P8106 Midterm - Code

Group 2: Kate Colvin (KAC2301), Jeong Yun (Lizy) Choi (JC6452), and

Exploratory Analysis

Loading in Data

```
load("dat1.RData")
load("dat2.RData")

dat1 <- dat1 %>% janitor::clean_names()
dat2 <- dat2 %>%janitor::clean_names()
```

Producing Summary Table

Training and test data have the same distribution of demographic characteristics; there is a difference in time since vaccination and log-transformed antibody levels between training and test data

```
# Combining data for summary table, data cleaning
dat1_com <- dat1 %>% mutate(set = "Training Data")
dat2_com <- dat2 %>% mutate(set = "Testing Data")
dat <- dat1_com %>%
  rbind(dat2 com) %>%
  rename(days_vaccinated = time) %>%
  mutate(race = as.character(race), smoking = as.character(smoking)) %>%
  mutate(race = case_match(
        race, "1" ~ "White", "2" ~ "Asian", "3" ~ "Black", "4" ~ "Hispanic"),
         gender = case_match(gender, 1 ~ "Male", 0 ~ "Female"),
         smoking = case_match(
           smoking, "0" ~ "Never", "1" ~ "Former", "2" ~ "Current"))
# Summary table
dat %>% select(!id) %>%
  tbl_summary(
   by = set,
   label = list(age = "Age", gender = "Gender", race = "Race", smoking = "Smoking",
                 height = "Height (cm)", weight = "Weight (kg)", bmi = "BMI",
                 diabetes = "Diabetes", hypertension = "Hypertension",
                 sbp = "Systolic Blood Pressure (mmHg)", ldl = "LDL Cholesterol (mg/dL)",
                 days vaccinated = "Time Since Vaccinated (days)",
                 log_antibody = "Log-Transformed Antibody Level")) %>%
  add_overall() %>% add_p() %>%
  modify_caption("Summary of Patient Testing and Training Data (N=6000)") %>%
  as_gt() %>% tab_options(table.font.size = 10)
```

Table 1: Summary of Patient Testing and Training Data (N=6000)

Characteristic	Overall $N = 6,000^{1}$	Testing Data $N = 1,000^{1}$	Training Data $N = 5{,}000^{1}$	$\mathbf{p} ext{-}\mathbf{value}^2$
Age	60.0 (57.0, 63.0)	60.0 (57.0, 63.0)	60.0 (57.0, 63.0)	0.9
Gender				0.7
Female	3,082 (51%)	509 (51%)	2,573 (51%)	
Male	2,918 (49%)	491 (49%)	2,427 (49%)	
Race				0.6
Asian	333 (5.6%)	55 (5.5%)	278 (5.6%)	
Black	1,235 (21%)	199 (20%)	1,036 (21%)	
Hispanic	548 (9.1%)	83 (8.3%)	465 (9.3%)	
White	3,884 (65%)	663 (66%)	3,221 (64%)	
Smoking				0.8
Current	589 (9.8%)	103 (10%)	486 (9.7%)	
Former	1,800 (30%)	296 (30%)	1,504 (30%)	
Never	3,611 (60%)	601 (60%)	3,010 (60%)	
Height (cm)	170.1 (166.1, 174.2)	170.2 (166.1, 174.2)	170.1 (166.1, 174.3)	0.7
Weight (kg)	80 (75, 85)	80 (75, 84)	80 (75, 85)	0.8
BMI	27.60 (25.80, 29.50)	27.60 (25.80, 29.60)	27.60 (25.80, 29.50)	0.9
Diabetes	929 (15%)	157 (16%)	772 (15%)	0.8
Hypertension	2,754 (46%)	456 (46%)	2,298 (46%)	0.8
Systolic Blood Pressure (mmHg)	130 (124, 135)	130 (124, 135)	130 (124, 135)	0.3
LDL Cholesterol (mg/dL)	110 (96, 124)	112 (96, 124)	110 (96, 124)	0.4
Time Since Vaccinated (days)	116 (82, 152)	171 (140, 205)	106 (76, 138)	< 0.001
Log-Transformed Antibody Level	10.06 (9.65, 10.45)	9.93 (9.50, 10.32)	10.09 (9.68, 10.48)	< 0.001

¹ Median (Q1, Q3); n (%)

Histograms of Differing Variables by Training and Test Set

```
# Antibody level
plot_sets <- dat %>%
  ggplot(aes(x = log_antibody,
             fill = set,
             color = set)) +
  geom_density(alpha = 0.3, linewidth = 1) +
  labs(x = "Log-Transformed Antibody Level",
       y = "Density",
       title = "Figure 1: Distribution of Log-Transformed Antibody Level, by Data Set") +
  theme_minimal()
# Time since vaccination (days)
plot_days <- dat %>%
  ggplot(aes(x = days_vaccinated,
            fill = set,
            color = set)) +
  geom_density(alpha = 0.3, linewidth = 1) +
  labs(x = "Time Since Vaccinated (days)",
       y = "Density",
       title = "Figure 2: Distribution of Days Since Vaccination, by Data Set") +
  theme minimal()
plot_sets
```

²Wilcoxon rank sum test; Pearson's Chi-squared test

Figure 1: Distribution of Log-Transformed Antibody Level, by Data Set

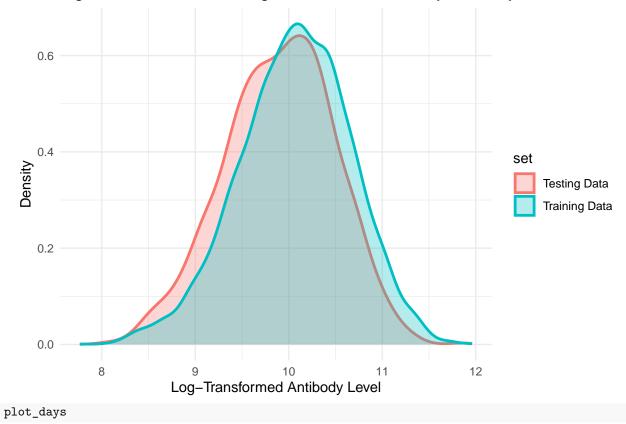
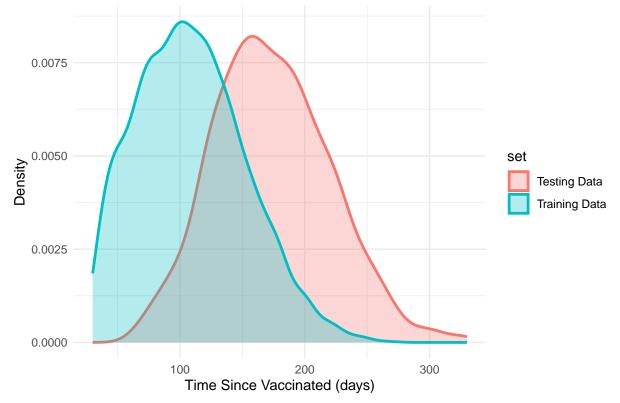
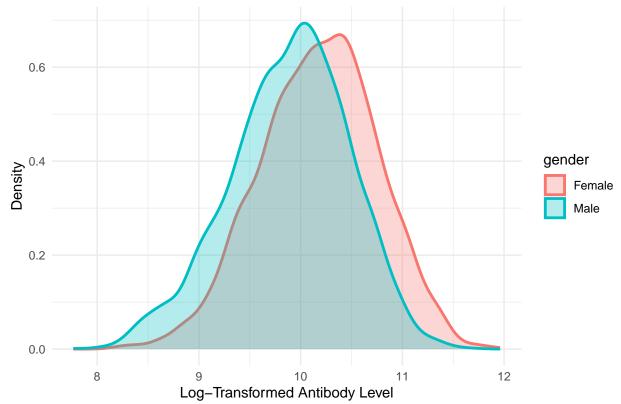


Figure 2: Distribution of Days Since Vaccination, by Data Set



Plots of Log-Transformed Antibody Level, by Categorical Variables

Figure 3: Distribution of Log-Transformed Antibody Level, by Gender



```
strip_markdown <- function(x) {gsub("\\*\\*", "", x)}

dat %>% select(gender, log_antibody) %>%
   tbl_summary(by = gender) %>% add_p() %>%
   modify_caption("Log-Transformed Antibody Level, by Gender") %>%
   as_kable() %>%
   footnote(general_title = "", general = "Median (Q1, Q3), Wilcoxon Rank Sum Test") %>%
   strip_markdown()
```

Table 2: Log-Transformed Antibody Level, by Gender

Characteristic	Female $N = 3,082$	$\mathrm{Male\ N} = 2{,}918$	p-value
log_antibody	$10.20\ (9.79,\ 10.58)$	9.93 (9.51, 10.30)	< 0.001

Median (Q1, Q3), Wilcoxon Rank Sum Test

Figure 4: Distribution of Log-Transformed Antibody Level, by Race

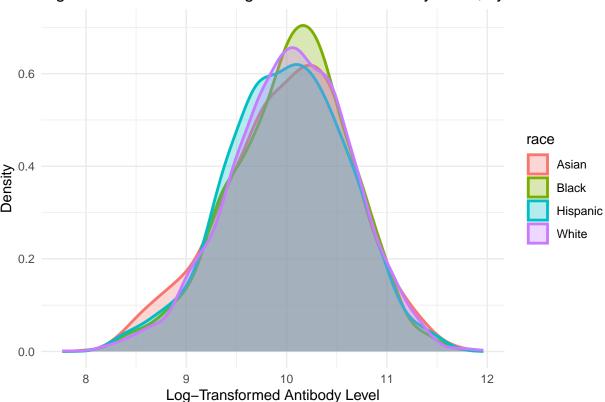


Table 3: Log-Transformed Antibody Level, by Race

Characteristic	Asian $N = 333$	Black $N = 1,235$	Hispanic $N = 548$	White $N = 3,884$	p-value
log_antibody	10.06 (9.62, 10.44)	10.08 (9.65, 10.44)	10.03 (9.61, 10.42)	10.06 (9.65, 10.46)	0.4

Median (Q1, Q3), Kruskal-Wallis Rank Sum Test

Figure 5: Distribution of Log-Transformed Antibody Level, by Smoking

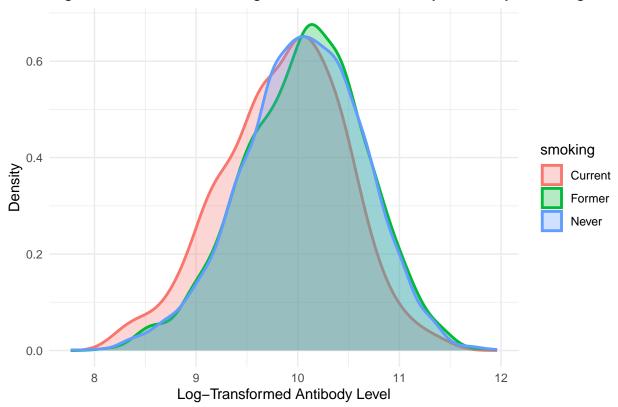


Table 4: Log-Transformed Antibody Level, by Smoking Status

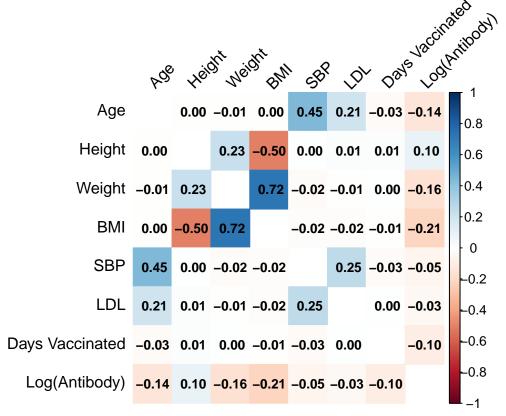
Characteristic	Current $N = 589$	Former $N = 1,800$	Never $N = 3,611$	p-value
log_antibody	9.91 (9.46, 10.28)	10.10 (9.66, 10.48)	10.07 (9.68, 10.46)	< 0.001

Median (Q1, Q3), Kruskal-Wallis Rank Sum Test

Correlation Matrix of Numerical Variables

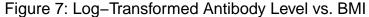
```
cor matrix <- dat %>%
  select(age, height, weight, bmi, sbp, ldl, days_vaccinated, log_antibody) %>%
  rename("Age" = age,
         "Height" = height,
         "Weight" = weight,
         "BMI" = bmi,
         "SBP" = sbp,
         "LDL" = 1d1,
         "Days Vaccinated" = days_vaccinated,
         "Log(Antibody)" = log_antibody) %>%
  cor()
cor_plot <- corrplot(cor_matrix,</pre>
                     main = "Figure 6: Correlation Matrix of Numerical Variables",
                     mar=c(0,0,1,0), cex.main = 1,
                     method = "color",
                     addCoef.col = "black",
                     tl.col = "black",
                     number.cex = 0.8,
                     tl.srt = 45,
                     order = 'original',
                     diag = F)
```





Plots of Log-Transformed Antibody Level vs. Selected Numerical Variables

```
# Antibody level vs. BMI
plot_bmi <- dat %>% ggplot(aes(x = bmi, y = log_antibody, fill = set, color = set)) +
  geom_point(alpha = 0.3, size = 2) +
  geom_smooth(method = "lm") +
  labs(y = "Log-Transformed Antibody Level", x = "BMI",
       title = "Figure 7: Log-Transformed Antibody Level vs. BMI") +
  theme minimal()
# Antibody level vs. Weight
plot_weight <- dat %>%
  ggplot(aes(x = weight, y = log_antibody, fill = set, color = set)) +
  geom_point(alpha = 0.3, size = 2) +
  geom smooth(method = "lm") +
  labs(y = "Log-Transformed Antibody Level", x = "Weight",
       title = "Figure 8: Log-Transformed Antibody Level vs. Weight") +
  theme minimal()
# Antibody level vs. Age
plot_age <- dat %>% ggplot(aes(x = age, y = log_antibody, fill = set, color = set)) +
  geom_point(alpha = 0.3, size = 2) + geom_smooth(method = "lm") +
  labs(y = "Log-Transformed Antibody Level", x = "Age",
       title = "Figure 9: Log-Transformed Antibody Level vs. Age") +
  theme_minimal()
plot_bmi
```



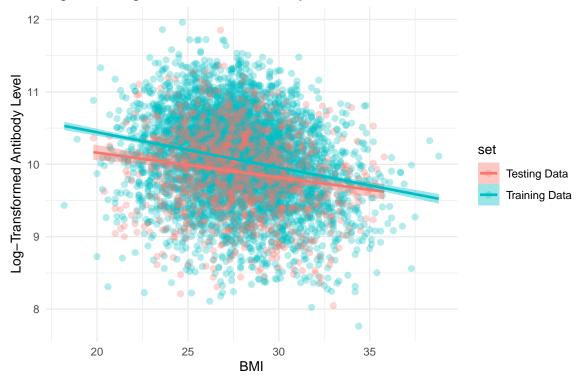
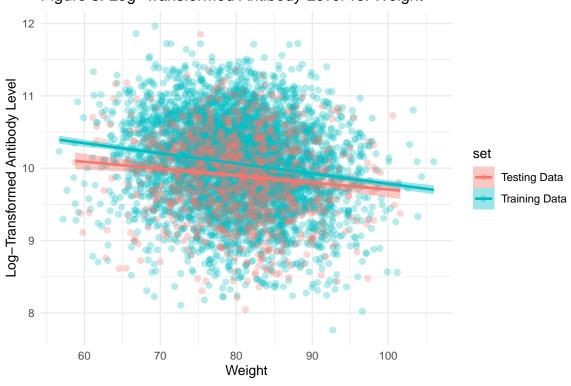
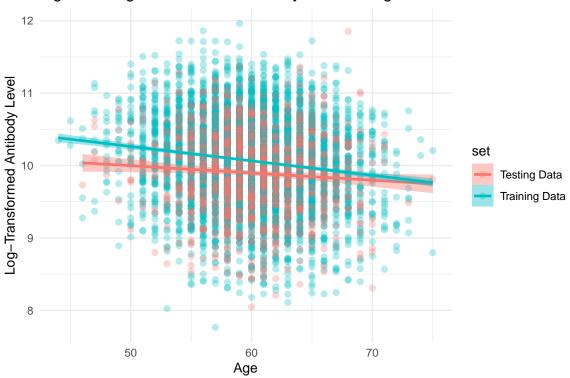


Figure 8: Log-Transformed Antibody Level vs. Weight



plot_age

Figure 9: Log-Transformed Antibody Level vs. Age



Model Training

Results