Homework 2

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Load data

```r
# Load data
ddh <- read.csv("https://raw.githubusercontent.com/sta440-fa23/class-files/main/homework-2/ddh.csv", hea

# Rename some variables
ddh <- ddh %>%
  mutate(delayed_fn = as.factor(delayed_fn))

levels(ddh$delayed_fn) <- c("IGF", "LGD")

# Look at data
head(ddh)
```

```
##   ID cold_ischemia r_height r_weight r_bmi r_age r_caucasian r_genderf
## 1  1           433    183.0     85.5  25.5    60           1         0
## 2  2           617    180.3     73.8  22.7    36           0         0
## 3  3           282    165.1     63.9  23.4    52           0         1
## 4  4           349    191.8    115.7  31.5    53           1         0
## 5  5           310    157.5     55.8  22.5    52           1         1
## 6  6           468    186.7     71.8  20.6    60           1         0
##   r_meld_assign r_meld_calc d_age d_cod d_caucasian d_genderf donorrisk sodium
## 1            25          10    13     3           1         1      1.15    155
## 2            18          11    56     1           0         0        NA    148
## 3            40          31    63     1           0         1      1.79    148
## 4            22          14    53     1           1         0      1.16    143
## 5            27          27    49     1           1         1      1.21    143
## 6            18          19    64     3           1         1        NA    145
##   steatosis sbp_lt_90 hemo_instability glucount glutwa glurange   glusd
## 1         0        60                1        5 213.44      191   76.94
## 2         0        NA               NA        3 232.20      193  105.19
## 3         0         0                1        4 143.59       26   11.70
## 4         0         5                1        3 129.67       73   36.64
## 5         0         5                1        6 158.27       53   21.27
## 6         0         0                1        4 207.62       79   37.70
##   delayed_fn
## 1        IGF
## 2        LGD
## 3        IGF
## 4        LGD
## 5        IGF
## 6        IGF
```

Figure 1

```r
# Boxplot for TWA
twa_plot <- ggplot(data=ddh,
        mapping=aes(y=glutwa, x=delayed_fn, fill=delayed_fn)) +
    geom_boxplot() +
    xlab("TWA") +
    ylab('Donor glucose measures, mg/DL') +
    scale_x_discrete(limits=c("IGF", "LGD")) +
    guides(fill=FALSE) +
    ylim(50, 500)

# Boxplot for Range
range_plot <- ggplot(data=ddh,
        mapping=aes(y=glurange, x=delayed_fn, fill=delayed_fn)) +
    geom_boxplot() +
    xlab("Range") +
    ylab(NULL) +
    scale_x_discrete(limits=c("IGF", "LGD")) +
    guides(fill=FALSE) +
    ylim(1, 1000) +
    scale_y_log10()

# Boxplot for SD
sd_plot <- ggplot(data=ddh,
        mapping=aes(y=glusd, x=delayed_fn, fill=delayed_fn)) +
    geom_boxplot() +
    xlab("SD") +
    ylab(NULL) +
    scale_x_discrete(limits=c("IGF", "LGD")) +
    guides(fill=FALSE) +
  ylim(1, 300) +
  scale_y_log10()

# Print plots
grid.arrange(twa_plot, range_plot, sd_plot, ncol = 3)
```
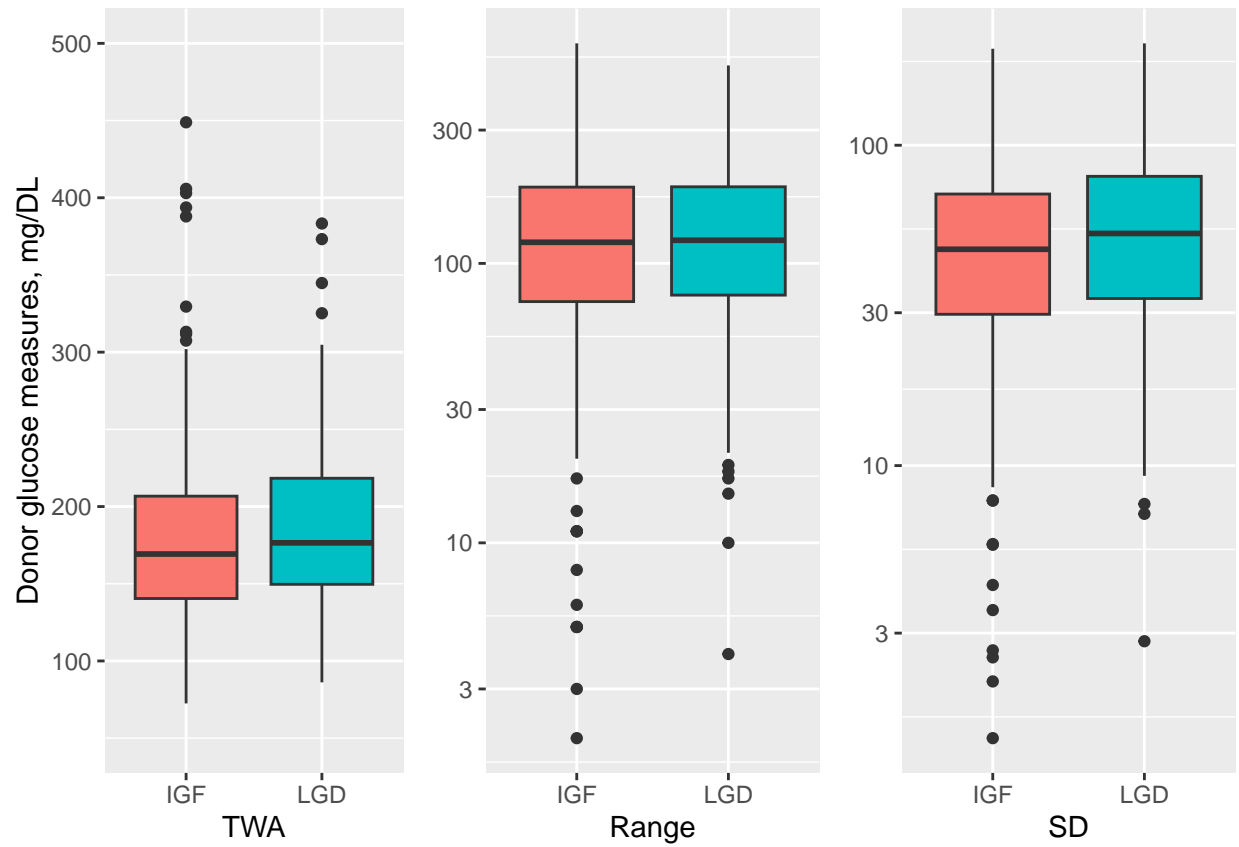
Table 2