Allometric relationships

Allometric relationships

- A linear allometric relationship is said to exist between two dimensional elements (X and Y) of an individual or population (in our case, a forest stand) when the relationship between them can be expressed in the following form:

$$\boldsymbol{Y = k\,X^{a}}$$

  - ✓ *a* - allometric constant, characterizes the individual in a certain environment
  - ✓ *k* - depends on the initial conditions and units of *Y* and *X*

Allometric relationships

- The allometric equation therefore describes one tree variable as a function of other tree variable following the model.
- Taking logarithms and then differentiating, it can be shown that the allometric equation assumes that the relative growth rate of one plant part is proportional to that of another

$$Y = k\, X^{a} \qquad \Leftrightarrow \qquad ln(Y) = \ln(k) + a\,\ln(X)$$

Allometric relationships

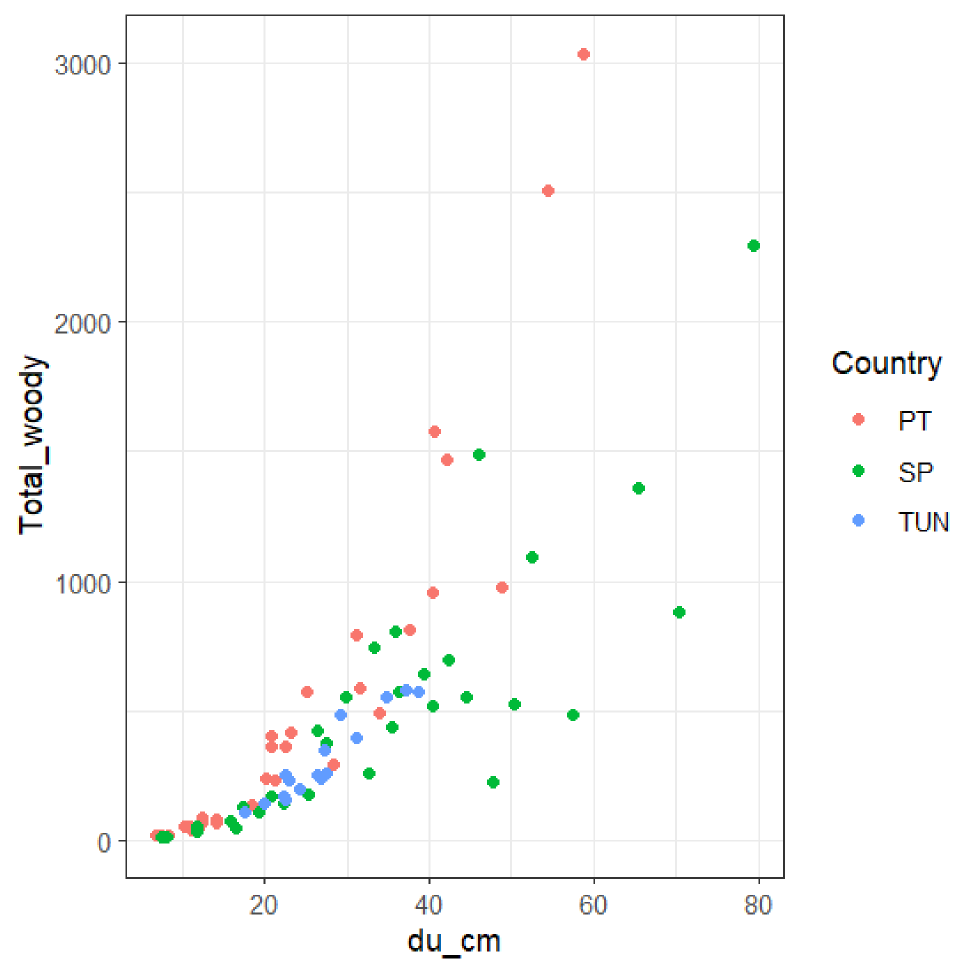
- The parameter *a* - allometric constant - is the coefficient of proportionality between the relative growth rates of the two plant parts

$$\frac{1}{Y}\frac{dY}{dt} = a\frac{1}{X}\frac{dX}{dt}$$

$$\int \frac{1}{Y}\frac{dY}{dt} = a\int \frac{1}{X}\frac{dX}{dt} \qquad \Rightarrow \qquad ln(Y) = k + a\,ln(X)$$

- *a* can, therefore, provide direct information on the partitioning of assimilates between plant parts

Allometric relationships



Allometric relationships

- The multiple allometric relationship is established between one tree variable and other tree variables (more than one):

$$Y = k\, X^{a}\, Z^{b}$$

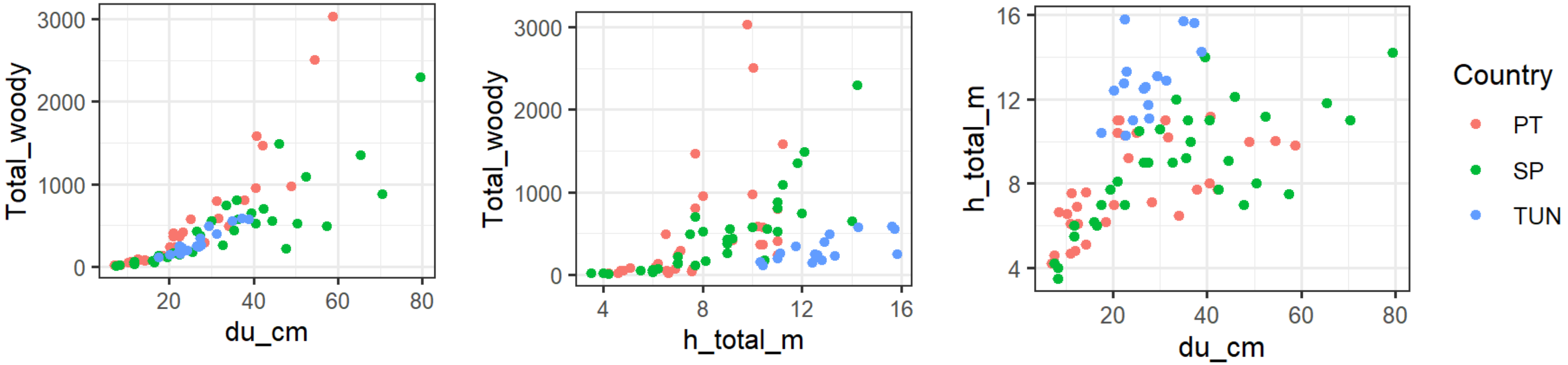
Allometric relationships

- Allometric relationships can also be established between forest stand variables
- The existence of allometric relationships between tree variables (or between stand variables) is very important for growth and yield modelling of trees and stands
- It is one of the biologic hypothesis that can be used in the formulation of models

Fitting an allometric model in R
Practice 2

1. Initial data analysis

   ✓ Descriptive analysis of the data. Location and dispersion measures. Look for tendencies. Look for errors. Data limitations… ggplot, summary(dados), geom_boxplot()…



Fitting an allometric model in R
Practice 2

1. Initial data analysis

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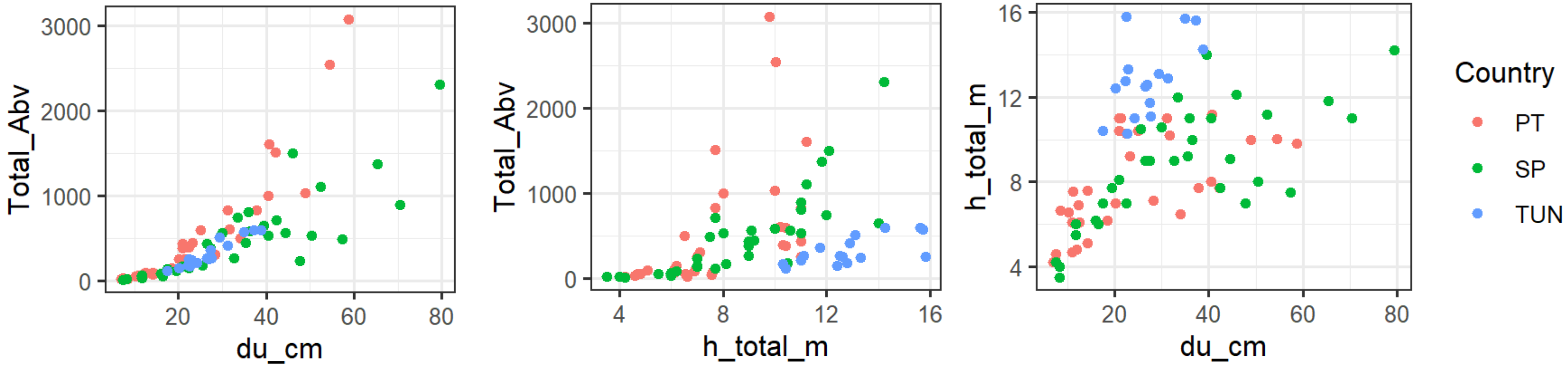

Fitting an allometric model in R
Practice 2

1. Initial data analysis

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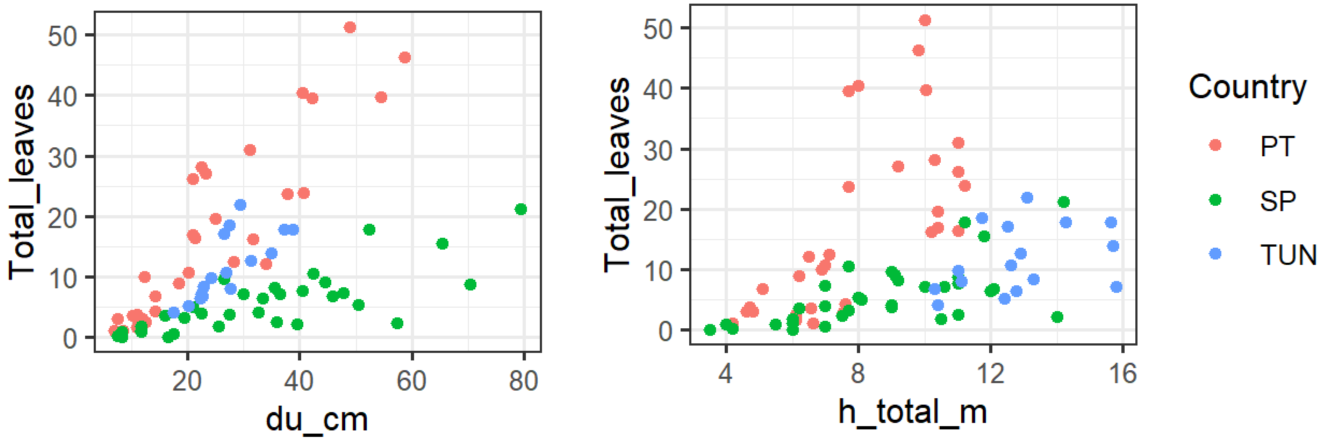

Fitting an allometric model in R
Practice 2

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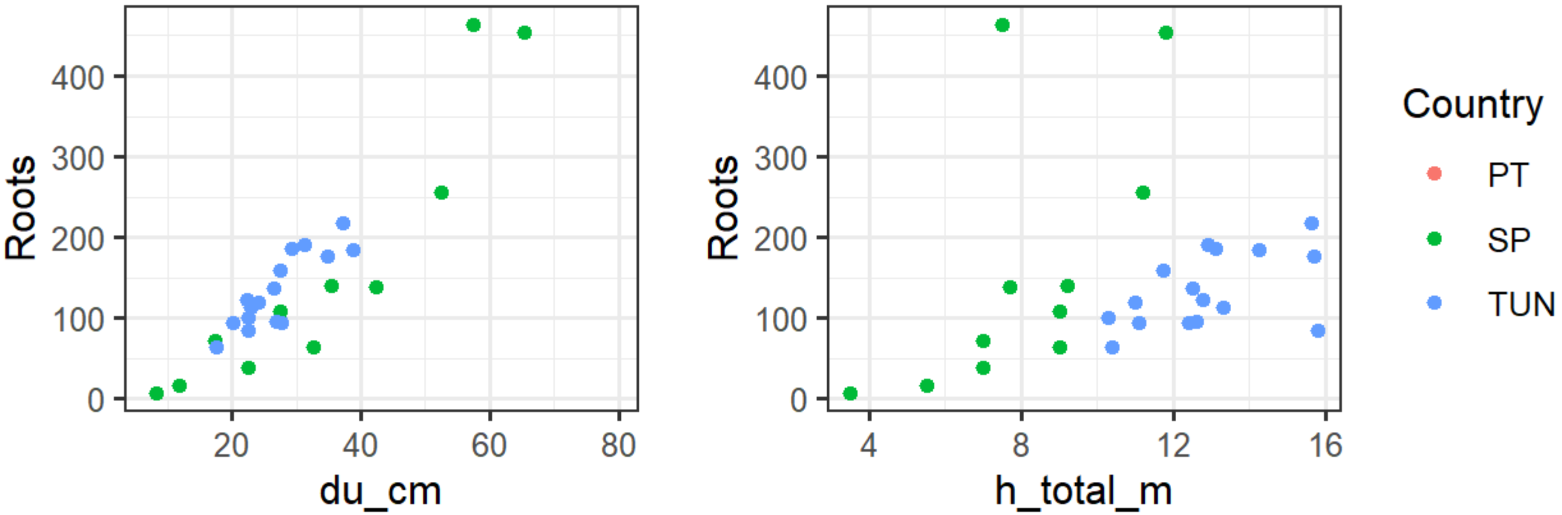


Fitting an allometric model in R
Practice 2

2. Fit the allometric model. Total_woody $= a\,du^{b}$. Look at model parameter significance. Are they significantly different from zero in the model?

Statistical Tests for Parameter Significance: t-test for each parameter βj (in this example a and b).

- The hypothesis for this test are:

$$H_0 : \beta_j = 0 \quad \text{(the parameter is not significant)}$$

$$H_1 : \beta_j \neq 0$$

- The t-statistic is computed as:

$$t_j = \frac{\hat{\beta}_j}{\mathrm{SE}(\hat{\beta}_j)}$$ ~ t student distribution with (n−k) degrees of freedom under H_0.

Fitting an allometric model in R
Practice 2

2. Fit the allometric model. Total_woody $= \boldsymbol{a\,du^{\,b}}$. Look at model parameter significance. Are they significantly different from zero in the model?

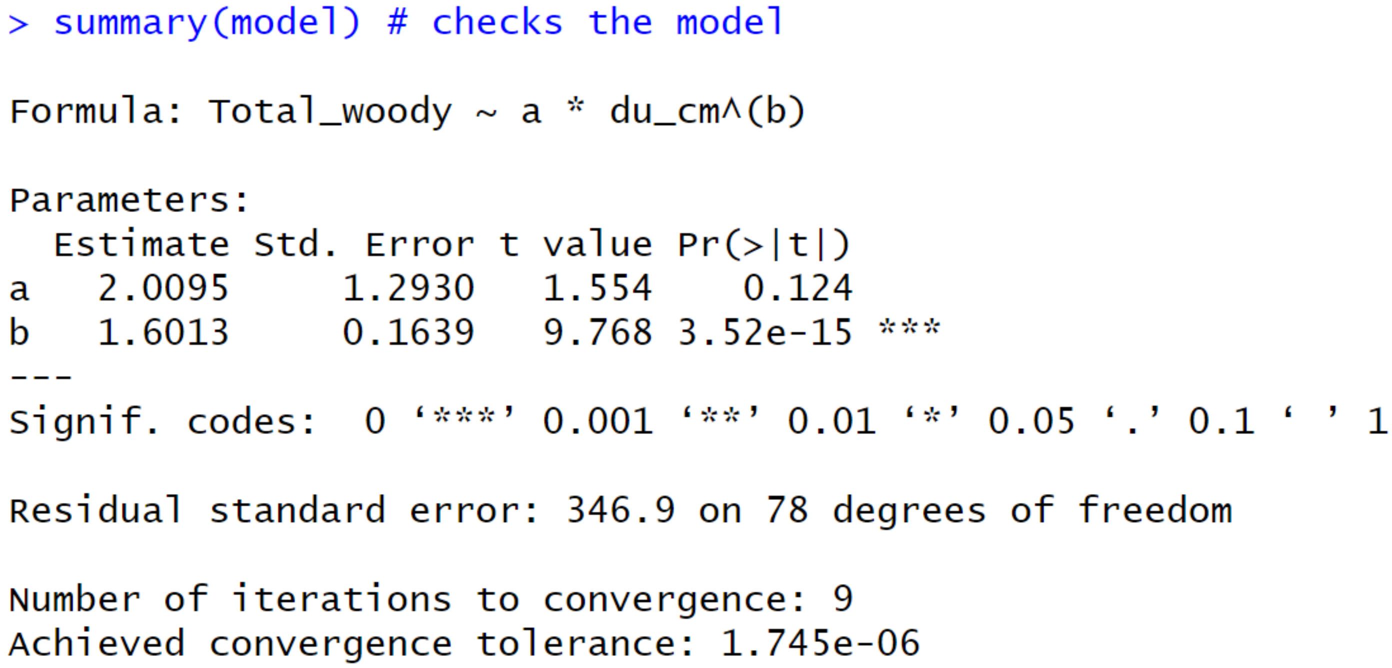
Statistical Tests for Parameter Significance: t-test for each parameter ßj (in this example a and b).

- The p-value is obtained as: $p = 2P(T > |t_j|)$

If p is small (e.g., $p < 0.05$), we reject H_0, indicating that parameter β_j is statistically significant.

Fitting an allometric model in R
Practice 2

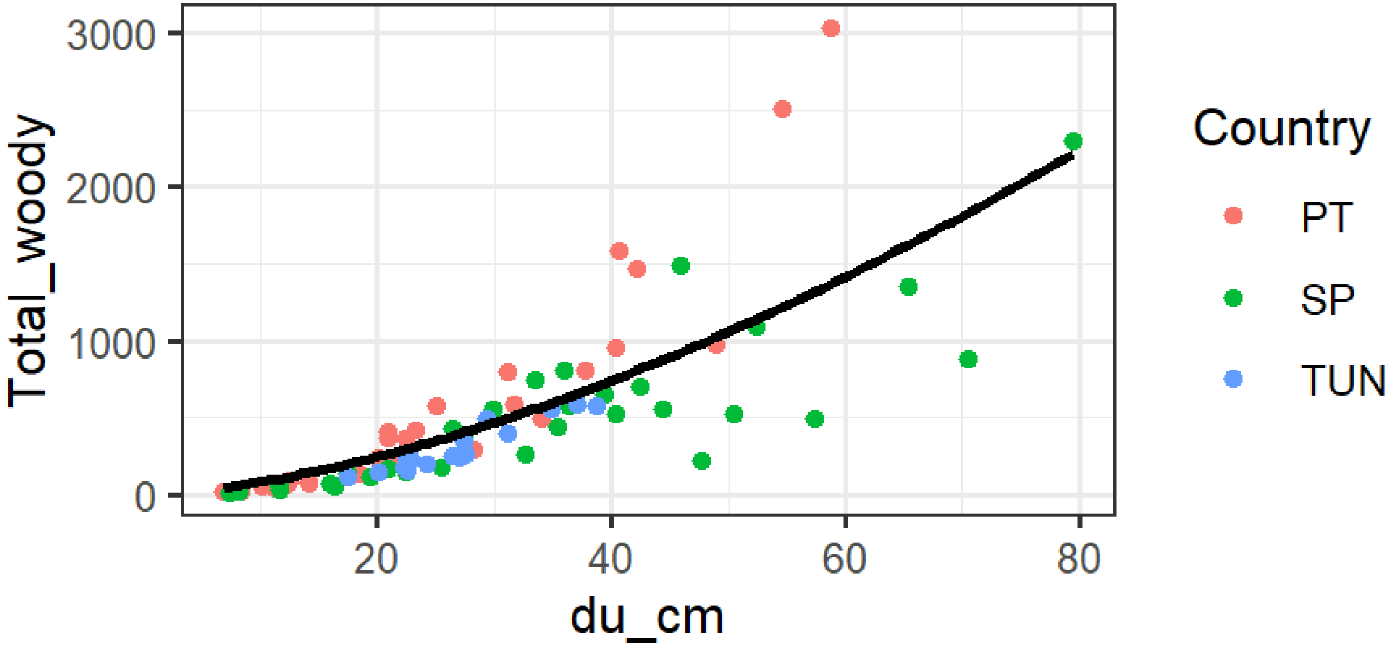
2. Fit the allometric model: Total_woody $= a\,du^{b}$. Look at model parameter significance. Are they significantly different from zero in the model?



```
> summary(model) # checks the model

Formula: Total_woody ~ a * du_cm^(b)

Parameters:
  Estimate Std. Error t value Pr(>|t|)
a   2.0095     1.2930   1.554    0.124
b   1.6013     0.1639   9.768 3.52e-15 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 346.9 on 78 degrees of freedom

Number of iterations to convergence: 9
Achieved convergence tolerance: 1.745e-06
```

Fitting an allometric model in R
Practice 2

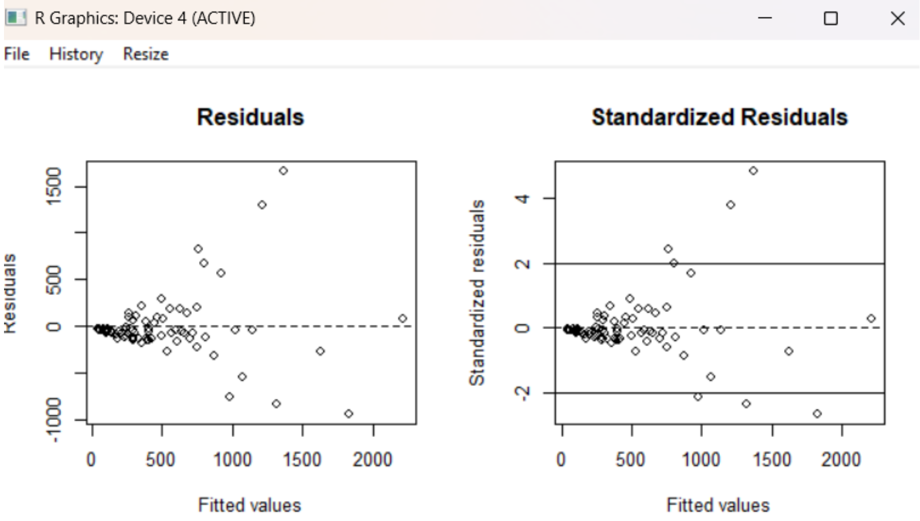
3. Look at model parameter estimates. Interpret them under biological meaning. Plot the estimates on the data.



Fitting an allometric model in R
Practice 2

4. Verify model conditions
    - ✓ Residuals distribution

```
# residuals plots
plot(nlsResiduals(model))
```

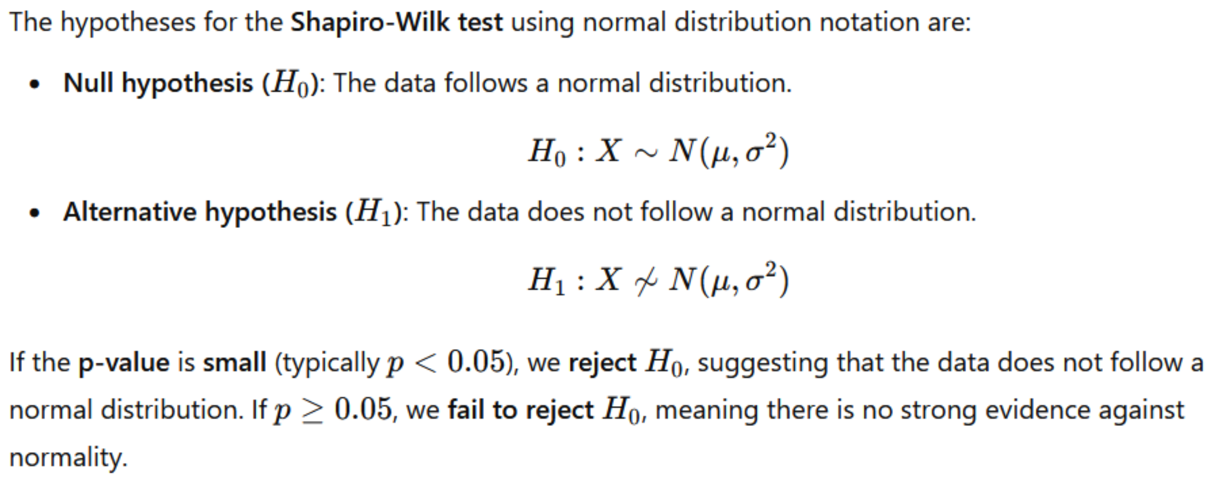


Fitting an allometric model in R
Practice 2

4. Verify model conditions

- ✓ Normality of the residuals

```
# normality test
shapiro.test(dados$Total_woody)
```



The hypotheses for the **Shapiro-Wilk test** using normal distribution notation are:

- **Null hypothesis** (H_0): The data follows a normal distribution.

$$H_0 : X \sim N(\mu, \sigma^2)$$

- **Alternative hypothesis** (H_1): The data does not follow a normal distribution.

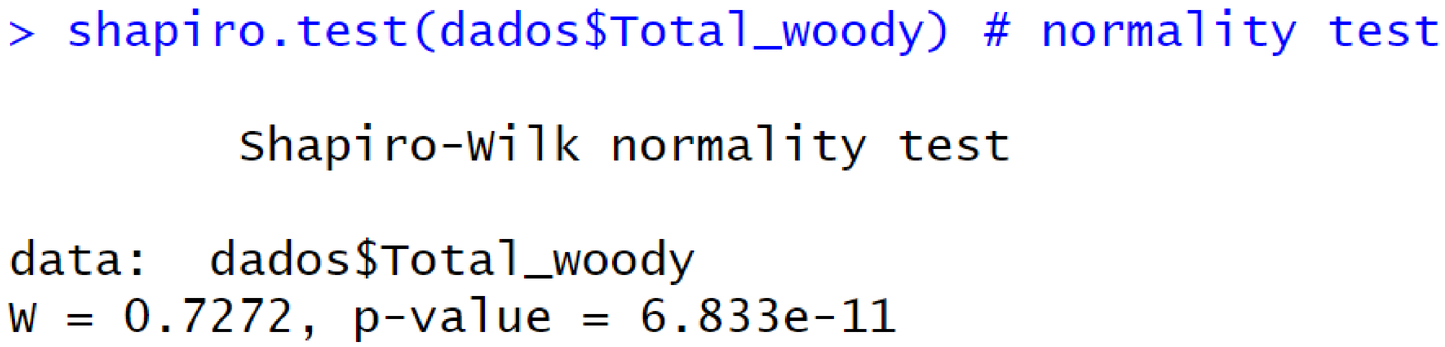
$$H_1 : X \not\sim N(\mu, \sigma^2)$$

If the **p-value** is **small** (typically $p < 0.05$), we **reject** H_0, suggesting that the data does not follow a normal distribution. If $p \geq 0.05$, we **fail to reject** H_0, meaning there is no strong evidence against normality.

Fitting an allometric model in R
Practice 2

4. Verify model conditions
   - ✓ Normality of the residuals

```
# normality test

shapiro.test(dados$Total_woody)
```



```
> shapiro.test(dados$Total_woody) # normality test

        Shapiro-Wilk normality test

data:  dados$Total_woody
W = 0.7272, p-value = 6.833e-11
```

Fitting an allometric model in R
Practice 2

4. Verify model conditions

✓ Normality of the errors

QQ plot (Quantile-Quantile plot) - graphical tool used to assess whether a dataset follows a specific theoretical distribution, such as a normal distribution. It compares the quantiles of the observed data with the quantiles of the theoretical distribution.

How it works:

- Quantiles of the observed data are plotted on the y-axis.
- Quantiles of the theoretical distribution (e.g., normal distribution) are plotted on the x-axis.
- The points on the plot represent pairs of quantiles from both datasets (observed vs. theoretical).

Fitting an allometric model in R
Practice 2

4. Verify model conditions
   - ✓ Normality of the errors

QQ plot (Quantile-Quantile plot) - graphical tool used to assess whether a dataset follows a specific theoretical distribution, such as a normal distribution. It compares the quantiles of the observed data with the quantiles of the theoretical distribution.

If the data is normally distributed (for example), the points will lie approximately on a straight line (usually a 45-degree line or a line with slope 1). If the points deviate significantly from the straight line, it suggests that the data does not follow the chosen theoretical distribution.

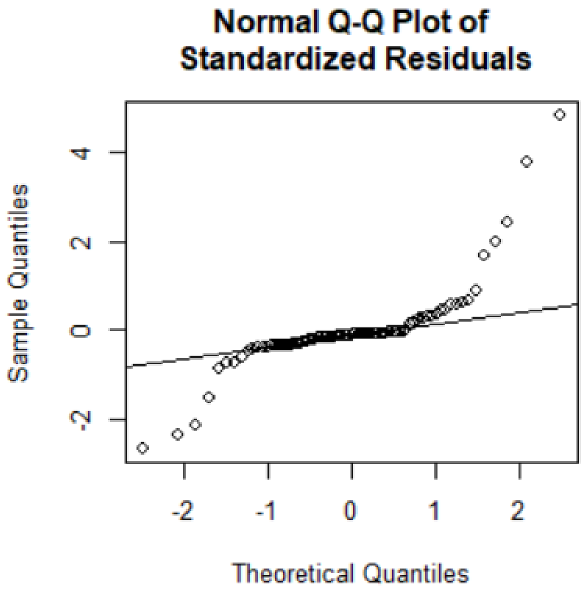
Fitting an allometric model in R
Practice 2

4. Verify model conditions

   - ✓ Normality of the errors

How to plot the QQ plot

Option 1) plot(nlsResiduals(model)))

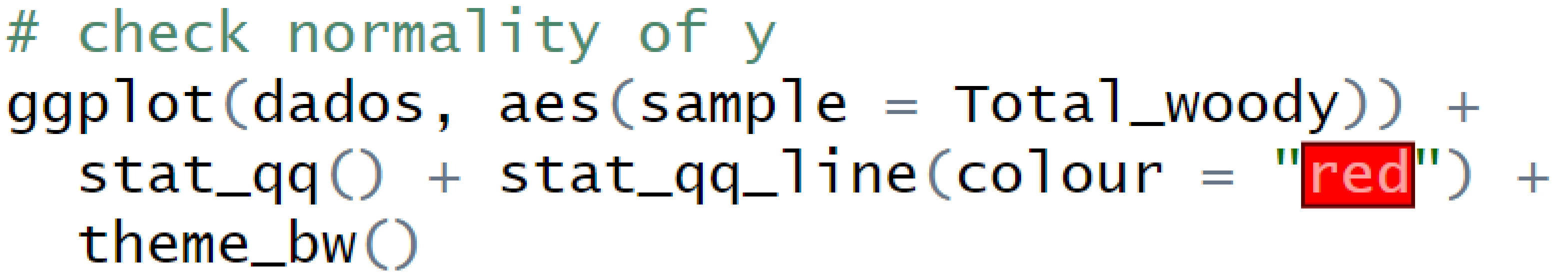


Fitting an allometric model in R
Practice 2

4. Verify model conditions
   - ✓ Normality of the errors

How to plot the QQ plot

Option 2) ggplot



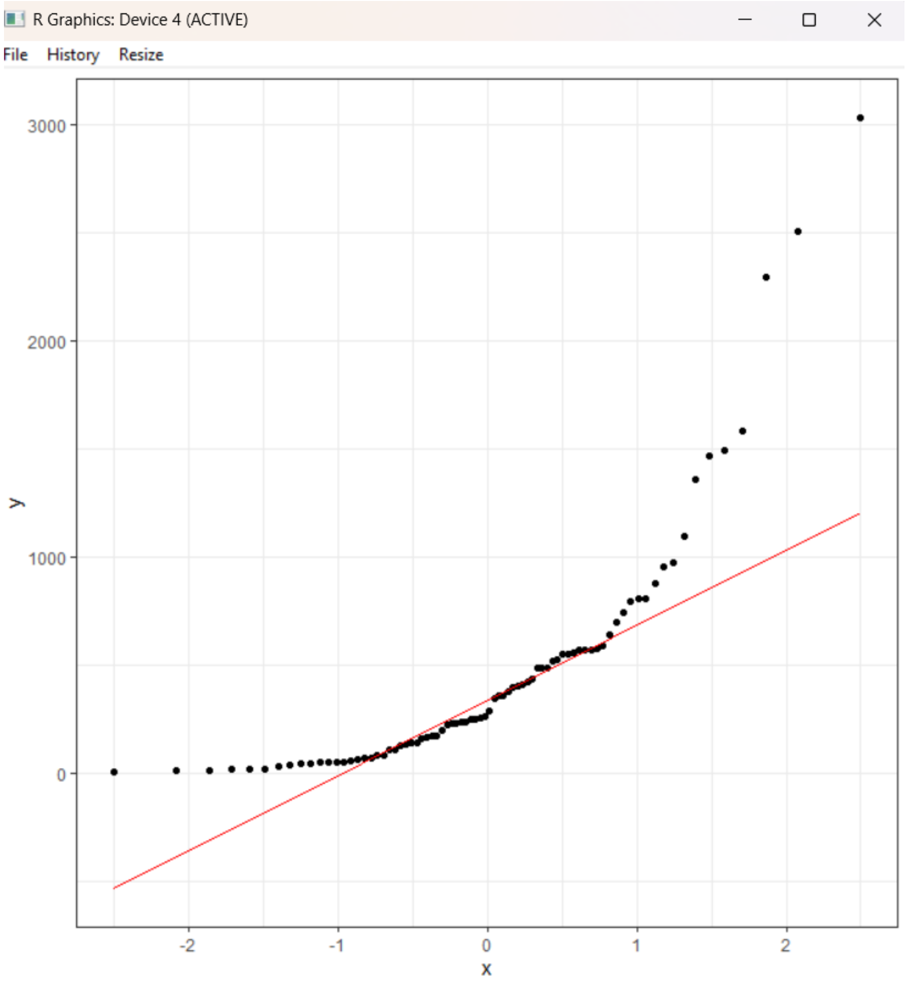
```
# check normality of y
ggplot(dados, aes(sample = Total_woody)) +
  stat_qq() + stat_qq_line(colour = "red") +
  theme_bw()
```

Fitting an allometric model in R
Practice 2

4. **Verify model conditions**
   - ✓ Normality of the errors

How to plot the QQ plot

Option 2) ggplot



Fitting an allometric model in R
Practice 2

4. Verify model conditions

   ✓ Normality of the errors

Key interpretations of a QQ plot:

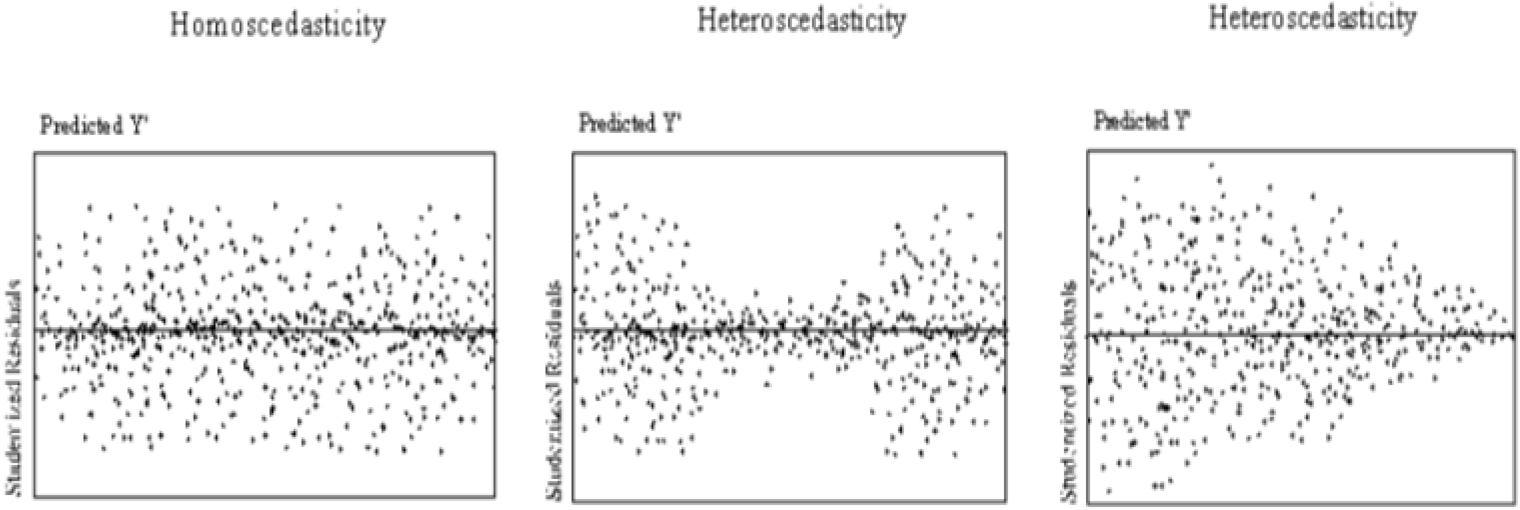
- Straight line: The data follows the specified distribution (e.g., normal).
- Curved pattern: Indicates skewness in the data.
- If the points bend upward at the ends, it suggests that the data has heavy tails (more extreme values than the normal distribution).
- If the points bend downward at the ends, it suggests light tails (fewer extreme values than the normal distribution).
- S-shaped or other patterns: Indicates that the data may not match the specified distribution at all.

Fitting an allometric model in R
Practice 2

4. Verify model conditions
   - ✓ Homoscedasticity: denotes the assumption that the variance of the residuals remains constant across all levels/range of the independent variable(s). Put simply, it signifies that the dispersion of residuals stays consistent, enhancing the accuracy and legitimacy of regression predictions. Heteroscedasticity, the violation of homoscedasticity, is present when the residual values varies across values of an independent variable.

Fitting an allometric model in R
Practice 2

4. Verify model conditions
    - Homoscedasticity: residuals (yy) versus independent variables (xx)



Fitting an allometric model in R
Practice 2

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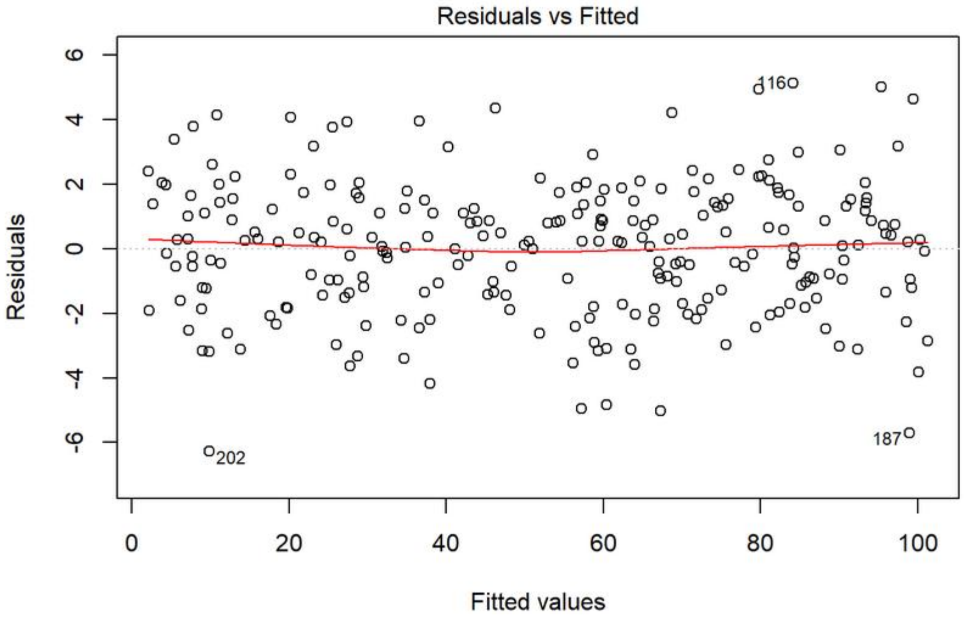
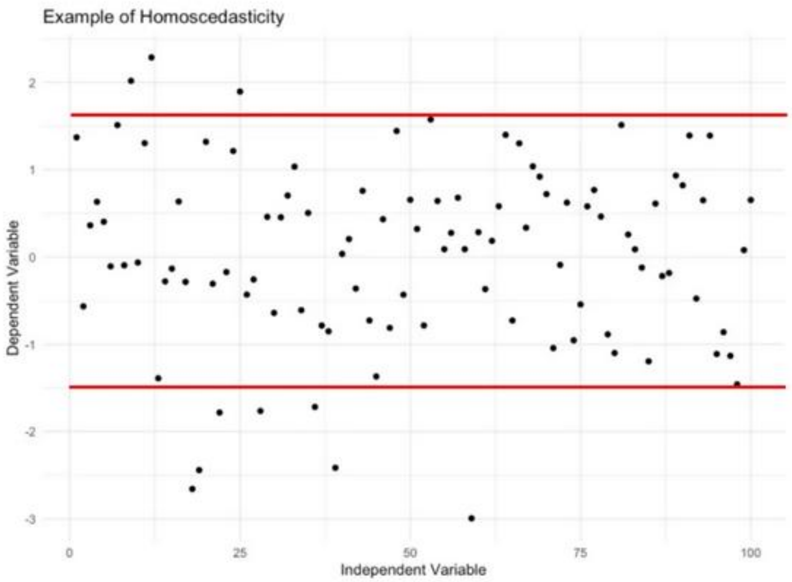
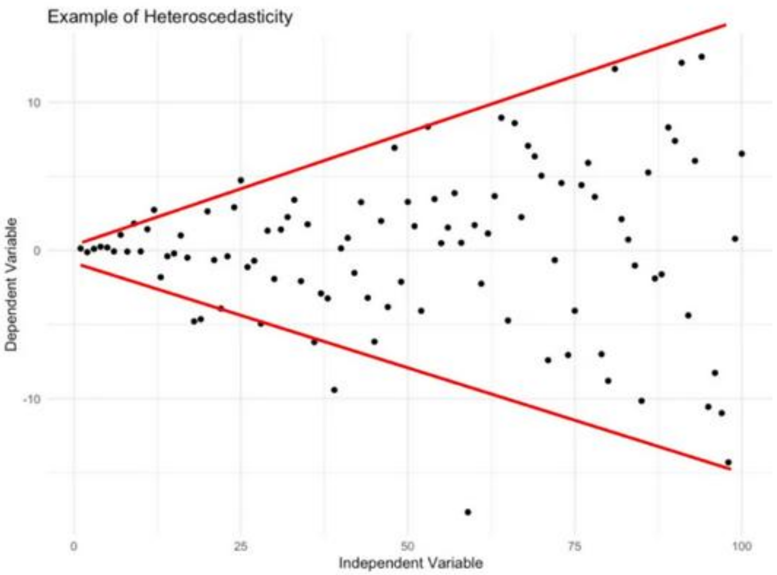


Fitting an allometric model in R
Practice 2

4. Verify model conditions
    - ✓ Homoscedasticity: residuals (yy) versus independent variables (xx)



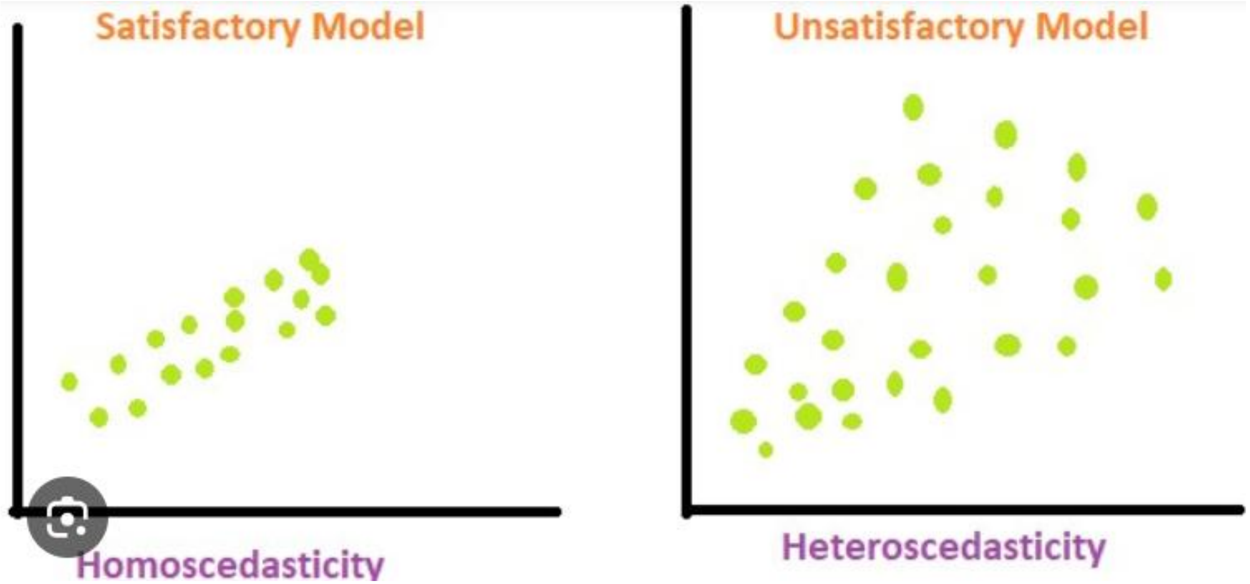
Example of Homoscedasticity



Example of Heteroscedasticity

Fitting an allometric model in R
Practice 2

4. Verify model conditions
   - ✓ Homoscedasticity: Observed values (yy) versus predicted values using the fitted model (xx)



Fitting an allometric model in R
Practice 2

4. Verify model conditions
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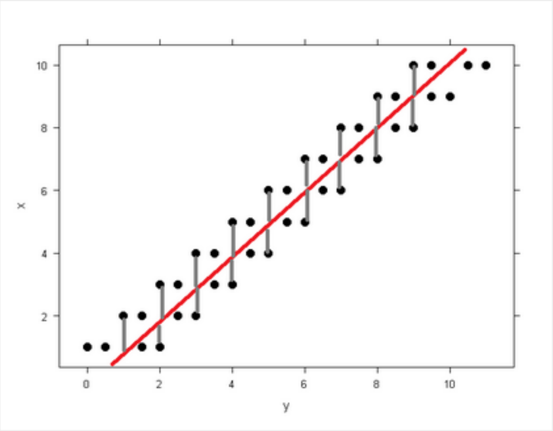
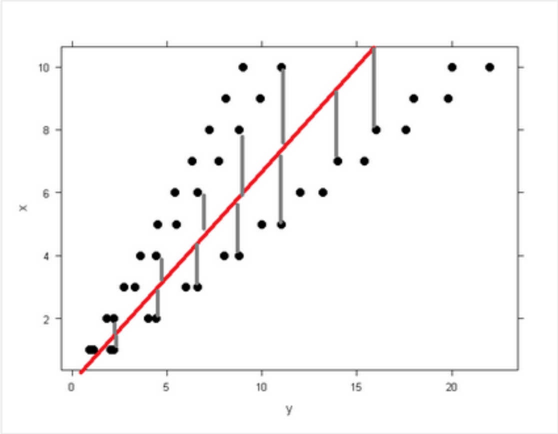
Scatter	Plots
Homoscedastic	Heteroscedastic
	

Additional reading

- MYERS, R. H. 1990. Classical and Modern Regression with Applications. Second edition. Duxbury Classic Series. Chapters 3, 5 and 6.
- Jorge, C.; Tomé, M.; Ruiz-Peinado, R.; Zribi, L.; Paulo, J.A. Quercus suber Allometry in the West Mediterranean Basin. Forests 2023, 14, 649. https://doi.org/10.3390/f14030649
- A.C. Correia, S.P. Faias, R. Ruiz-Peinado, F. Chianucci, A. Cutini, L. Fontes, M.C. Manetti, G. Montero, P. Soares, M. Tomé. 2018. Generalized biomass equations for Stone pine (Pinus pinea L.) across the Mediterranean basin. Forest Ecology and Management, Volume 429, Pages 425-436, https://doi.org/10.1016/j.foreco.2018.07.037
- https://ademos.people.uic.edu/Chapter12.html