

BL6024 Assessment

All scripts must be fully annotated and completely reproducible. Marks for each bit are in brackets, in bold, after each.

Install and load the 'MEMSS' package and use the 'RatPupWeight' dataframe contained within it. To load it, just type `data(RatPupWeight)` into R after you have installed and loaded the MEMSS package.

1. Accounting for the effect of treatment, is there a difference in mean pup weight between the sexes? **(10 marks)**
2. Make an appropriate plot that illustrates the difference in mean pup weight between each of the sexes *within* each treatment. **(10 marks)**
3. A) Accounting for the fact that multiple pups were measured within each litter, determine if sex and litter size affect pup weight. Conduct all appropriate model and significance checks. **(20 marks)**.

B) What percentage of total variance is explained by variation within litters? **(10 marks)**
4. Using a generalized linear model (GLM) with an appropriate link function, determine if sex, treatment and weight and all possible two-way interactions between them affect litter size. Start with a model with main effects and interactions, and then simplify it using backwards model selection. Conduct all appropriate model and significance checks. **(20 marks)**. Bonus marks: is there underdispersion or overdispersion in your final best model, and why? **(10 marks)**
5. Generate a plot with weight on the x-axis and litter size (Lsize) on the y-axis, and then plot the predicted effects (on the original data scale) from the best model from step 4. Note you need to back-transform from the link scale here, i.e. the resulting predicted effects will be curves. Colour code the data points and predicted curves to highlight any statistically significant main effects or interactions involving categorical variables from the final minimum adequate model. **(20 marks)** You can use ggplot or base R here!