

Comparison using R

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2024-07-19

Importing Data Set for Analysis

For today's analysis we'll be using "chickwts" built in data set of R.

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2    3.5.1      v tibble    3.2.1
## v lubridate  1.9.3      v tidyr     1.3.1
## v purrr      1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
data("chickwts")
df <- chickwts
unique(df$feed)
```

```
## [1] horsebean linseed  soybean  sunflower meatmeal  casein
## Levels: casein horsebean linseed meatmeal soybean sunflower
```

```
mean_data <- group_by(df, feed) %>% summarise(weight_mean= mean(weight),
                                              sd = sd(weight)) %>%
  arrange(desc(weight_mean))
print(mean_data)
```

```
## # A tibble: 6 x 3
##   feed      weight_mean    sd
##   <fct>          <dbl> <dbl>
## 1 sunflower      329.  48.8
## 2 casein         324.  64.4
## 3 meatmeal      277.  64.9
## 4 soybean       246.  54.1
## 5 linseed       219.  52.2
## 6 horsebean     160.  38.6
```

ANOVA on 'Chickwts' Data Set

```
library(tidyverse)
library(stats)
library(multcomp)
```

```
## Loading required package: mvtnorm

## Loading required package: survival

## Loading required package: TH.data

## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##   select

##
## Attaching package: 'TH.data'

## The following object is masked from 'package:MASS':
##
##   geyser
```

```
library(multcompView)
tibble(mean_data)
```

```
## # A tibble: 6 x 3
##   feed      weight_mean    sd
##   <fct>          <dbl> <dbl>
## 1 sunflower      329.  48.8
## 2 casein         324.  64.4
## 3 meatmeal       277.  64.9
## 4 soybean        246.  54.1
## 5 linseed        219.  52.2
## 6 horsebean      160.  38.6
```

```
anova <- aov(weight ~ feed, data=df)
```

```
summary(anova)
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## feed         5  231129    46226   15.37 5.94e-10 ***
## Residuals    65  195556     3009
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

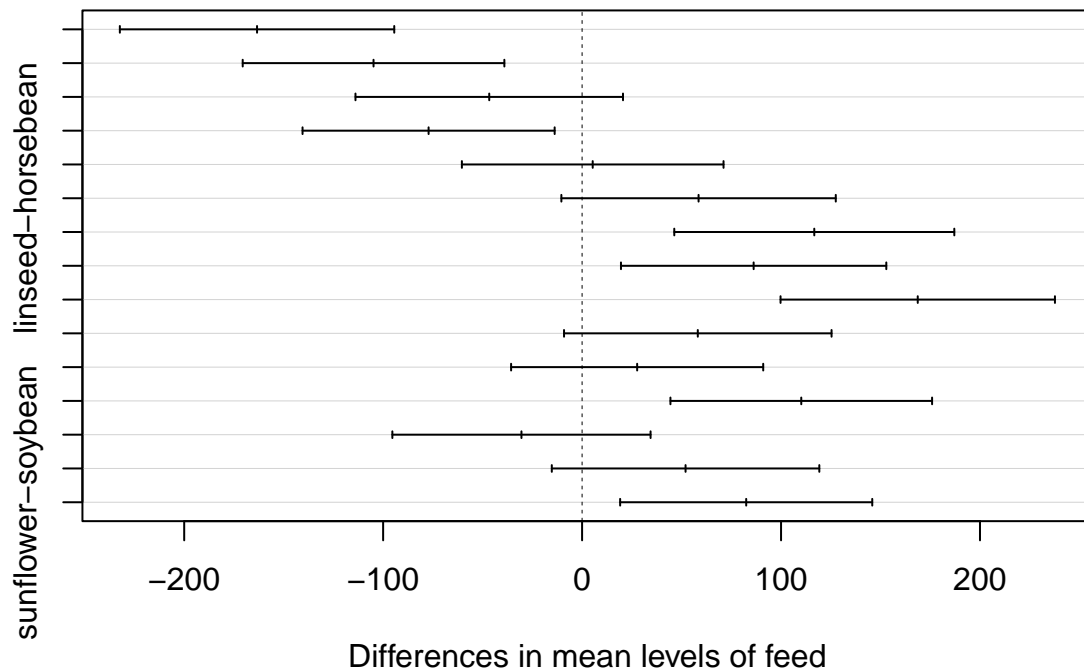
```
tukey <- TukeyHSD(anova)
tukey
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = weight ~ feed, data = df)
##
## $feed
##
```

	diff	lwr	upr	p adj
horsebean-casein	-163.383333	-232.346876	-94.41979	0.0000000
linseed-casein	-104.833333	-170.587491	-39.07918	0.0002100
meatmeal-casein	-46.674242	-113.906207	20.55772	0.3324584
soybean-casein	-77.154762	-140.517054	-13.79247	0.0083653
sunflower-casein	5.333333	-60.420825	71.08749	0.9998902
linseed-horsebean	58.550000	-10.413543	127.51354	0.1413329
meatmeal-horsebean	116.709091	46.335105	187.08308	0.0001062
soybean-horsebean	86.228571	19.541684	152.91546	0.0042167
sunflower-horsebean	168.716667	99.753124	237.68021	0.0000000
meatmeal-linseed	58.159091	-9.072873	125.39106	0.1276965
soybean-linseed	27.678571	-35.683721	91.04086	0.7932853
sunflower-linseed	110.166667	44.412509	175.92082	0.0000884
soybean-meatmeal	-30.480519	-95.375109	34.41407	0.7391356
sunflower-meatmeal	52.007576	-15.224388	119.23954	0.2206962
sunflower-soybean	82.488095	19.125803	145.85039	0.0038845

```
plot(TukeyHSD(anova))
```

95% family-wise confidence level



Visualization of results through 'Barplots'

Lettering of results

```
library(multcomp)
library(multcompView)
group_letters <- multcompLetters4(anova, tukey)
group_letters

## $feed
## sunflower casein meatmeal soybean linseed horsebean
##          "a"      "a"      "ab"      "b"      "bc"      "c"
```

Adding letters to data frame of results

```
library(tidyverse)
group_letters <- as.data.frame.list(group_letters$feed)

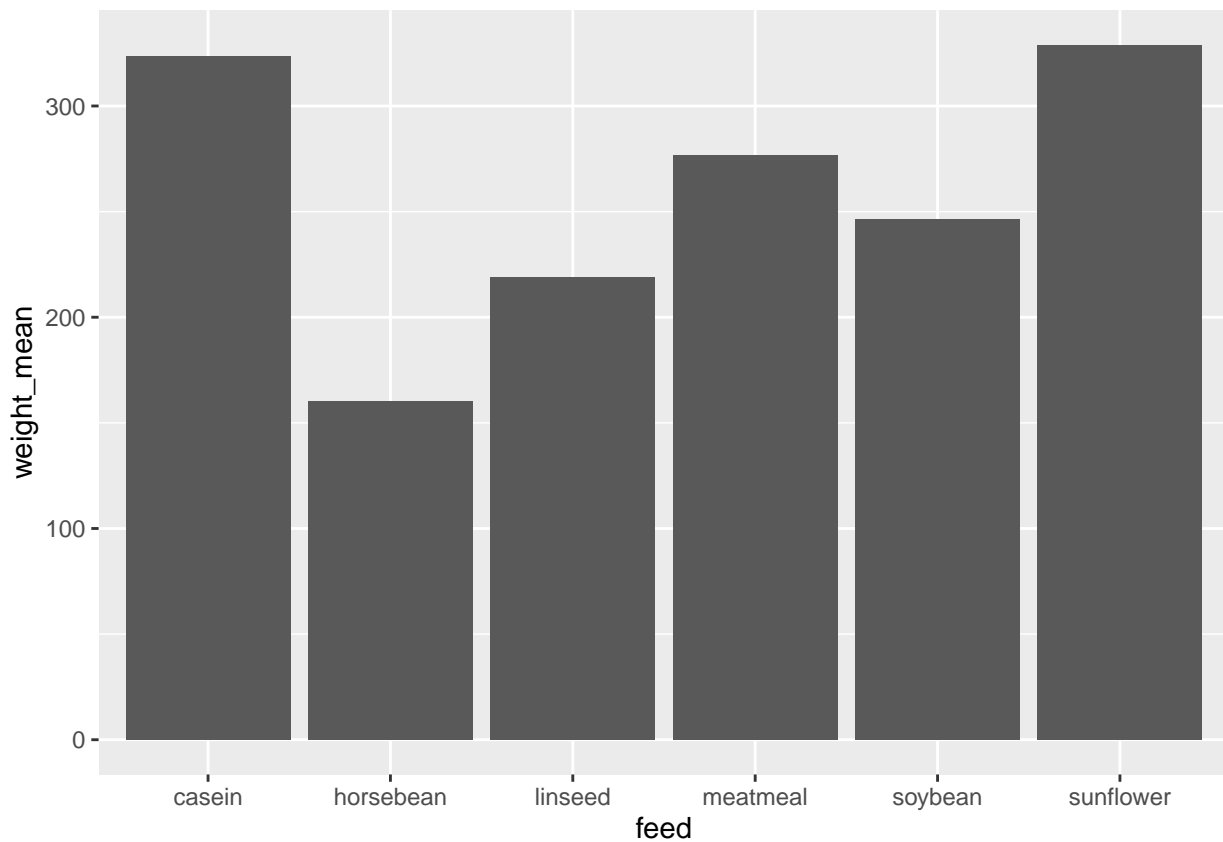
mean_data$group_letters <- group_letters$Letters

tibble(mean_data)
```

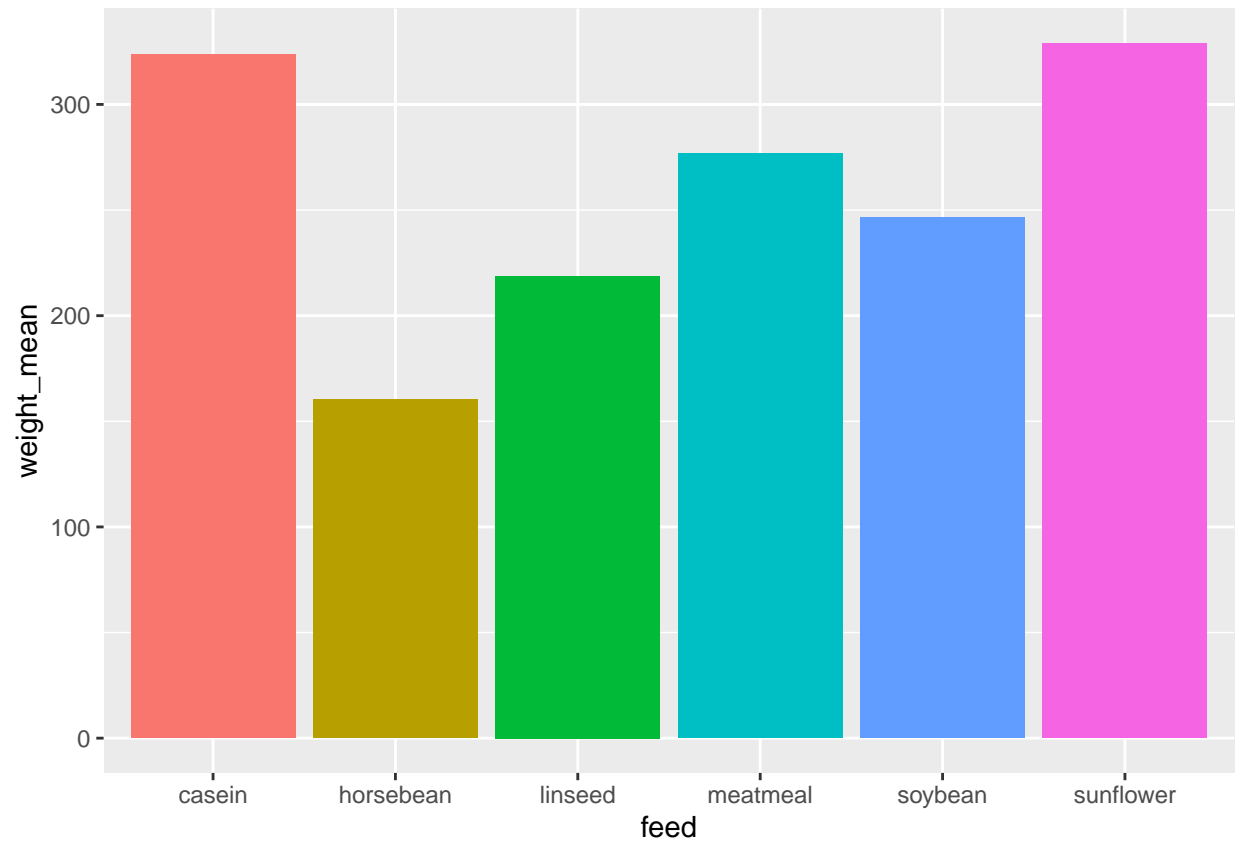
```
## # A tibble: 6 x 4
##   feed      weight_mean    sd group_letters
##   <fct>      <dbl> <dbl> <chr>
## 1 sunflower    329.  48.8 a
## 2 casein       324.  64.4 a
## 3 meatmeal     277.  64.9 ab
## 4 soybean      246.  54.1 b
## 5 linseed      219.  52.2 bc
## 6 horsebean    160.  38.6 c
```

Creating 'barplots' using ggplot2

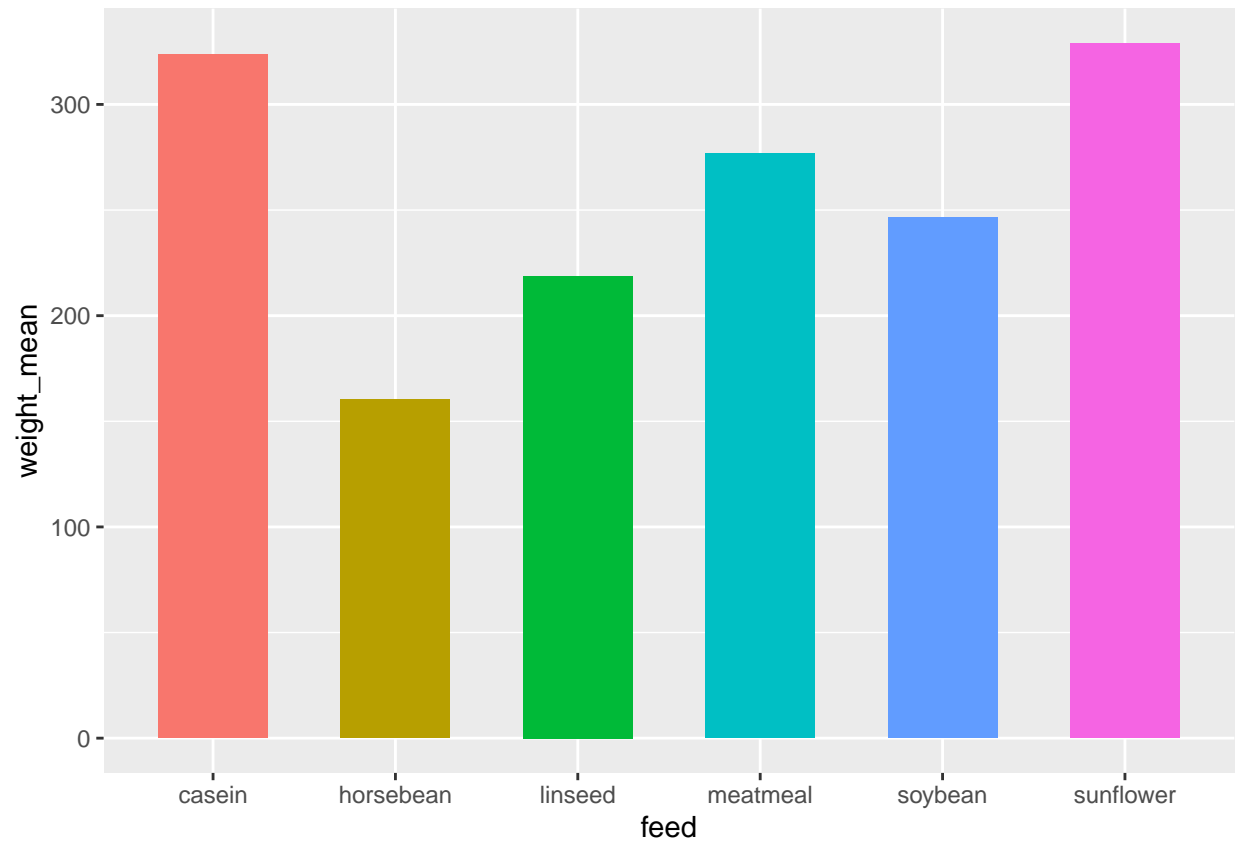
```
library(ggplot2)
library(RColorBrewer)
library(ggthemes)
ggplot(mean_data, mapping = aes(x=feed, y=weight_mean))+
  geom_bar(stat = "identity")
```



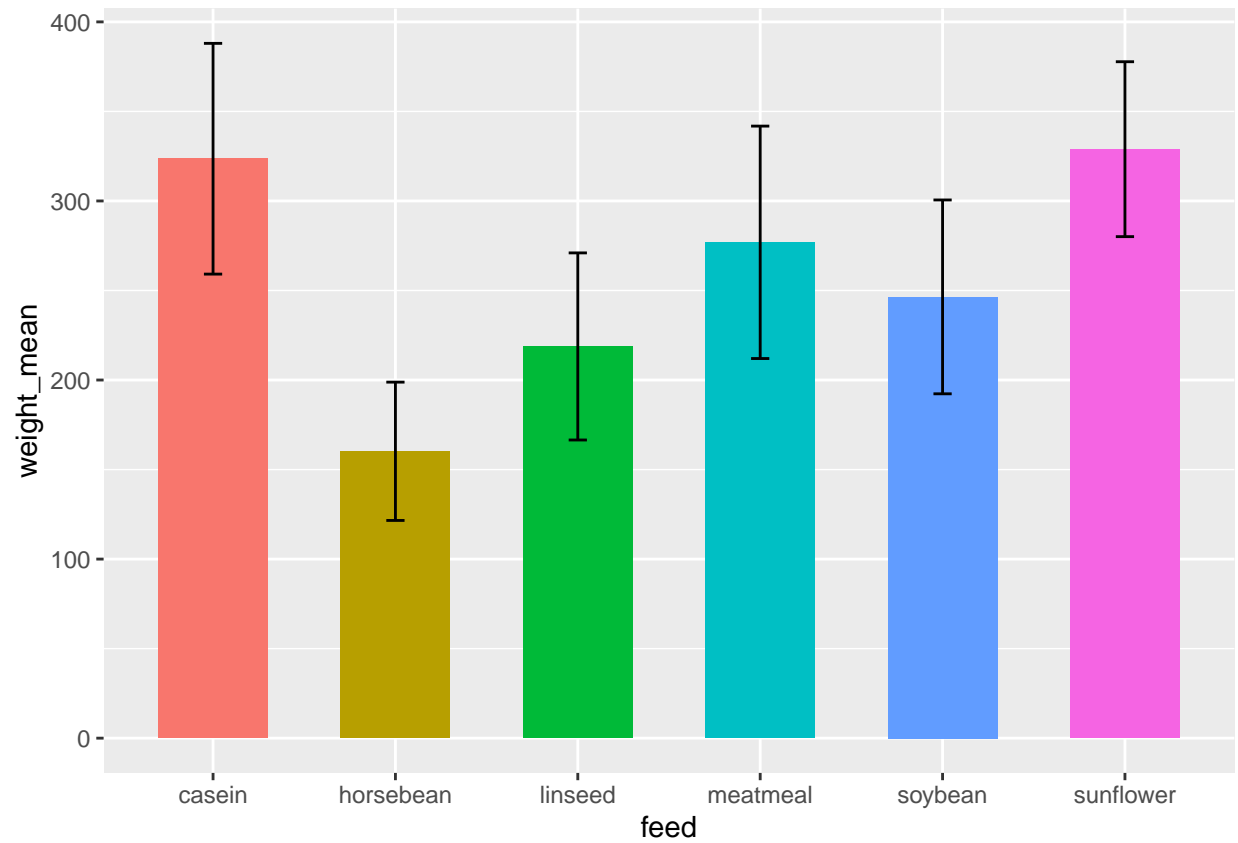
```
ggplot(mean_data, mapping = aes(x=feed, y=weight_mean))+
  geom_bar(stat = "identity", aes(fill = feed), show.legend = FALSE)
```



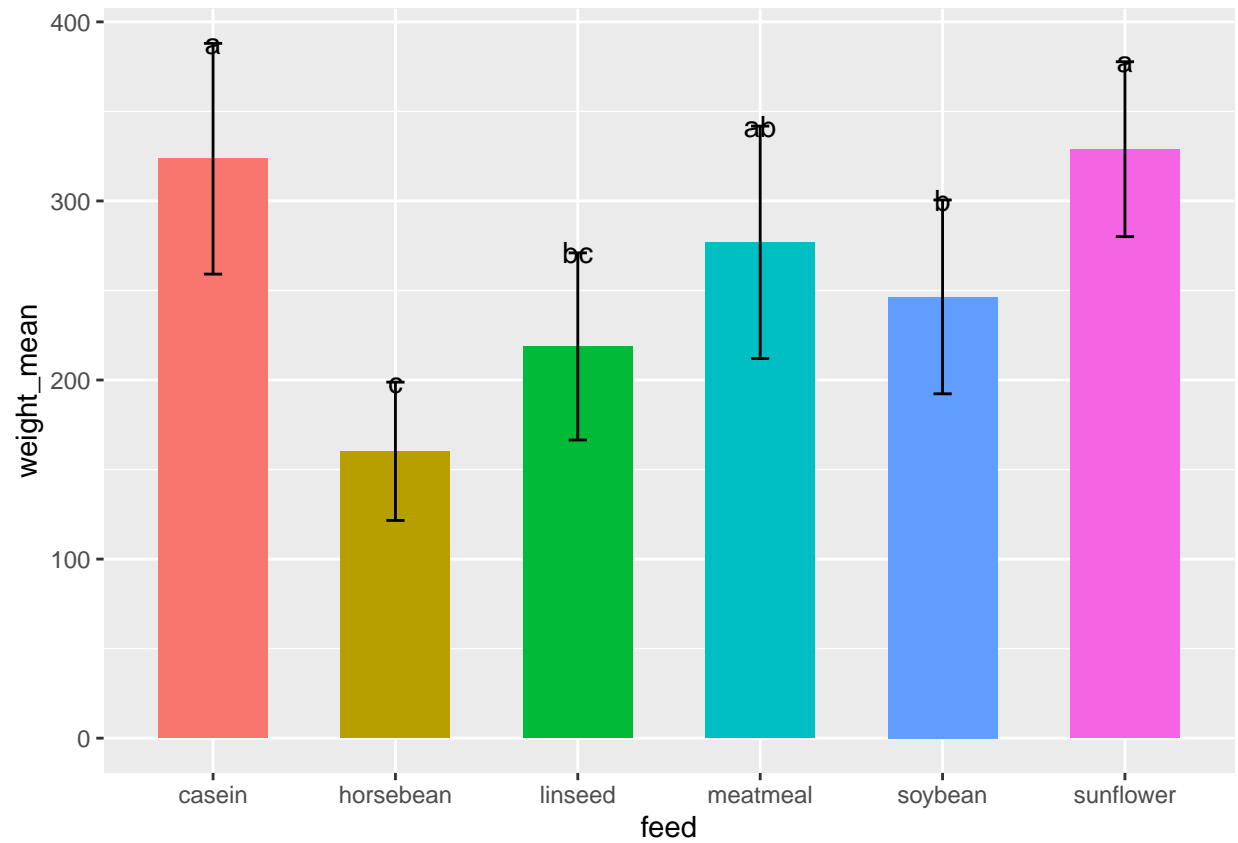
```
ggplot(mean_data, mapping = aes(x=feed, y=weight_mean))+  
  geom_bar(stat = "identity", aes(fill = feed), show.legend = FALSE, width = 0.6)
```



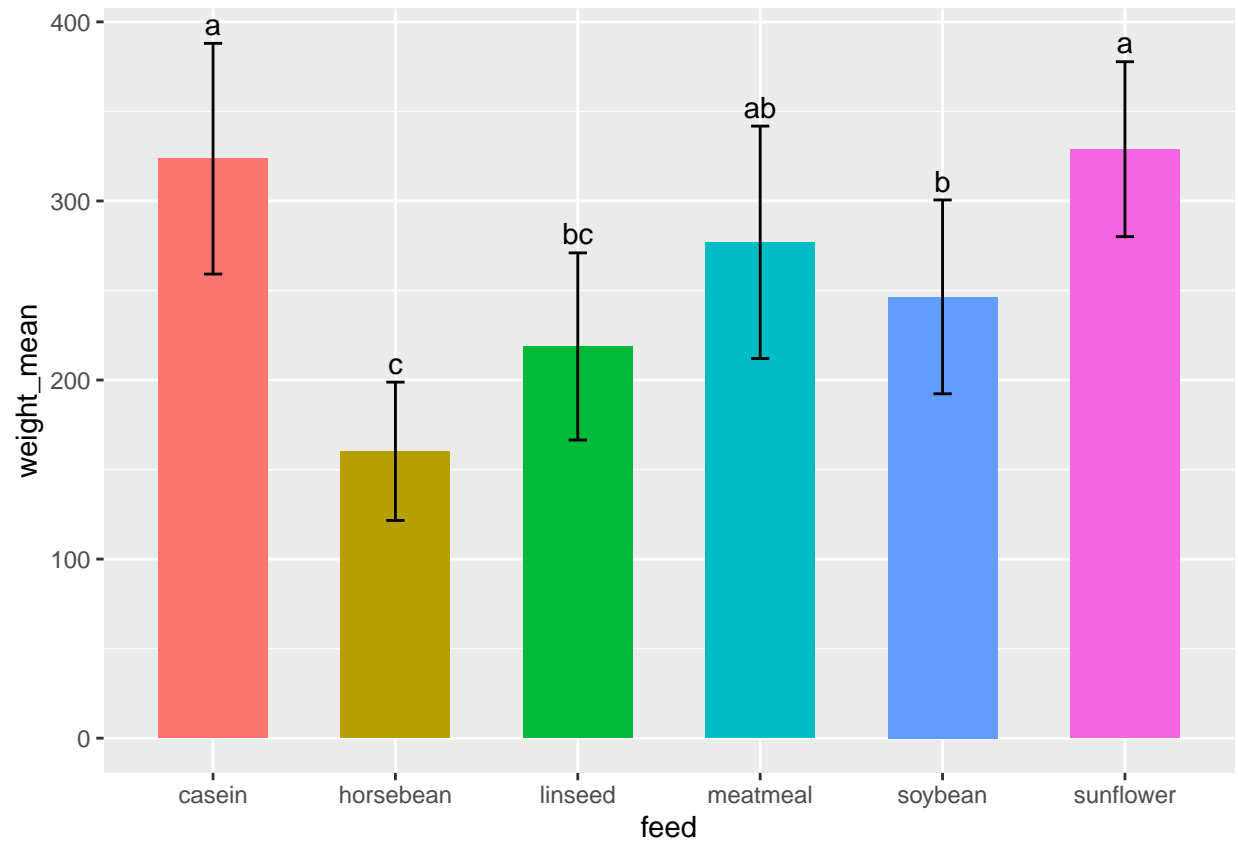
```
ggplot(mean_data, mapping = aes(x=feed, y=weight_mean))+  
  geom_bar(stat = "identity", aes(fill = feed), show.legend = FALSE, width = 0.6)+  
  geom_errorbar(aes(ymin = weight_mean-sd, ymax = weight_mean+sd), width= 0.1)
```



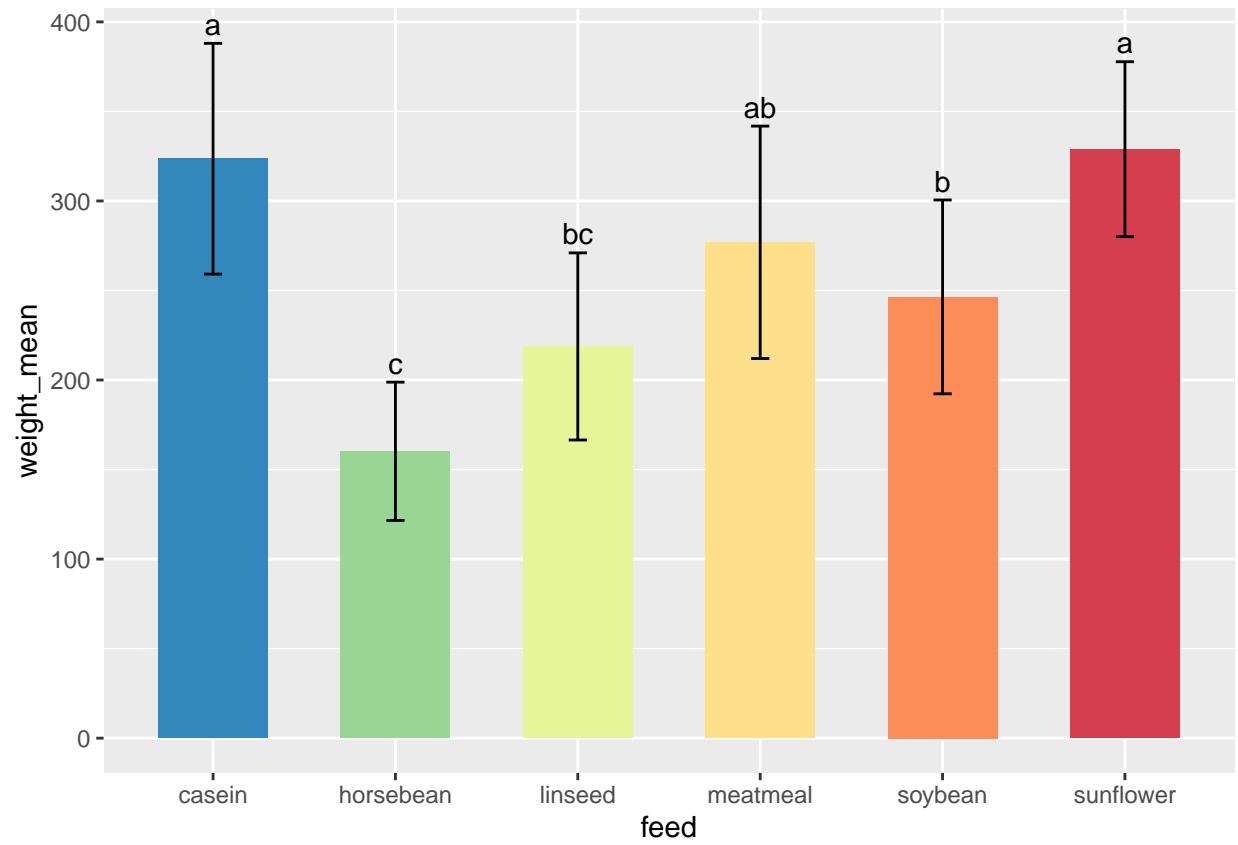
```
ggplot(mean_data, mapping = aes(x=feed, y=weight_mean))+  
  geom_bar(stat = "identity", aes(fill = feed), show.legend = FALSE, width = 0.6)+  
  geom_errorbar(aes(ymin = weight_mean-sd, ymax = weight_mean+sd), width= 0.1)+  
  geom_text(aes(label = group_letters, y= weight_mean+sd))
```

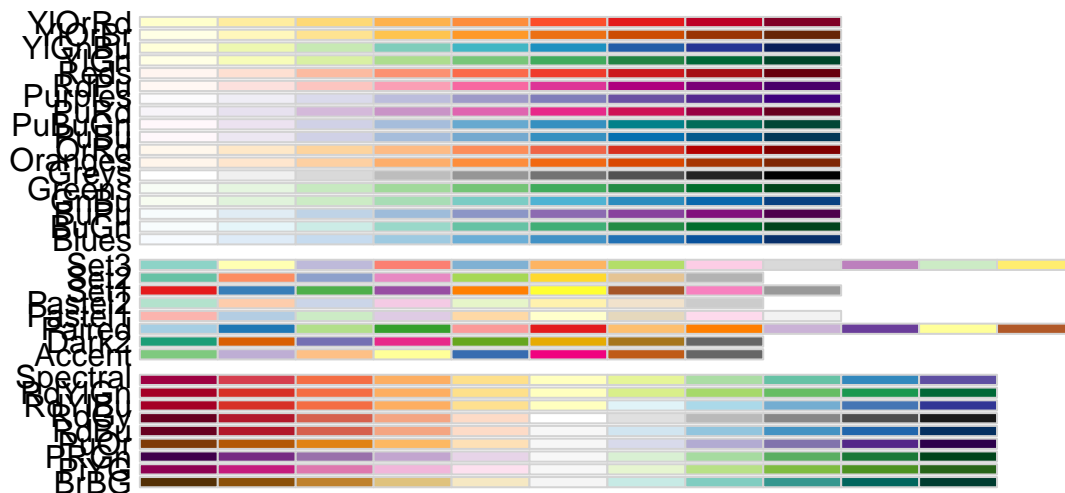
```
ggplot(mean_data, mapping = aes(x=feed, y=weight_mean))+  
  geom_bar(stat = "identity", aes(fill = feed), show.legend = FALSE, width = 0.6)+  
  geom_errorbar(aes(ymin = weight_mean-sd, ymax = weight_mean+sd), width= 0.1)+  
  geom_text(aes(label = group_letters, y= weight_mean+sd), vjust= -0.4)
```



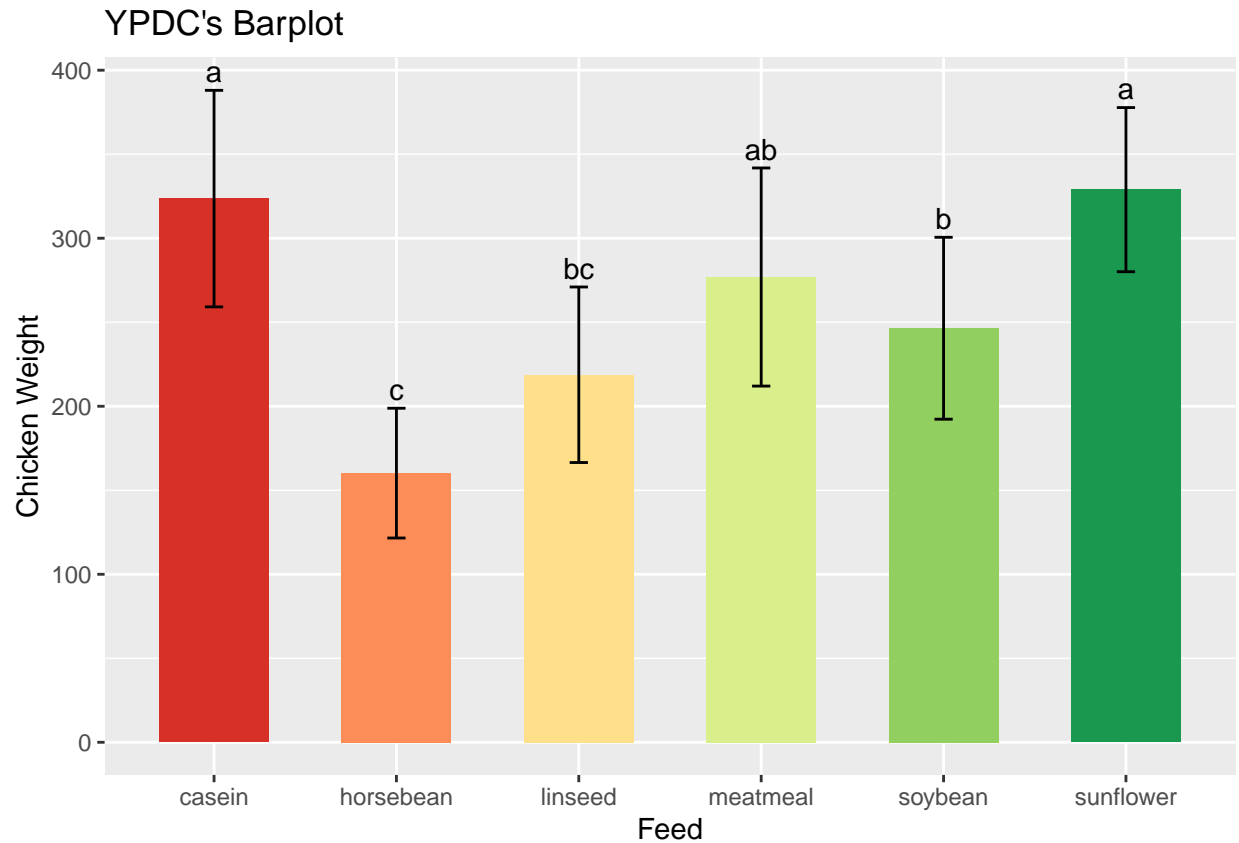
```
ggplot(mean_data, mapping = aes(x=feed, y=weight_mean))+
  geom_bar(stat = "identity", aes(fill = feed), show.legend = FALSE, width = 0.6)+
  geom_errorbar(aes(ymin = weight_mean-sd, ymax = weight_mean+sd), width= 0.1)+
  geom_text(aes(label = group_letters, y= weight_mean+sd), vjust= -0.4)+
  scale_fill_brewer(palette = "Spectral", direction = -1)
```



```
display.brewer.all()
```

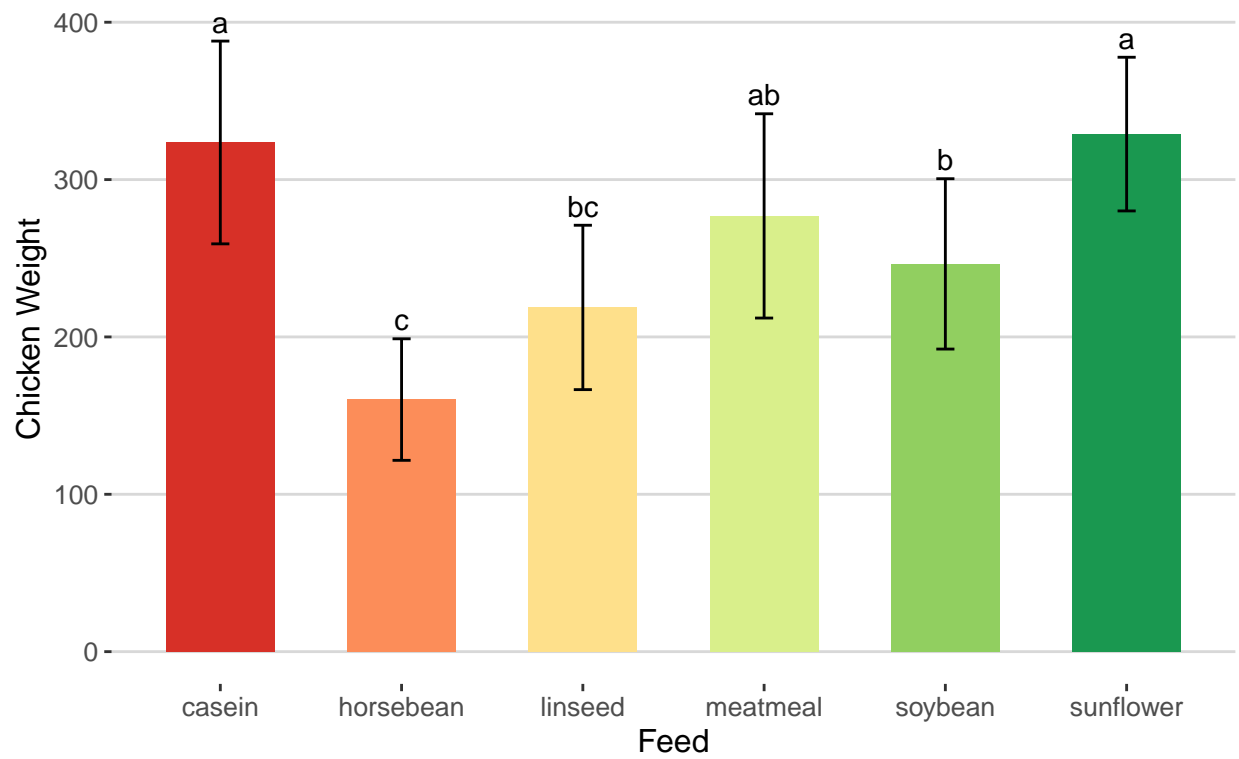


```
ggplot(mean_data, mapping = aes(x=feed, y=weight_mean))+
  geom_bar(stat = "identity", aes(fill = feed), show.legend = FALSE, width = 0.6)+
  geom_errorbar(aes(ymin = weight_mean-sd, ymax = weight_mean+sd), width= 0.1)+
  geom_text(aes(label = group_letters, y= weight_mean+sd), vjust= -0.4)+
  scale_fill_brewer(palette = "RdYlGn", direction = 1)+
  labs(title = "YPDC's Barplot", x="Feed", y="Chicken Weight", fill= "Feed Type")
```



```
p <- ggplot(mean_data, mapping = aes(x=feed, y=weight_mean))+
  geom_bar(stat = "identity", aes(fill = feed), show.legend = FALSE, width = 0.6)+
  geom_errorbar(aes(ymin = weight_mean-sd, ymax = weight_mean+sd), width= 0.1)+
  geom_text(aes(label = group_letters, y= weight_mean+sd), vjust= -0.4)+
  scale_fill_brewer(palette = "RdYlGn", direction = 1)+
  labs(title = "YPDC's Barplot", x="Feed", y="Chicken Weight", fill= "Feed Type")+
  ylim(0,410)+ ggthemes::theme_hc() ;p
```

YPDC's Barplot



```
tiff("barplot.tiff", units = "in", width = 10, height = 9, res = 300, compression = "lzw")
p
dev.off()
```

```
## pdf
## 2
```