

# Calecopal Plots

Heili Lowman

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## “calecopal” exploration

The following script will demonstrate the available color palettes as part of the “calecopal” package written by An Bui, Ana Sofia Guerra, and yours truly. For more info, go to <https://github.com/an-bui/calecopal>.

Palettes for which only 5 colors exist have plots using a truncated version of the dataset created using the “chickwts” dataset and “tidyverse” package.

NOTE: This document contains no continuous color palettes although that is a functionality of the package.

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```
library(tidyverse) # Loads tidyverse.
```

```
## -- Attaching packages ----- tidyverse 1.2.1 --
```

```
## v ggplot2 3.2.0    v purrr  0.3.3
## v tibble  2.1.3    v dplyr  0.8.1
## v tidyr   0.8.3    v stringr 1.4.0
## v readr   1.3.1    v forcats 0.4.0
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(datasets) # Loads datasets automatically available in R.
```

```
library(calecopal) # Loads color palettes.
```

```
data() # Explores freely available data.
```

```
# We're going to first use the chickwts dataset to explore discrete color packages rather than continuous
```

```
#View(chickwts) # Pulls up chosen dataset.
```

```
chicks <- chickwts %>% # Takes original dataset and then...
```

```
  group_by(feed) %>% # Groups all data by "feed" column and then...
```

```
  summarize(meanW = mean(weight, na.rm = TRUE)) %>% # Calculates the mean weight of chicks and then ...
```

```
  ungroup() # Removes grouping so it doesn't cause formatting issues later.
```

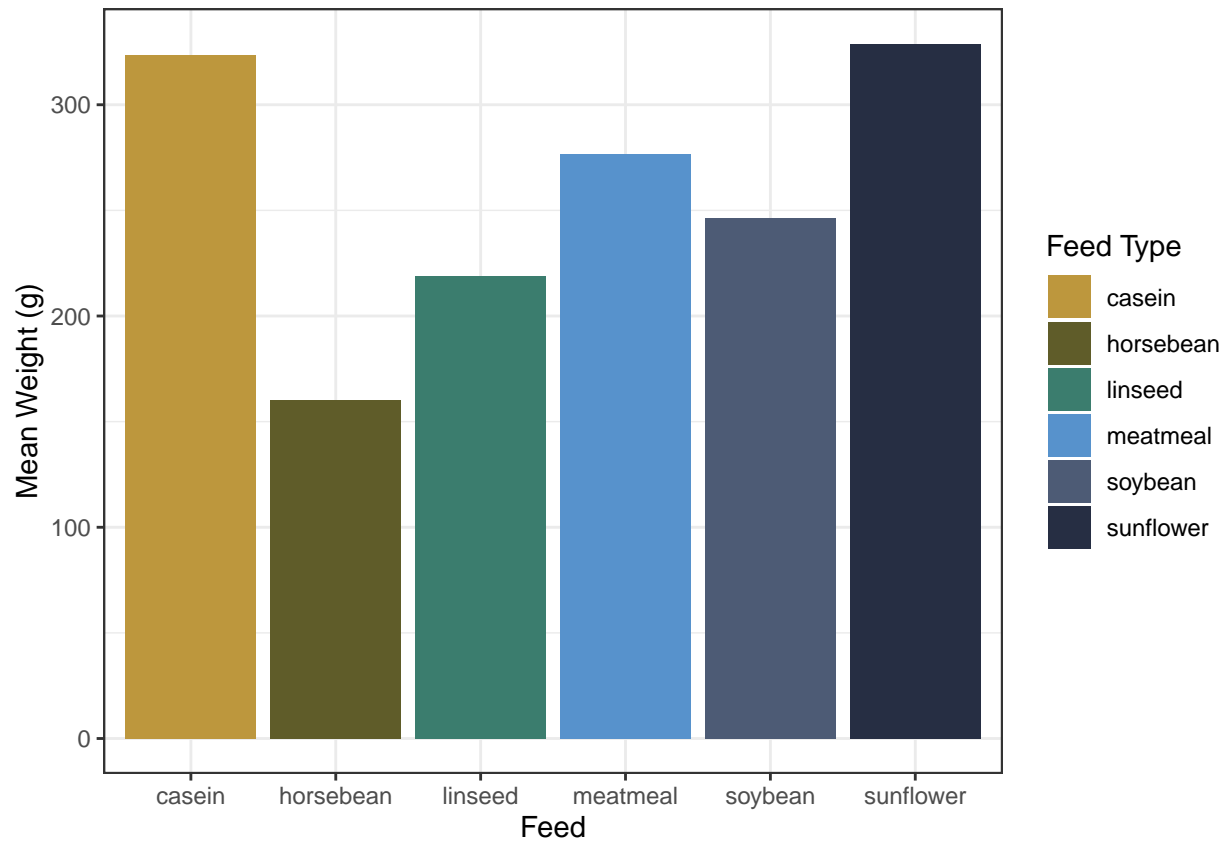
```
#View(chicks) # Displays newly created dataset.
```

```
names(cal_palettes) # Take a look at the available palettes. 22 in total.
```

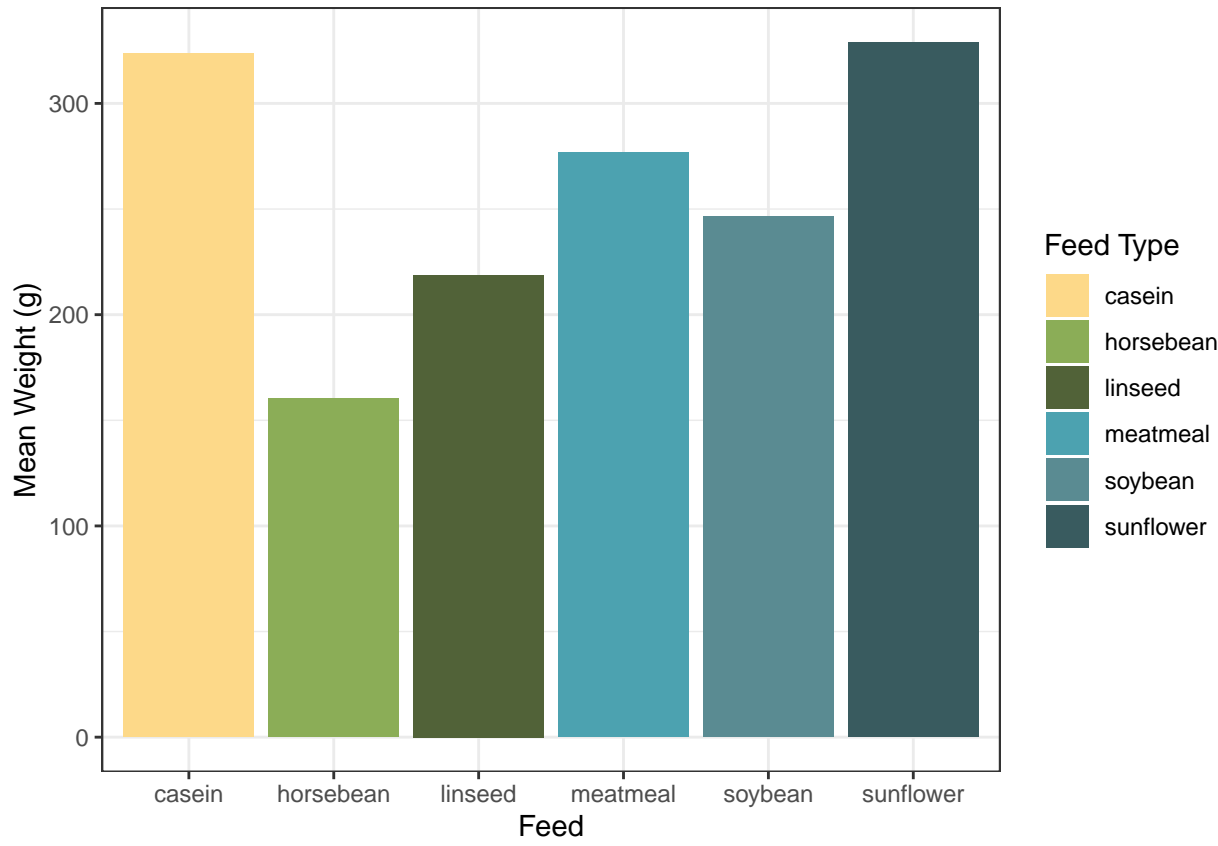
```
## [1] "sierra1"    "sierra2"    "chaparral1" "chaparral2"
## [5] "chaparral3" "conifer"    "desert"     "wetland"
## [9] "oak"        "kelp1"      "kelp2"      "coastaldune1"
## [13] "coastaldune2" "superbloom1" "superbloom2" "superbloom3"
## [17] "sbchannel"   "lake"       "fire"       "agriculture"
## [21] "bigsur"     "figmtn"
```

## sierra1

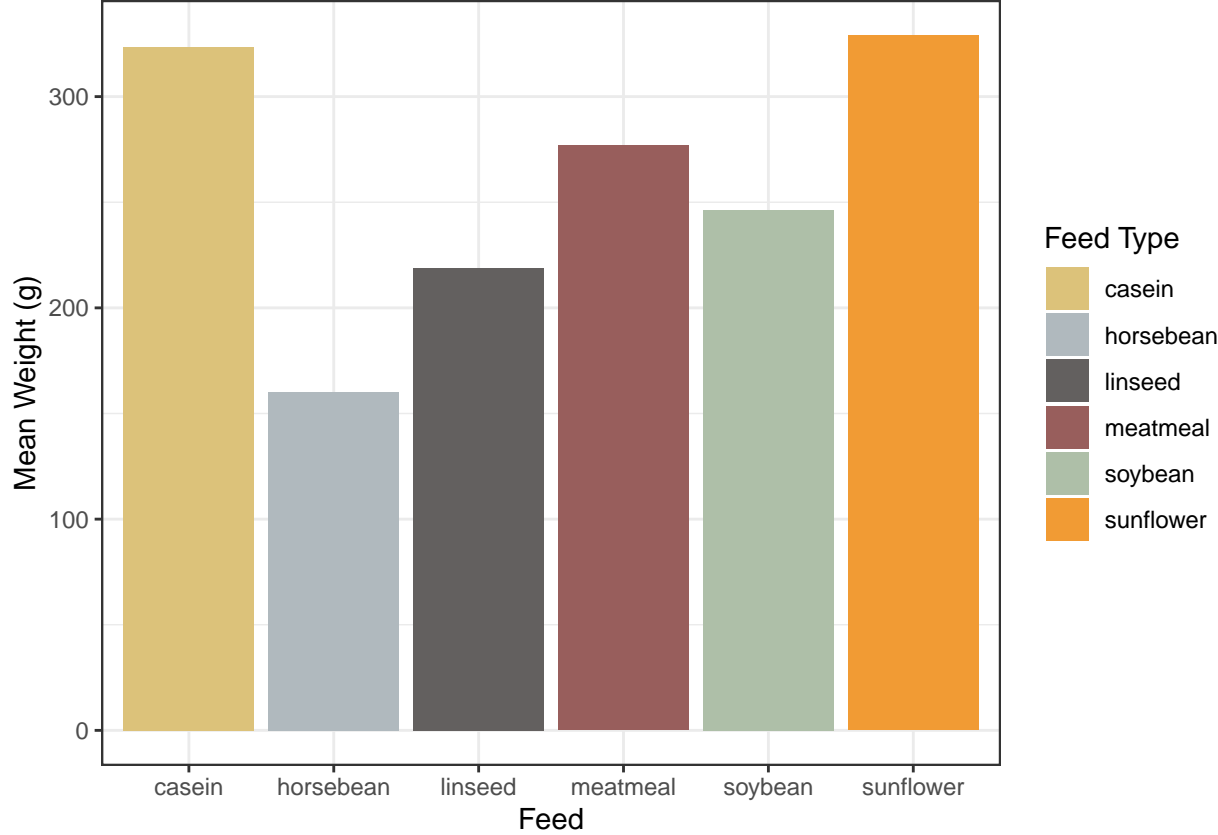
```
plot1 <- ggplot(chicks, aes(feed, meanW, fill = feed)) + # Creates basic plot.  
  geom_bar(stat = "identity") + # Specifies bar plot.  
  scale_fill_manual(name = "Feed Type", values = cal_palette("sierra1")) + # Uses calecopal palette.  
  theme_bw() + # Removes most gridlines.  
  xlab("Feed") + # Renames x axis.  
  ylab("Mean Weight (g)") # Renames y axis.  
  
plot1 # Displays plot.
```



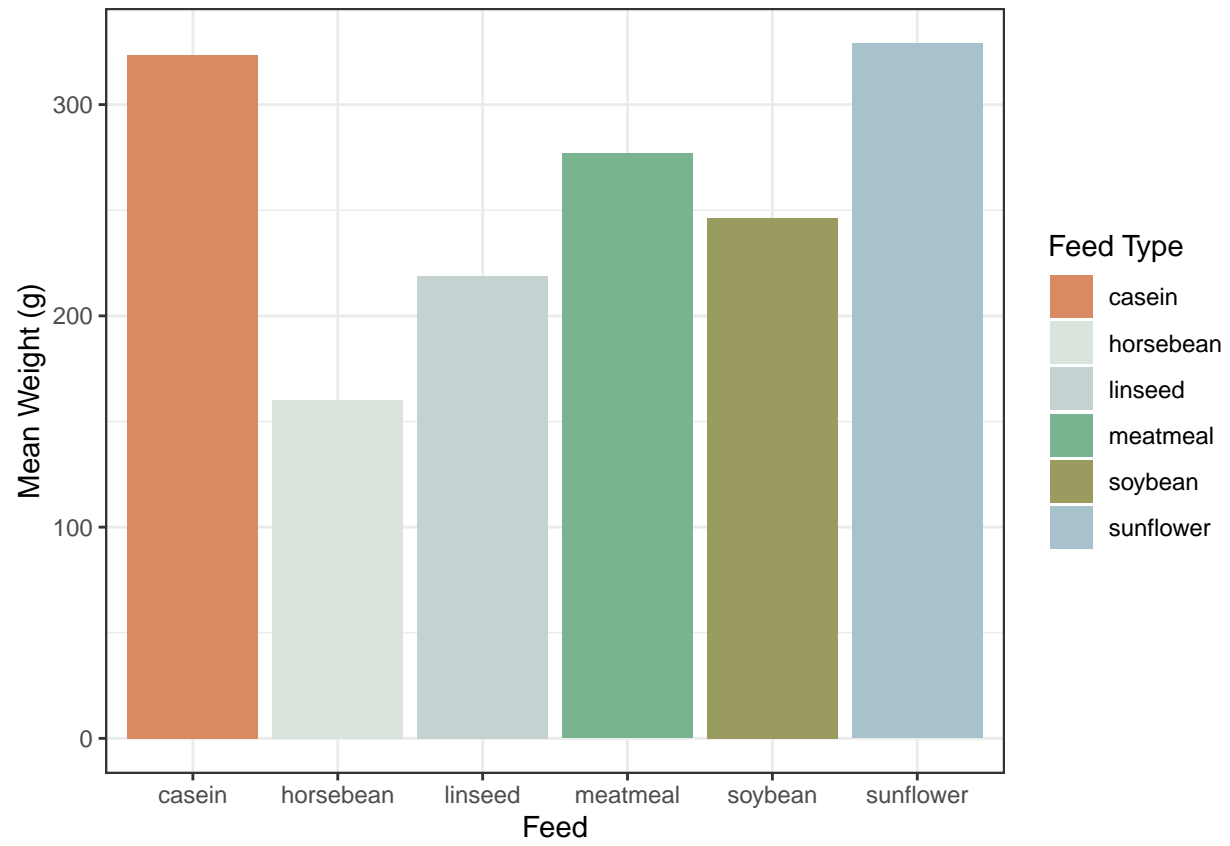
sierra2



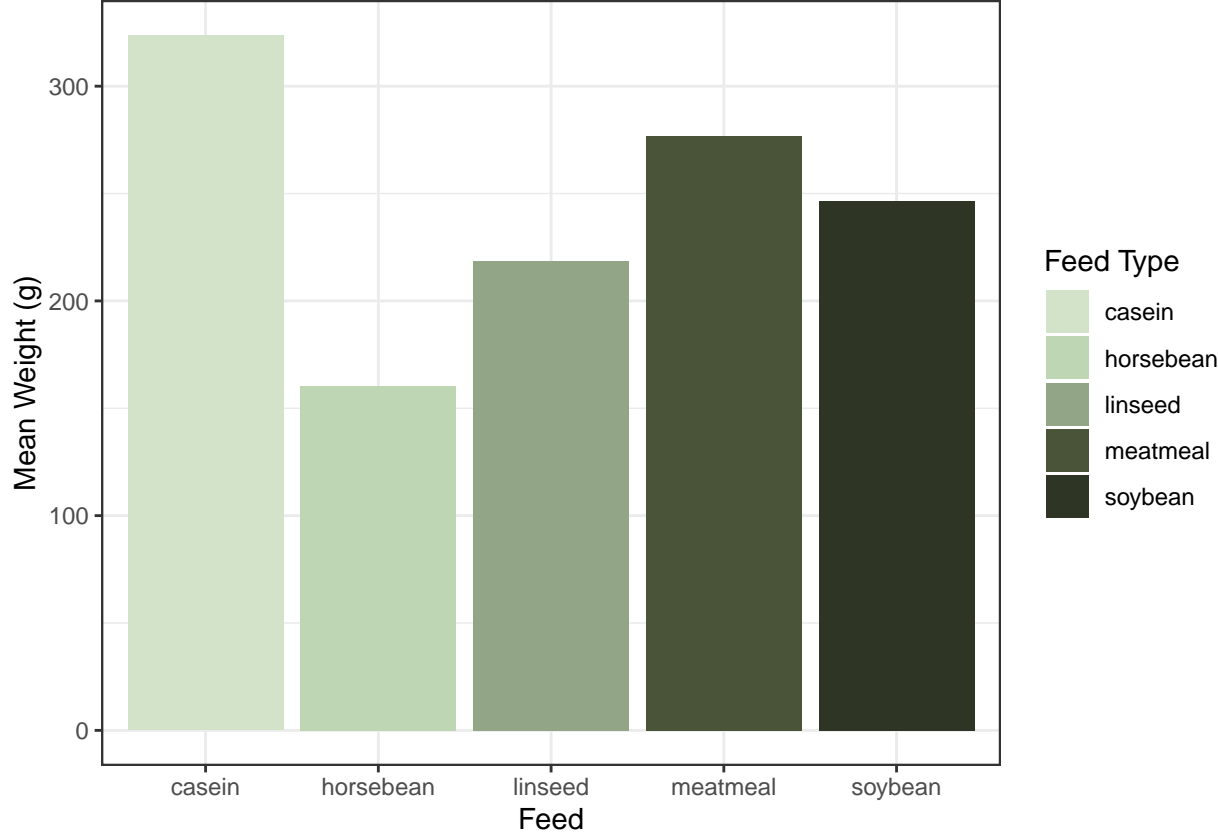
chaparral1



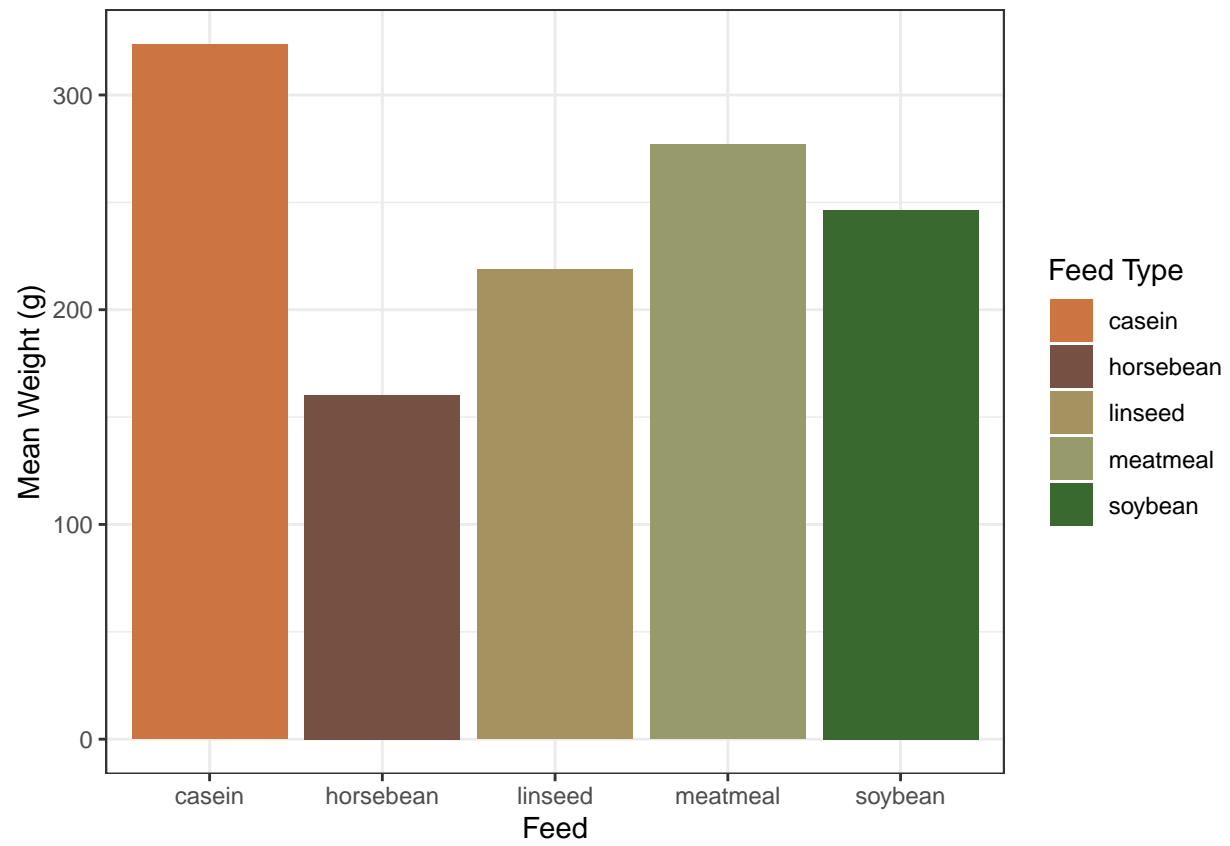
chaparral2



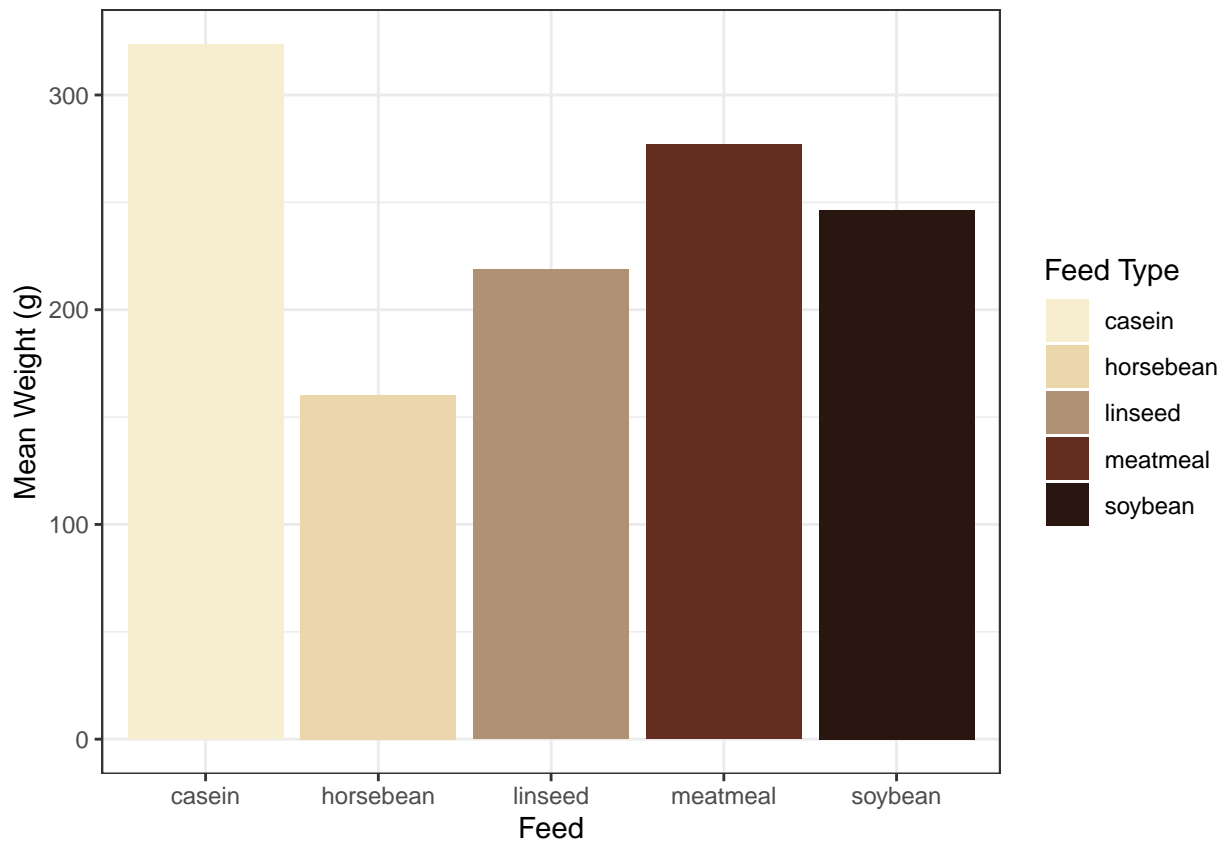
chaparral3



conifer

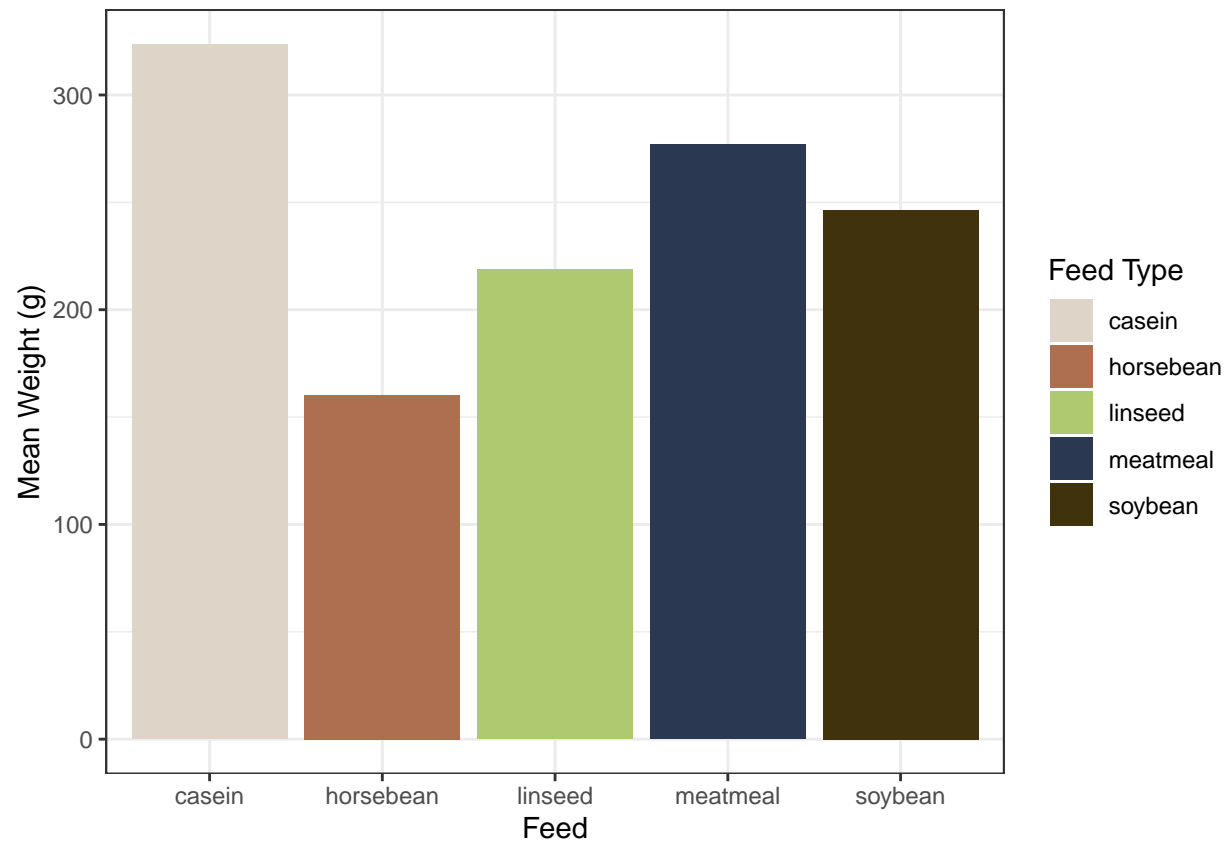


desert

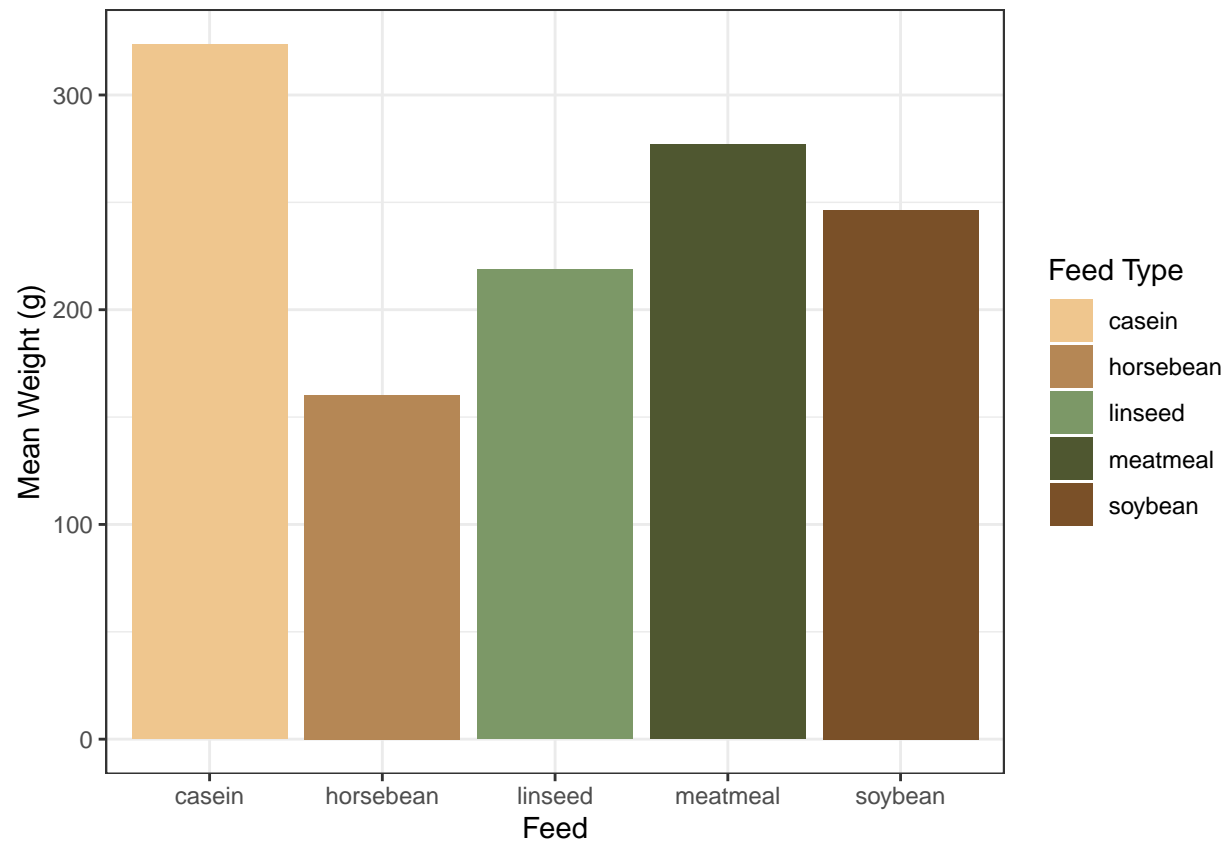




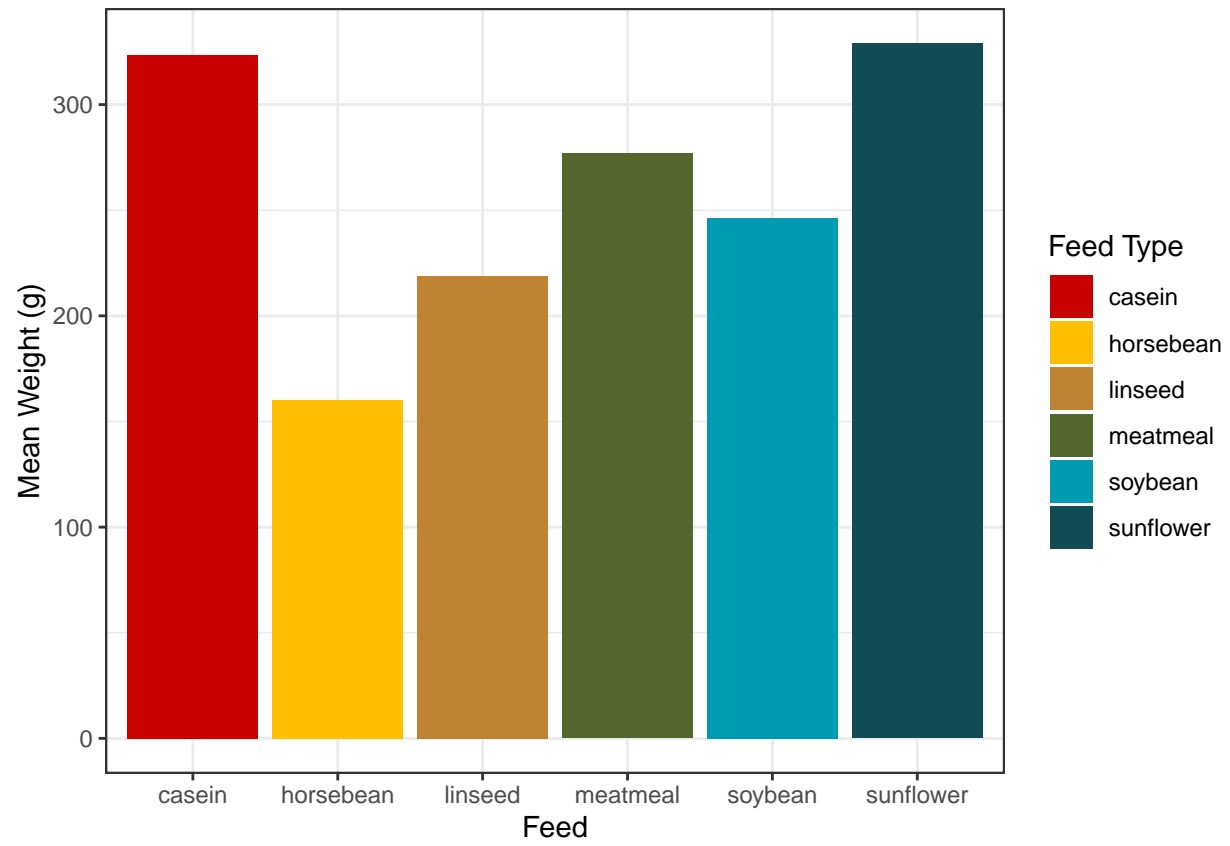
wetland



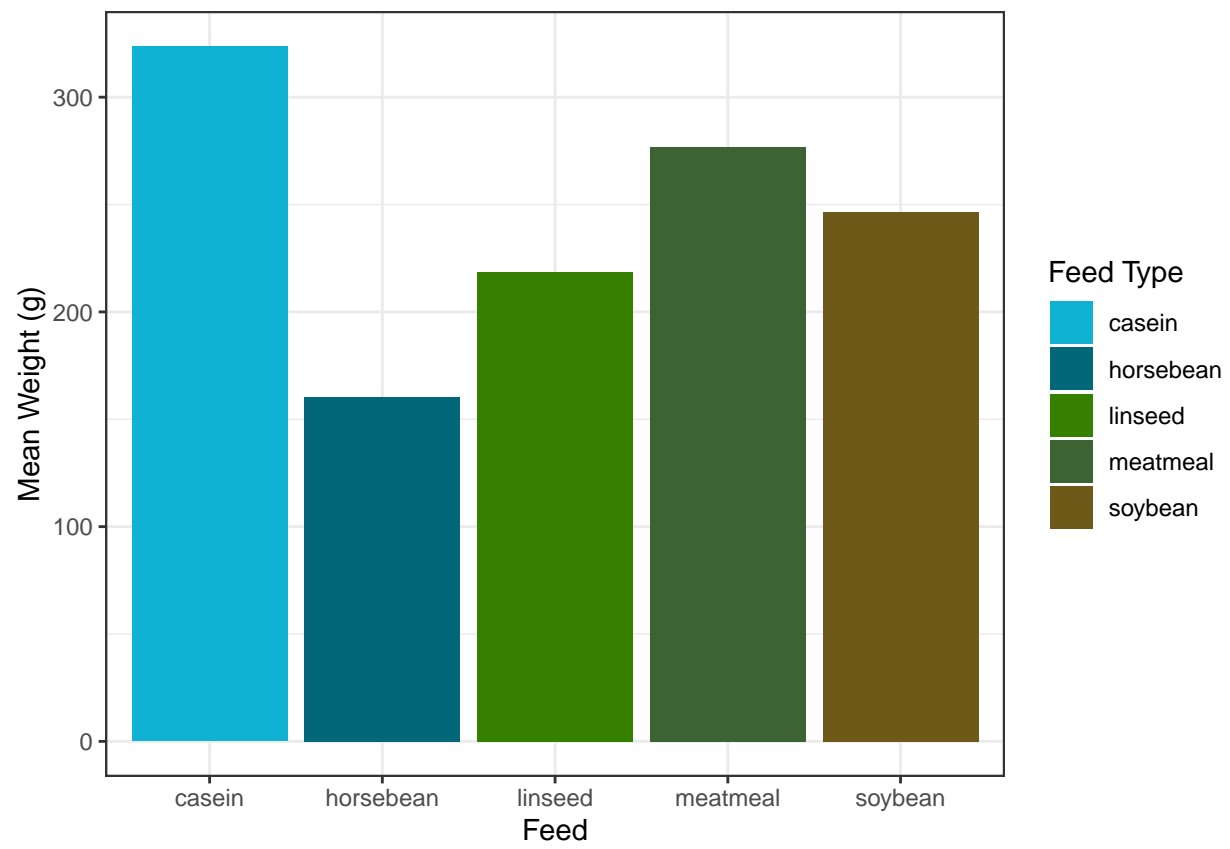
oak



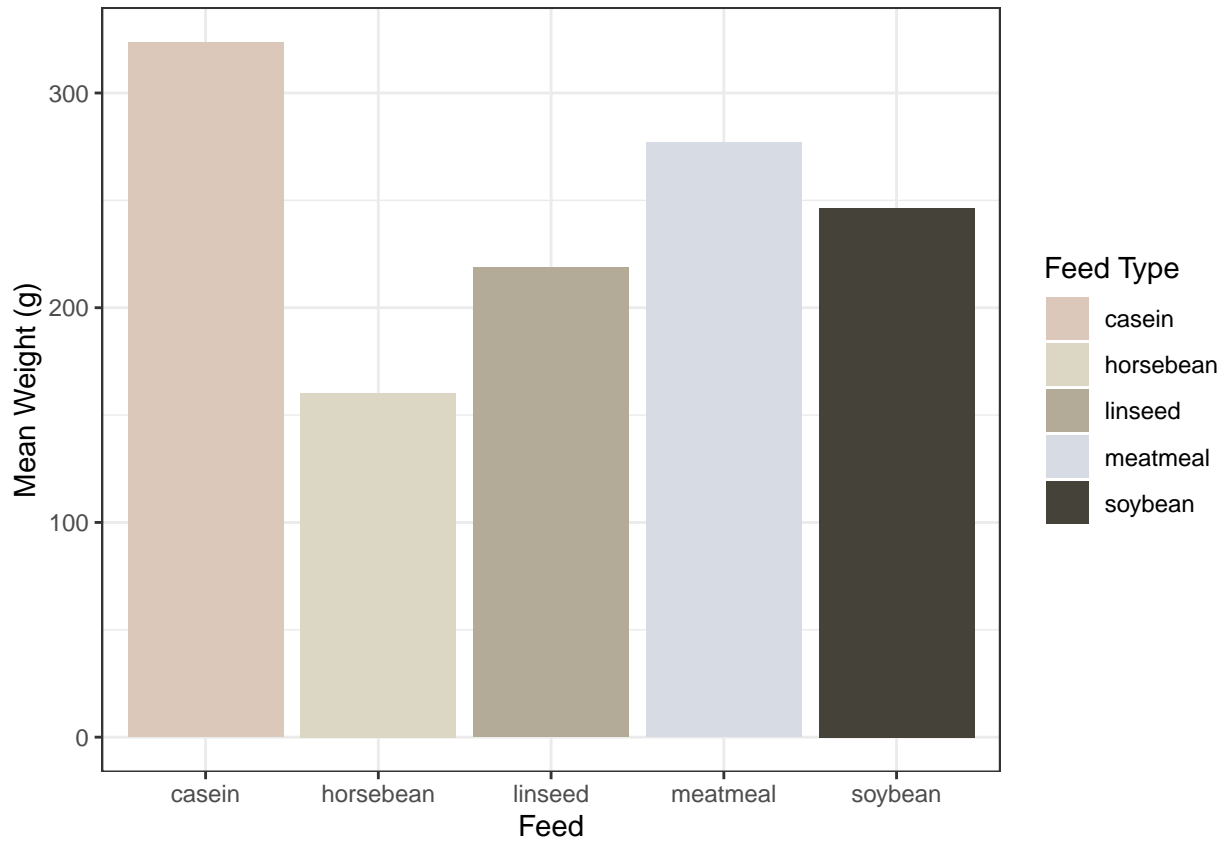
kelp1



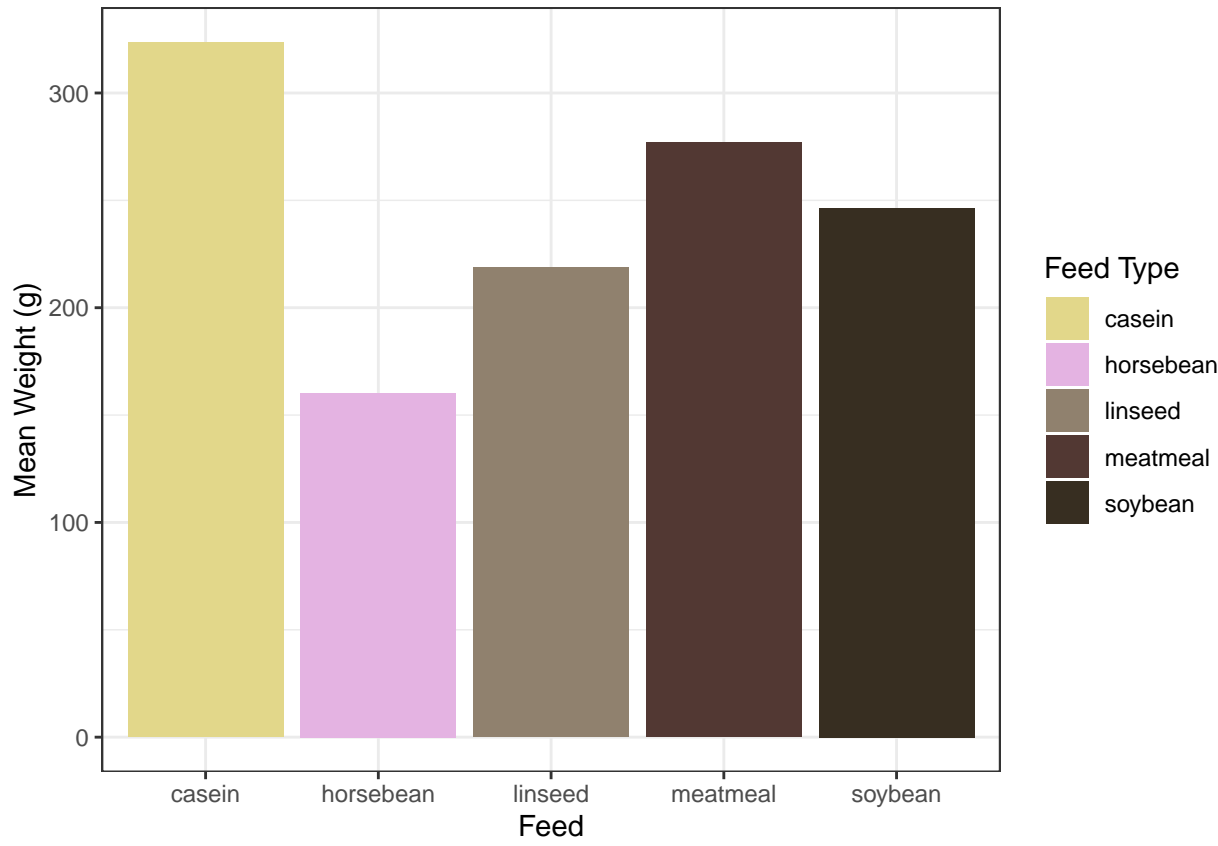
kelp2



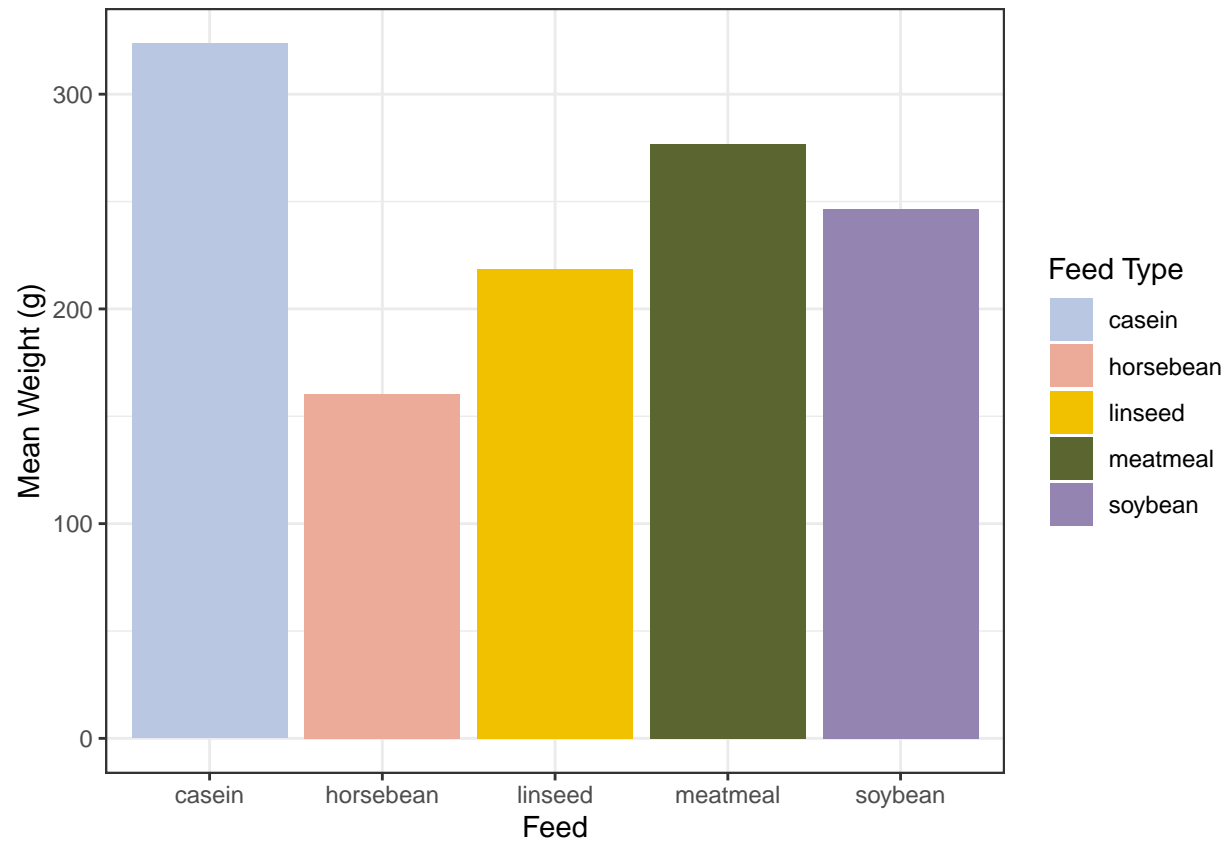
coastaldune1



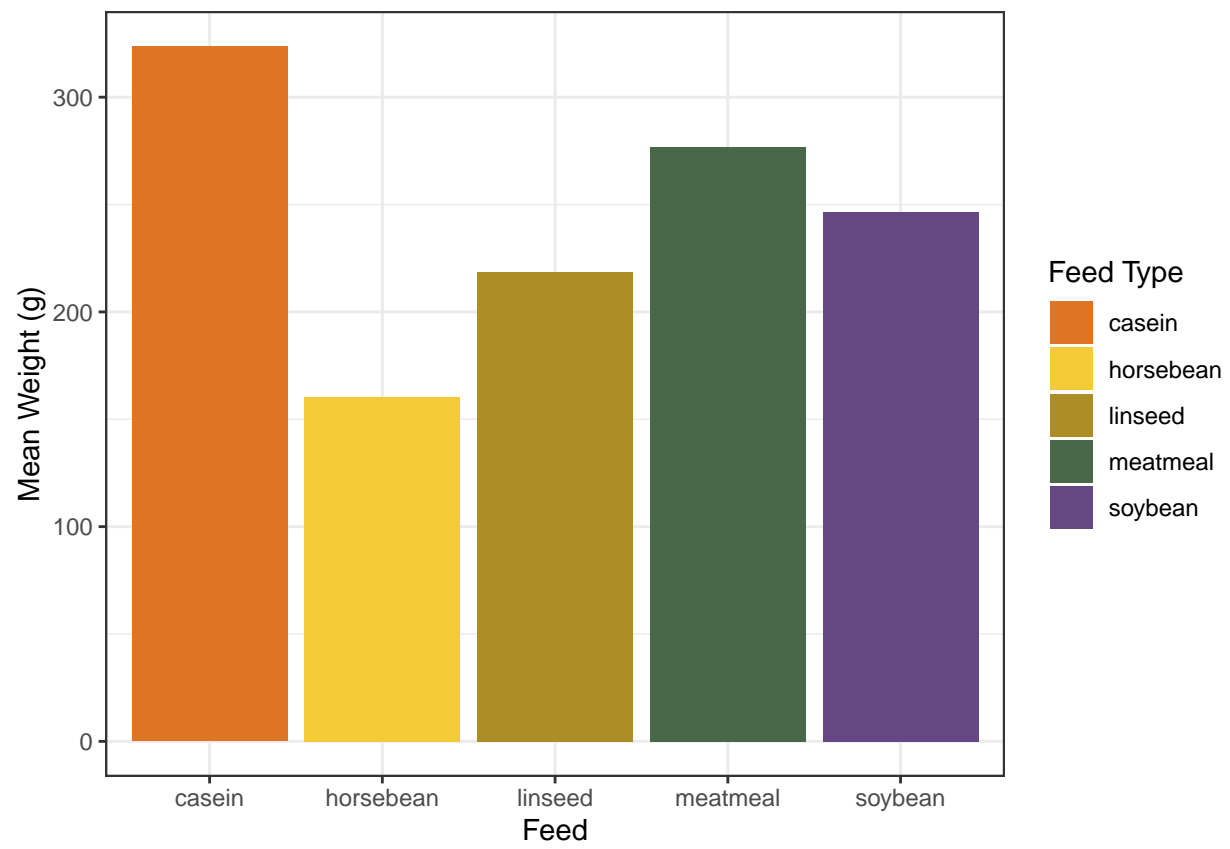
coastaldune2



superbloom1

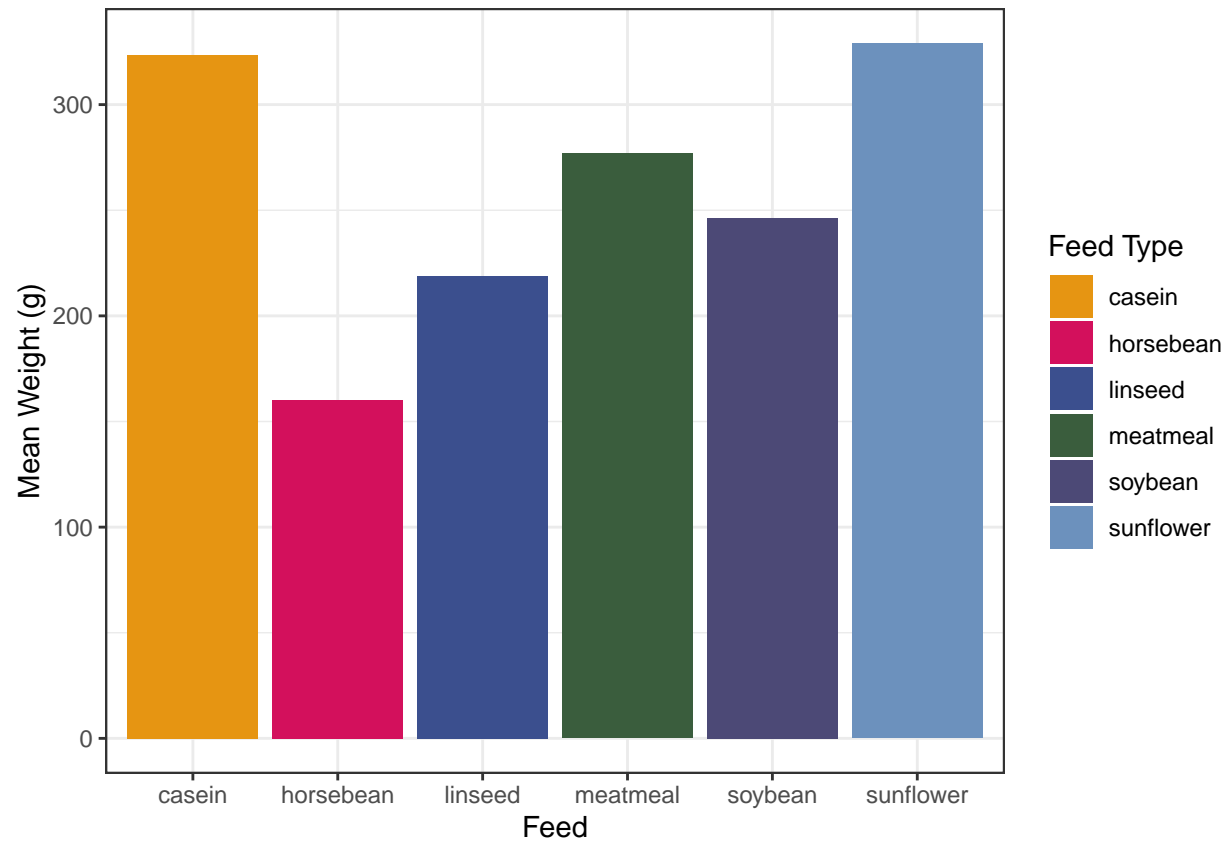


superbloom2

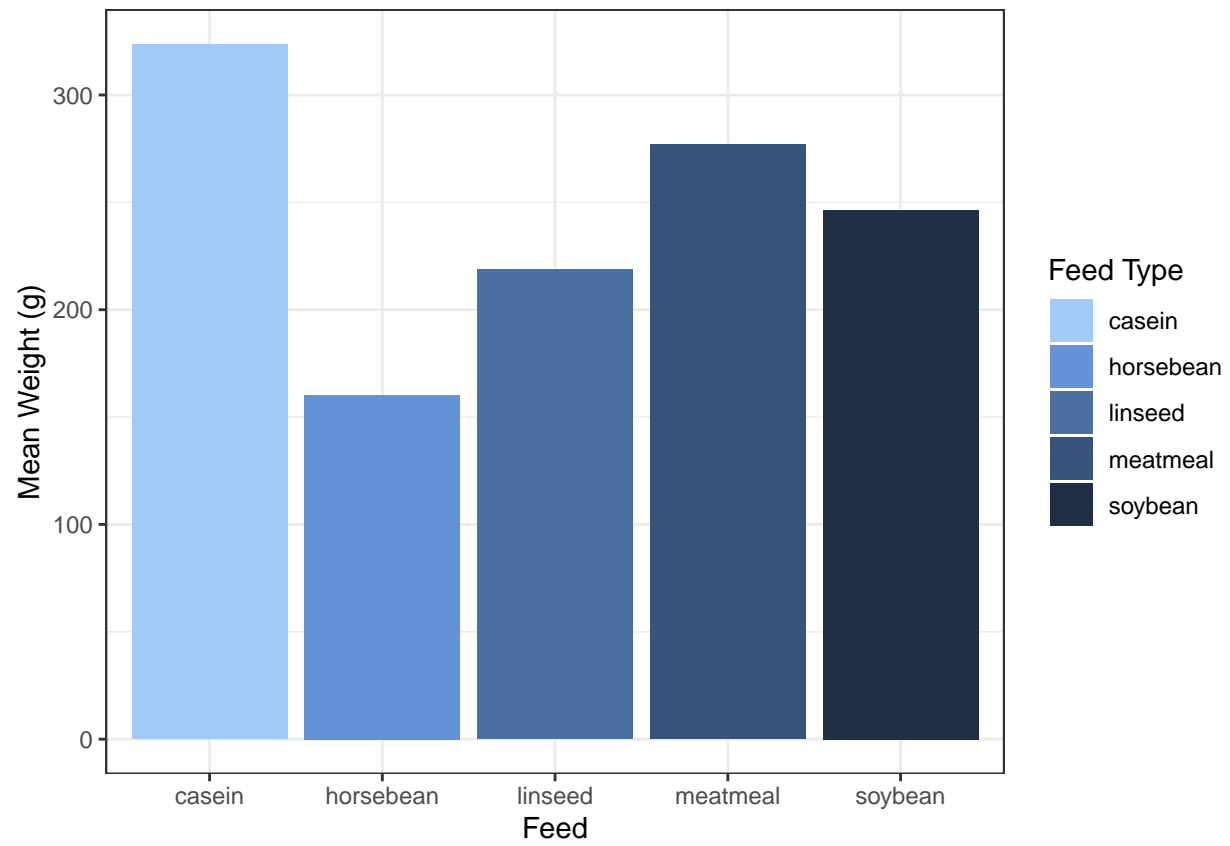




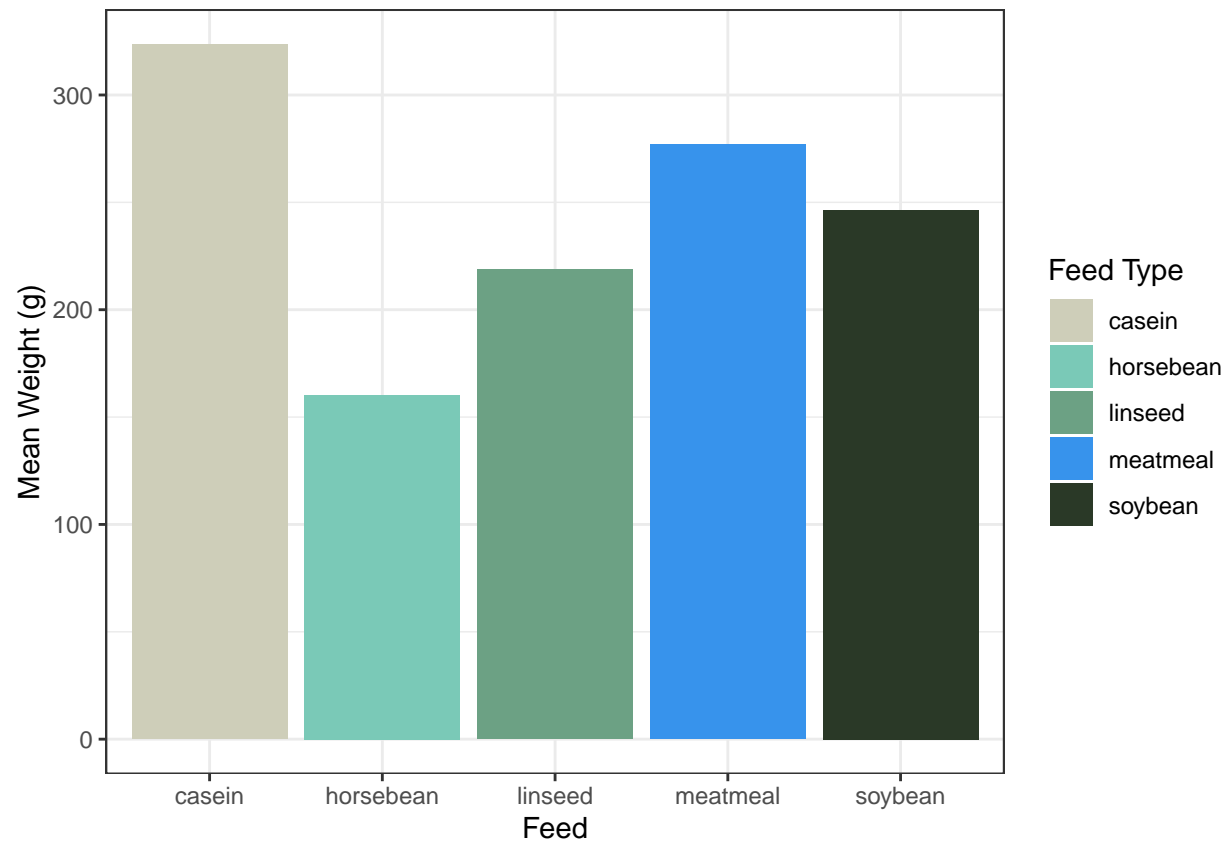
superbloom3



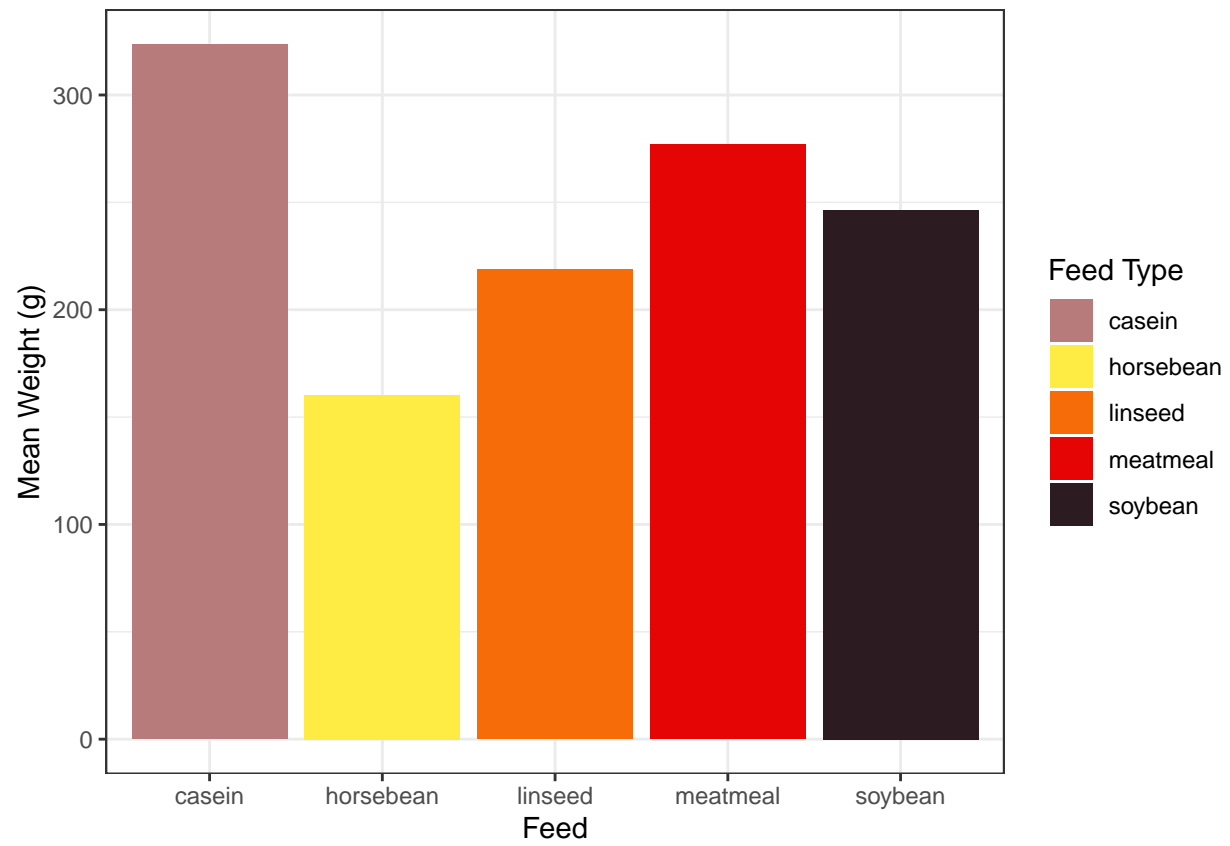
sbchannel



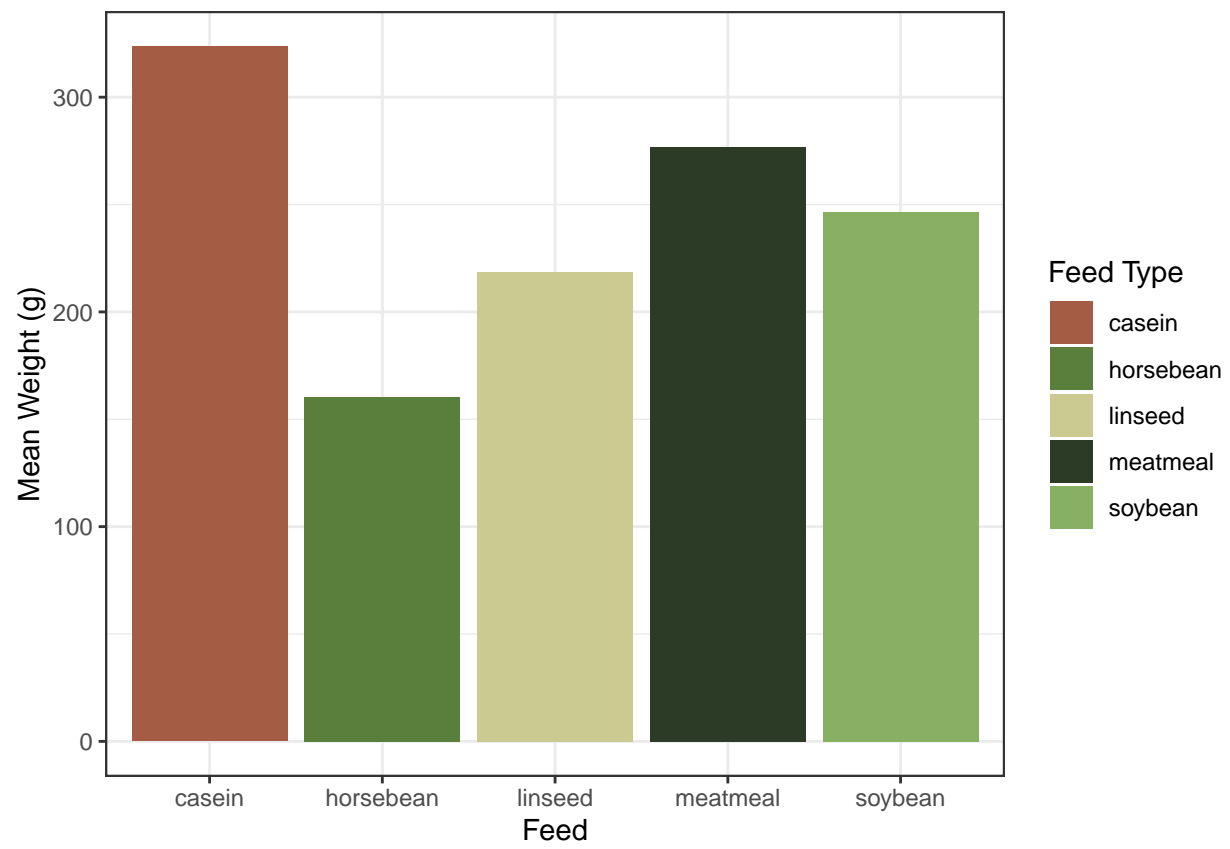
lake



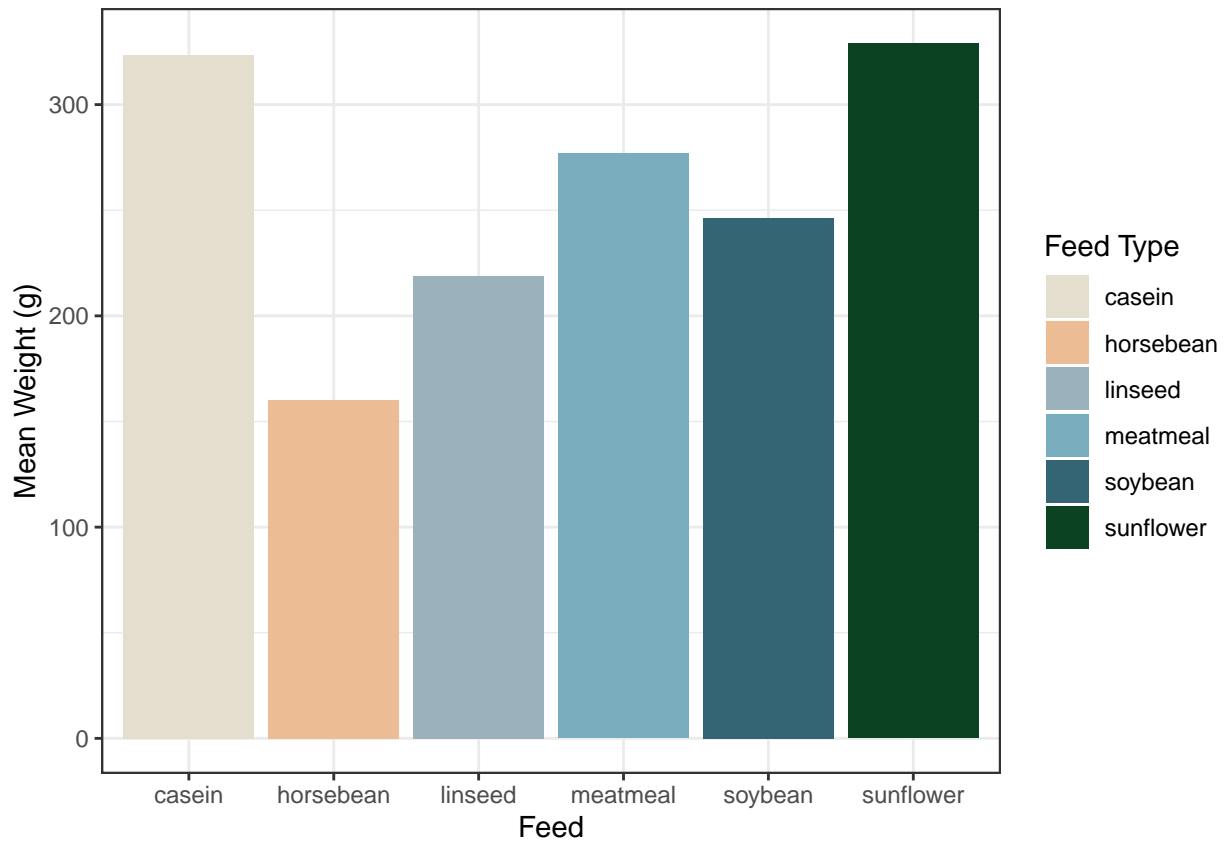
fire



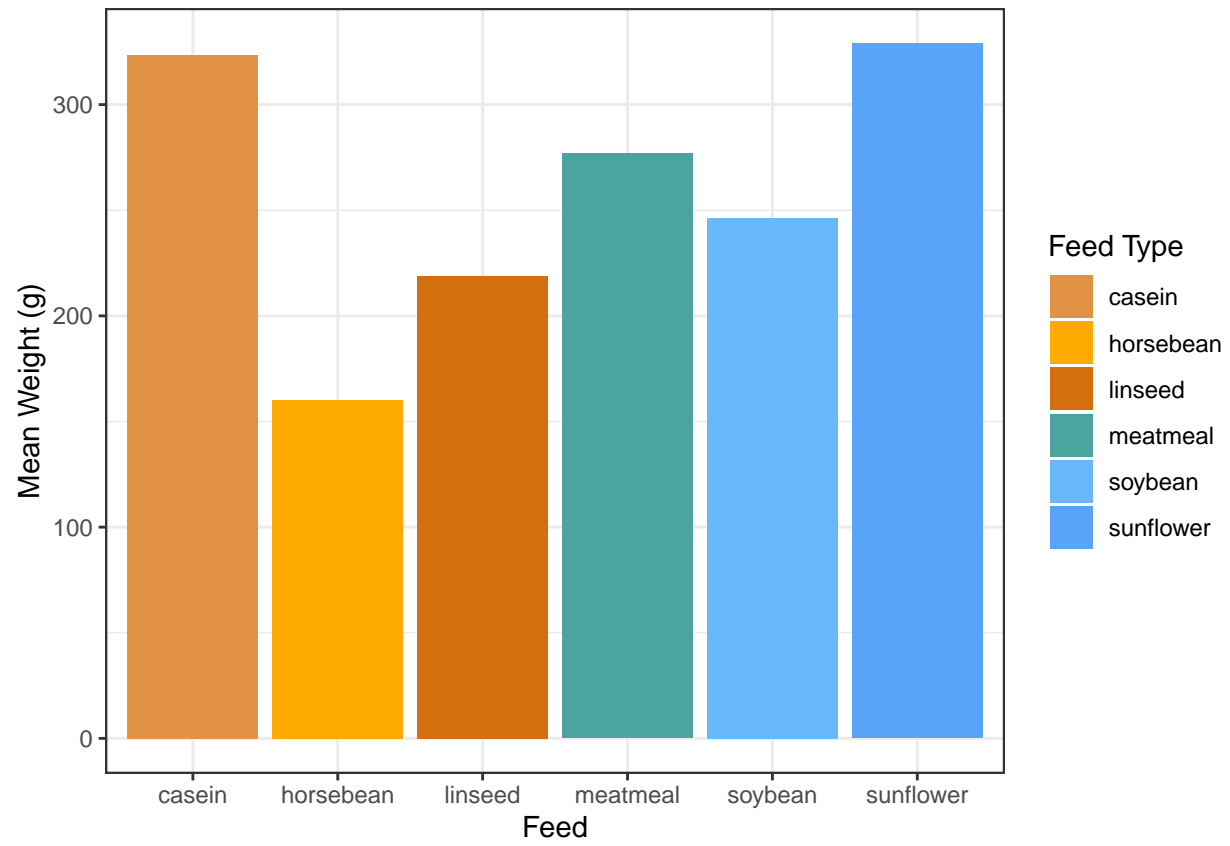
## agriculture



bigsur



figmtn



End of R Markdown file.