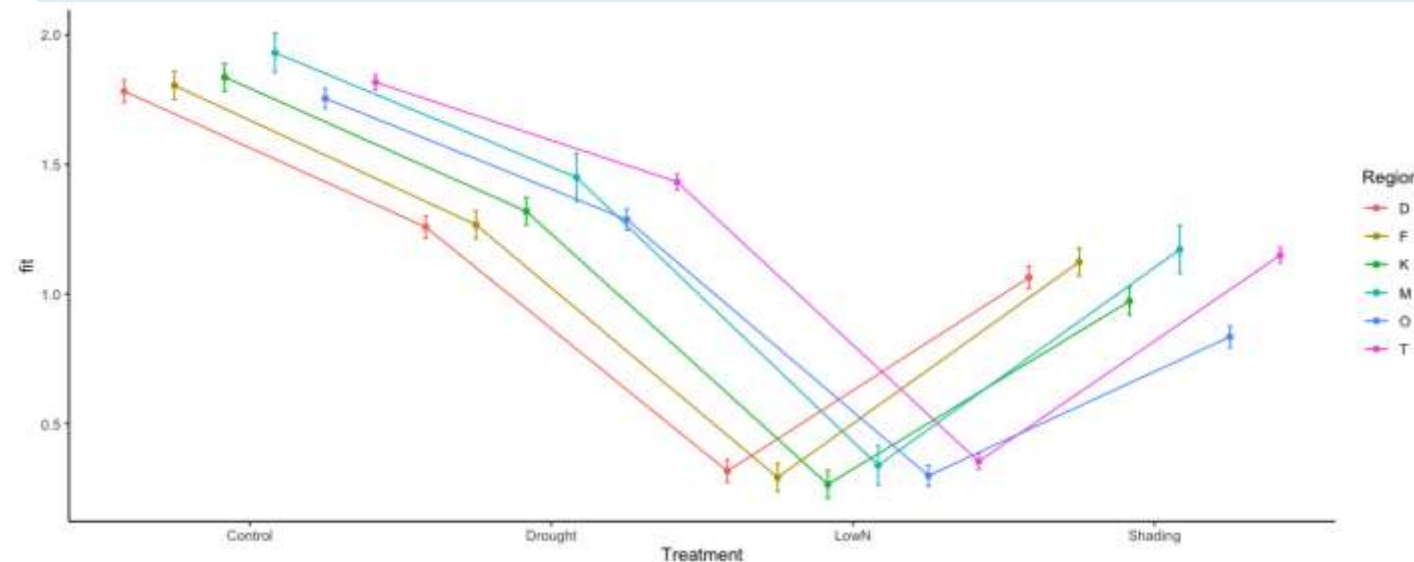
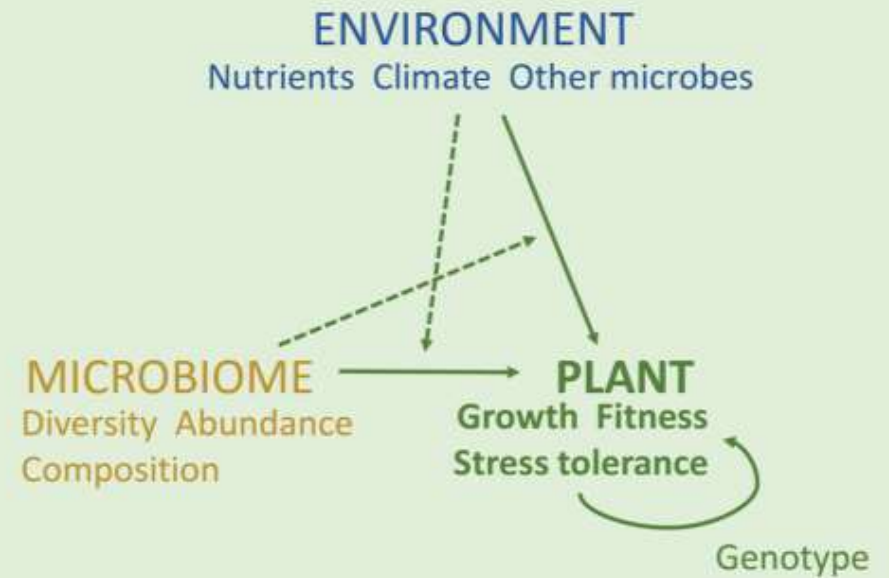


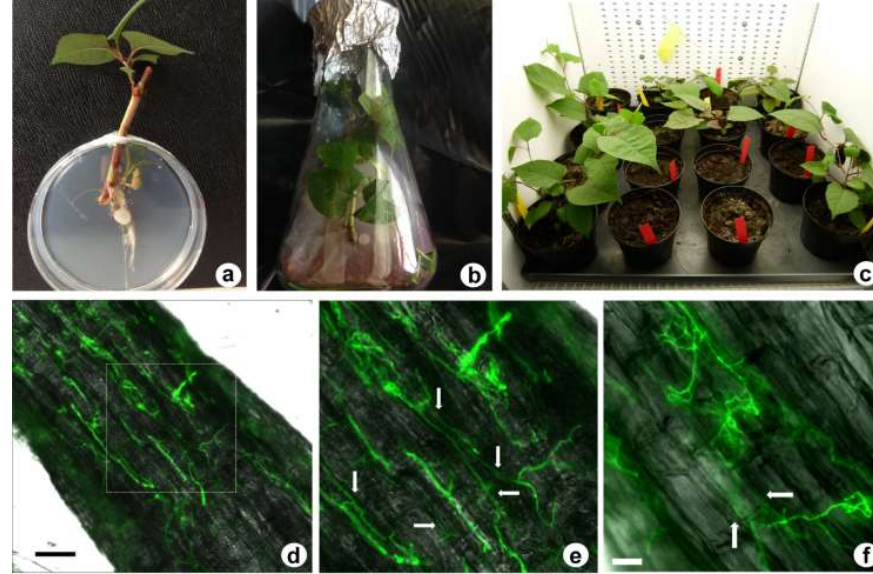
# Plant perspective

## Plot region effect

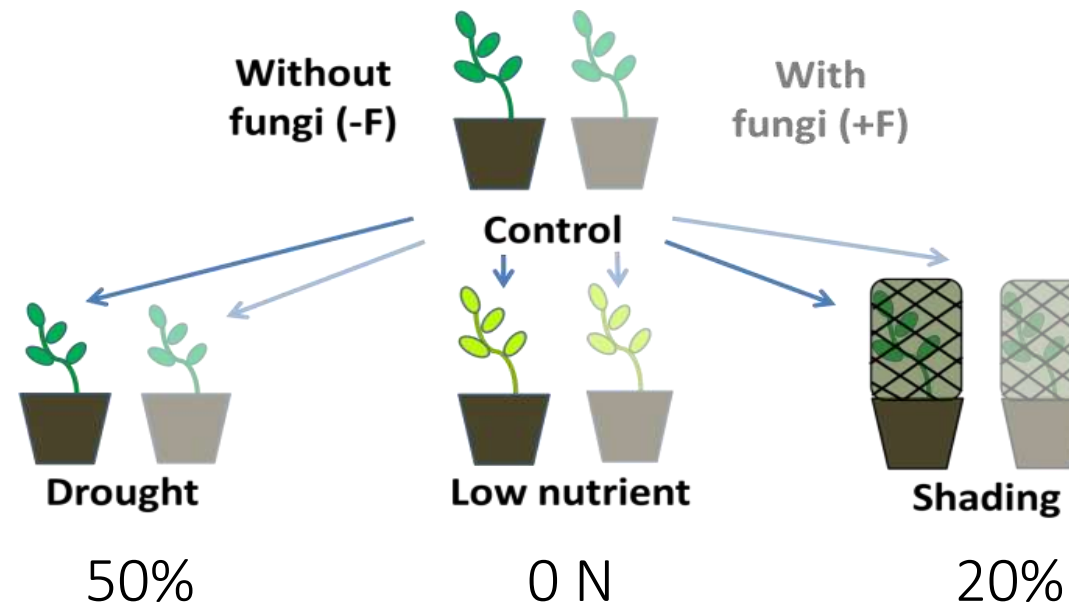
```
efreg <- effect("Region:Treatment",model3)
efreg <- as.data.frame(efreg)
efreg
```

```
g5<- ggplot(data=efreg, aes(x=Treatment, y=fit, colour=Region
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1), p
  geom_line(position=position_dodge(width=1))+
  geom_point(position=position_dodge(width=1))+
  theme_classic()
g5
```

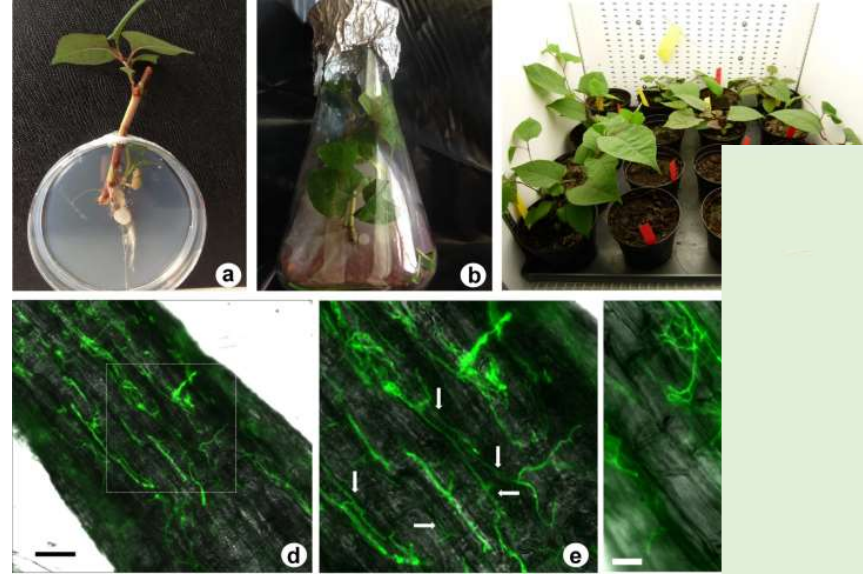




# Colonization ~ Environment

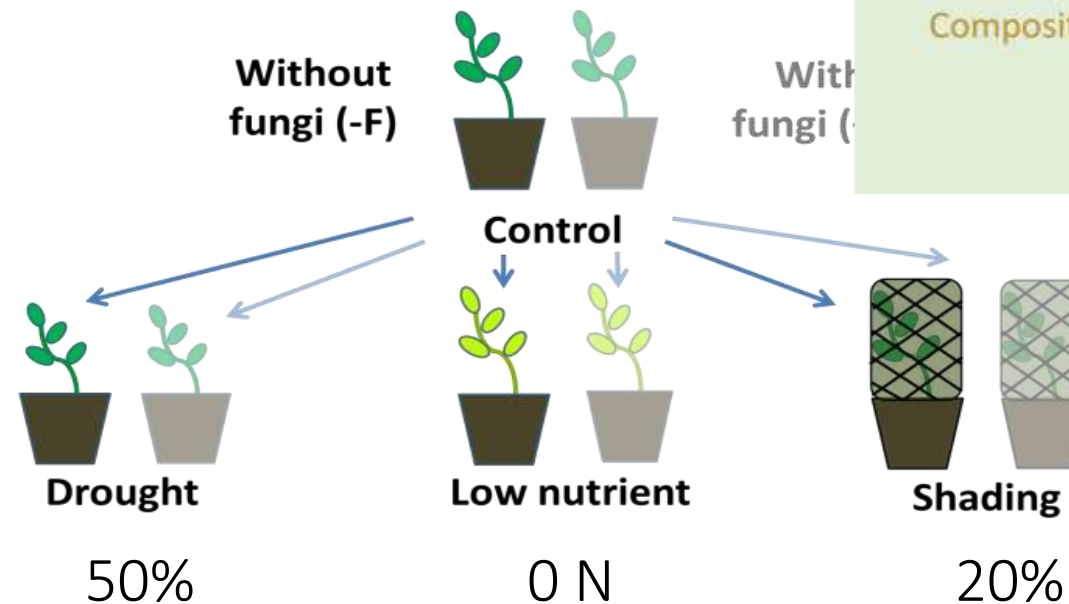
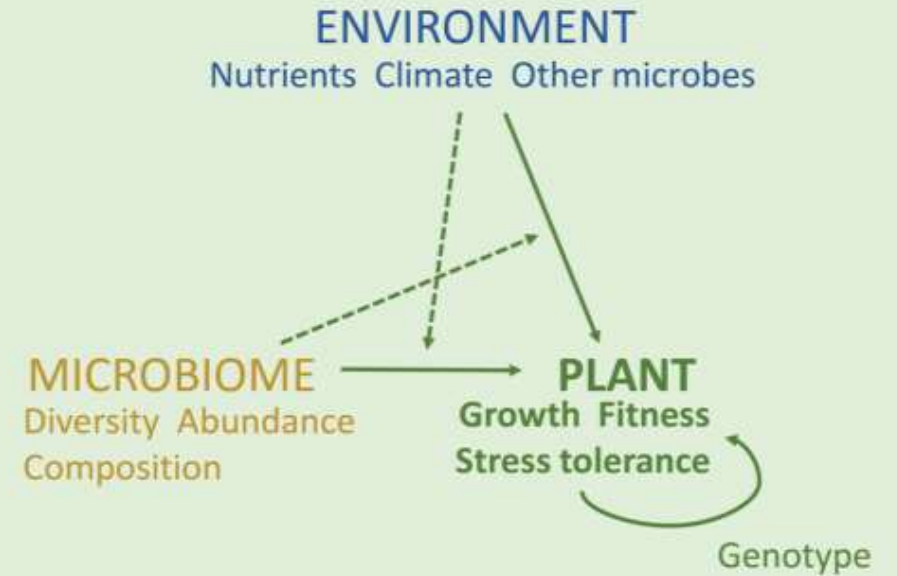






# Colonization ~ Envir

## Plant perspective

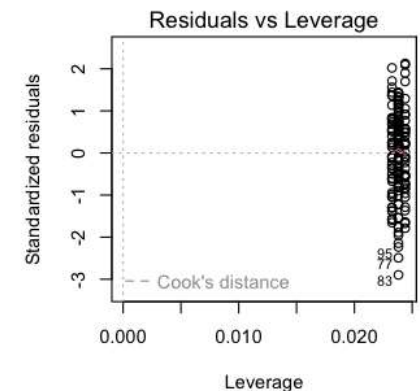
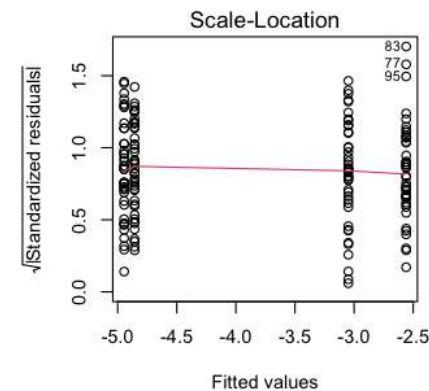
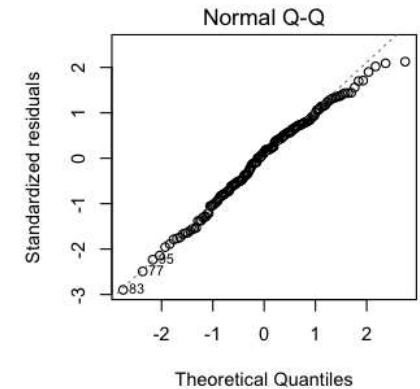
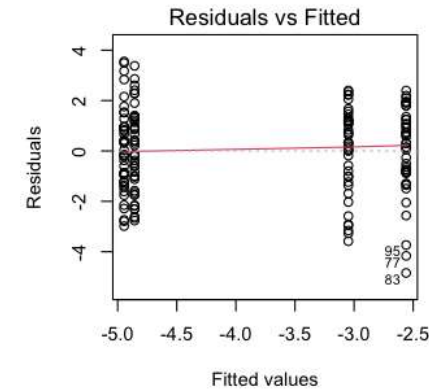


# Test the response of colonization to plant stress

```
model4<- lm (log(log(RawFungusPlant+1)*100) ~ Treatment, data = dt)
summary(model4)
anova(model4)
plot(model4)
```

## Analysis of Variance Table

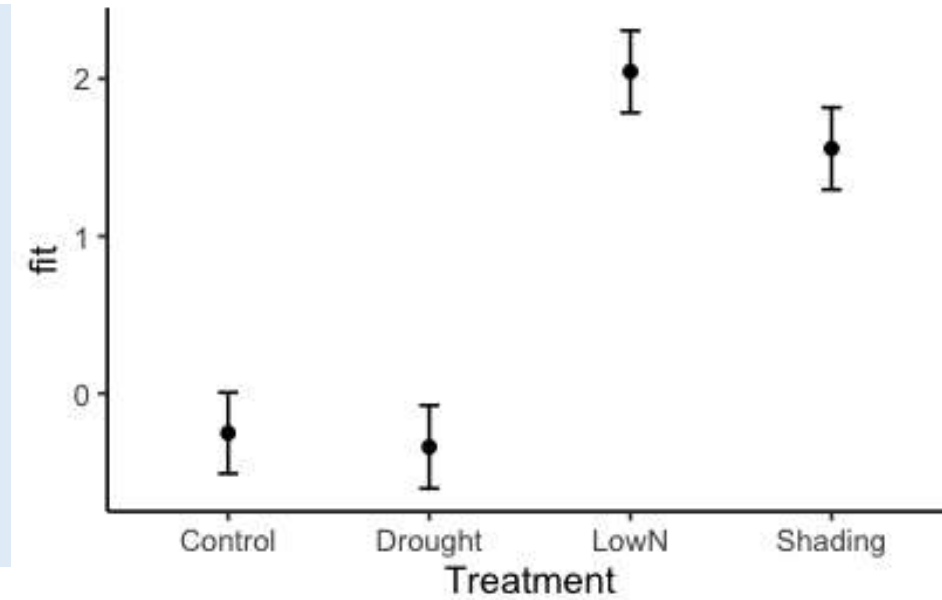
```
Response: log(log(RawFungusPlant + 1) * 100)
          Df Sum Sq Mean Sq F value    Pr(>F)
Treatment   3 189.72    63.24  22.111 4.479e-12 ***
Residuals 164  469.05     2.86
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



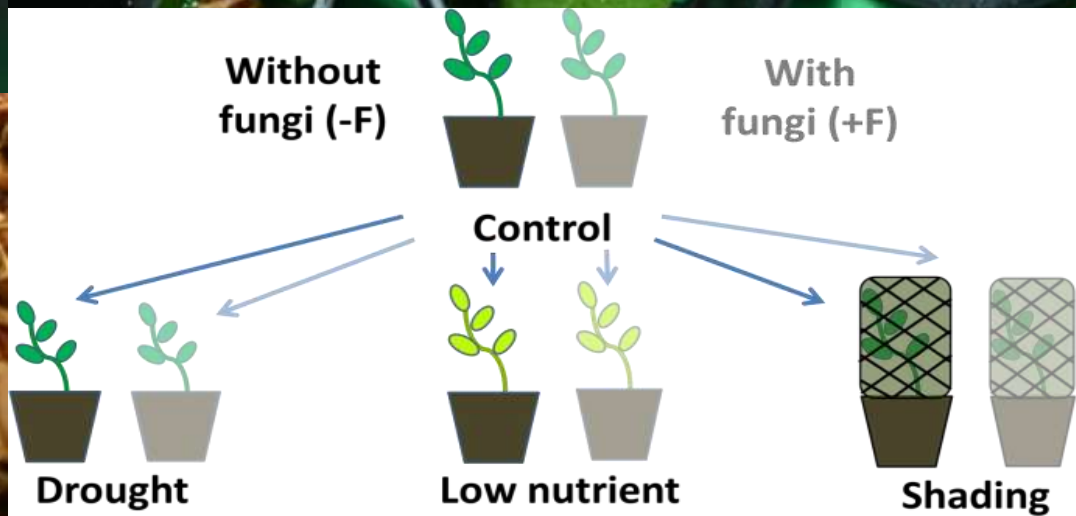
## Plot colonization by treatments

```
efcol <- effect("Treatment",model4)
efcol <- as.data.frame(efreg)
efcol

g4<- ggplot(data=efcol, aes(x=Treatment, y=fit))+
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1))+
  geom_line()+
  geom_point()+
  theme_classic()
g4
```



# Further interactions



# Test palatability by inoculation

```
model5<- lm (log(Perc_eat+1) ~ Fungus*Treatment, data = dt)
summary(model5)
anova(model5)
plot(model5)
```

Call:

```
lm(formula = log(Perc_eat + 1) ~ Fungus * Treatment, data = dt)
```

Residuals:

Min	1Q	Median	3Q	Max
-2.66963	-0.97623	-0.05173	0.90414	2.78778

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	0.3004	0.5799	0.518	0.60537
Funguswith	1.5269	0.7233	2.111	0.03688 *
TreatmentDrought	0.2436	0.7393	0.329	0.74237
TreatmentLowN	1.7899	0.6399	2.797	0.00602 **
TreatmentShading	2.0824	0.6332	3.289	0.00133 **
Funguswith:TreatmentDrought	-1.2778	0.9346	-1.367	0.17414
Funguswith:TreatmentLowN	-0.8016	0.8202	-0.977	0.33037
Funguswith:TreatmentShading	-1.6155	0.8172	-1.977	0.05041 .

---

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

Residual standard error: 1.297 on 118 degrees of freedom

(159 observations deleted due to missingness)

Multiple R-squared: 0.2597, Adjusted R-squared: 0.2158

F-statistic: 5.913 on 7 and 118 DF, p-value: 6.619e-06



# Test palatability by inoculation

```
model5<- lm (log(Perc_eat+1) ~ Fungus*Treatment, data = dt)
summary(model5)
anova(model5)
plot(model5)
```

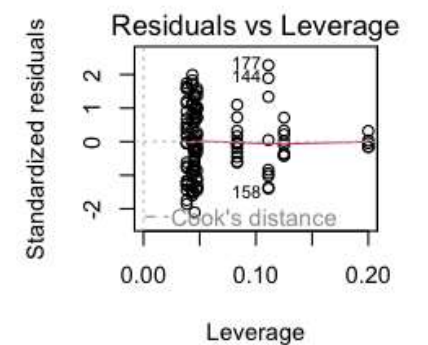
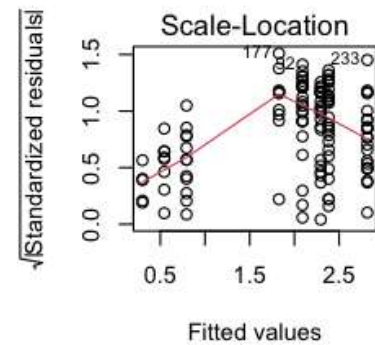
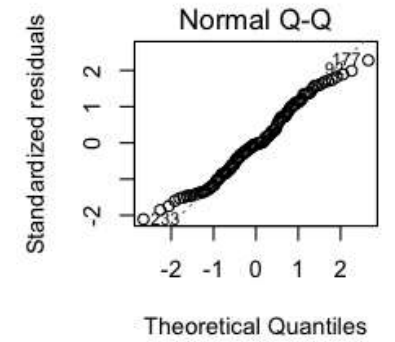
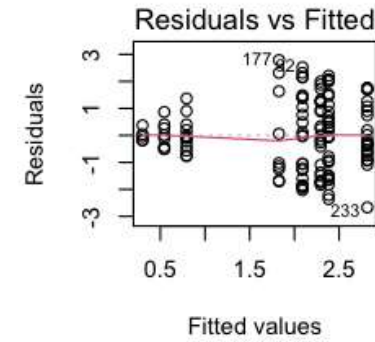
Analysis of Variance Table

Response: log(Perc\_eat + 1)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Fungus	1	2.083	2.0833	1.2389	0.2679
Treatment	3	59.392	19.7972	11.7732	8.399e-07 ***
Fungus:Treatment	3	8.129	2.7096	1.6114	0.1904
Residuals	118	198.423	1.6815		

---

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



## Plot palatability by inoculation

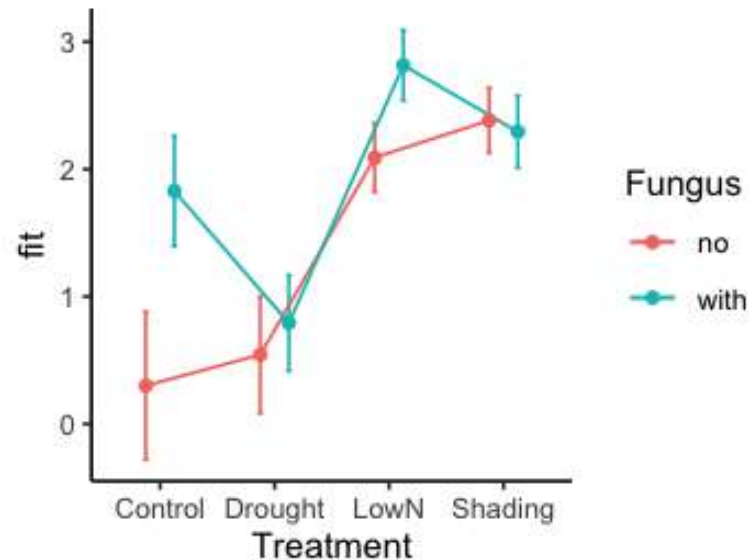
```
efherb <- effect("Fungus:Treatment",model5)
efherb <- as.data.frame(efherb)
efherb
```

```
g5<- ggplot(data=efherb, aes(x=Treatment, y=fit, colour=Fungus, group=Fungus))+
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1), position=position_dodge(width=0.5))+
  geom_line(position=position_dodge(width=0.5))+
  geom_point(position=position_dodge(width=0.5))+
  theme_classic()
g5
```

# Plot palatability by inoculation

```
efherb <- effect("Fungus:Treatment",model5)
efherb <- as.data.frame(efherb)
efherb
```

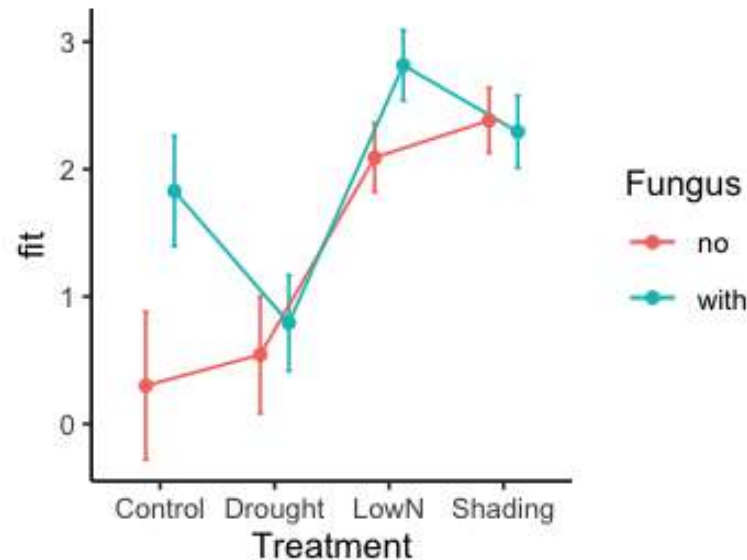
```
g5<- ggplot(data=efherb, aes(x=Treatment, y=fit, colour=Fungus, group=Fungus))+
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1), position=position_dodge(width=0.5))+
  geom_line(position=position_dodge(width=0.5))+
  geom_point(position=position_dodge(width=0.5))+
  theme_classic()
g5
```



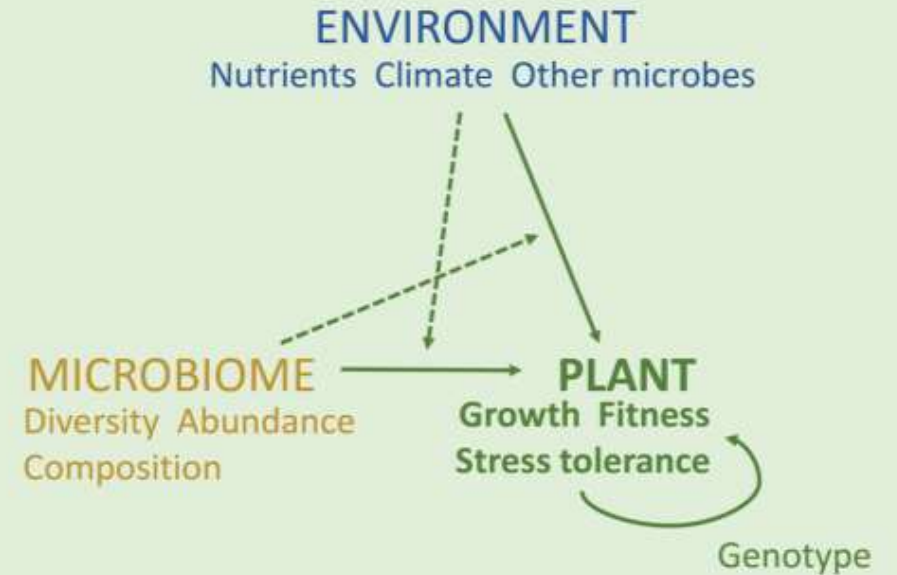
# Plot palatability by inoculation

```
efherb <- effect("Fungus:Treatment",model5)
efherb <- as.data.frame(efherb)
efherb
```

```
g5<- ggplot(data=efherb, aes(x=Treatment, y=fit, colour=Fungus))
  geom_errorbar(aes(ymin=fit-se, ymax=fit+se, width = 0.1),
  geom_line(position=position_dodge(width=0.5))+
  geom_point(position=position_dodge(width=0.5))+
  theme_classic()
g5
```



## Plant perspective



# Test palatability by colonization

```
model6<- lm (log(log(Perc_eat+1)) ~ RawFungusPlant, data = dt)
summary(model6)
anova(model6)
plot(model6)
```

Call:

```
lm(formula = log(log(Perc_eat + 1)) ~ RawFungusPlant, data = dt)
```

Residuals:

Min	1Q	Median	3Q	Max
-3.8771	-0.5118	0.4316	0.8158	1.3659

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	0.1604	0.1575	1.019	0.3117
RawFungusPlant	1.0836	0.5757	1.882	0.0639 .

---

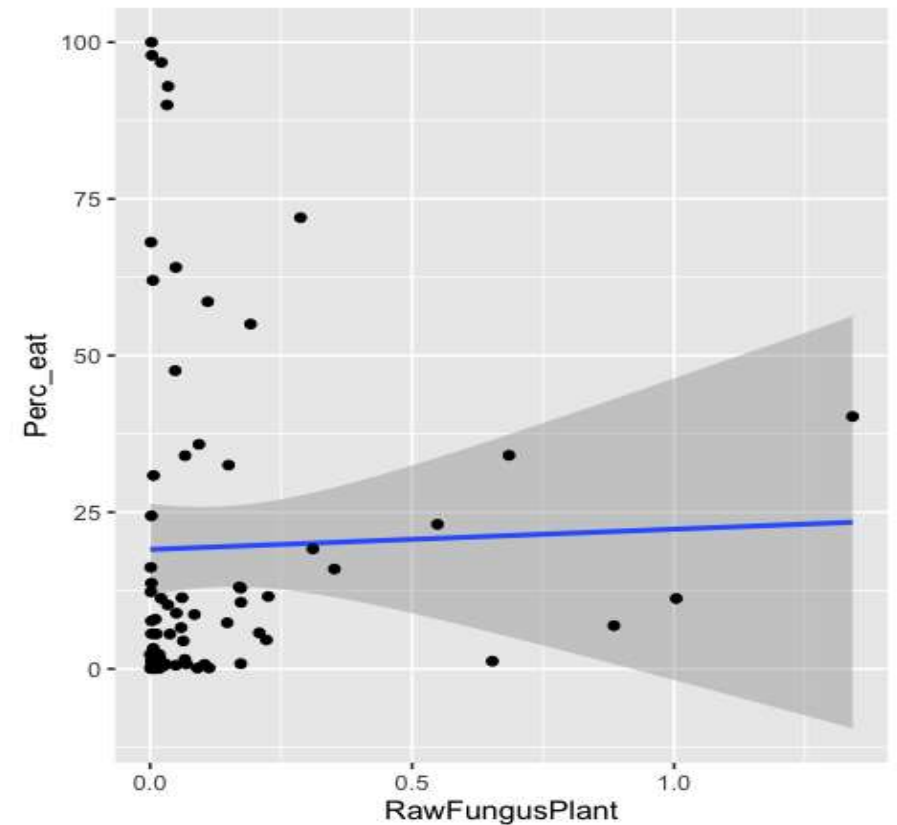
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.195 on 72 degrees of freedom

(211 observations deleted due to missingness)

Multiple R-squared: 0.04689, Adjusted R-squared: 0.03365

F-statistic: 3.542 on 1 and 72 DF, p-value: 0.06387



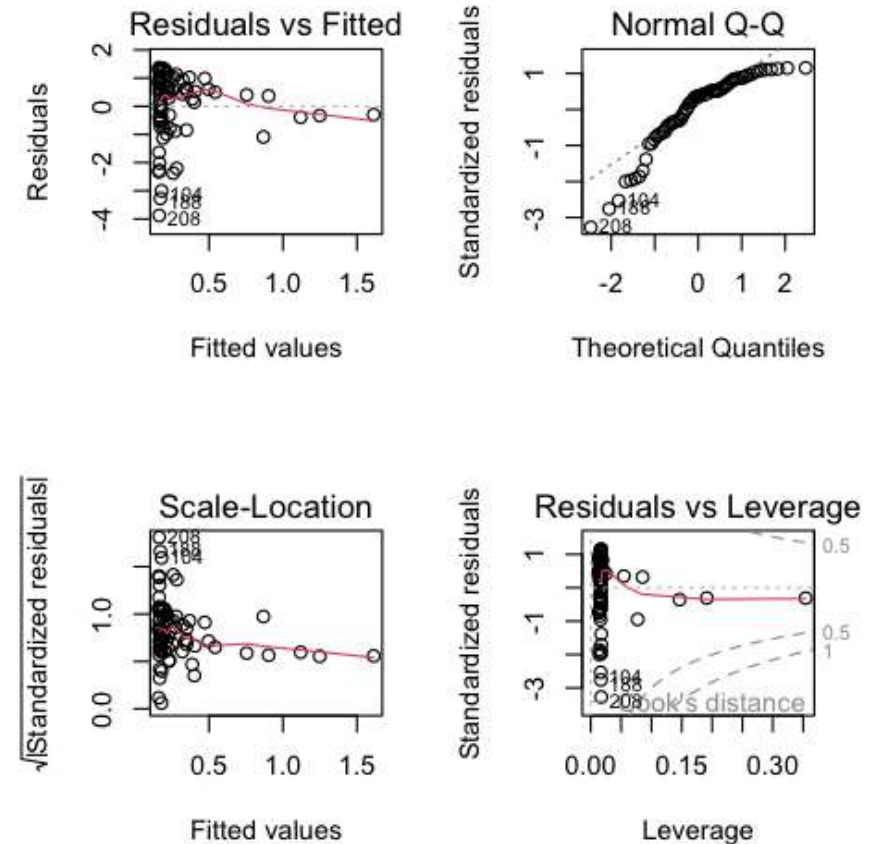


# Test palatability by colonization

```
model6<- lm (log(Perc_eat+1) ~ RawFungusPlant*Treatment, data = dt)
summary(model6)
anova(model6)
plot(model6)
```

Analysis of Variance Table

```
Response: log(log(Perc_eat + 1))
              Df Sum Sq Mean Sq F value Pr(>F)
RawFungusPlant 1   5.061   5.0610   3.5421 0.06387 .
Residuals      72 102.876   1.4288
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

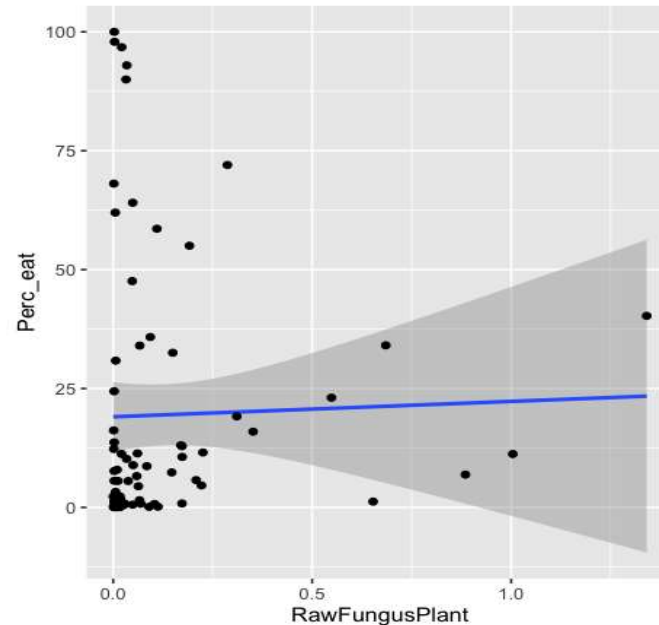


# Test palatability by colonization

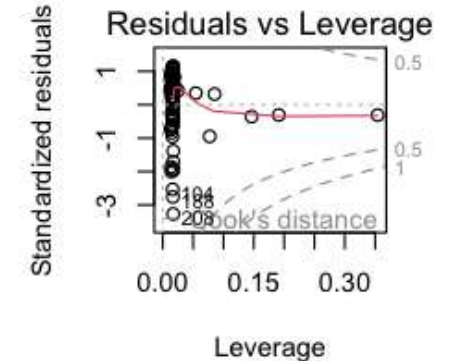
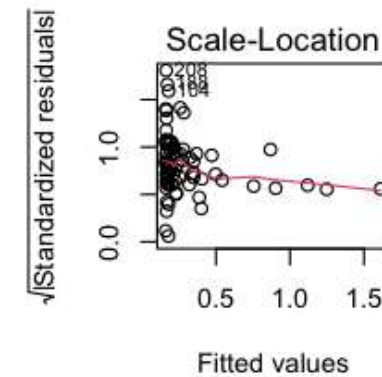
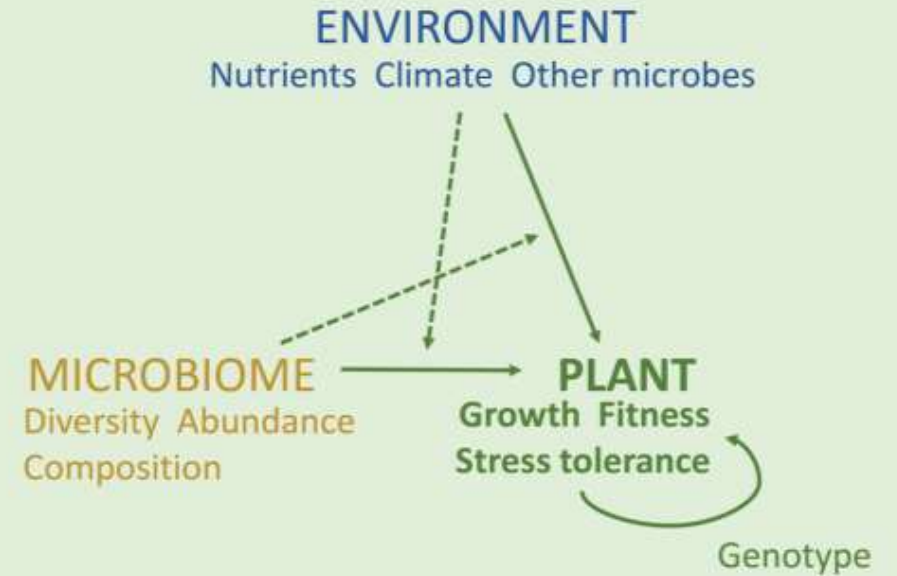
```
model6<- lm (log(Perc_eat+1) ~ RawFungusPlant*Treatment, dat  
summary(model6)  
anova(model6)  
plot(model6)
```

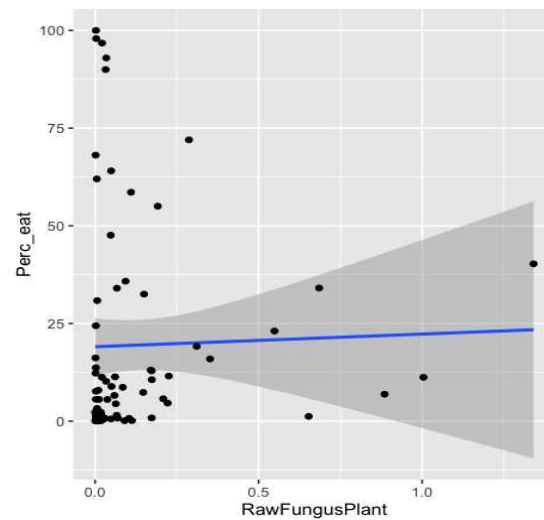
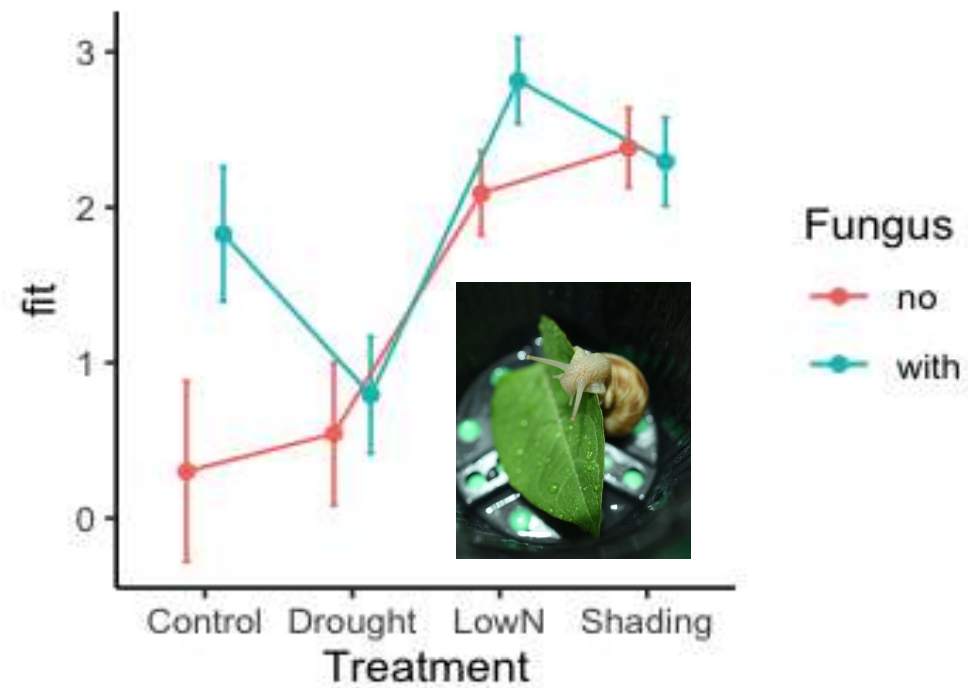
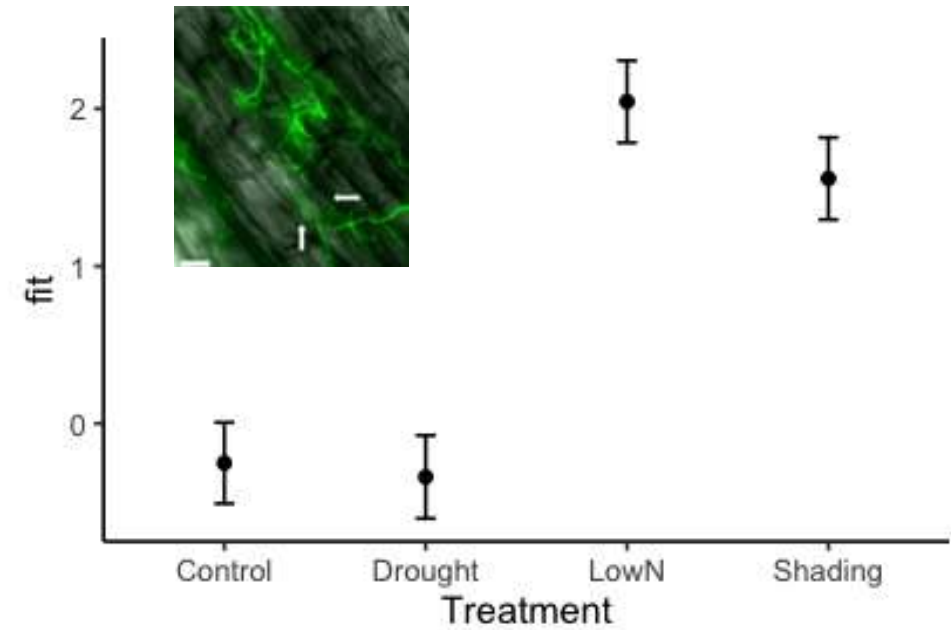
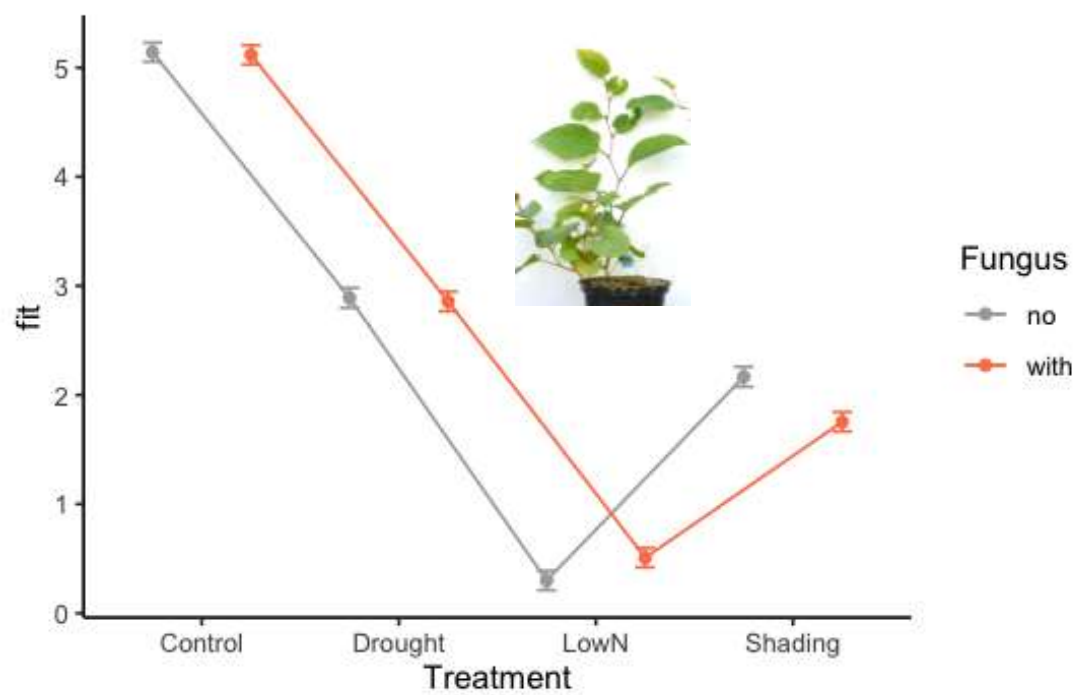
Analysis of Variance Table

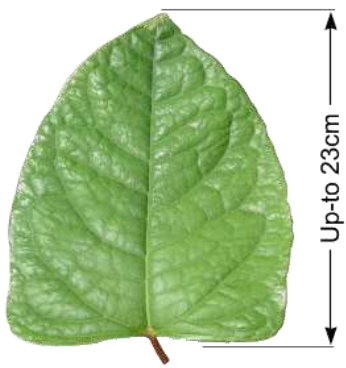
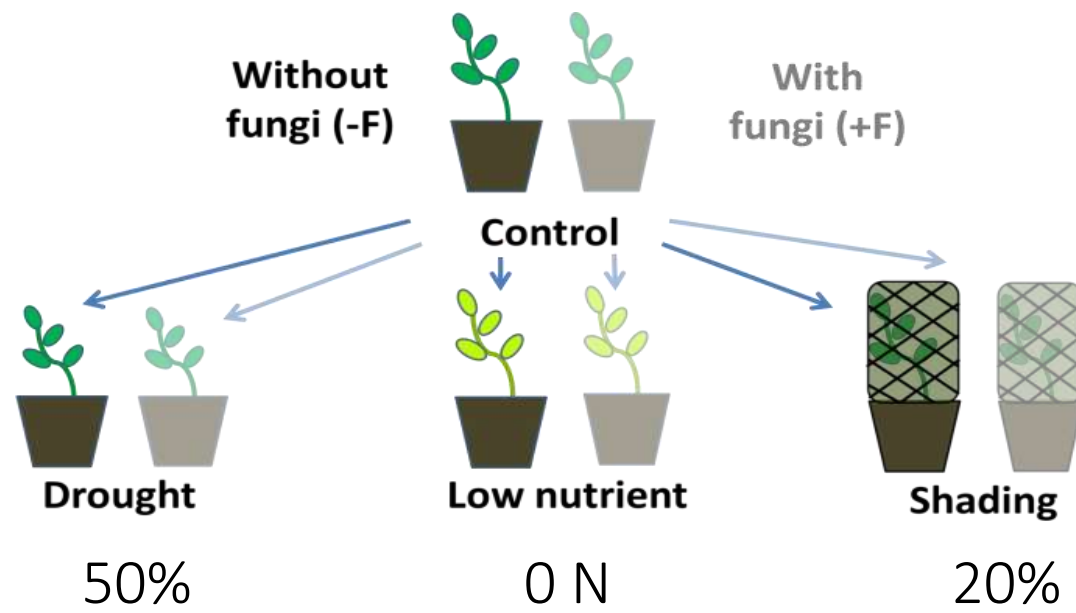
```
Response: log(log(Perc_eat + 1))  
          Df Sum Sq Mean Sq F value Pr(>F)  
RawFungusPlant 1    5.061   5.0610   3.5421 0.06387 .  
Residuals    72  102.876   1.4288  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



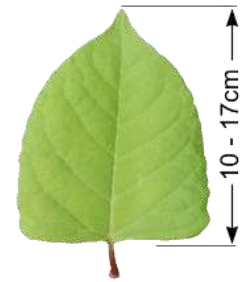
## Plant perspective







Bohemian knotweed  
(*Fallopia × bohemica*)



Japanese knotweed  
(*Fallopia japonica*)

