Introduction to statistics in R

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Summary

In this lecture:

1. The stepwise process to analyze your data
2. Application
3. Practical on your own
4. Conclusion

Summary

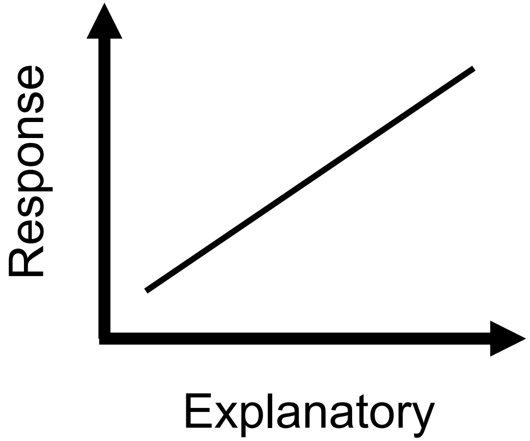
In this lecture:

1. **The stepwise process to analyze your data**

Summary

In this lecture:

1. **The stepwise process to analyze your data**
   Focus on linear models with continuous predictors.



Steps to analyze your data

Check your data structure

1. What are your variables?
    - i. What is your response variable?
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2. How are your data distributed?
3. How do you expect your response variable to be distributed?

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Build your hypothesis

1. What do you want to test?
2. What data distribution will you use?
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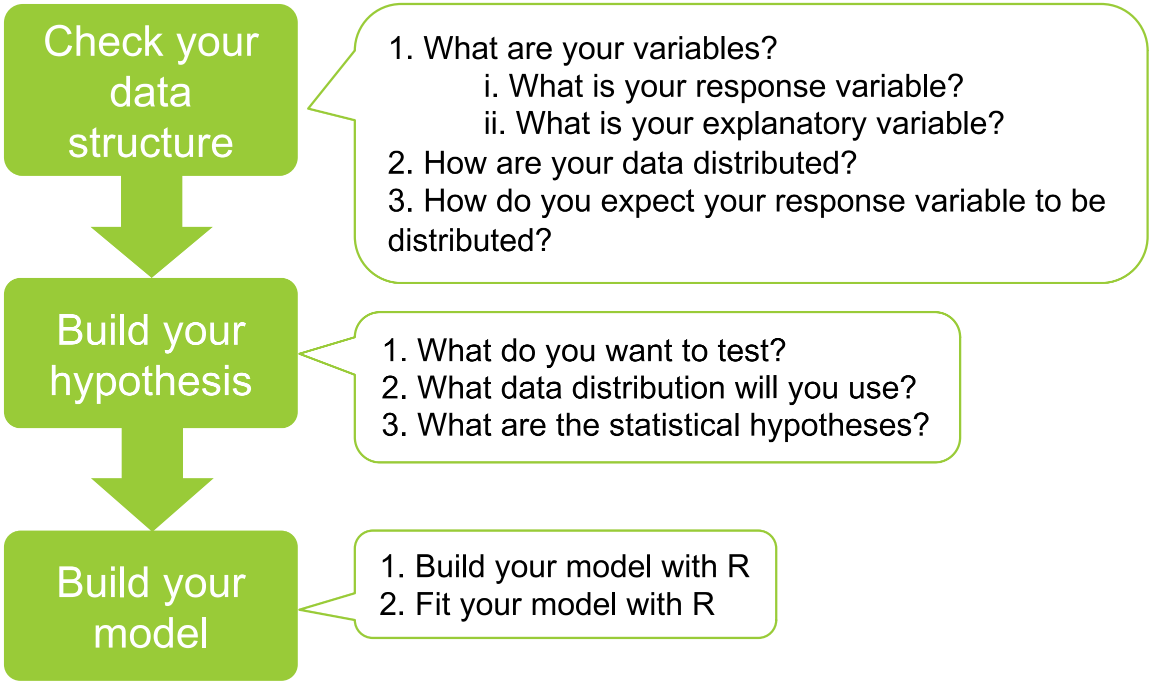

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1. Build your model with R
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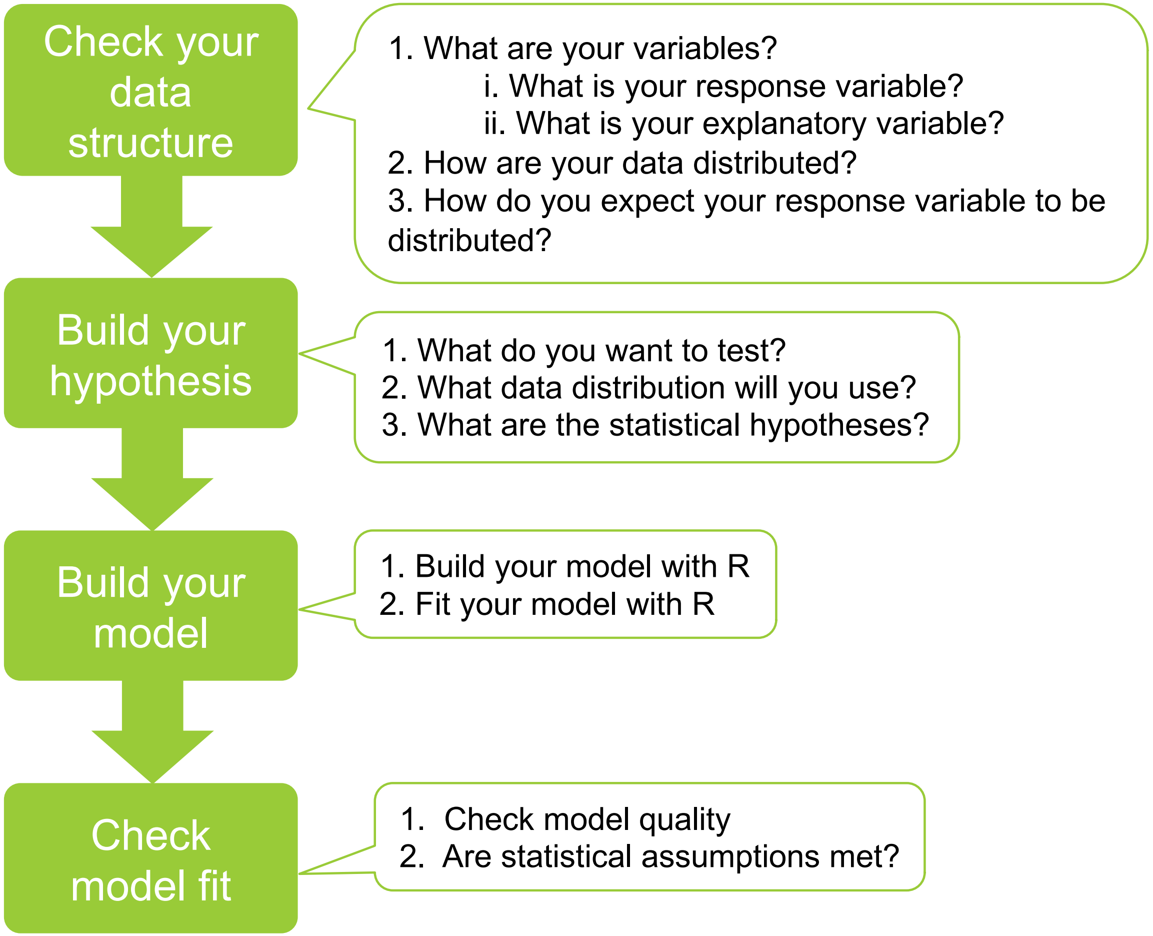

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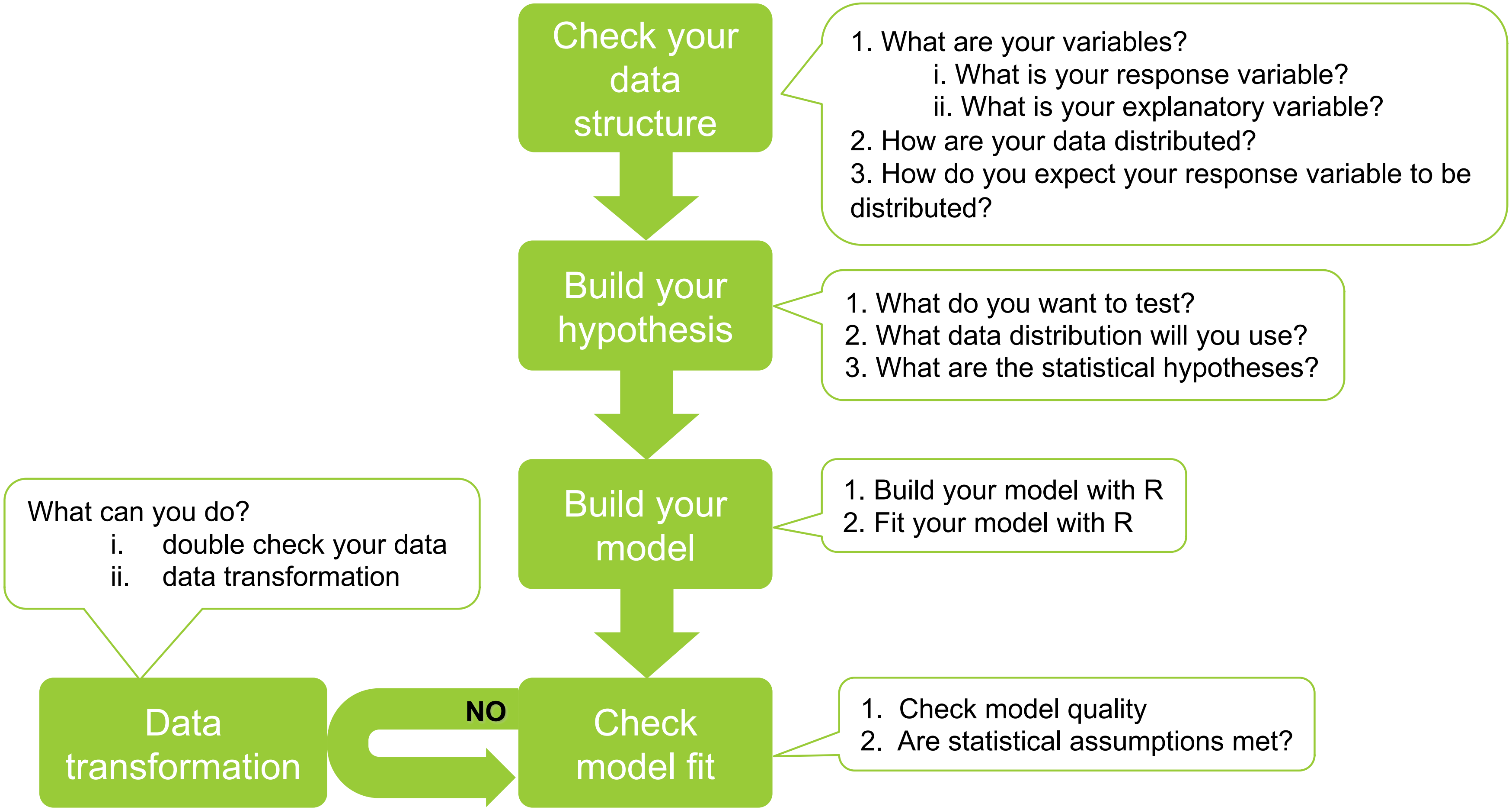
Check model fit

1. Check model quality
2. Are statistical assumptions met?

Steps to analyze your data



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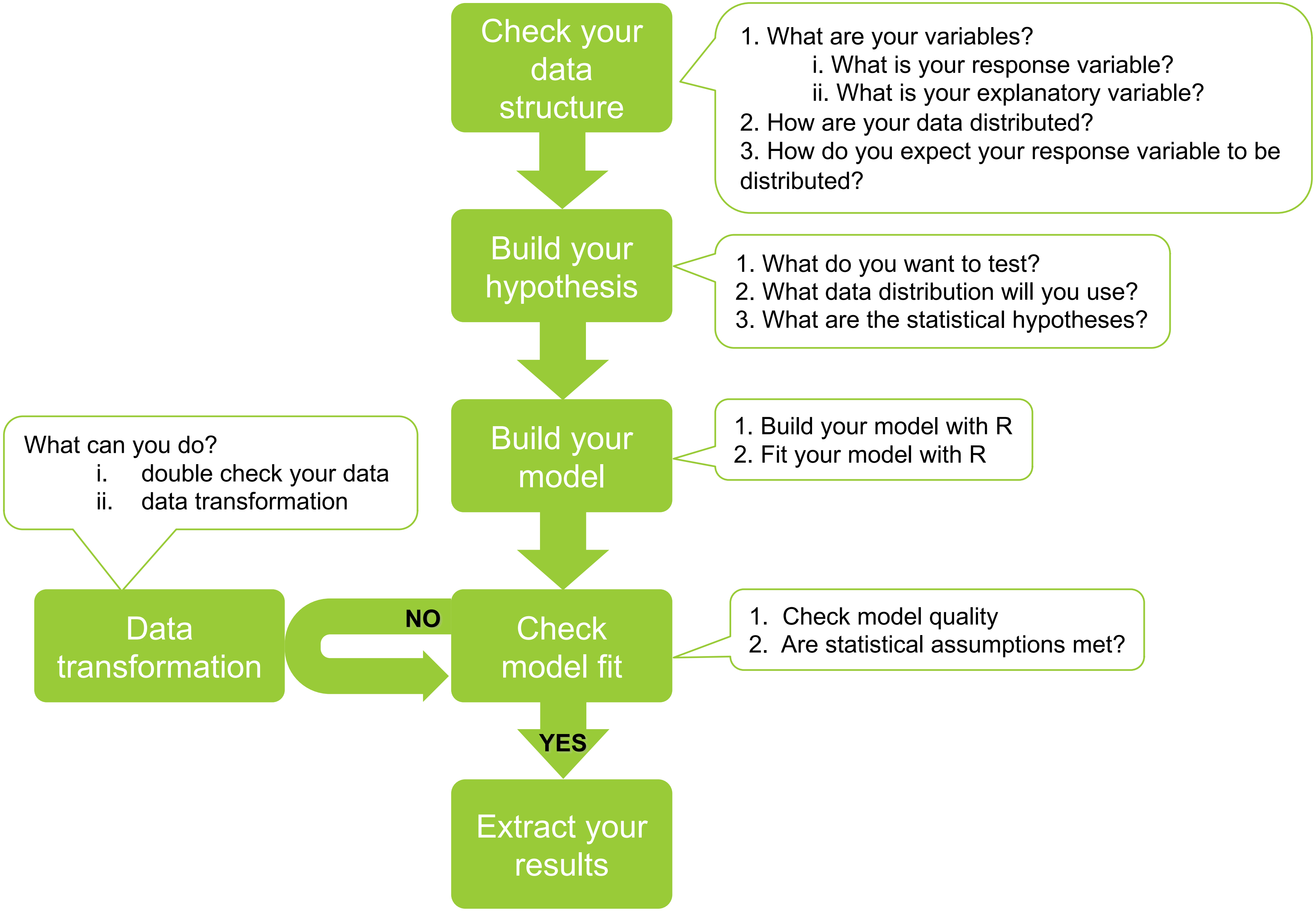
Data transformation

What can you do?

- i. double check your data
- ii. data transformation

Steps to analyze your data



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Data transformation

What can you do?
    i. double check your data
    ii. data transformation

YES

Extract your results

Summary

In this lecture:

1. The stepwise process to analyze your data
2. Application

Who to do that using RStudio

- **You need**
    - RStudio
    - R version 4.0 or higher
    - The following packages:
        - Data handling: **dplyr**
        - Model quality checks: **performance** (needed with **see**)
        - Extract your results: **ggeffects**
        - Plot: **ggplot2** (join the course from Steph for more details)
    - A dataset to analyze

Example: tree diversity effect on litterfall and decomposition

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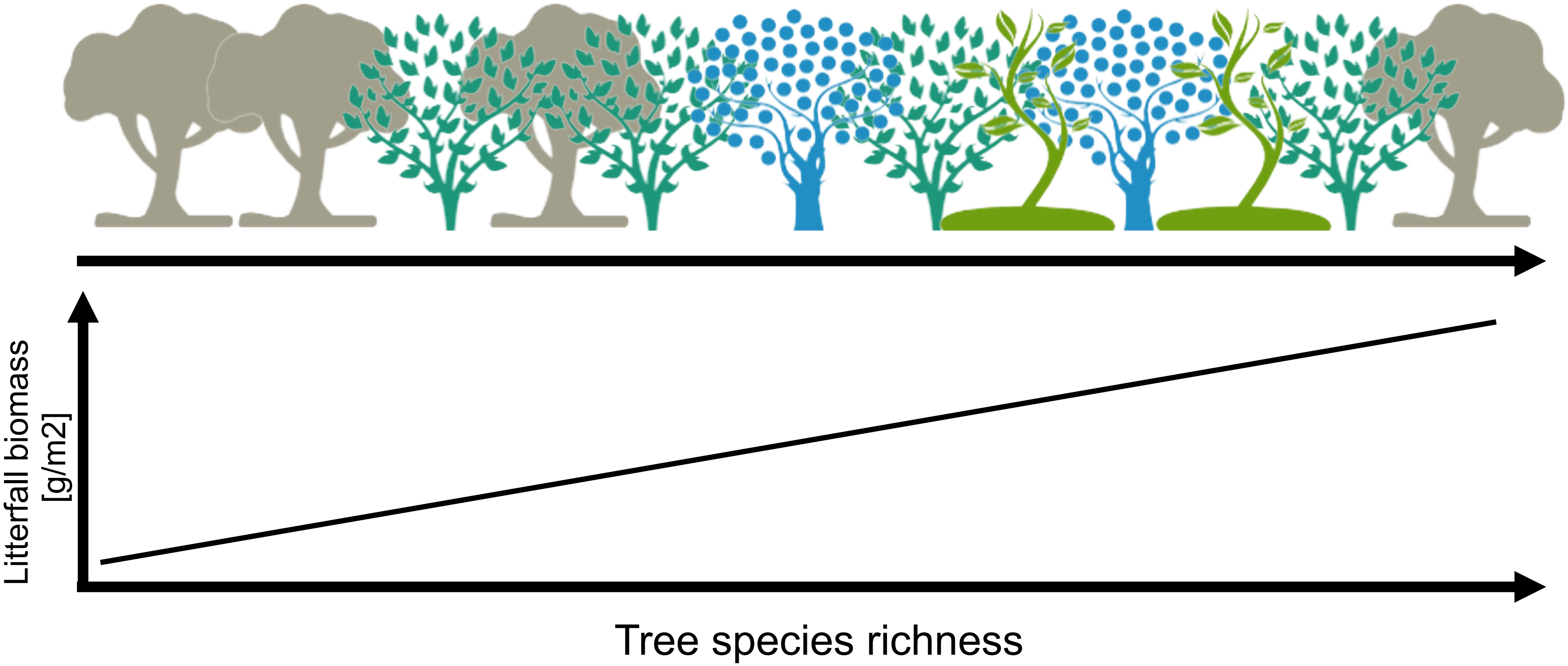
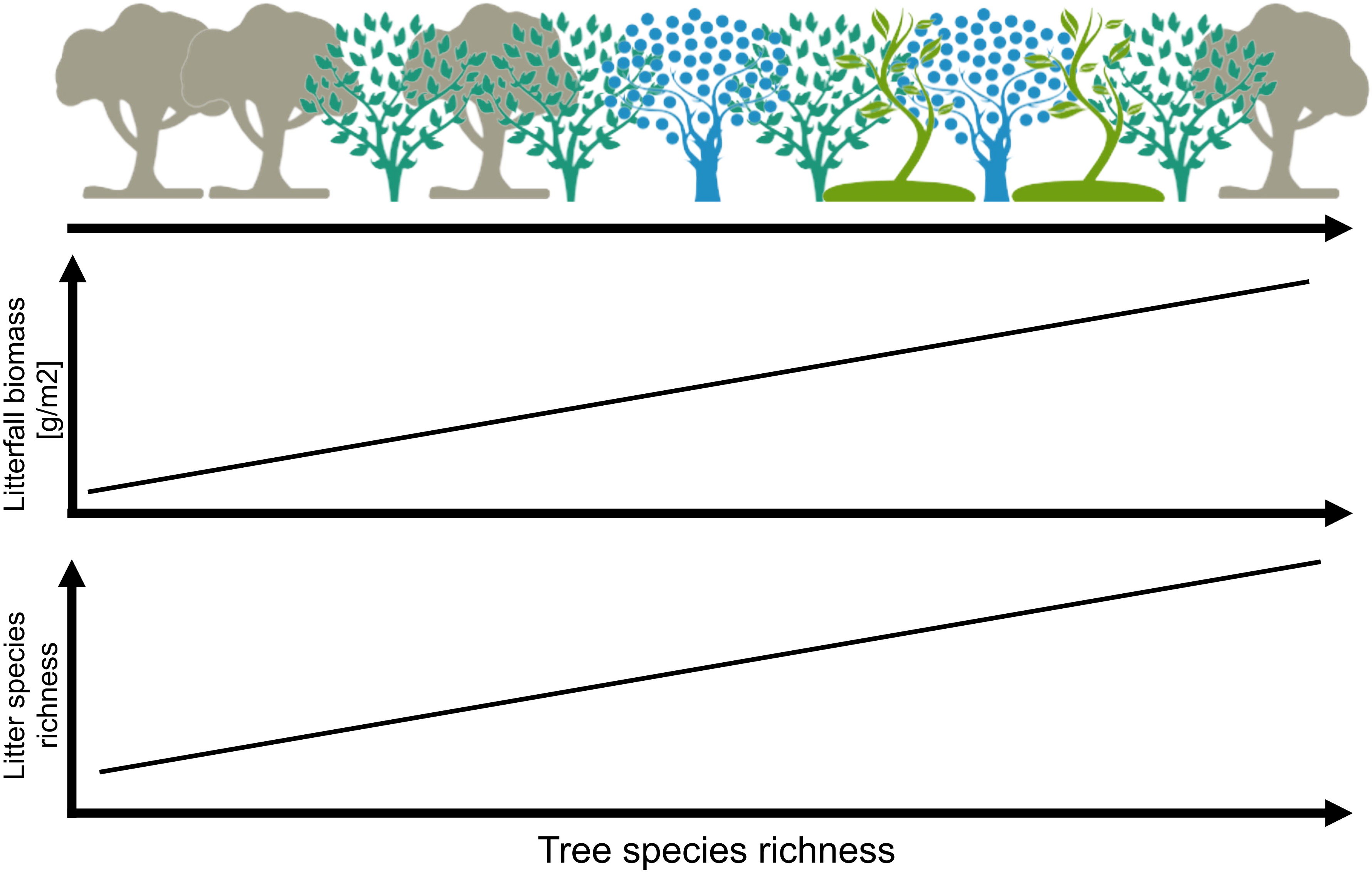


Example: tree diversity effect on litterfall and decomposition



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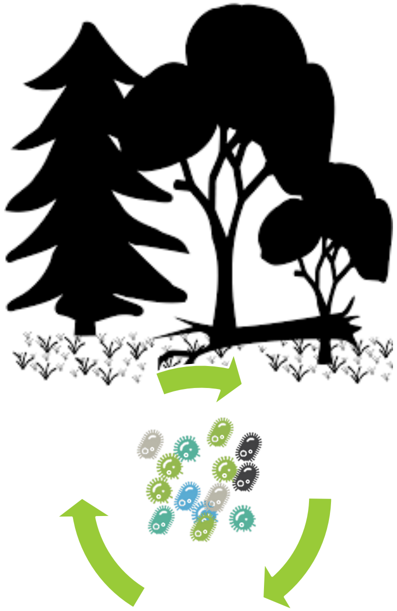

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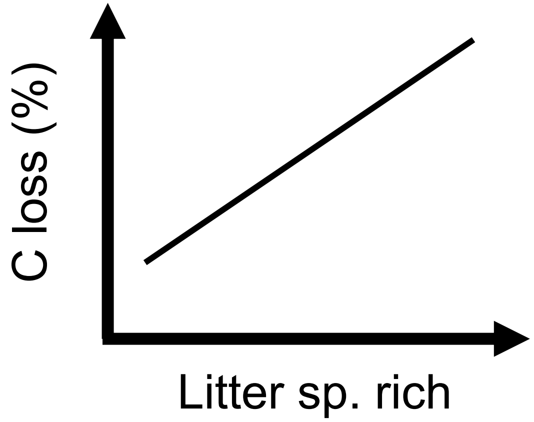

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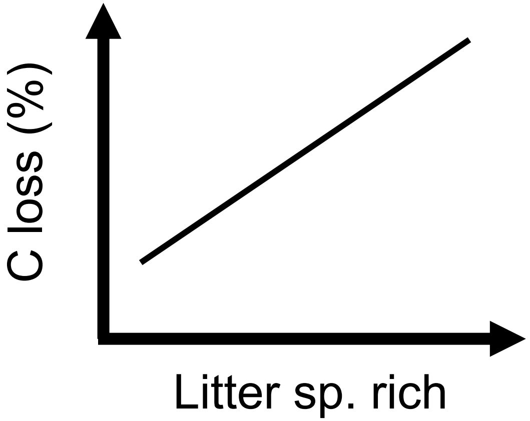

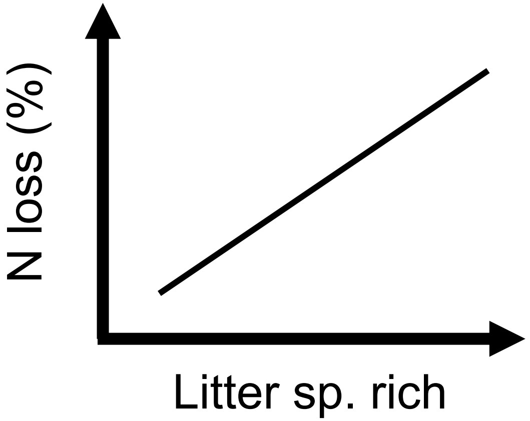

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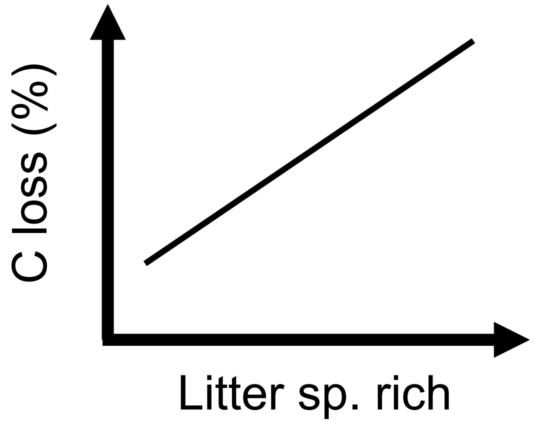

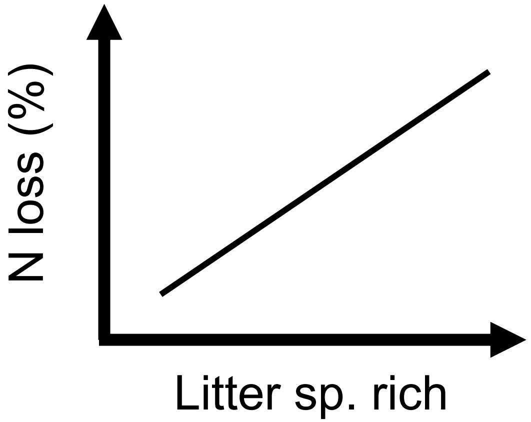

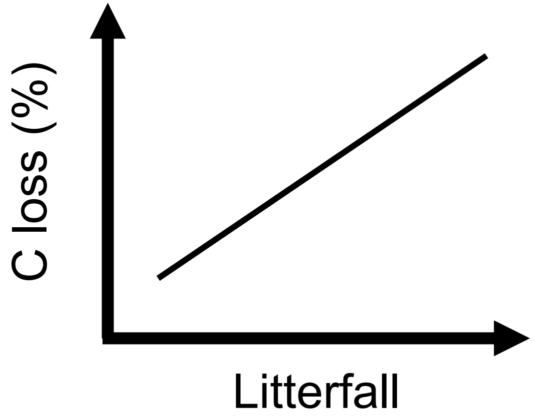

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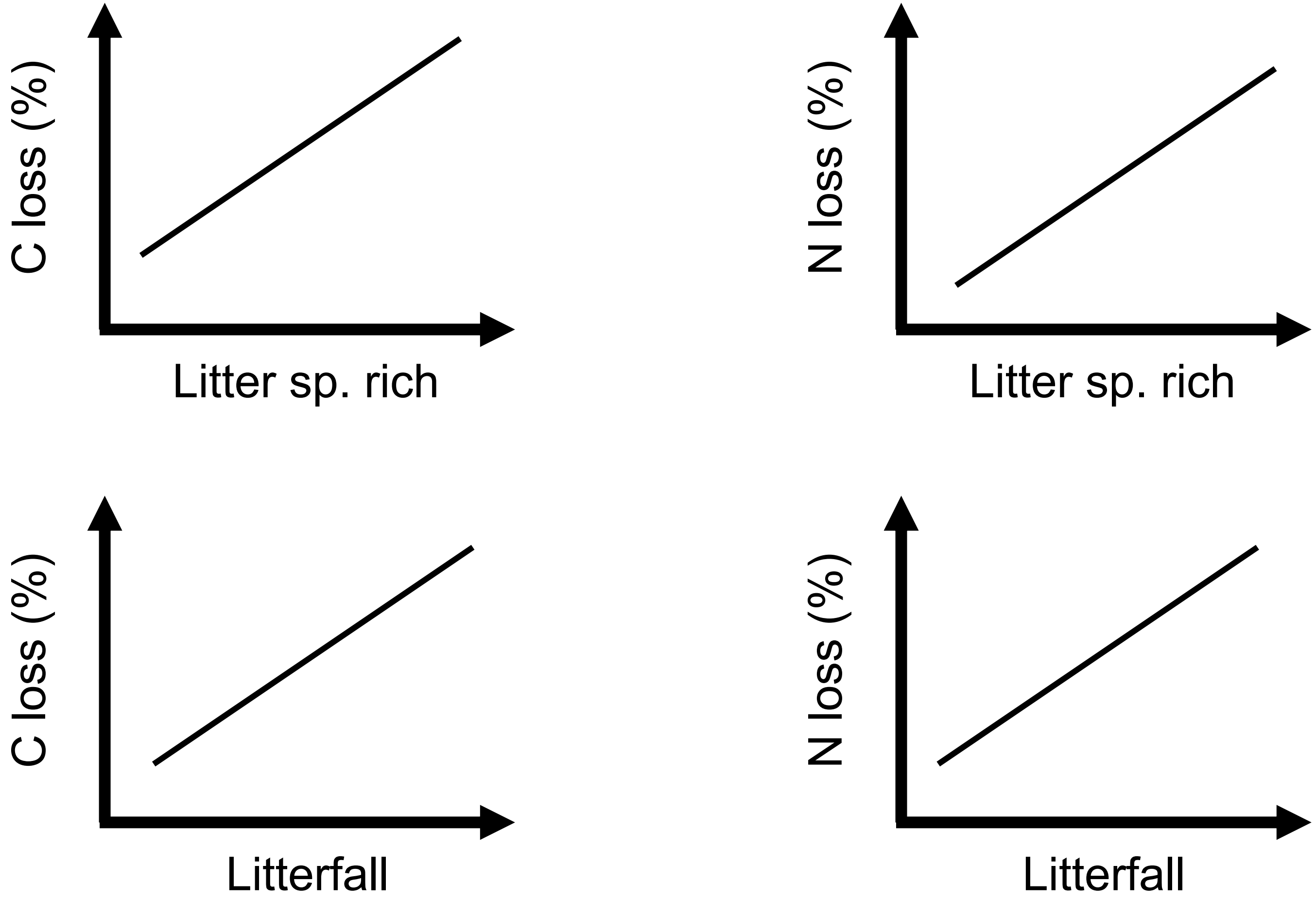
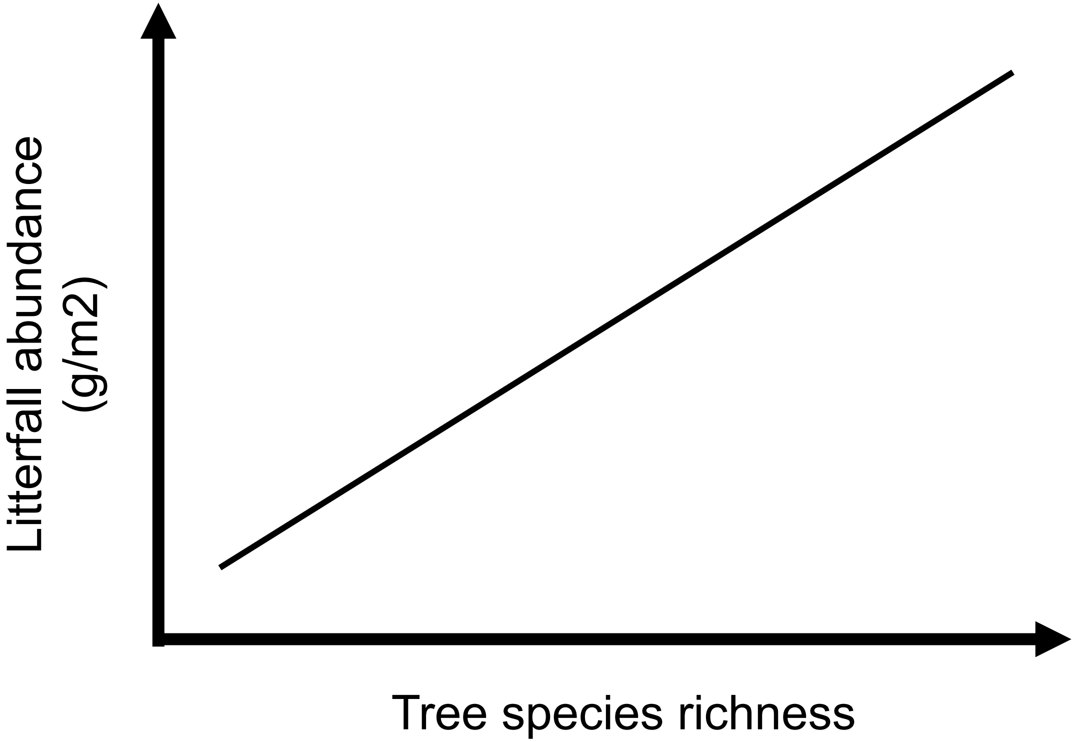


Example: tree diversity effect on litterfall abundance



Check your data structure

Check your data structure

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Check your data structure

1. load your data in a dataset called df:

File type	R function [package]	Example
.csv	read.csv(file = ‘name.csv’)	df = read.csv(file = “my-data.csv”)
.txt	read.delim(file = ‘name.txt’)	df = read.txt(file = “my-data.txt”)
.xlsx	read_xlsx(path = ‘name.xlsx’, sheet = “sheet.name”) [package: readxl]	df = read_xlsx(path = “my-data.xlsx”, sheet = “rawdata”)

Check your data structure

1. load your data in a dataset called df:

	TSP	litterfall	neigh.sp.rich
1	1-E34	73.98	1
2	10-G17	21.82	1
3	100-Q21	71.98	2
4	101-Q21	38.18	2
5	102-P26	66.06	2
6	103-P26	35.30	2
7	105-O6	22.71	3
8	11-O27	123.49	1
9	112-H31	147.98	2
10	113-H31	102.94	2
11	115-T17	292.50	2
12	116-I27	15.19	2
13	117-I27	22.12	3
14	118-I27	37.39	3
15	119-S18	91.97	2

Check your data structure

1. load your data in a dataset called df
2. what are your variables?

TSP

Litterfall

neigh.sp.rich

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1	1-E34	73.98	1
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Check your data structure

1. load your data in a dataset called df
2. what are your variables?

Variable name	Measure	Type	Expected range	Expected distribution
TSP	Sample name			
litterfall	Quantity of litter in gram fall on 1 m2			
neigh.sp.rich	Number of species in the surrounding			

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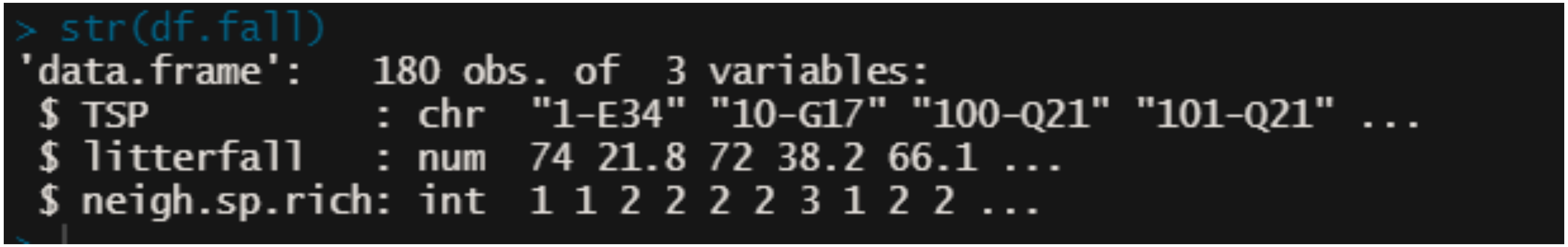
```
str(df)
```



```
> str(df.fall)
'data.frame':	180 obs. of  3 variables:
 $ TSP          : chr  "1-E34" "10-G17" "100-Q21" "101-Q21" ...
 $ litterfall   : num  74 21.8 72 38.2 66.1 ...
 $ neigh.sp.rich: int  1 1 2 2 2 2 3 1 2 2 ...
```

Check your data structure

1. load your data in a dataset called df
2. what are your variables?

Variable name	Measure	Type	Expected range	Expected distribution
TSP	Sample name	Character		
litterfall	Quantity of litter in gram fall on 1 m2	Numeric		
neigh.sp.rich	Number of species in the surrounding	Integer		

Check your data structure

1. load your data in a dataset called df
2. what are your variables?

Variable name	Measure	Type	Expected range	Expected distribution
TSP	Sample name	Character	All sample names	
litterfall	Quantity of litter in gram fall on 1 m2	Numeric	0 – 500 g/m2	
neigh.sp.rich	Number of species in the surrounding	Integer	[1;12]	

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1. load your data in a dataset called df
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Variable name	Measure	Type	Expected range	Expected distribution
TSP	Sample name	Character	All sample names	-
litterfall	Quantity of litter in gram fall on 1 m2	Numeric	0 – 500 g/m2	Normal
neigh.sp.rich	Number of species in the surrounding	Integer	[1;12]	-

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DANGER ZONE

Your data are not Normally distributed, your residuals should be!

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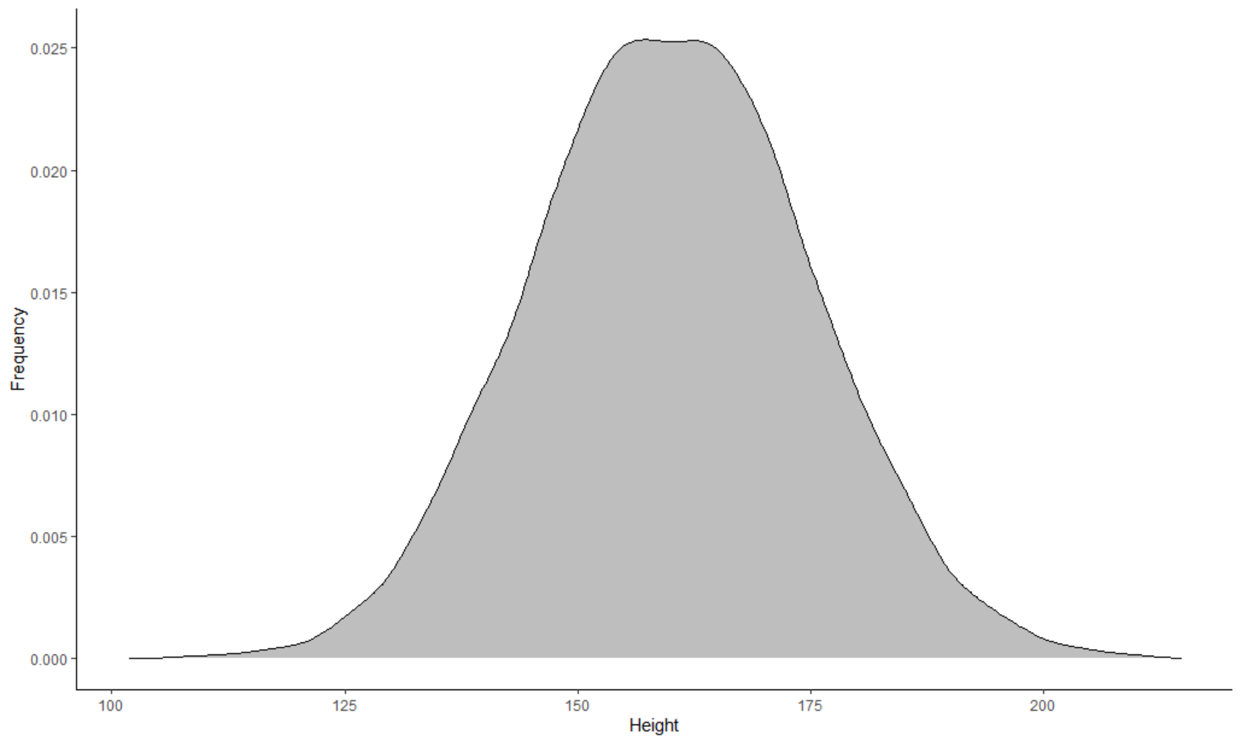
Your data are not Normally distributed, your residuals should be!
Let takes people height as example:



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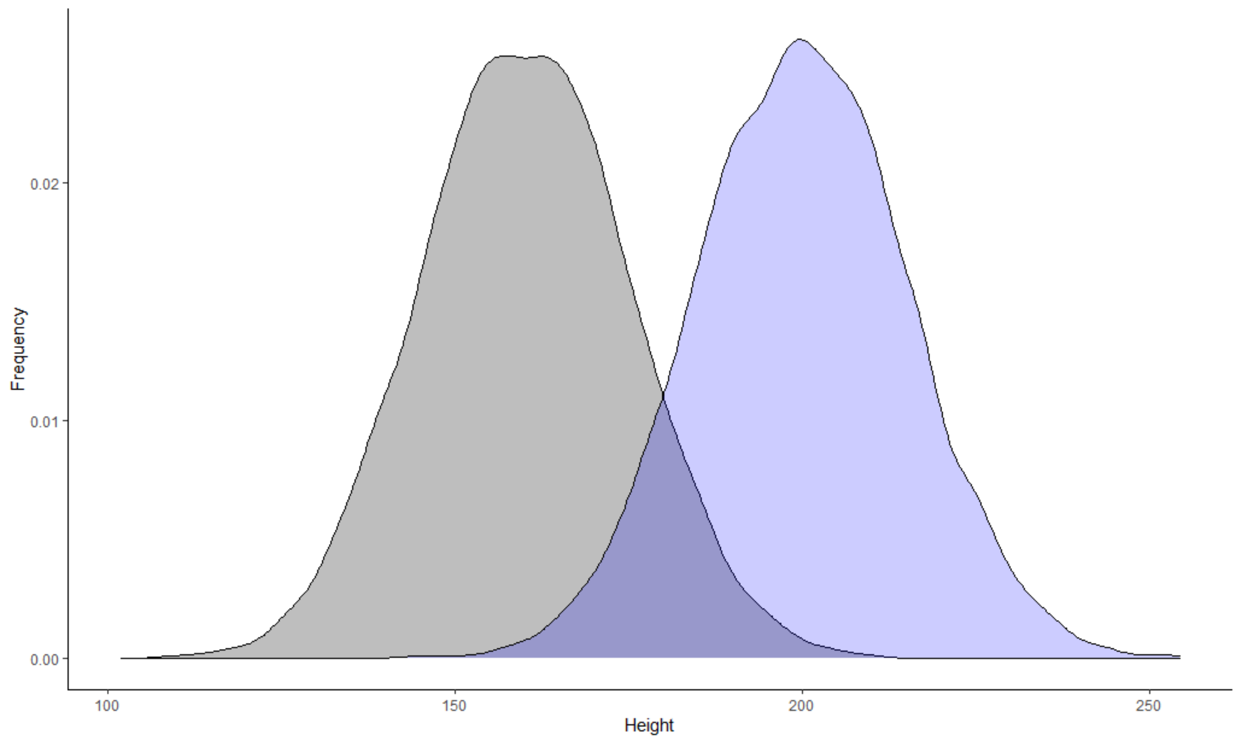
Let takes people height as example, drinking your soup makes you grow up



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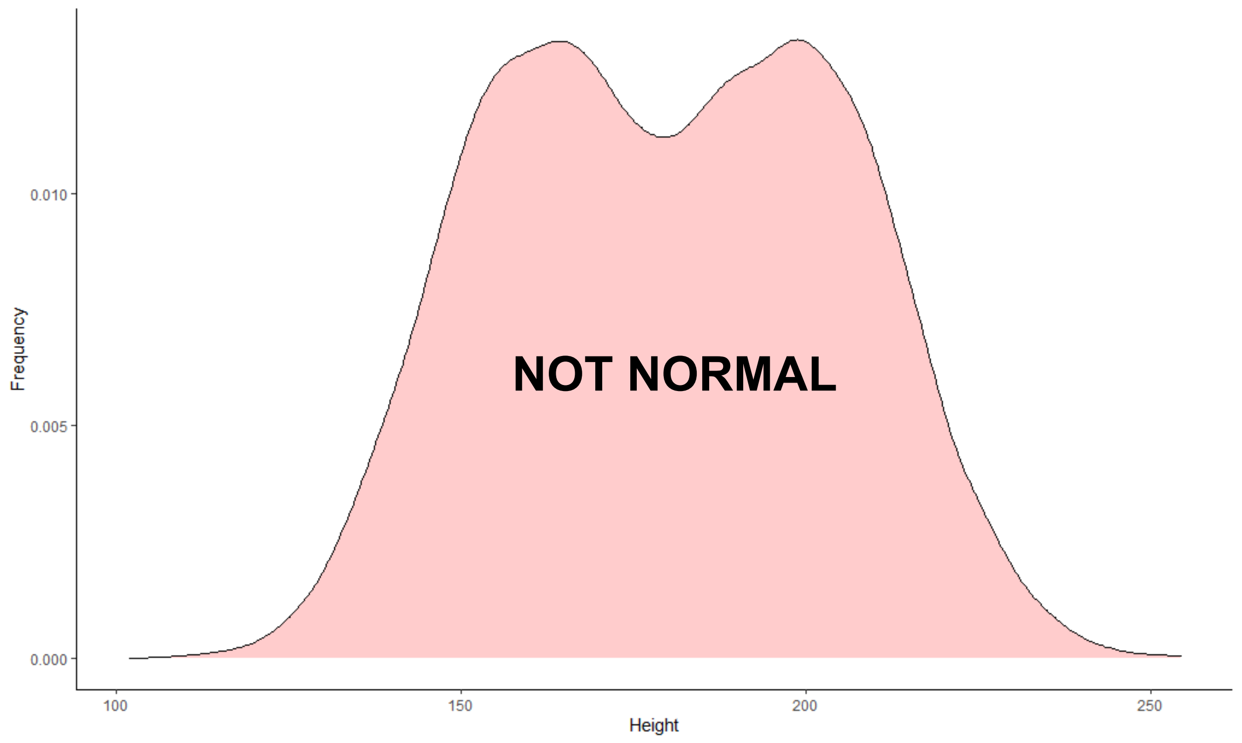


Check your data structure

DANGER ZONE

Height should follow a normal distribution
Therefore, your residuals should follow a normal distribution
Your population **DOES NOT** follow a normal distribution

(Same goes with other distribution types!)

Check your data structure

1. load your data in a data called df
2. what are your variables?
3. how are your variables distributed?
    1. Missing values

WARNING DANGER ZONE

Only keep complete rows:

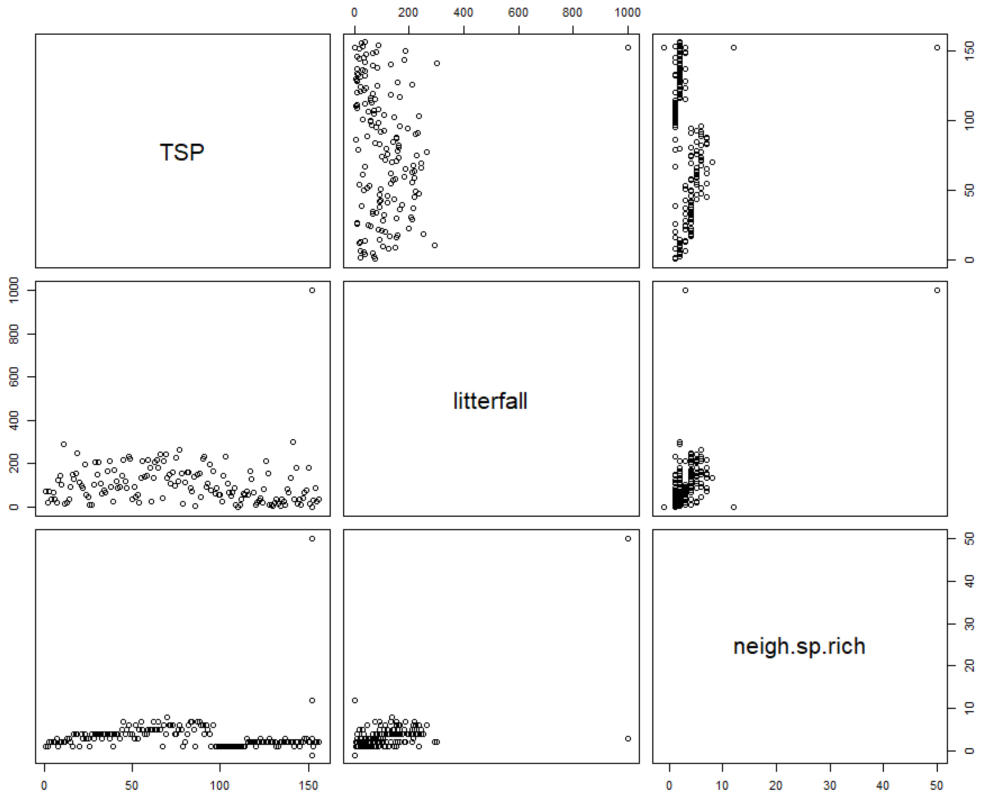
```
df = df[complete.cases(),]
```

Check your data structure

1. load your data in a data called df
2. what are your variables?
3. how are your variables distributed?

Quick and dirty

```
plot(df)
```



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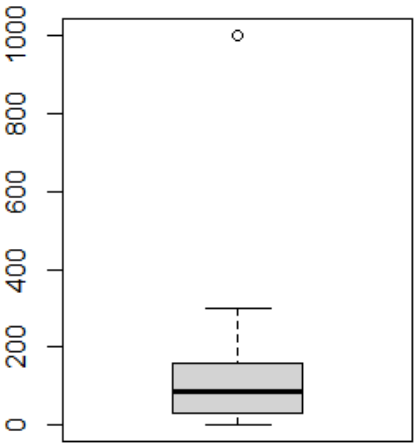
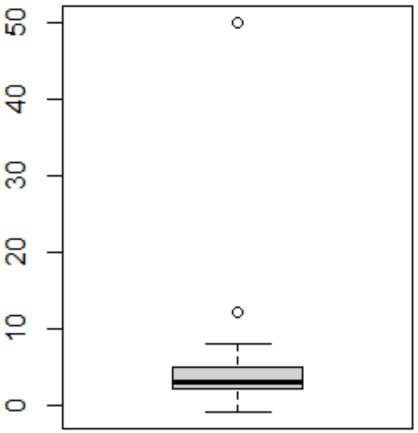
```
boxplot(df$litterfall)
```

Litterfall



neigh.sp.rich



Check your data structure

1. load your data in a data called df
2. what are your variables?
3. how are your variables distributed?
    1. Control data out of range:

```
df[df$litterfall<0 | df$litterfall>500,]
```

Conditions on rows

All columns

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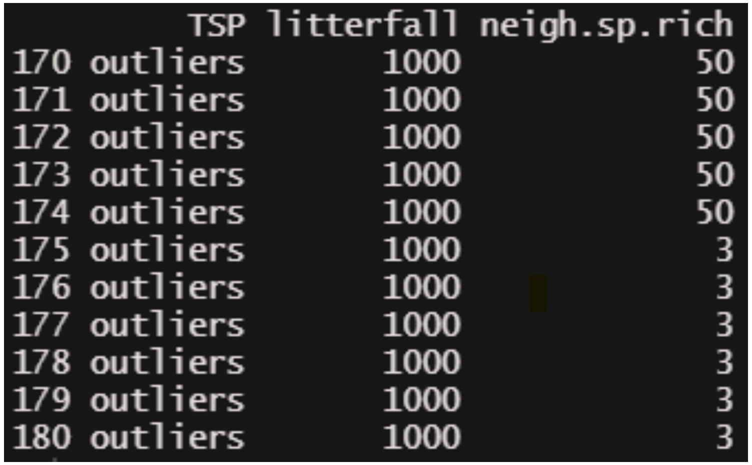

```
             TSP litterfall neigh.sp.rich
170 outliers       1000            50
171 outliers       1000            50
172 outliers       1000            50
173 outliers       1000            50
174 outliers       1000            50
175 outliers       1000             3
176 outliers       1000             3
177 outliers       1000             3
178 outliers       1000             3
179 outliers       1000             3
180 outliers       1000             3
```

Check your data structure

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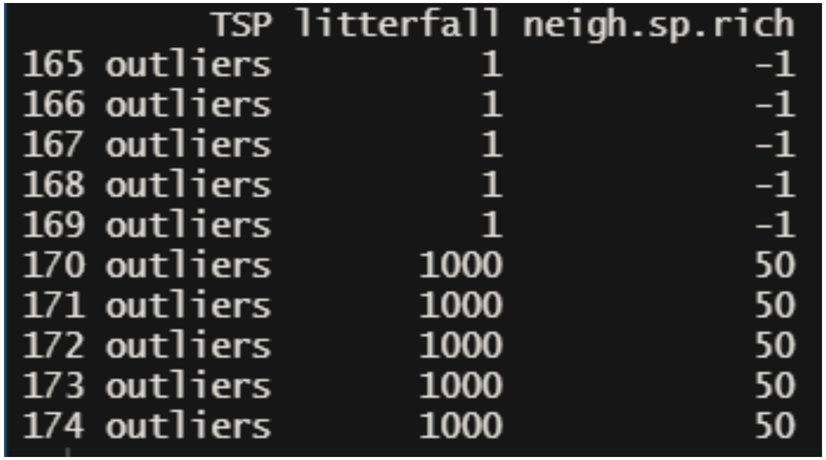
    1. Control data out of range:

```
df[df$neigh.sp.rich<1 | df$neigh.sp.rich>12,]
```



```
         TSP litterfall neigh.sp.rich
165 outliers          1            -1
166 outliers          1            -1
167 outliers          1            -1
168 outliers          1            -1
169 outliers          1            -1
170 outliers       1000            50
171 outliers       1000            50
172 outliers       1000            50
173 outliers       1000            50
174 outliers       1000            50
```

Check your data structure

1. load your data in a data called df
2. what are your variables?
3. how are your variables distributed?
    1. Control data out of range
    2. Correct if typos or remove

Write the opposite conditional:

```
df[df$neigh.sp.rich>=1 & df$neigh.sp.rich<=12,]
```

Leave R to do it for you:

```
df[!(df$neigh.sp.rich<1 | df$neigh.sp.rich>12),]
```

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WARNING DANGER ZONE
You will overwrite your data in r keep a safe copy
df.raw = df

```
df = df[!(df$neigh.sp.rich<1 | df$neigh.sp.rich>12),]
   df = df[!(df$litterfall<0 | df$litterfall>500),]
```

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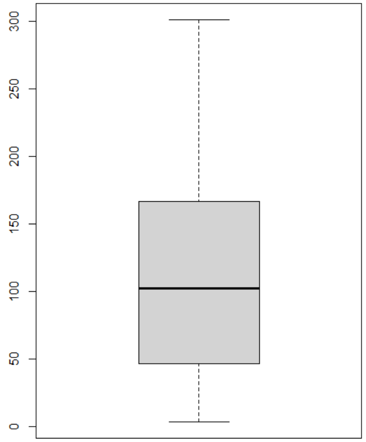
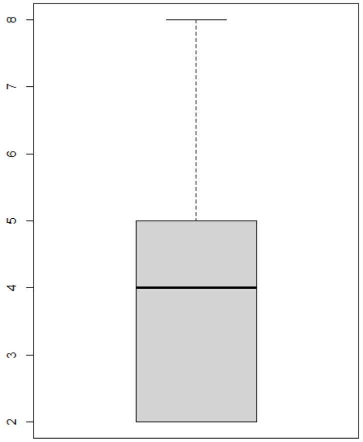
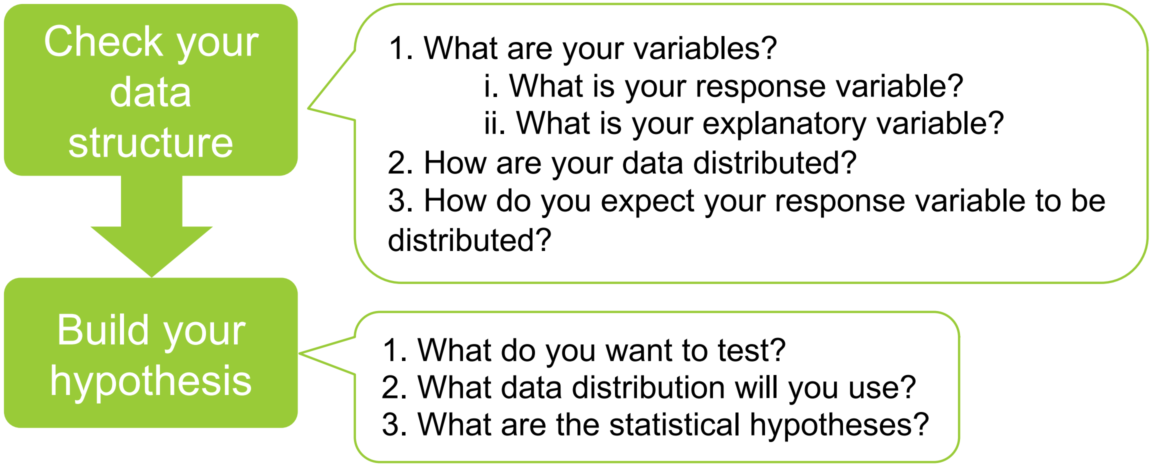
Litterfall



neigh.sp.rich



Build your hypothesis



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2. What data distribution will you use?
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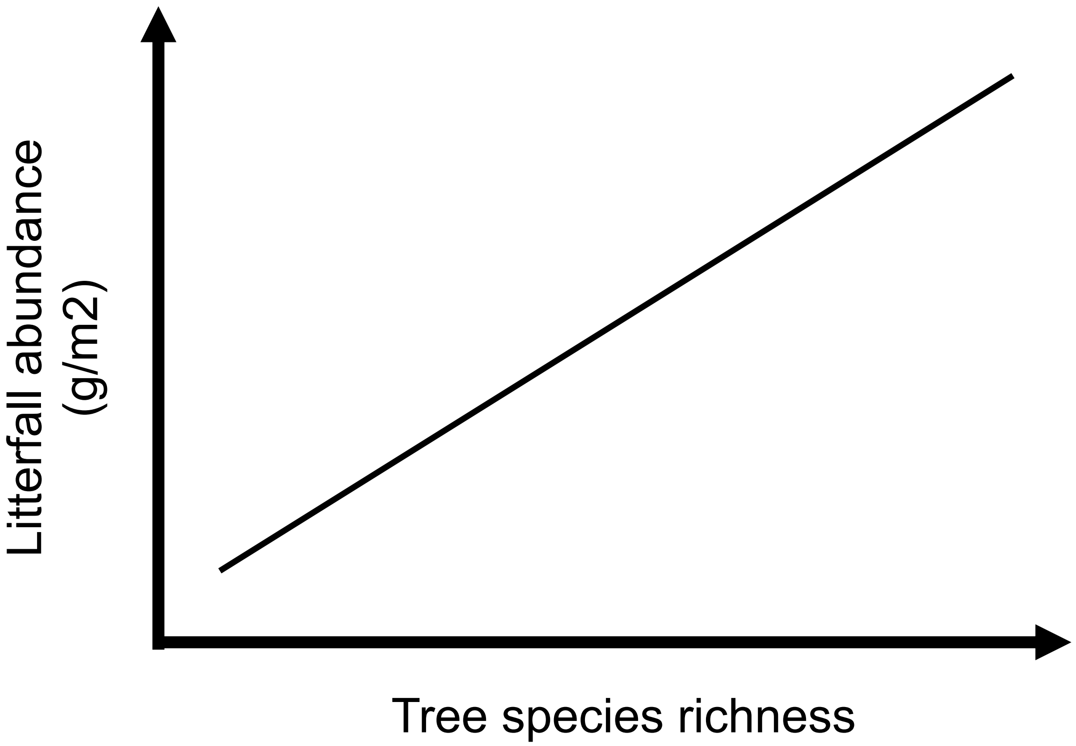
Build your hypothesis

1. what do you want to test?



Build your hypothesis

1. what do you want to test?

Tree species richness increase litterfall

Build your hypothesis

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Tree species richness increase litterfall

“litterfall” increase with “neigh.sp.rich”

Build your hypothesis

1. what do you want to test?

Tree species richness increase litterfall

“litterfall” increase with “neigh.sp.rich”

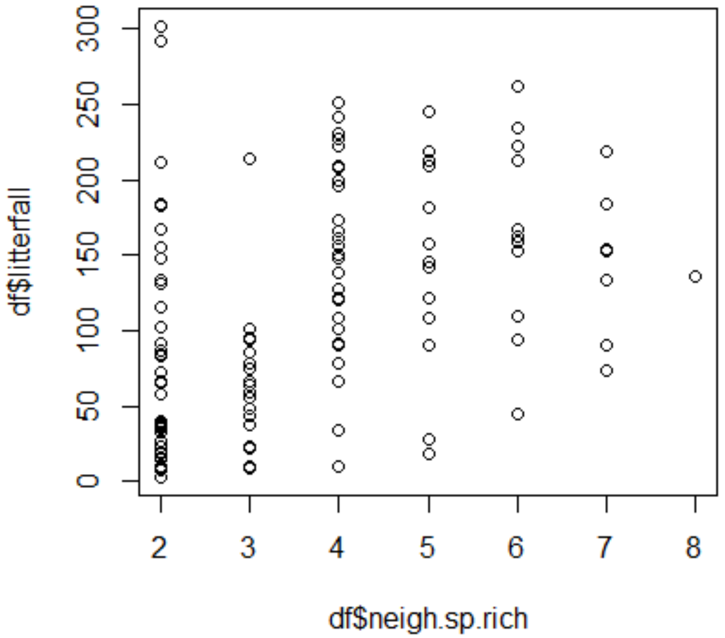
$$litterfall \sim \mu + \alpha \times neigh.sp.rich + \varepsilon$$

H0: $\alpha = 0$, $litterfall \sim \mu + \varepsilon$

H1: $\alpha \neq 0$, $litterfall \sim \mu + \alpha \times neigh.sp.rich + \varepsilon$

Build your hypothesis

1. what do you want to test?
   take a look at your data: `plot(df$litterfall ~ df$neigh.sp.rich)`



Build your hypothesis

1. what do you want to test?
2. what distribution will you use? How do you expect your data to fall around your mean

$$litterfall \sim \mu \; + \; \alpha \times neigh.sp.rich + \; \varepsilon$$

Build your hypothesis

1. what do you want to test?
2. what distribution will you use? How do you expect your data to fall around your mean

$$litterfall \sim \mu + \alpha \times neigh.sp.rich + \varepsilon$$

$$\varepsilon \hookrightarrow N(0, \sigma)$$

Build your hypothesis

1. what do you want to test?
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Build your hypothesis

1. what do you want to test?
2. what distribution will you use?
3. what are you statistical hypotheses?

i. Independence

ii. Random sampling

iii. Normally distributed error: $\varepsilon \hookrightarrow N(0, \sigma)$

iv. Equal variances (homoscedasticity)

v. Linearity

vi. Predictors are fixed

Build your hypothesis

1. what do you want to test?
2. what distribution will you use?
3. what are you statistical hypotheses?

   most control by your experiment structure

- i. Independence
- ii. Random sampling
- iii. Normally distributed error: $\varepsilon \hookrightarrow N(0, \sigma)$
- iv. Equal variances (homoscedasticity)
- v. Linearity
- vi. Predictors are fixed

Build your model in R

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1. What do you want to test?
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Build your model

1. Build your model with R
2. Fit your model with R

Build your model in R

1. build your model

Build your model in R

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Function: `lm()` (`glm()` for other residual distribution)

Build your model in R

1. build your model

Function: `lm()` (`glm()` for other residual distribution)

Formula: `y ~ x`

Build your model in R

1. build your model

Function: `lm()` (`glm()` for other residual distribution)

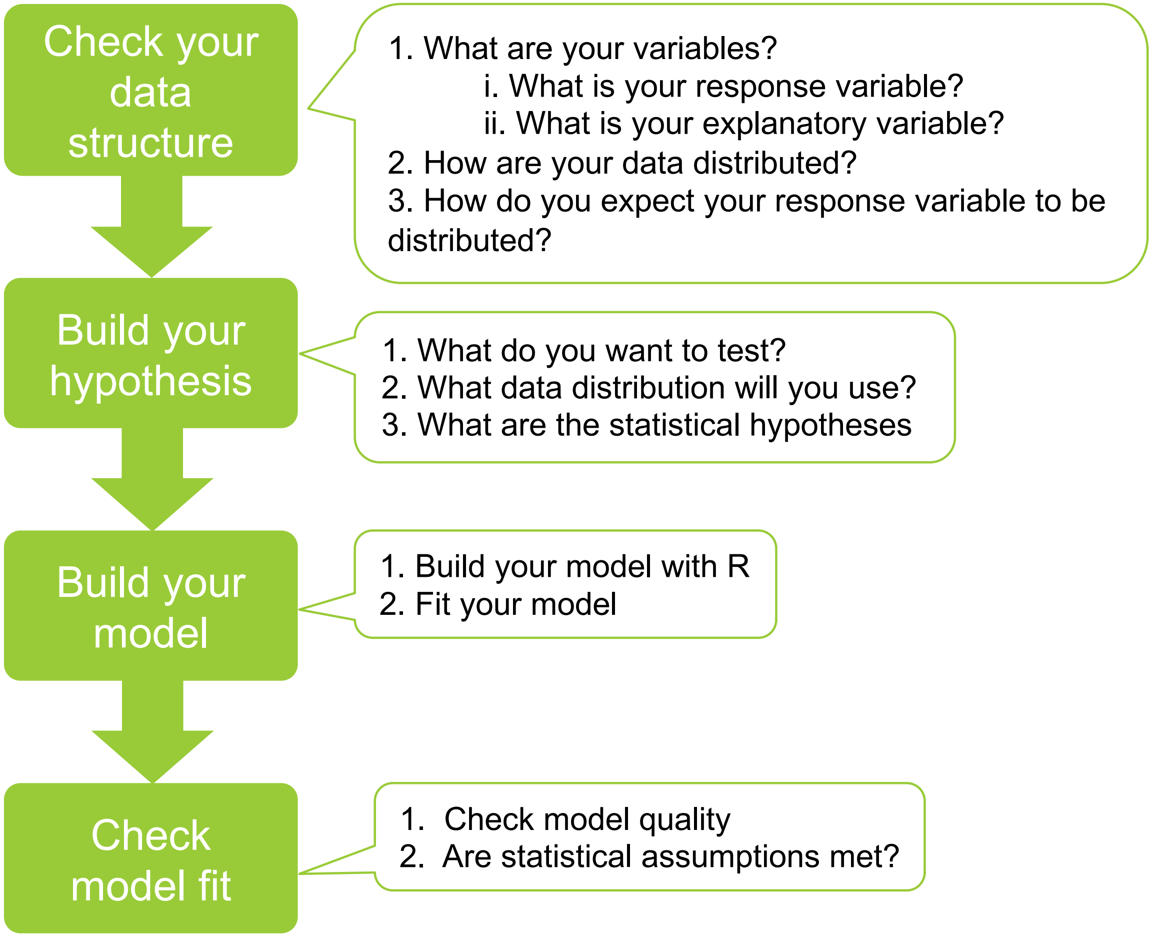
Formula: `y ~ x`

Together: `lm(formula = litterfall ~ neigh.sp.rich, data = df)`

2. fit the model to your data:

```
mod = lm(formula = litterfall ~ neigh.sp.rich, data = df)
```

Check the model fit



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Check the model fit

Check the model quality and the assumptions: the **performance** package

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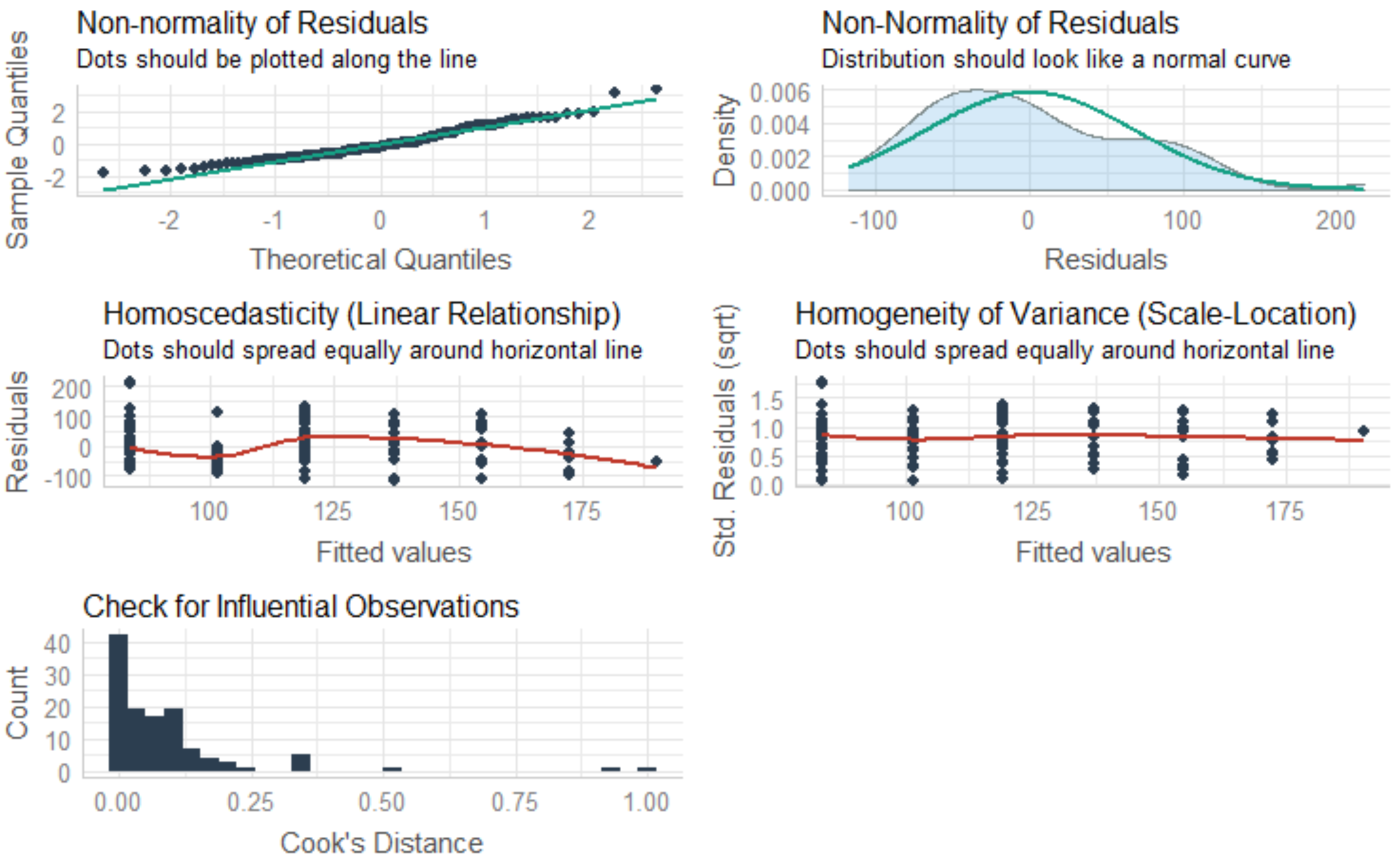
```



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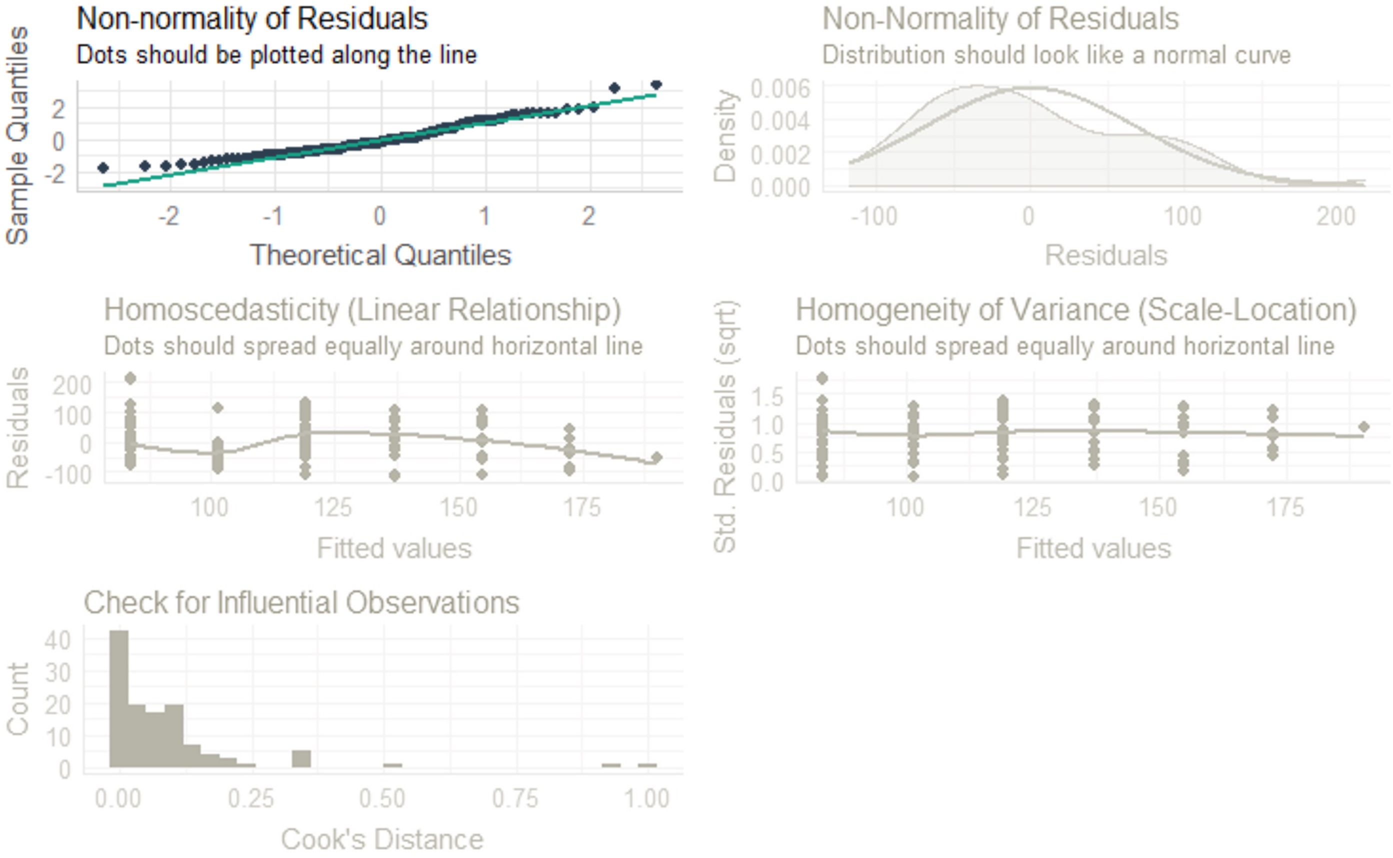

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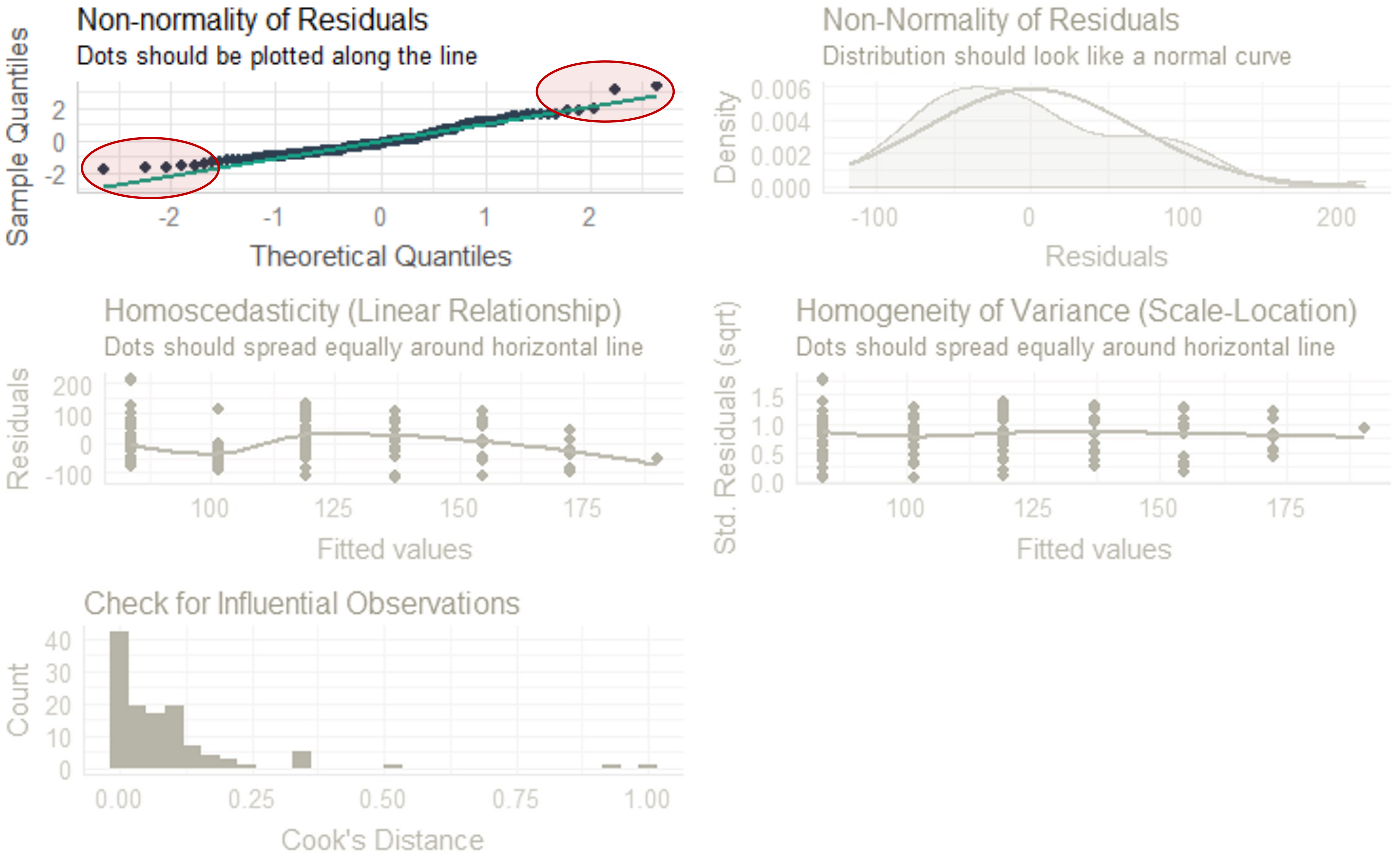

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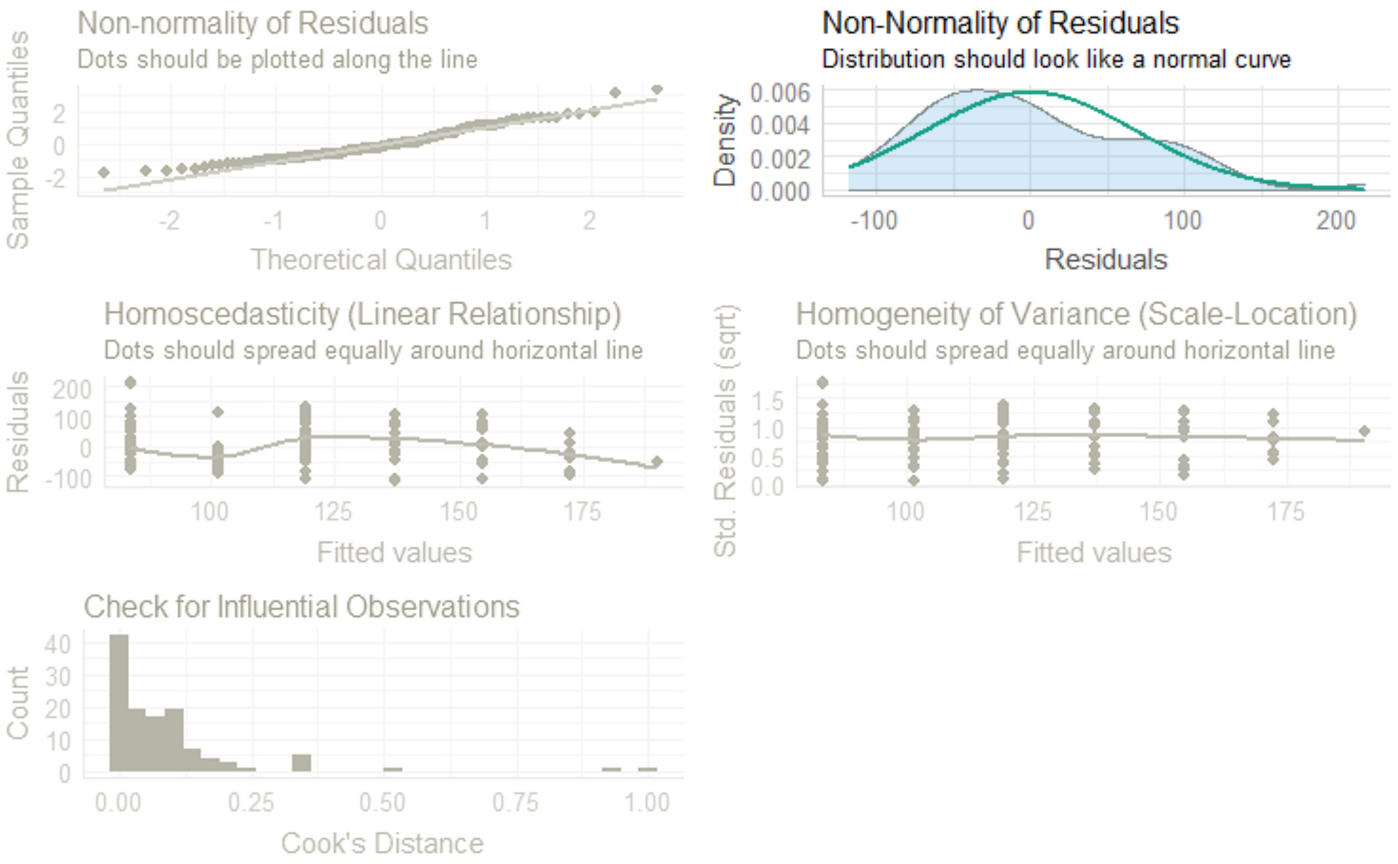

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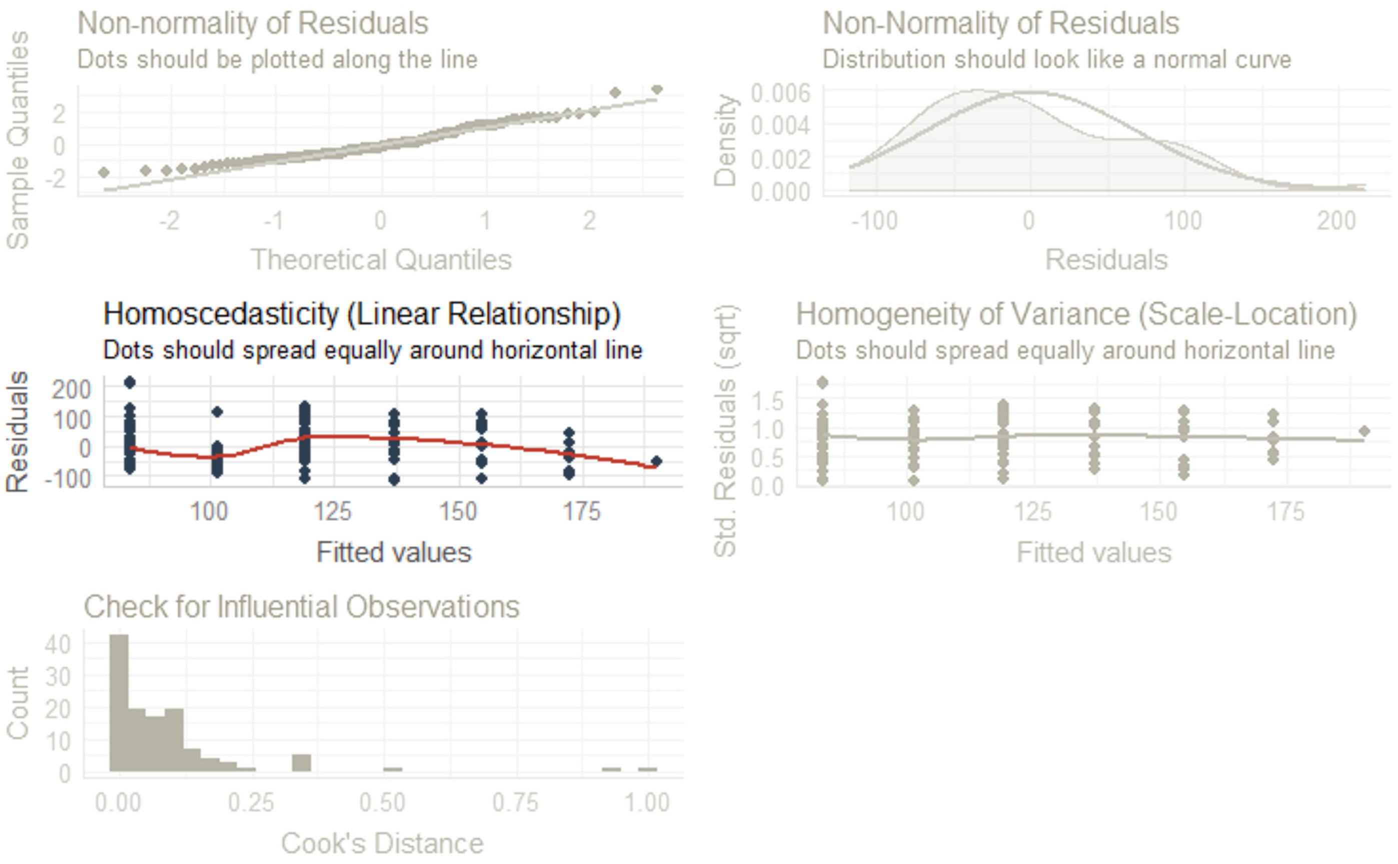

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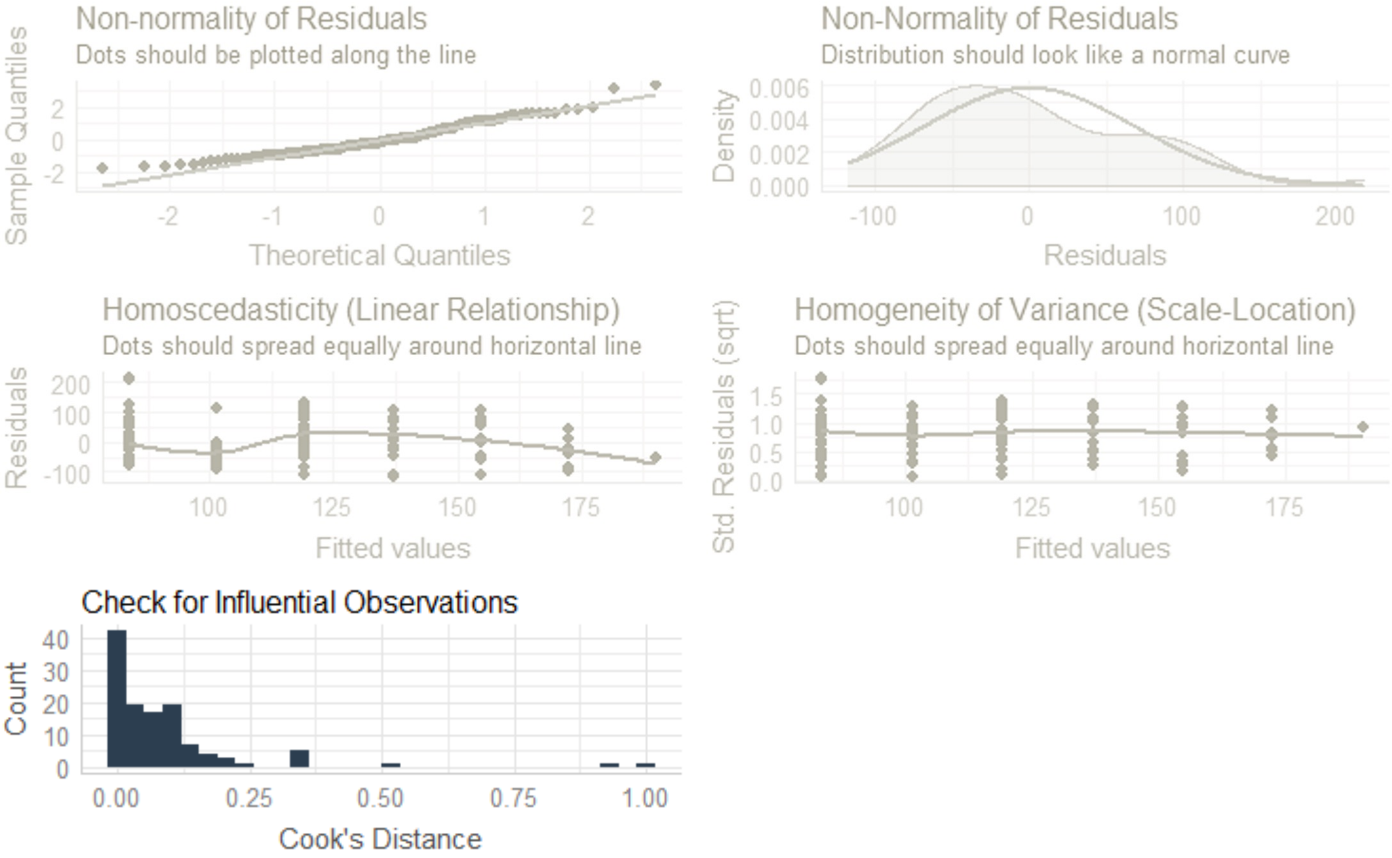
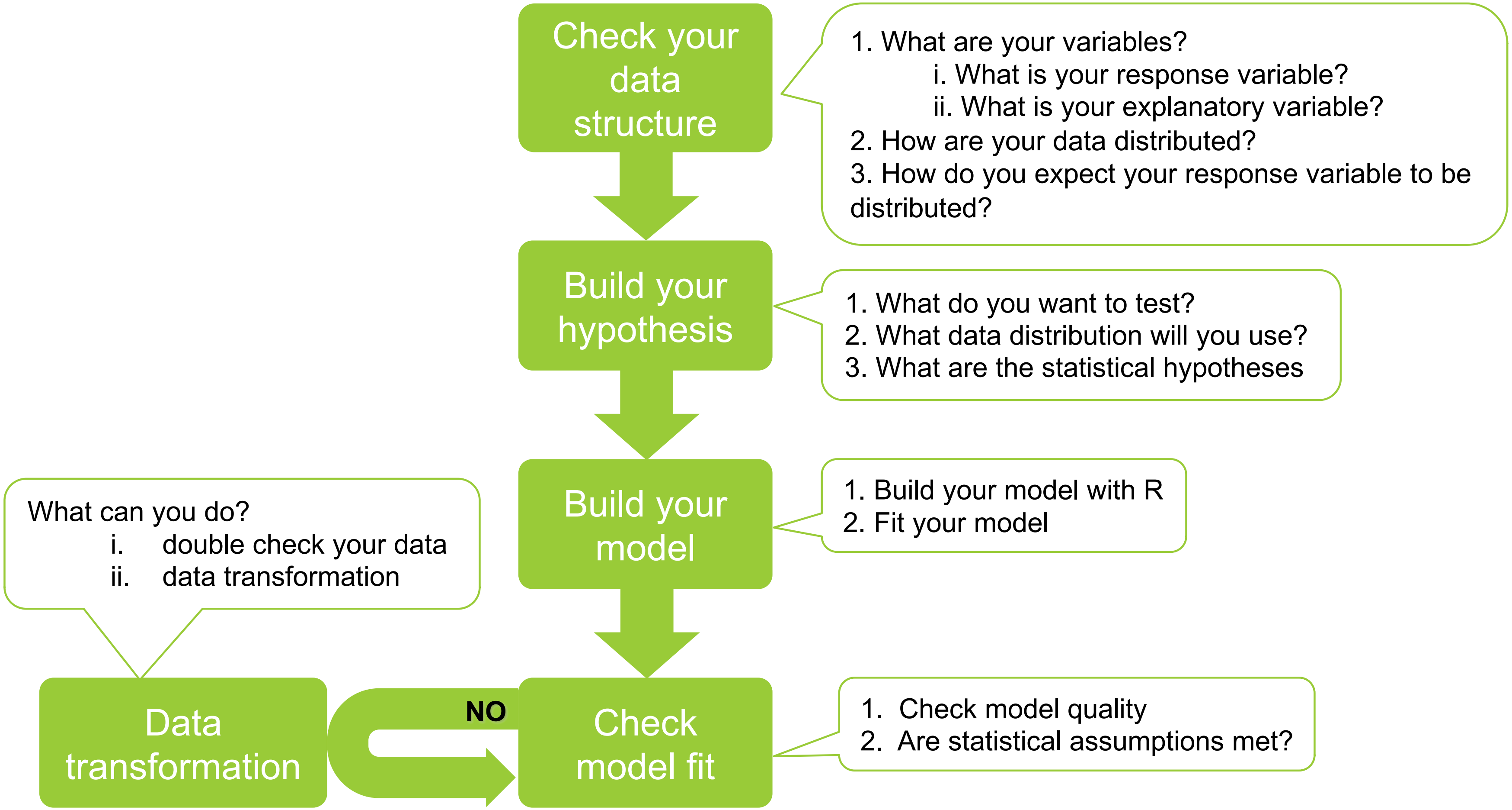


Data transformation and outliers



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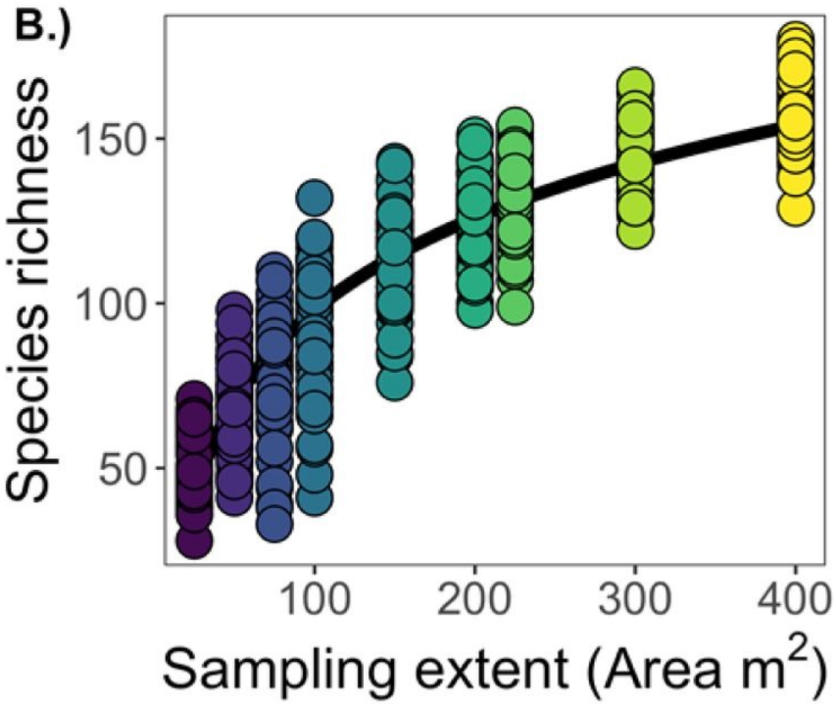

Barry et al 2019

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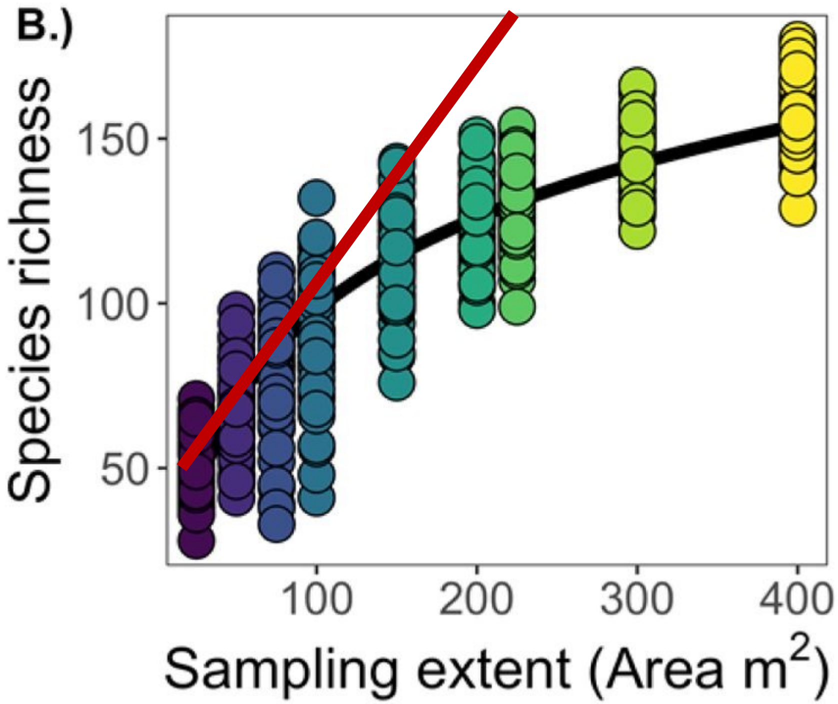

Barry et al 2019

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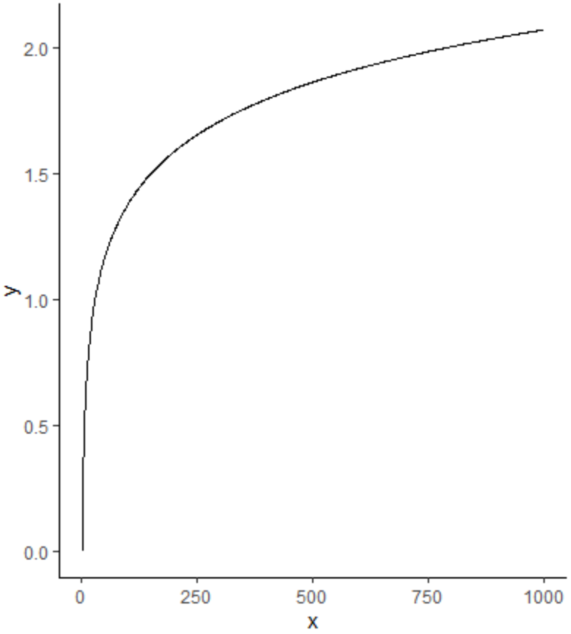

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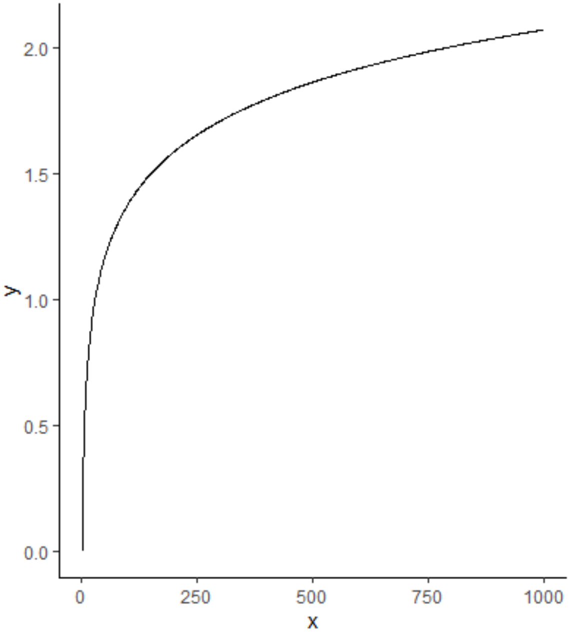

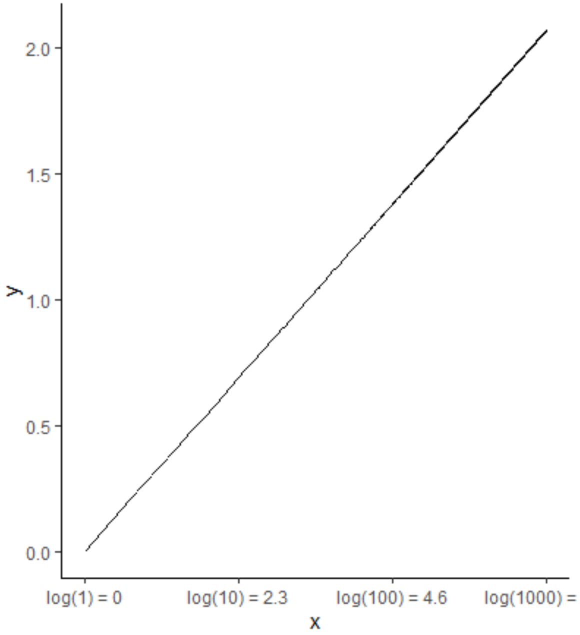

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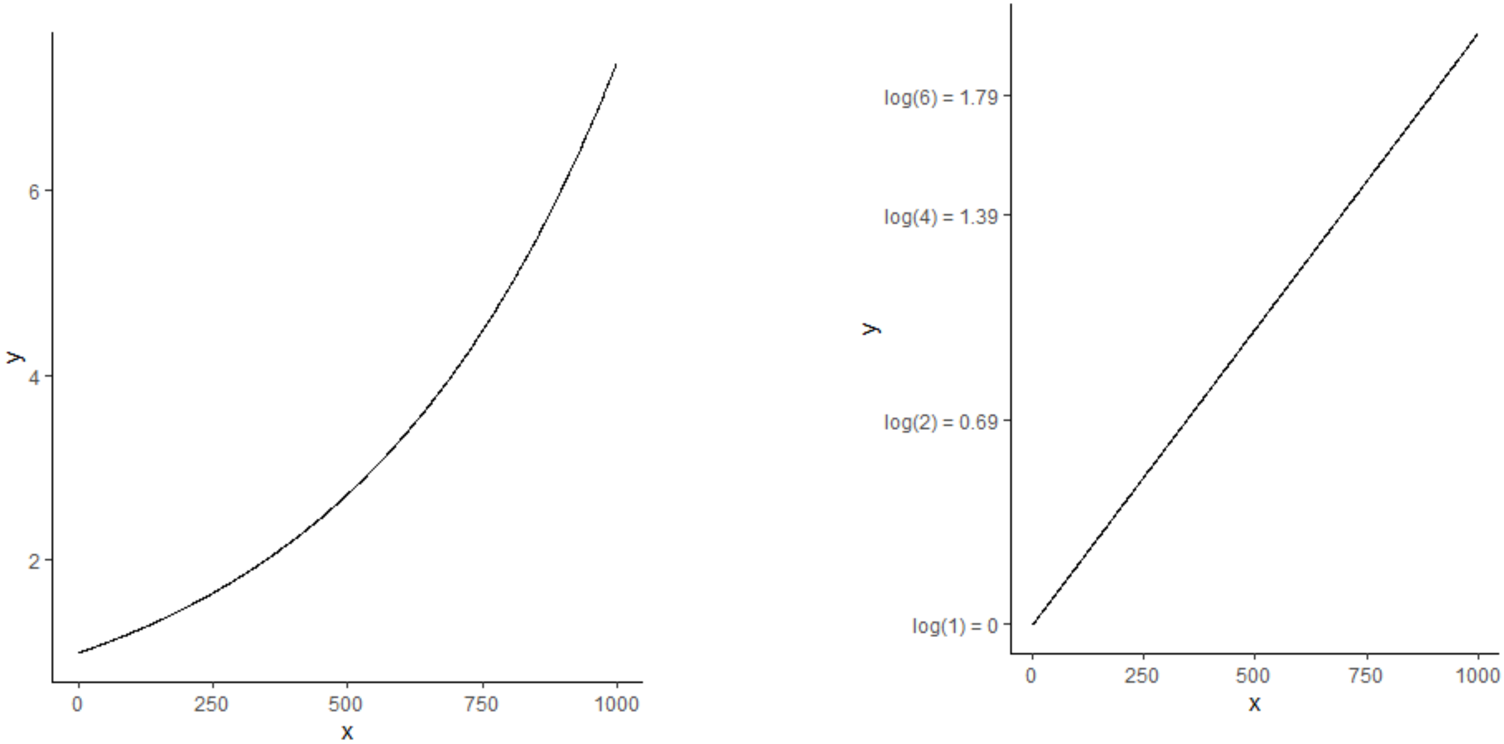

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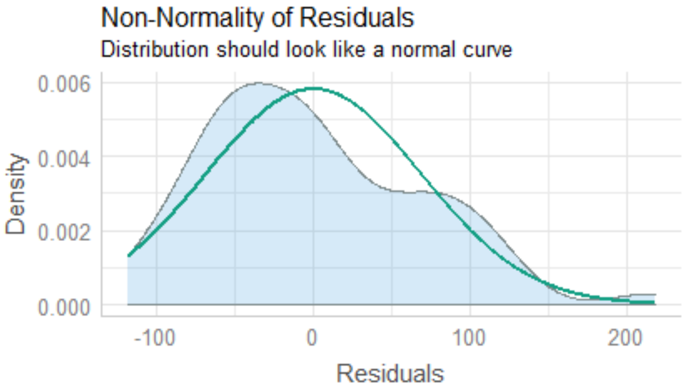

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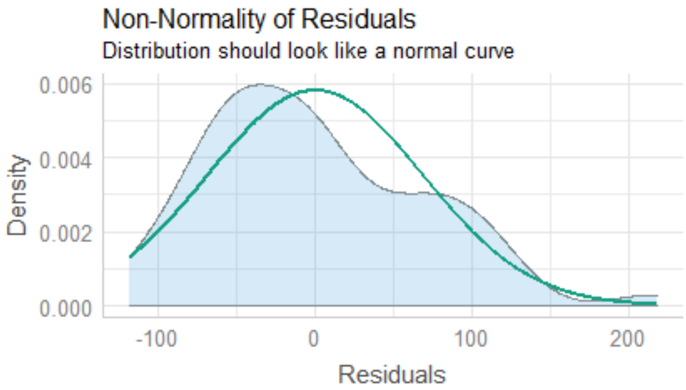
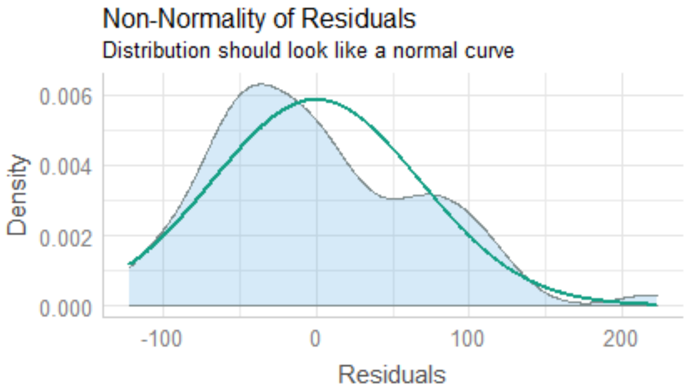


log-transformation explanatory variable



Data transformation and outliers

Check outliers with performance: `check_outliers(mod)`
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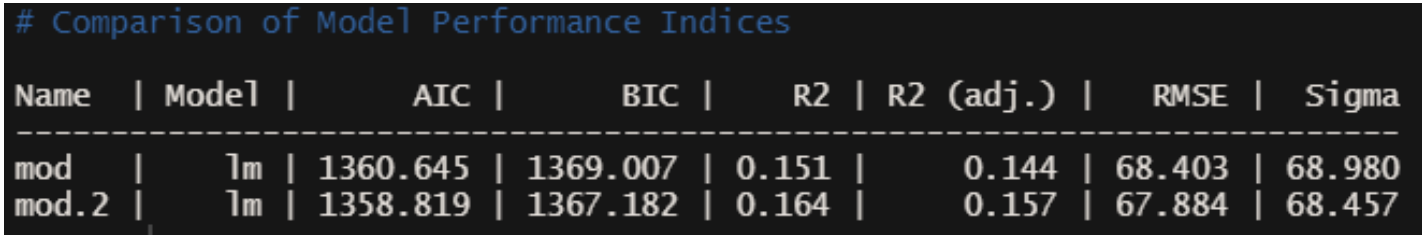
Compare the models quality: `compare_performance(mod, mod.log)`



```
# Comparison of Model Performance Indices

Name  | Model |      AIC |      BIC |    R2 | R2 (adj.) |   RMSE |  Sigma
---------------------------------------------------------------------------
mod   |    lm | 1360.645 | 1369.007 | 0.151 |     0.144 | 68.403 | 68.980
mod.2 |    lm | 1358.819 | 1367.182 | 0.164 |     0.157 | 67.884 | 68.457
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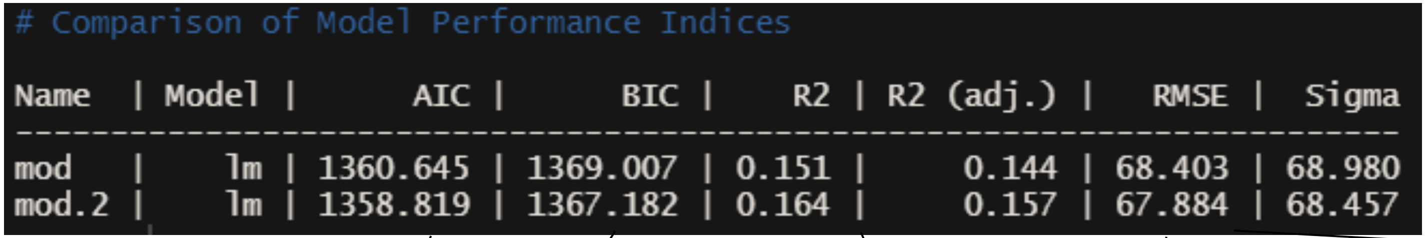

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```

AIC: fit quality – weighted by the number of variables

BIC: fit quality – weighted by the number of variables and the sample size

R: fit quality – part of variance explained

RMSE: Mean Root Standard Error – standard error of the residuals

Sigma: residual standard error

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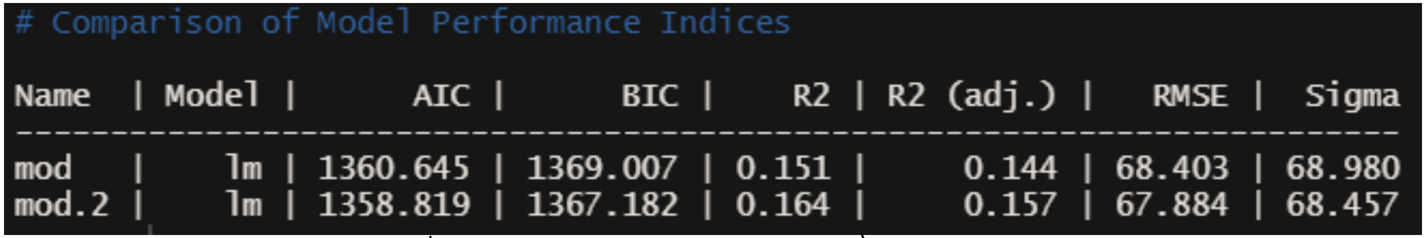

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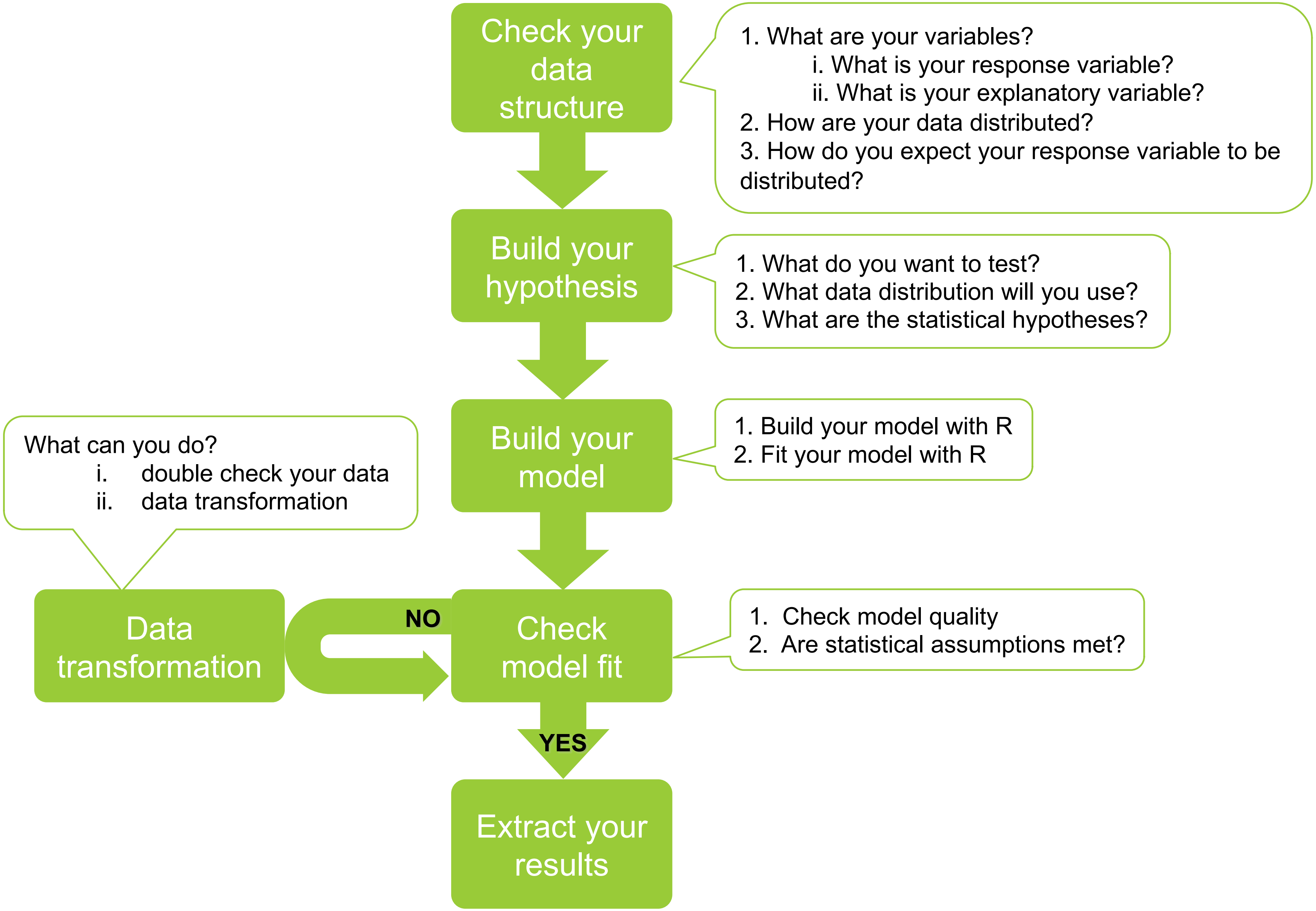
AIC: fit quality – weighted by the number of variables

R: fit quality – part of variance explained

$\Delta AIC > [2,8]$: the model are different
Can be completed by ANOVA (see following lecture)

Extract your results



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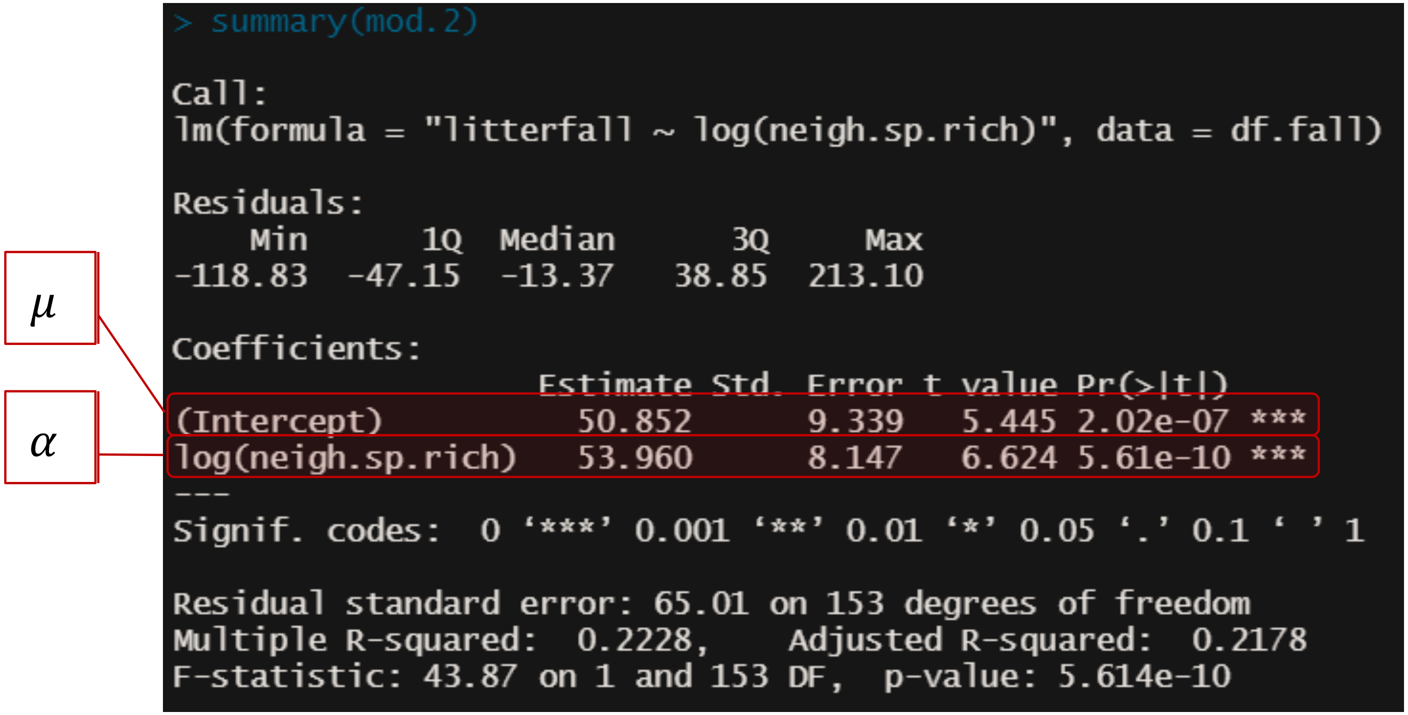
YES

Extract your results

Extract your results

`summary(mod)`

$$litterfall \sim \mu + \alpha \times \log(neigh.sp.rich) + \varepsilon$$



```
> summary(mod.2)

Call:
lm(formula = "litterfall ~ log(neigh.sp.rich)", data = df.fall)

Residuals:
    Min      1Q  Median      3Q     Max 
-118.83  -47.15  -13.37   38.85  213.10 

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)    
(Intercept)          50.852      9.339   5.445 2.02e-07 ***
log(neigh.sp.rich)   53.960      8.147   6.624 5.61e-10 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 65.01 on 153 degrees of freedom
Multiple R-squared:  0.2228,	Adjusted R-squared:  0.2178 
F-statistic: 43.87 on 1 and 153 DF,  p-value: 5.614e-10
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Mean litterfall when diversity null = 50.852 +/- 18.304 g/m2 (Estimate +/- 1.96 x SE)
Effect species richness = 53.960 +/- 15.958 g/m2/log(#species)

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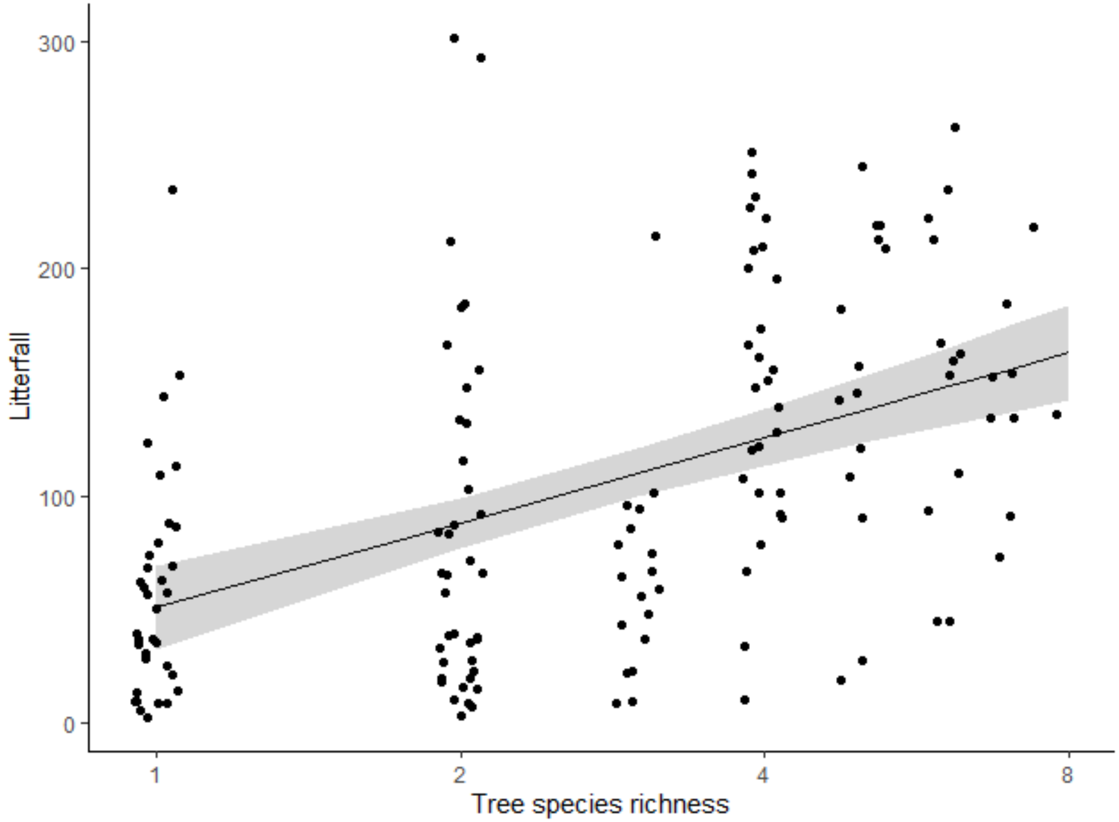

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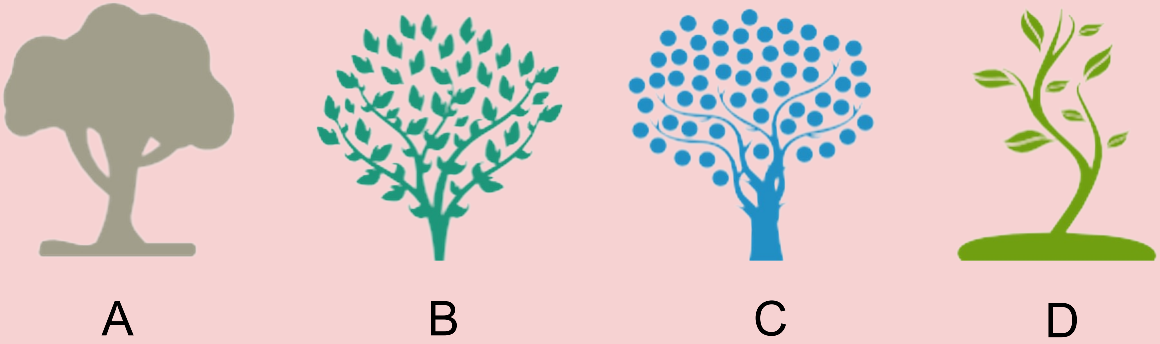
DANGER ZONE: the factors



```
lm(formula = litterfall ~ species, data = df)
```

Extract your results

```
summary(mod)
```

DANGER ZONE: the factors

A

B

C

D

```
lm(formula = litterfall ~ species, data = df)
```

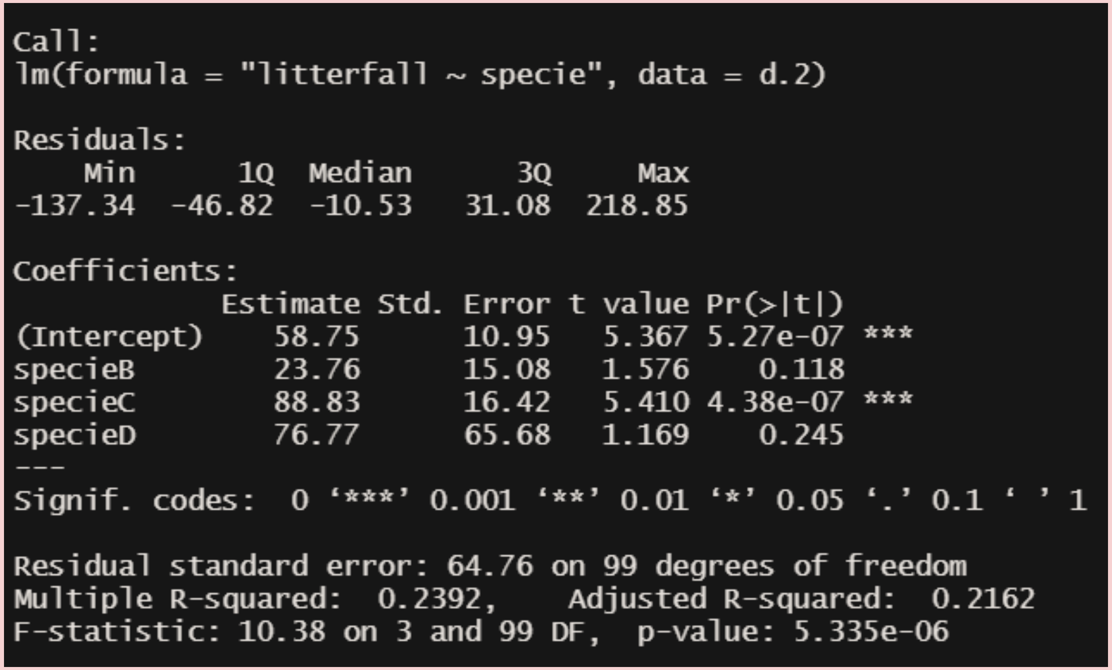
$$litterfall \sim \alpha_A \times specie_A + \alpha_B \times specie_B + \alpha_C \times specie_C + \alpha_D \times specie_D + \varepsilon$$

$specie_i$ is 0 or 1

Extract your results

`summary(mod)`

DANGER ZONE: the factors



```
Call:
lm(formula = "litterfall ~ specie", data = d.2)

Residuals:
    Min      1Q  Median      3Q     Max 
-137.34  -46.82  -10.53   31.08  218.85 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)    58.75      10.95   5.367 5.27e-07 ***
specieB        23.76      15.08   1.576    0.118    
specieC        88.83      16.42   5.410 4.38e-07 ***
specieD        76.77      65.68   1.169    0.245    
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Residual standard error: 64.76 on 99 degrees of freedom
Multiple R-squared:  0.2392,    Adjusted R-squared:  0.2162 
F-statistic: 10.38 on 3 and 99 DF,  p-value: 5.335e-06
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$$litterfall \sim \alpha_A \times specie_A + \alpha_B \times specie_B + \alpha_C \times specie_C + \alpha_D \times specie_D + \varepsilon$$

Extract your results

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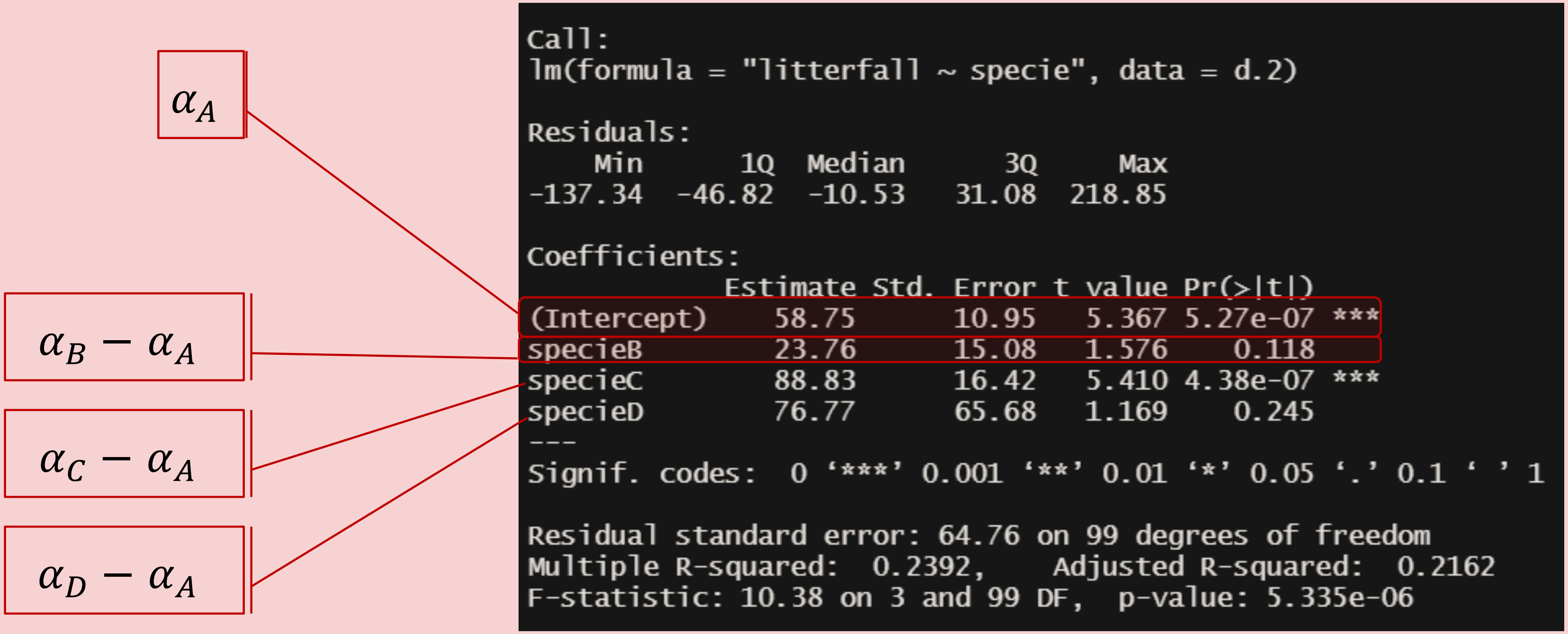
DANGER ZONE: the factors



α_A

$\alpha_B - \alpha_A$

$\alpha_C - \alpha_A$

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$$litterfall \sim \alpha_A \times specie_A + \alpha_B \times specie_B + \alpha_C \times specie_C + \alpha_D \times specie_D + \varepsilon$$

If you like to test the differences between the different factors you need to do an ANOVA and a Tukey test

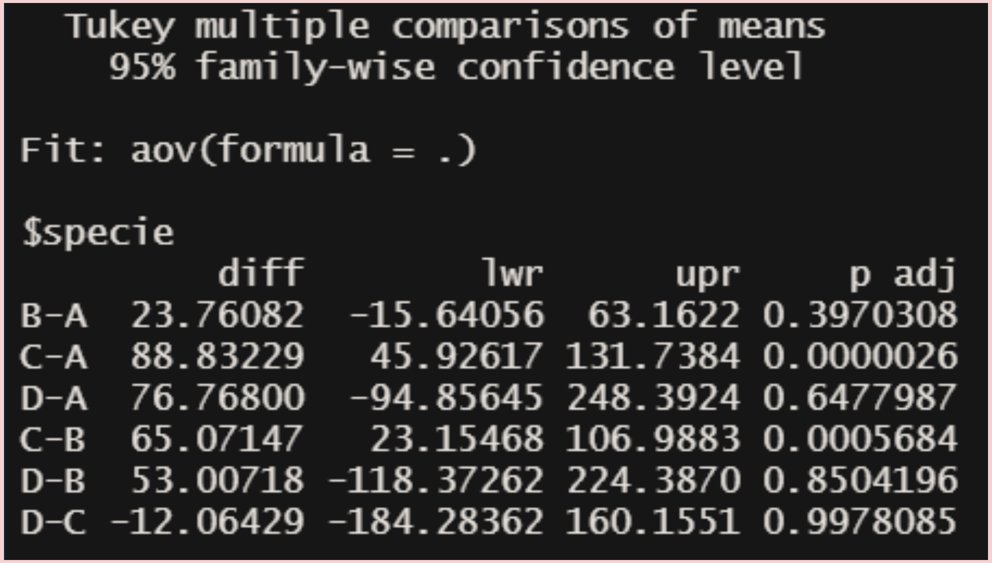
Extract your results

```
summary(mod)
```

DANGER ZONE: the factors

If you like to test the differences between the different factors you need to do an ANOVA and a Tukey test

```
mod = lm(formula = litterfall ~ species, data = df)
mod.aov = aov(mod)
TukeyHSD(mod.aov)
```



```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = .)

$specie
         diff        lwr      upr     p adj
B-A  23.76082  -15.64056  63.1622 0.3970308
C-A  88.83229   45.92617 131.7384 0.0000026
D-A  76.76800  -94.85645 248.3924 0.6477987
C-B  65.07147   23.15468 106.9883 0.0005684
D-B  53.00718 -118.37262 224.3870 0.8504196
D-C -12.06429 -184.28362 160.1551 0.9978085
```

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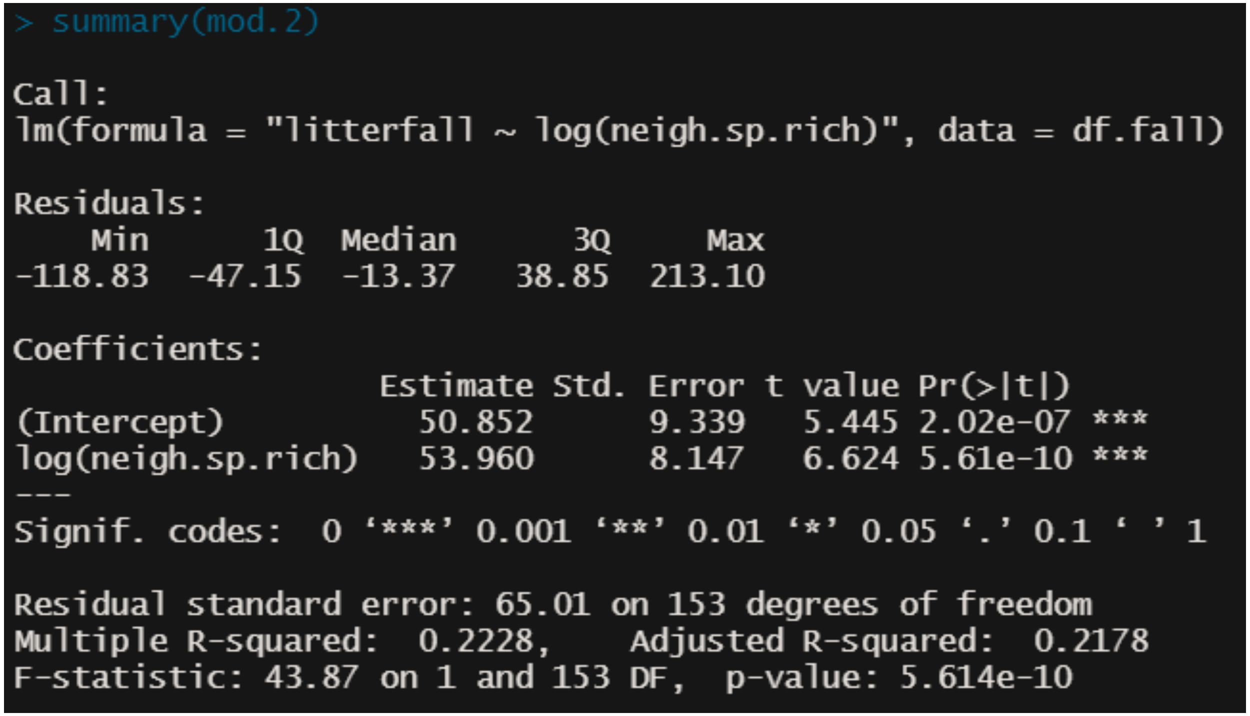

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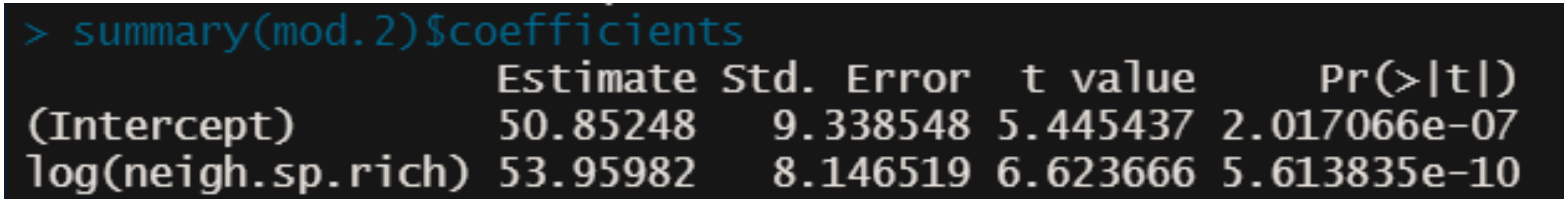
Extract your results

`summary(mod)`

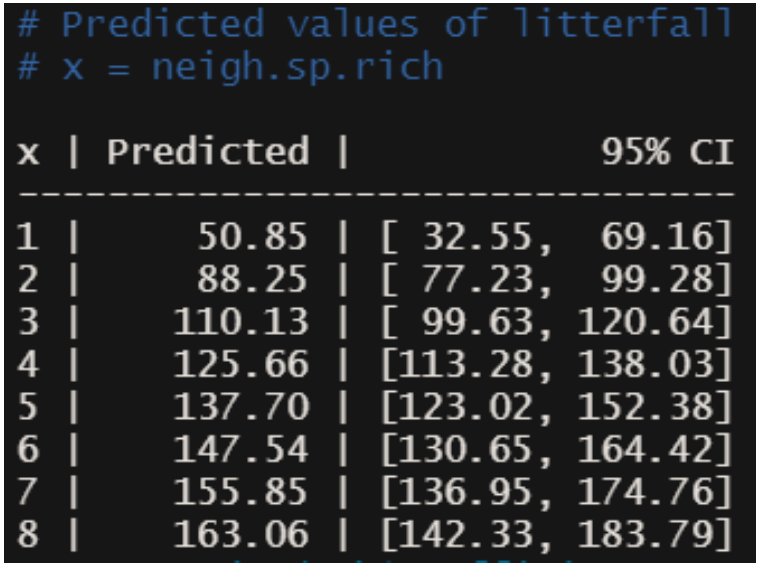
Extract the coefficients: `summary(mod)$coefficients`



```
> summary(mod.2)$coefficients
                  Estimate Std. Error  t value     Pr(>|t|)
(Intercept)       50.85248   9.338548 5.445437 2.017066e-07
log(neigh.sp.rich) 53.95982   8.146519 6.623666 5.613835e-10
```

To extract the predictions from your models: ggeffect package

`pred = ggpredict(model = mod, terms = 'neigh.sp.rich’)`



```
# Predicted values of litterfall
# x = neigh.sp.rich

x | Predicted |           95% CI
--------------------------------
1 |     50.85 | [ 32.55,  69.16]
2 |     88.25 | [ 77.23,  99.28]
3 |    110.13 | [ 99.63, 120.64]
4 |    125.66 | [113.28, 138.03]
5 |    137.70 | [123.02, 152.38]
6 |    147.54 | [130.65, 164.42]
7 |    155.85 | [136.95, 174.76]
8 |    163.06 | [142.33, 183.79]
```

Summary

In this lecture:

1. The stepwise process to analyses your data
2. Application on an example with R
3. Practical on your own

Your time to play