

Mob grazing data pull

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2025-01-31

Data summary

year	spring pregraze	summer	fall pregraze
2017	18	native grass equation	17
2018	18	36	18
2019	35	36	no data collected

Notes

- For 2019 summer, the bottle codes were incorrectly labelled as 80000s instead of 90000s. We corrected this just in the sheet, inferring that 80000s were impossible due to no bottle codes being made for those and other factors.
- For 2019 summer, we inferred crop and timing based on treatment info, NIRS values and plot ordering. the crop and timing was not originally included in bottle code
- For 2019 spring pregraze, we inferred crop and timing info based on treatment info and plot ordering. Bottle codes where phosphorous column = P were not included as these are microplots
- For summer 2017, native grass equation was used which does not predict ADF or protein preventing forage quality determination. See 30Jan2025 datapull for native grass data for summer harvest 2017 and compare with bottle codes in 2017 fieldwork log. [2017 data for summer and fall pregraze](#)
- Final data file = [Mob.jpb.v1](#), sheet = final

Calculating forage quality parameters

```
library(tidyverse)

source("functions_nir.R")

read.csv("mob.jpb.v1.xlsx - final (1).csv") -> dat

# tidy.nir.report function does not work because I messed with dataframe slightly. Copying the

dat %>%
  rename_all(., tolower) %>%
  select(1:35) %>% # take out the unnecessary columns
  mutate(
    code = `bottle.code`,
    drymatter = dry.matter,
    protein = `protein.dry.basis`,
    adf = `adf.dry.basis`,
    ndf = `ndf.dry.basis`,
    ndf48h = ndfd48.as.is) %>%
  select(code, drymatter, protein, adf, ndf, ndf48h) %>%
  mutate(
    # protein = protein * drymatter / 100, already dry basis
    # adf = adf * drymatter / 100,
    # ndf = ndf * drymatter / 100,
    ndf48h = ndf48h * drymatter / 100) -> dat1

calc.rfq.rfv(dat1) -> dat2

dat %>%
  select(1:8) %>% # take out the unnecessary columns
  mutate(code = bottle.code) %>%
  filter(code != "NA") %>% # the NA values were kicking out left_join issue
  left_join(dat2) %>%
  select(1:6, protein, adf, ndf, ndf48h, rfq.grass, rfq.legume, rfv) %>%
  write.csv("mobGrazing_forageQuality_30Jan2025.csv",
    row.names = F)
```