.Prac #5 - FINAL

This first experiment was designed to compare total plant dry mass over time in *Arabidopsis* in response to nitrogen availability. The aim of the study was to determine if nitrogen availability influenced plant growth.

For the experiment 100 *Arabidopsis* plants were grown in soil for 21 days then randomised to one of 4 hydroponic tanks. The tanks had either 0.2mM (2 tanks) or 2mM (2 tanks) nitrate as the nitrogen source. Plants were harvested and dried at either 10 days or 24 days. (Because the measurements were destructive repeat measurements were not possible.)

1. Identify the statistical framework for this experiment:  
   outcome measure:  
   experimental factors:  
   blocking factors:  
   Specify the fixed component of the model:  
   Why is it important to take into account the blocking structure in the model?
2. Import the data “Prac 5 Arabidopsis nitrogen.csv”. Look at the structure (str()) of the data and change data types to factors, as needed.
3. Visualise the data using ggplot2. The outcome measure of interest is PlantDM. Comment on within-group variation. What happens if you log-transform the outcome measure PlantDM?
4. Fit a linear model with no random effects. What can you infer about:  
   (a) the nitrogen effect  
   (b) the time effect  
   (c) nitrogen by time interaction
5. Repeat 4. using a linear mixed model. How does your inference change?
6. Get estimated marginal means (emmeans) for Nitrogen and Time, as well as estimates for each treatment condition.
7. Look at residual plots and comment upon whether the model assumptions are reasonable.

You are testing the efficacy of a growth regulator on plant height. You have 3 large tables in a greenhouse where you can arrange your plants in a 6X6 grid. You plan to test 6 doses that you will apply to the plants weekly. You plan to use the final plant height at 8 weeks as your outcome measure.

1. Identify the statistical framework for this experiment:  
   outcome measure:  
   experimental factors:  
   blocking factors:  
   Specify the fixed component of the model:  
   Why is it important to take into account the blocking structure in the model?
2. Import the data “Prac 5 plant growth.csv”. Look at the structure (str()) of the data and change data types to factors, as needed.
3. Visualise the data using ggplot2. Comment on the patterns you observe.
4. Fit a linear model with no random effects. What can you infer about the Dose effect?
5. Repeat 4. using a linear mixed model. How does your inference change?
6. Get estimated marginal means (emmeans) for each Dose, and compare mean height between doses.
7. Look at residual plots and comment upon whether the model assumptions are reasonable.

Nematode infection may have serious consequences to plant health. This experiment was conducted in order to assess which genes are relevant to host response. Using the model organism legume *Medicago Truncatula,* three candidate genes were identified and selectively knocked out to create three mutant lines. Wild type and mutant plants were grown in a greenhouse in three separate experiments. In each experiment, half of the plants were infected with nematodes. Several phenotypic measurements were made after 8 weeks. For our analysis, we will focus on assessing the effect of mutation and infection on plant weight.

1. Identify the statistical framework for this experiment:  
   outcome measure:  
   experimental factors:  
   blocking factors:  
   Specify the fixed component of the model:  
   Why is it important to take into account the blocking structure in the model?
2. Import the data “Prac 5 nematode.csv”. Look at the structure (str()) of the data and change data types to factors, as needed.
3. Visualise the data using ggplot2. Comment on the patterns you observe.
4. Fit a linear model with no random effects. What can you infer about the effect on infection on the plants? Is this effect modulated for the mutant plants?
5. Repeat 4. using a linear mixed model. How does your inference change?
6. Get estimated marginal mean plant weight (emmeans) for each infection status and genotype.
7. Look at residual plots and comment upon whether the model assumptions are reasonable.

This experiment was conducted to quantify the effect of temperature on leaf respiration in banana trees, and the differential effect of temperature between genotypes. Twenty (20) banana plants were grown in each of 4 sheds, 10 plants of genotype A and 10 plants of genotype B. For each plant, four “plugs” were sampled from a designated leaf. A plug was exposed to 1 of 4 temperatures (low, medium, high and very high), and respiration recorded.

1. Identify the statistical framework for this experiment:  
   outcome measure:  
   experimental factors:  
   blocking factors:  
   Specify the fixed component of the model:  
   Why is it important to take into account the blocking structure in the model?
2. Import the data “Prac 5 respiration.csv”. Look at the structure (str()) of the data and change data types to factors, as needed.
3. Visualise the data using ggplot2. Comment on the patterns you observe.
4. Fit a linear model with no random effects. What do you infer about the effect on temperature on respiration? Does this effect differ between genotypes?
5. Repeat 4. using a linear mixed model. How does your inference change?
6. Get estimated marginal mean respiration (emmeans) for each temperature and genotype.
7. Look at residual plots and comment upon whether the model assumptions are reasonable.