ENTMLGY 6702 Entomological Techniques and Data Analysis Boxplots and points

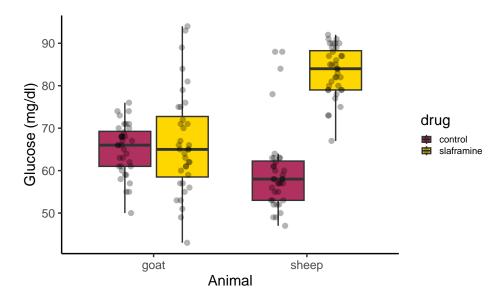
Load in the glucose_df.txt dataset.

```
gluc_df <- read.table("glucose_df.txt", sep="\t", header=T)
summary(gluc_df)</pre>
```

```
diet
                                                           drug
##
        rep
                      animal
                                                       Length:144
##
  Min. : 1.00
                  Length: 144
                                     Length: 144
   1st Qu.: 3.75
                  Class :character
                                     Class : character
                                                       Class :character
##
  Median: 6.50
                  Mode :character
                                     Mode :character
                                                       Mode :character
  Mean : 6.50
##
   3rd Qu.: 9.25
##
   Max.
          :12.00
##
      glucose
## Min.
          :43.00
## 1st Qu.:59.00
## Median :66.00
## Mean
         :68.65
## 3rd Qu.:79.00
## Max. :94.00
```

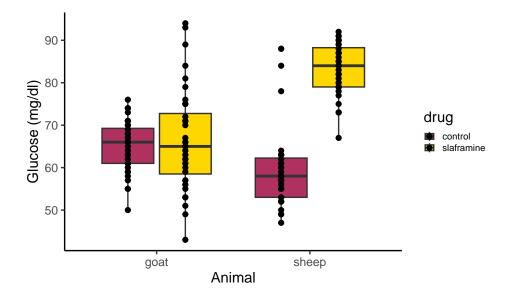
Option 1: Using jittering. Note that the alpha command in making the points transparent as well.

```
library(tidyverse)
ggplot(gluc_df, mapping=aes( y=glucose, x=animal, fill=drug))+
geom_boxplot(outlier.color=NA)+
geom_point(position = position_jitterdodge( jitter.width = 0.1), alpha=0.3)+
    theme_classic()+
ylab("Glucose (mg/dl)")+
xlab("Animal")+
theme(legend.text=element_text(size=7))+
theme(legend.key.size = unit(0.3, 'cm'))+
scale_fill_manual(values=c("maroon", "gold"))
```



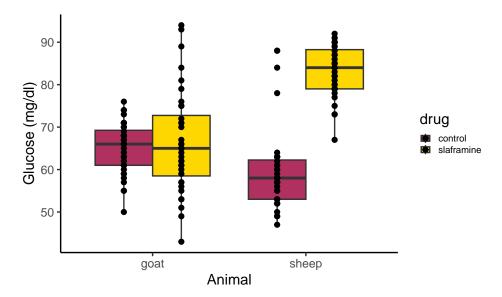
Option 2: Use width = 0.75, but ensure you have fill=drug in the first line when first making the call to ggplot().

```
ggplot(gluc_df, mapping=aes( y=glucose, x=animal, fill=drug))+
geom_boxplot( outlier.color=NA)+
    geom_point(position=position_dodge(width=0.75))+
ylab("Glucose (mg/dl)")+
xlab("Animal")+
theme_classic()+
theme(legend.text=element_text(size=7))+
theme(legend.key.size = unit(0.3, 'cm'))+
scale_fill_manual(values=c("maroon", "gold"))
```



Option 3 (and a bit more on how this works): when making a grouped boxplot, ggplot (under the hood) is imposing a "dodge" (moving and spacing out the boxes for display). To ensure that the points are perfectly on top of the plots, we need to use the same exact dodge value.

```
ggplot(gluc_df, mapping=aes( y=glucose, x=animal, fill=drug))+
geom_boxplot(position=position_dodge(width=0.75), outlier.color=NA)+
    geom_point(position=position_dodge(width=0.75))+
ylab("Glucose (mg/dl)")+
xlab("Animal")+
theme_classic()+
theme(legend.text=element_text(size=7))+
theme(legend.key.size = unit(0.3, 'cm'))+
scale_fill_manual(values=c("maroon", "gold"))
```



Option 4: you can organize your points nicely as well, if ya like.

```
ggplot(gluc_df, mapping=aes( y=glucose, x=animal, fill=drug))+
geom_boxplot(position=position_dodge(width=0.75), outlier.color=NA)+
geom_dotplot(binaxis = "y", stackdir = "center", binwidth = 3,
    position=position_dodge(0.75), dotsize=0.4, alpha=1)+
ylab("Glucose (mg/dl)")+
xlab("Animal")+
theme_classic()+
theme(legend.text=element_text(size=7))+
theme(legend.key.size = unit(0.3, 'cm'))+
scale_fill_manual(values=c("maroon", "gold"))
```

