Homework 2

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Load data

```
# 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_1 = as.factor(delayed_fn))

levels(ddh$delayed_fn_1) <- c("IGF", "LGD")

# Look at data
#head(ddh)
```

Figure 1: Deceased donor hyperglycemia and liver graft dysfunction

```
# Boxplot for TWA
twa_plot <- ggplot(data=ddh,
        mapping=aes(y=glutwa, x=delayed_fn_1, fill=delayed_fn_1)) +
      geom_boxplot() +
      xlab("TWA") +
      ylab(NULL) +
      scale_x_discrete(limits=c("IGF", "LGD")) +
      guides(fill=FALSE) +
      ylim(50, 500) +
      theme_classic() +
  scale_fill_manual(values=c("#FFFFFF", "#808080"))

# Boxplot for Range
range_plot <- ggplot(data=ddh,
        mapping=aes(y=glurange, x=delayed_fn_1, fill=delayed_fn_1)) +
      geom_boxplot() +
      xlab("Range") +
      ylab(NULL) +
      scale_x_discrete(limits=c("IGF", "LGD")) +
      guides(fill=FALSE) +
      ylim(1, 1000) +
      scale_y_log10() +
      theme_classic() +
  scale_fill_manual(values=c("#FFFFFF", "#808080"))
```

```
# Boxplot for SD
sd_plot <- ggplot(data=ddh,
        mapping=aes(y=glusd, x=delayed_fn_1, fill=delayed_fn_1)) +
      geom_boxplot() +
      xlab("SD") +
      ylab(NULL) +
      scale_x_discrete(limits=c("IGF", "LGD")) +
      guides(fill=FALSE) +
  ylim(1, 300) +
  scale_y_log10() +
  theme_classic() +
  scale_fill_manual(values=c("#FFFFFF", "#808080"))

# Print plots
grid.arrange(twa_plot, range_plot, sd_plot, ncol = 3, top='Donor glucose measures, mg/dL')
```

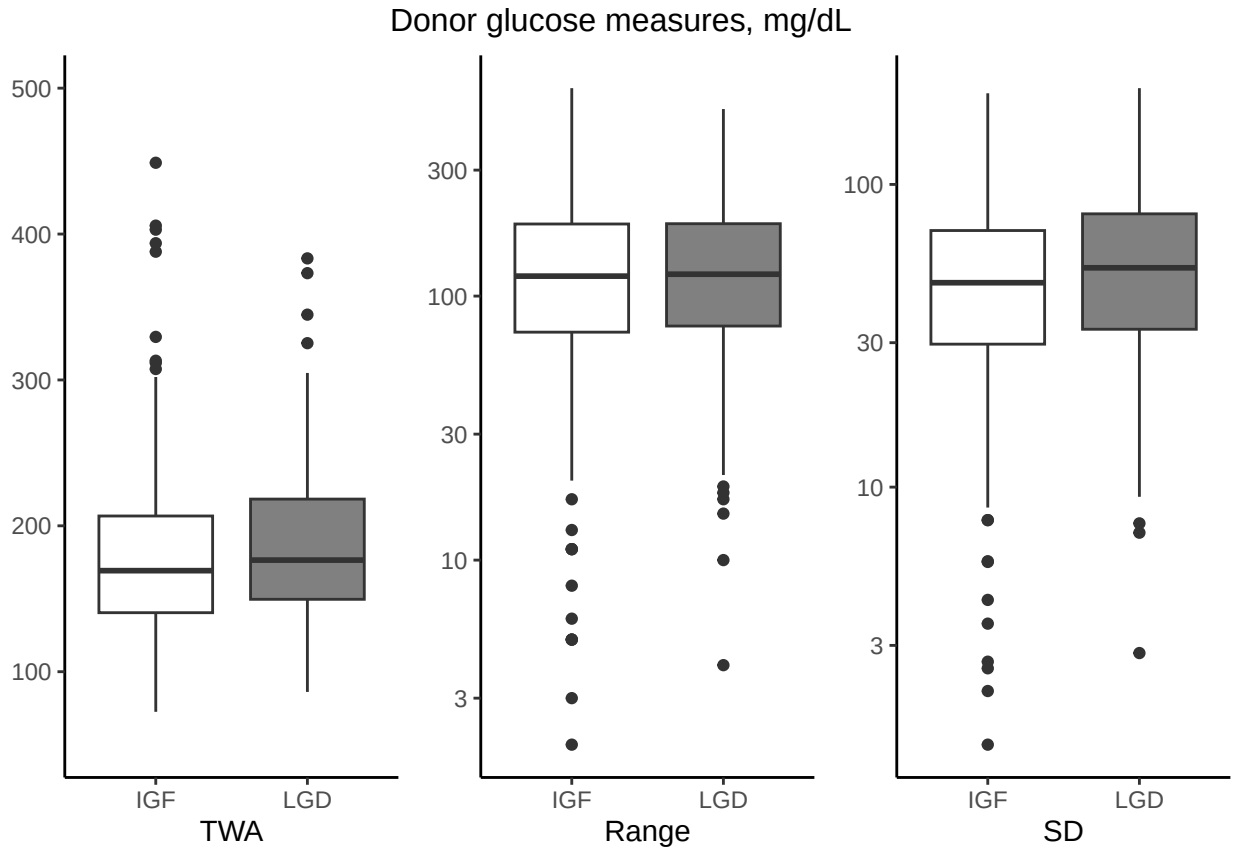

Table 2

```
# Fit models
unadjusted_model <- glm(delayed_fn ~ log(glutwa),
                        data = ddh,
                        family = "binomial")
```

```r
adjusted_model <- glm(delayed_fn ~ log(glutwa) + d_age + d_cod + r_meld_calc + hemo_instability,
                      data = ddh,
                      family = "binomial")

unadjusted_results <- tidy(unadjusted_model)
adjusted_results <- tidy(adjusted_model)

# Function to calculate results
calc_results <- function(coeff, a=0.05) {
  alpha <- a
  z_value <- qnorm(1 - alpha / 2)  # Calculate z-value for CI

  odds_ratio <- exp(coeff$estimate)
  lower_ci <- exp(coeff$estimate - z_value * coeff$std.error)
  upper_ci <- exp(coeff$estimate + z_value * coeff$std.error)
  p_value <- coeff$p.value

  return(data.frame(Odds_Ratio = odds_ratio, Lower_CI = lower_ci, Upper_CI = upper_ci, P_Value = p_valu
}

# Format results
unadj_twa <- unadjusted_results %>%
  filter(term == "log(glutwa)") %>%
  calc_results(a=0.05)
adj_twa <- adjusted_results %>%
  filter(term == "log(glutwa)") %>%
  calc_results(a=0.05)

# Make table
results_table <- rbind(
  data.frame(Exposure = "Time-weighted average", Model = "Unadjusted", unadj_twa),
  data.frame(Exposure = "Time-weighted average", Model = "Adjusted", adj_twa)
)

results_table$CI <- paste0("(", results_table$Lower_CI, ", ", results_table$Upper_CI, ")")

final_table <- results_table %>%
    select(Exposure, Model, Odds_Ratio, CI, P_Value)

# Print the table
kable(final_table, digits = 2)
```

Primary exposure

Exposure	Model	Odds_Ratio	CI	P_Value
Time-weighted average	Unadjusted	1.76	(0.918024179948013, 3.39248917541442)	0.09
Time-weighted average	Adjusted	1.63	(0.824025163536009, 3.21987836857906)	0.16

```r
# Fit models
unadjusted_model <- glm(delayed_fn ~ log(glurange),
```

```
                        data = ddh,
                        family = "binomial")

adjusted_model <- glm(delayed_fn ~ log(glurange) + d_age + d_cod + r_meld_calc + hemo_instability,
                      data = ddh,
                      family = "binomial")

unadjusted_results <- tidy(unadjusted_model)
adjusted_results <- tidy(adjusted_model)

# Function to calculate results
calc_results <- function(coeff, a=0.05) {
  alpha <- a
  z_value <- qnorm(1 - alpha / 2)  # Calculate z-value for CI

  odds_ratio <- exp(coeff$estimate)
  lower_ci <- exp(coeff$estimate - z_value * coeff$std.error)
  upper_ci <- exp(coeff$estimate + z_value * coeff$std.error)
  p_value <- coeff$p.value

  return(data.frame(Odds_Ratio = odds_ratio, Lower_CI = lower_ci, Upper_CI = upper_ci, P_Value = p_valu
}

# Format results
unadj_twa <- unadjusted_results %>%
  filter(term == "log(glurange)") %>%
  calc_results(a=0.025)
adj_twa <- adjusted_results %>%
  filter(term == "log(glurange)") %>%
  calc_results(a=0.025)

# Make table
results_table <- rbind(
  data.frame(Exposure = "Range", Model = "Unadjusted", unadj_twa),
  data.frame(Exposure = "Range", Model = "Adjusted", adj_twa)
)

results_table$CI <- paste0("(", results_table$Lower_CI, ", ", results_table$Upper_CI, ")")

final_table <- results_table %>%
    select(Exposure, Model, Odds_Ratio, CI, P_Value)

# Print the table
kable(final_table, digits = 2)
```

Secondary exposure: Range

Exposure	Model	Odds_Ratio	CI	P_Value
Range	Unadjusted	1.05	(0.803412580954879, 1.3690311560956)	0.69
Range	Adjusted	1.08	(0.81788117434853, 1.42414799859332)	0.54

```r
# Fit models
unadjusted_model <- glm(delayed_fn ~ log(glusd),
                        data = ddh,
                        family = "binomial")

adjusted_model <- glm(delayed_fn ~ log(glusd) + d_age + d_cod + r_meld_calc + hemo_instability,
                      data = ddh,
                      family = "binomial")

unadjusted_results <- tidy(unadjusted_model)
adjusted_results <- tidy(adjusted_model)

# Function to calculate results
calc_results <- function(coeff, a=0.05) {
  alpha <- a
  z_value <- qnorm(1 - alpha / 2)  # Calculate z-value for CI

  odds_ratio <- exp(coeff$estimate)
  lower_ci <- exp(coeff$estimate - z_value * coeff$std.error)
  upper_ci <- exp(coeff$estimate + z_value * coeff$std.error)
  p_value <- coeff$p.value

  return(data.frame(Odds_Ratio = odds_ratio, Lower_CI = lower_ci, Upper_CI = upper_ci, P_Value = p_valu
}

# Format results
unadj_twa <- unadjusted_results %>%
  filter(term == "log(glusd)") %>%
  calc_results(a=0.025)
adj_twa <- adjusted_results %>%
  filter(term == "log(glusd)") %>%
  calc_results(a=0.025)

# Make table
results_table <- rbind(
  data.frame(Exposure = "SD", Model = "Unadjusted", unadj_twa),
  data.frame(Exposure = "SD", Model = "Adjusted", adj_twa)
)

results_table$CI <- paste0("(", results_table$Lower_CI, ", ", results_table$Upper_CI, ")")

final_table <- results_table %>%
    select(Exposure, Model, Odds_Ratio, CI, P_Value)

# Print the table
kable(final_table, digits = 2)
```

Secondary exposure: SD

Exposure	Model	Odds_Ratio	CI	P_Value
SD	Unadjusted	1.17	(0.866576504087504, 1.58986667695158)	0.24
SD	Adjusted	1.20	(0.875882487131345, 1.63209400457053)	0.20