

Assignment 2

Your Name

2025-09-03

Goal of this assignment

The goals of this assignment are to:

- Review treatment structure and design structure of designed experiments.
- Analyze data generated by a designed experiment using statistical software.

Please complete exercises (1) and (2), rename the Rmd file to “Assignment2_YourLastName.Rmd” (e.g., “Assignment2_Smith.Rmd”), your name in the header, and knit the Rmd to an html file or pdf file. Please submit that html or pdf file on CANVAS by Wednesday, September 10th by midnight. You may work in pairs, but each one of you will have to submit your own file.

Formatting:

Please make sure that your knitted pdf or html document does not include unnecessary warnings/messages. For the statistical models, you can use \LaTeX code embedded in your Rmd, or paste a picture. You can check the raw Rmd files from the lectures (including \LaTeX code) at https://github.com/stat870/fall2025/tree/main/_notes. Otherwise, you can check out the Rmd cheatsheet or the `knitr::include_graphics()` function.

1.

Below are two snippets from peer-reviewed papers. For all, identify the treatment structure, the design structure, or mention if this information is unclear or unavailable.

1a. Plasma concentrations of substance P and cortisol in beef calves after castration or simulated castration

2.

The data in the code below correspond to a multi-environment trial of sorghum, with 18 genotypes in 6 environments

2a.

Write the statistical model that best represents the data generating process.

```
library(tidyverse)
library(agridat)
library(glmmTMB)
data("omer.sorghum")
df <- omer.sorghum
model1 <- glmmTMB(yield ~ 1 + gen + env + (1|env:rep),
                  data = df)
```