***2.5 Statistical Analysis (rough draft)***

Each of the 10 treatment combinations (Display Time, Cutting Technique) were tested and measured for microbial information in each of three batches, with two independent replicates per treatment in each batch. The physiochemical measurements also were measured in a similar experimental design, but an experimental unit was instead each fabricated steak. A linear mixed effects model was used to treat batch as a random effect (1 | Batch), which allows the data to be modeled in a nested structure through batch. An ANOVA could not replicate a similar statistical analysis due to its independence assumption being violated. Additionally, accounting for random effects allows a more thorough generalization of the analysis results to a larger population since random effects account for within and between batch variability. Finally, since the data included repeated measures (multiple steaks from the same cow would hold the assumption that two cuts from one cow are more similar than two cuts from different cows) a linear mixed effects model handles this within-subject association.

Mathematically, the linear mixed effects model included cutting method, display time, and muscle type (only for the physiochemical measurements) as well as all possible interaction terms across these factors as fixed effects. Each model was then analyzed post hoc to determine which groups were significantly different across combinations of display time and cutting technique at (P < 0.5). For physiochemical measurements, these differences were conditioned on the muscle type to emphasize the interaction between cutting technique and display time within each muscle type.