Appendix: R Code

```
knitr::opts_chunk$set(echo = FALSE, warning=FALSE, message=FALSE)
library(tidyverse)
library(knitr)

data <- read.csv("S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Study Data/REPOWERFinalDataStacked2020

data <- filter(data, time %in% c(0, 6, 24))


# Initial data subsets by timepoint
data_0mo <- filter(data, time==0)
data_6mo <- filter(data, time==6)
data_24mo <- filter(data, time==24)

# Subset IWQOL by timepoint
iwqol_0mo <- data_0mo$iwqoltotal
iwqol_6mo <- data_6mo$iwqoltotal
iwqol_24mo <- data_24mo$iwqoltotal


# Calculate change in IWQOL for each patient at each timepoint
iwqol_delta_0to6 <- iwqol_6mo - iwqol_0mo
iwqol_delta_0to24 <- iwqol_24mo - iwqol_0mo


# Add change from 0 to 6 months to base data set (3 timepoint = 3 reps)
data <- data %>%
  mutate(iwqol_delta_0to6 = rep(iwqol_delta_0to6, each=3))


# Add change from 0 to 24 months to base data set (3 timepoint = 3 reps)
data <- data %>%
  mutate(iwqol_delta_0to24 = rep(iwqol_delta_0to24, each=3))

#head(data[, c("study_id", "time", "iwqoltotal", "iwqol_delta_0to6", "iwqol_delta_0to24")])


# Add comorbidity count and proxy for 2+ comorbidities to dataset
comorbidities <- c("bmh_high_cholest", "bmh_asthma", "bmh_respiratory",
                   "bmh_colitiscrohns", "bmh_hip", "bmh_knee", "bmh_gallblad",
                   "bmh_heartfail", "bmh_angin", "bmh_stroke", "bmh_claud",
                   "bmh_arthritis", "bmh_hyperthy", "bmh_hypothy", "bmh_hypertens",
                   "bmh_pain_wlkmin20", "bmh_diabetes", "bmh_cancer")

data <- data %>%
  mutate(comorbidities_num = rowSums(across(comorbidities))) %>%
```

```r
  mutate(two_plus_comorbidities = ifelse(comorbidities_num >= 2, 1, 0))


# Add mental health disorder count and proxy for 1+ mental health disorders to dataset
mental_health_vars <- c("bmh_depression", "bmh_anxiety", "bmh_othermental")

data <- data %>%
  mutate(mental_health_num = rowSums(across(mental_health_vars))) %>%
  mutate(mental_health = ifelse(mental_health_num >= 1, 1, 0))


#head(data[, c("study_id", "time", "comorbidities_num", "two_plus_comorbidities",
#              "mental_health_num", "mental_health")])



# Calculate BMIs for all timepoints
data$bmi_all <- round((data$weight_kg*2.20462/data$height^2)*703, digits=1)

#head(data[,c("time", "weight_kg", "height", "bmi", "bmi_all")])


# Update subsets
data_0mo <- filter(data, time==0)
data_6mo <- filter(data, time==6)
data_24mo <- filter(data, time==24)

# Calculate delta BMI (relative to 0 mo)
bmi_0mo <- data_0mo$bmi_all
bmi_6mo <- data_6mo$bmi_all
bmi_24mo <- data_24mo$bmi_all


# Calculate change in IWQOL for each patient at each timepoint
bmi_delta_0to0 <- bmi_0mo - bmi_0mo
bmi_delta_0to6 <- bmi_6mo - bmi_0mo
bmi_delta_0to24 <- bmi_24mo - bmi_0mo

# Add change to base data set
data_0mo <- data_0mo %>%
  mutate(bmi_delta = bmi_delta_0to0)

data_6mo <- data_6mo %>%
  mutate(bmi_delta = bmi_delta_0to6)

data_24mo <- data_24mo %>%
  mutate(bmi_delta = bmi_delta_0to24)

data <- rbind(data_0mo, data_6mo, data_24mo)
data <- data[order(data$study_id, data$time),]

write.csv(data, "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Study Data/data_OR.csv",
          row.names=FALSE)
```

```r
knitr::opts_chunk$set(echo = FALSE, warning=FALSE, message=FALSE, options(digits=3))
library(tidyverse)
library(knitr)
library(lme4)
library(lmerTest)
library(kableExtra)
library(broom.mixed)
library(broom)
library(MASS)
library(pROC)
library(car)
library(fBasics)

data <- read.csv("S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Study Data/data_OR.csv",
                 na.strings="NA")

data$treatment_arm <- relevel(factor(data$treatment_arm), ref="In-clinic individual")

data_0mo <- filter(data, time==0)
data_6mo <- filter(data, time==6)
data_24mo <- filter(data, time==24)

predictors <- c("sex", "age", "rurality", "bmi", "mental_health",
                "two_plus_comorbidities", "treatment_arm",
                "weight_chng_per", "SITE", "Affiliation")

outcomes <- c("iwqoltotal", "iwqol_delta_0to6", "iwqol_delta_0to24")

data_6mo_na_rm <- drop_na(data_6mo[, names(data) %in% c(predictors, outcomes)])
data_24mo_na_rm <- drop_na(data_24mo[, names(data) %in% c(predictors, outcomes)])


# Affiliation fixed, site random

# Only affiliation and site
model.affil <- lmer(iwqoltotal ~  Affiliation  + (1 | SITE), data_0mo)
anova.affil <- anova(model.affil, type = "III")
p.affil <- anova.affil[1,6]


# Treatment arm
model.treat <- lmer(iwqoltotal ~  Affiliation + treatment_arm + (1 | SITE), data_0mo)
anova.treat <- anova(model.treat, type = "III")
p.treat <- anova.treat[2,6]
#summary(model.treat)
  # lower QoL in-clinic individual group at baseline


# Age
model.age <- lmer(iwqoltotal ~ Affiliation + age + (1 | SITE), data_0mo)
anova.age <- anova(model.age, type = "III")
p.age <- anova.age[2,6]
```

```r
# Sex
model.sex <- lmer(iwqoltotal ~ Affiliation + sex + (1 | SITE), data_0mo)
anova.sex <- anova(model.sex, type = "III")
p.sex <- anova.sex[2,6]


# Rurality
model.rural <- lmer(iwqoltotal ~ Affiliation + rurality + (1 | SITE), data_0mo)
anova.rural <- anova(model.rural, type = "III")
p.rural <- anova.rural[2,6]

# bmi (initial)
model.bmi <- lmer(iwqoltotal ~ Affiliation + bmi + (1 | SITE), data_0mo)
anova.bmi <- anova(model.bmi, type = "III")
p.bmi <- anova.bmi[2,6]


# Mental health disorders
model.mental <- lmer(iwqoltotal ~ Affiliation + mental_health + (1 | SITE), data_0mo)
anova.mental <- anova(model.mental, type = "III")
p.mental <- anova.mental[2,6]

# 2+ comorbidities
model.comorbid <- lmer(iwqoltotal ~ Affiliation + two_plus_comorbidities + (1 | SITE),
                       data_0mo)
anova.comorbid <- anova(model.comorbid, type = "III")
p.comorbid <- anova.comorbid[2,6]


p.table <- rbind(p.affil, p.treat, p.age, p.sex, p.rural, p.bmi, p.mental, p.comorbid)
colnames(p.table) <- c("p-value")

rownames(p.table) <- c("Affliation", "Treatment Arm", "Age", "Sex", "Rurality", "BMI",
                       "Mental Health Disorder(s)", "Comorbidities (2+)")

kable(p.table, linesep = "",
      caption = "Univariate Table - IWQOL Total at 0 Months",
      col.names = c("Variable", "p-value")) %>%
  kable_styling(latex_options = "striped")

write.csv(p.table,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/0mo_Univariate.csv")


# All variables
#------------------------
model.0mo.full <- lmer(iwqoltotal ~ Affiliation + treatment_arm + age + sex + rurality +
                         bmi + mental_health + two_plus_comorbidities + (1 | SITE),
                       data_0mo)

table.0mo.full <- anova(model.0mo.full)

rownames(table.0mo.full) <- c("Affliation", "Treatment Arm", "Age", "Sex", "Rurality",
```

```
                              "BMI", "Mental Health Disorder(s)", "Comorbidities (2+)")

kable(table.0mo.full, linesep = "",
      caption = "Full Model - IWQOL Total at 0 Months",
      col.names = c("Variable", "Sum Sq", "Mean Sq", "Num DF",
                    "Den DF", "F value", "Pr(>F)")) %>%
  kable_styling(latex_options = "striped")

write.csv(table.0mo.full,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/0mo_FullModel.csv")


# Remove age
#------------------------
model.0mo.reduced1 <- lmer(iwqoltotal ~ Affiliation + treatment_arm + sex + rurality +
                             bmi + mental_health + two_plus_comorbidities + (1 | SITE),
                           data_0mo)

table.0mo.reduced1 <- anova(model.0mo.reduced1)

rownames(table.0mo.reduced1) <- c("Affliation", "Treatment Arm", "Sex", "Rurality",
                                  "BMI", "Mental Health Disorder(s)", "Comorbidities (2+)")

kable(table.0mo.reduced1, linesep = "",
      caption = "Reduced Model 1 - Remove Age - IWQOL Total at 0 Months",
      col.names = c("Variable", "Sum Sq", "Mean Sq", "Num DF",
                    "Den DF", "F value", "Pr(>F)")) %>%
  kable_styling(latex_options = "striped")



# Remove comorbidites
#------------------------
model.0mo.reduced2 <- lmer(iwqoltotal ~  Affiliation + treatment_arm + sex + rurality +
                             bmi + mental_health + (1 | SITE), data_0mo)

table.0mo.reduced2 <- anova(model.0mo.reduced2)

rownames(table.0mo.reduced2) <- c("Affiliation", "Treatment Arm", "Sex", "Rurality",
                                  "BMI", "Mental Health Disorder(s)")

kable(table.0mo.reduced2, linesep = "",
      caption = "Reduced Model 2 - Remove Comorbidities - IWQOL Total at 0 Months",
      col.names = c("Variable", "Sum Sq", "Mean Sq", "Num DF",
                    "Den DF", "F value", "Pr(>F)")) %>%
  kable_styling(latex_options = "striped")



# Remove affiliation
#------------------------
model.0mo.reduced3 <- lmer(iwqoltotal ~ treatment_arm + sex + rurality + bmi +
                             mental_health + (1 | SITE), data_0mo)
```

```
table.0mo.reduced3 <- anova(model.0mo.reduced3)

rownames(table.0mo.reduced3) <- c("Treatment Arm", "Sex", "Rurality",
                                  "BMI", "Mental Health Disorder(s)")

kable(table.0mo.reduced3, linesep = "",
      caption = "Reduced Model 3 - Remove Affiliation - IWQOL Total at 0 Months",
      col.names = c("Variable", "Sum Sq", "Mean Sq", "Num DF",
                    "Den DF", "F value", "Pr(>F)")) %>%
  kable_styling(latex_options = "striped")


# Remove treatment arm
#-----------------------
model.0mo.reduced4 <- lmer(iwqoltotal ~ sex + rurality + bmi + mental_health + (1 | SITE),
                           data_0mo)

table.0mo.reduced4 <- anova(model.0mo.reduced4)

rownames(table.0mo.reduced4) <- c("Sex", "Rurality", "BMI", "Mental Health Disorder(s)")

kable(table.0mo.reduced4, linesep = "",
      caption = "Final Reduced Model - IWQOL Total at 0 Months",
      col.names = c("Variable", "Sum Sq", "Mean Sq", "Num DF",
                    "Den DF", "F value", "Pr(>F)")) %>%
  kable_styling(latex_options = "striped")

write.csv(table.0mo.reduced4,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/0mo_ReducedModel.csv")


vif.0mo <- data.frame(vif(model.0mo.reduced4))

rownames(vif.0mo) <- c("Sex", "Rurality", "BMI", "Mental Health Disorder(s)")

kable(vif.0mo, linesep = "",
      caption = "Variance Inflation Factors for the Final Model - IWQOL Total at 0 Months",
      col.names = c("Variable", "GVIF", "DF", "GVIF^(1/(2*DF))")) %>%
  kable_styling(latex_options = "striped")

write.csv(vif.0mo,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/0mo_VIF.csv")


# Estimates and CIs
# ---------------------
beta_estimates_0mo <- data.frame(fixef(model.0mo.reduced4))
colnames(beta_estimates_0mo) <- "Beta Estimate"

CI_bounds_0mo <- data.frame(confint(model.0mo.reduced4))
CI_bounds_0mo <- CI_bounds_0mo[-c(1:2), ]        # Remove ".sig01", ".sigma"
CIs_0mo <- data.frame(apply(CI_bounds_0mo, 1, function(ci)
  paste0("[", round(ci[1], 2), ", ", round(ci[2], 2), "]")))
```

```r
colnames(CIs_0mo) <- "95 Percent Confidence Interval"

final_model_results_0mo <- cbind(beta_estimates_0mo, CIs_0mo)

rownames(final_model_results_0mo) <- c("Intercept", "Male", "Large Rural", "Small Rural",
                                       "BMI", "Mental Health Disorder(s)")

kable(final_model_results_0mo, linesep = "",
      caption = "Estimates and 95 Percent Confidence Intervals - IWQOL Total at 0 Months") %>%
  kable_styling(latex_options = "striped")

write.csv(final_model_results_0mo,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/0mo_Estimates.csv")


#final_vars <- c("sex", "rurality", "bmi", "mental_health")

sum_sex_mean <- aggregate(data_0mo$iwqoltotal, list(data_0mo$sex), FUN=mean)
sum_sex_sd <- aggregate(data_0mo$iwqoltotal, list(data_0mo$sex), FUN=sd)
sum_sex <- merge(sum_sex_mean, sum_sex_sd, by=c("Group.1"))

sum_rurality_mean <- aggregate(data_0mo$iwqoltotal,
                               list(data_0mo$rurality), FUN=mean)
sum_rurality_sd <- aggregate(data_0mo$iwqoltotal,
                             list(data_0mo$rurality), FUN=sd)
sum_rurality <- merge(sum_rurality_mean, sum_rurality_sd, by=c("Group.1"))

sum_mental_health_mean <- aggregate(data_0mo$iwqoltotal,
                                    list(data_0mo$mental_health), FUN=mean)
sum_mental_health_sd <- aggregate(data_0mo$iwqoltotal,
                                  list(data_0mo$mental_health), FUN=sd)
sum_mental_health <- merge(sum_mental_health_mean, sum_mental_health_sd, by=c("Group.1"))


sum_table_0mo <- rbind(sum_sex, sum_rurality, sum_mental_health)
colnames(sum_table_0mo) <- c("Variable", "Mean", "Std Deviation")
sum_table_0mo$Variable[6:7] <- c("No Mental Health Disorder", "Mental Health Disorder(s)")
sum_table_0mo <- sum_table_0mo[c(1:3, 5, 4, 6:7), ]


kable(sum_table_0mo, linesep = "", row.names = FALSE,
      caption = "Variable Summary Table - IWQOL Total at 0 Months") %>%
  kable_styling(latex_options = "striped")


# Only affiliation and site
model.affil <- lmer(iwqol_delta_0to6 ~  Affiliation  + (1 | SITE), data_6mo)
anova.affil <- anova(model.affil, type = "III")
p.affil <- anova.affil[1,6]


# Treatment arm
model.treat <- lmer(iwqol_delta_0to6 ~  Affiliation + treatment_arm + (1 | SITE),
```

```
                    data_6mo)
anova.treat <- anova(model.treat, type = "III")
p.treat <- anova.treat[2,6]


# Age
model.age <- lmer(iwqol_delta_0to6 ~ Affiliation + age + (1 | SITE), data_6mo)
anova.age <- anova(model.age, type = "III")
p.age <- anova.age[2,6]


# Sex
model.sex <- lmer(iwqol_delta_0to6 ~ Affiliation + sex + (1 | SITE), data_6mo)
anova.sex <- anova(model.sex, type = "III")
p.sex <- anova.sex[2,6]


# Rurality
model.rural <- lmer(iwqol_delta_0to6 ~ Affiliation + rurality + (1 | SITE),
                    data_6mo)
anova.rural <- anova(model.rural, type = "III")
p.rural <- anova.rural[2,6]


# bmi (initial)
model.bmi <- lmer(iwqol_delta_0to6 ~ Affiliation + bmi + (1 | SITE), data_6mo)
anova.bmi <- anova(model.bmi, type = "III")
p.bmi <- anova.bmi[2,6]


# Mental health disorders
model.mental <- lmer(iwqol_delta_0to6 ~ Affiliation + mental_health + (1 | SITE),
                     data_6mo)
anova.mental <- anova(model.mental, type = "III")
p.mental <- anova.mental[2,6]


# 2+ comorbidities
model.comorbid <- lmer(iwqol_delta_0to6 ~ Affiliation + two_plus_comorbidities
                       + (1 | SITE), data_6mo)
anova.comorbid <- anova(model.comorbid, type = "III")
p.comorbid <- anova.comorbid[2,6]


# Percent Weight Change
model.weight <- lmer(iwqol_delta_0to6 ~  Affiliation + weight_chng_per
                     + (1 | SITE), data_6mo)
anova.weight <- anova(model.weight, type = "III")
p.weight <- anova.weight[2,6]


p.table <- rbind(p.affil, p.treat, p.age, p.sex, p.rural, p.bmi,
                 p.mental, p.comorbid, p.weight)
```

```r
colnames(p.table) <- c("p-value")

rownames(p.table) <- c("Affliation", "Treatment Arm", "Age", "Sex", "Rurality", "BMI",
                       "Mental Health Disorder(s)", "Comorbidities (2+)",
                       "Percent Weight Change")

kable(p.table, linesep = "", caption = "Univariate Table - Change in IWQOL at 6 Months",
      col.names = c("Variable", "p-value")) %>%
  kable_styling(latex_options = "striped")

write.csv(p.table,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/6mo_Univariate.csv")


# All variables
# -----------------------
model.6mo.full <- lmer(iwqol_delta_0to6 ~ age + sex + mental_health + weight_chng_per
                       + (1 | SITE), data_6mo)

table.6mo.full <- anova(model.6mo.full)

rownames(table.6mo.full) <- c("Age", "Sex", "Mental Health Disorder(s)",
                              "Percent Weight Change")

kable(table.6mo.full, linesep = "",
      caption = "Full Model - Change in IWQOL at 6 Months",
      col.names = c("Variable", "Sum Sq", "Mean Sq", "Num DF",
                    "Den DF", "F value", "Pr(>F)")) %>%
  kable_styling(latex_options = "striped")

write.csv(table.6mo.full,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/6mo_FullModel.csv")


# Remove comorbidities
# -----------------------
model.6mo.reduced1 <- lmer(iwqol_delta_0to6 ~ sex + mental_health + weight_chng_per
                           + (1 | SITE), data_6mo)

table.6mo.reduced1 <- anova(model.6mo.reduced1)

rownames(table.6mo.reduced1) <- c("Sex", "Mental Health Disorder(s)", "Percent Weight Change")

kable(table.6mo.reduced1, linesep = "",
      caption = "Final Reduced Model - Change in IWQOL at 6 Months",
      col.names = c("Variable", "Sum Sq", "Mean Sq", "Num DF",
                    "Den DF", "F value", "Pr(>F)")) %>%
  kable_styling(latex_options = "striped")

write.csv(table.6mo.reduced1,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/6mo_ReducedModel.csv")
```

```r
vif.6mo <- data.frame(vif(model.6mo.reduced1))
rownames(vif.6mo) <- c("Sex", "Mental Health Disorder(s)", "Percent Weight Change")
colnames(vif.6mo) <- "VIF"

kable(vif.6mo, linesep = "",
      caption = "Variance Inflation Factors for the Final Model - Change in IWQOL at 6 Months",
      col.names = c("Variable", "VIF")) %>%
  kable_styling(latex_options = "striped")

write.csv(vif.6mo,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/6mo_VIF.csv")


# Estimates and CIs
# ---------------------
beta_estimates_6mo <- data.frame(fixef(model.6mo.reduced1))
colnames(beta_estimates_6mo) <- "Beta Estimate"

CI_bounds_6mo <- data.frame(confint(model.6mo.reduced1))
CI_bounds_6mo <- CI_bounds_6mo[-c(1:2), ]        # Remove ".sig01", ".sigma"
CIs_6mo <- data.frame(apply(CI_bounds_6mo, 1, function(ci)
  paste0("[", round(ci[1], 2), ", ", round(ci[2], 2), "]")))
colnames(CIs_6mo) <- "95 Percent Confidence Interval"

final_model_results_6mo <- cbind(beta_estimates_6mo, CIs_6mo)

rownames(final_model_results_6mo) <- c("Intercept", "Male", "Mental Health Disorder(s)",
                                       "Percent Weight Change")

kable(final_model_results_6mo, linesep = "",
      caption = "Estimates and 95 Percent Confidence Intervals - Change in IWQOL at 6 Months",
      col.names = c("Variable", "Beta Estimate", "95 Percent Confidence Interval")) %>%
  kable_styling(latex_options = "striped")

write.csv(final_model_results_6mo,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/6mo_Estimates.csv")


#final_vars <- c("sex", "mental_health", "weight_chng_per")

sum_sex_mean <- aggregate(data_6mo_na_rm$iwqol_delta_0to6,
                          list(data_6mo_na_rm$sex), FUN=mean)
sum_sex_sd <- aggregate(data_6mo_na_rm$iwqol_delta_0to6,
                        list(data_6mo_na_rm$sex), FUN=sd)
sum_sex <- merge(sum_sex_mean, sum_sex_sd, by=c("Group.1"))


sum_mental_health_mean <- aggregate(data_6mo_na_rm$iwqol_delta_0to6,
                                    list(data_6mo_na_rm$mental_health), FUN=mean)
sum_mental_health_sd <-aggregate(data_6mo_na_rm$iwqol_delta_0to6,
                                 list(data_6mo_na_rm$mental_health), FUN=sd)
sum_mental_health <- merge(sum_mental_health_mean, sum_mental_health_sd, by=c("Group.1"))
```

```r
sum_table_6mo <- rbind(sum_sex, sum_mental_health)
colnames(sum_table_6mo) <- c("Variable", "Mean", "Std Deviation")
sum_table_6mo$Variable[3:4] <- c("No Mental Health Disorder", "Mental Health Disorder(s)")

kable(sum_table_6mo, linesep = "", row.names = FALSE,
      caption = "Variable Summary Table - Change in IWQOL at 6 Months") %>%
  kable_styling(latex_options = "striped")


# Only affiliation and site
model.affil <- lmer(iwqol_delta_0to24 ~  Affiliation  + (1 | SITE), data_24mo)
anova.affil <- anova(model.affil, type = "III")
p.affil <- anova.affil[1,6]


# Treatment arm
model.treat <- lmer(iwqol_delta_0to24 ~  Affiliation + treatment_arm
                    + (1 | SITE), data_24mo)
anova.treat <- anova(model.treat, type = "III")
p.treat <- anova.treat[2,6]
#summary(model.treat)


# Age
model.age <- lmer(iwqol_delta_0to24 ~ Affiliation + age + (1 | SITE), data_24mo)
anova.age <- anova(model.age, type = "III")
p.age <- anova.age[2,6]


# Sex
model.sex <- lmer(iwqol_delta_0to24 ~ Affiliation + sex + (1 | SITE), data_24mo)
anova.sex <- anova(model.sex, type = "III")
p.sex <- anova.sex[2,6]


# Rurality
model.rural <- lmer(iwqol_delta_0to24 ~ Affiliation + rurality + (1 | SITE), data_24mo)
anova.rural <- anova(model.rural, type = "III")
p.rural <- anova.rural[2,6]


# bmi (initial)
model.bmi <- lmer(iwqol_delta_0to24 ~ Affiliation + bmi + (1 | SITE), data_24mo)
anova.bmi <- anova(model.bmi, type = "III")
p.bmi <- anova.bmi[2,6]


# Mental health disorders
model.mental <- lmer(iwqol_delta_0to24 ~ Affiliation + mental_health
                     + (1 | SITE), data_24mo)
anova.mental <- anova(model.mental, type = "III")
p.mental <- anova.mental[2,6]
```

```r
# 2+ comorbidities
model.comorbid <- lmer(iwqol_delta_0to24 ~ Affiliation + two_plus_comorbidities
                       + (1 | SITE), data_24mo)
anova.comorbid <- anova(model.comorbid, type = "III")
p.comorbid <- anova.comorbid[2,6]


# Percent Weight Change
model.weight <- lmer(iwqol_delta_0to6 ~  Affiliation + weight_chng_per
                     + (1 | SITE), data_24mo)
anova.weight <- anova(model.weight, type = "III")
p.weight <- anova.weight[2,6]


p.table <- rbind(p.affil, p.treat, p.age, p.sex, p.rural,
                 p.bmi, p.mental, p.comorbid, p.weight)
colnames(p.table) <- c("p-value")

rownames(p.table) <- c("Affliation", "Treatment Arm", "Age", "Sex", "Rurality", "BMI",
                       "Mental Health Disorder(s)", "Comorbidities (2+)",
                       "Percent Weight Change")

kable(p.table, linesep = "",
      caption = "Univariate Table - Change in IWQOL at 24 Months",
      col.names = c("Variable", "p-value")) %>%
  kable_styling(latex_options = "striped")

write.csv(p.table,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/24mo_Univariate.csv")


# Full model
# ----------------------
model.24mo.full <- lmer(iwqol_delta_0to24 ~ age + sex + mental_health + weight_chng_per
                        + (1 | SITE), data_24mo)

table.24mo.full <- anova(model.24mo.full)

rownames(table.24mo.full) <- c("Age", "Sex", "Mental Health Disorder(s)",
                               "Percent Weight Change")

kable(table.24mo.full, linesep = "",
      caption = "Full Model - Change in IWQOL at 24 Months",
      col.names = c("Variable", "Sum Sq", "Mean Sq", "Num DF",
                    "Den DF", "F value", "Pr(>F)")) %>%
  kable_styling(latex_options = "striped")

write.csv(table.24mo.full,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/24mo_FullModel.csv")


# Remove age
# ---------------------
```

```r
model.24mo.reduced1 <- lmer(iwqol_delta_0to24 ~ sex + mental_health + weight_chng_per
                            + (1 | SITE), data_24mo)

table.24mo.reduced1 <- anova(model.24mo.reduced1)

rownames(table.24mo.reduced1) <- c("Sex", "Mental Health Disorder(s)",
                                   "Percent Weight Change")

kable(table.24mo.reduced1, linesep = "",
      caption = "Final Reduced Model - Change in IWQOL at 24 Months",
      col.names = c("Variable", "Sum Sq", "Mean Sq", "Num DF",
                    "Den DF", "F value", "Pr(>F)")) %>%
  kable_styling(latex_options = "striped")

write.csv(table.24mo.reduced1,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/24mo_ReducedModel.csv")


vif.24mo <- data.frame(vif(model.24mo.reduced1))

rownames(vif.24mo) <- c("Sex", "Mental Health Disorder(s)", "Percent Weight Change")
colnames(vif.24mo) <- "VIF"

kable(vif.24mo, linesep = "",
      caption = "Variance Inflation Factors for the Final Model - Change in IWQOL at 24 Months",
      col.names = c("Variable", "VIF")) %>%
  kable_styling(latex_options = "striped")

write.csv(vif.24mo,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/24mo_VIF.csv")


# Estimates and CIs
# ---------------------
beta_estimates_24mo <- data.frame(fixef(model.24mo.reduced1))
colnames(beta_estimates_24mo) <- "Beta Estimate"

CI_bounds_24mo <- data.frame(confint(model.24mo.reduced1))
CI_bounds_24mo <- CI_bounds_24mo[-c(1:2), ]        # Remove ".sig01", ".sigma"
CIs_24mo <- data.frame(apply(CI_bounds_24mo, 1, function(ci)
  paste0("[", round(ci[1], 2), ", ", round(ci[2], 2), "]")))
colnames(CIs_24mo) <- "95 Percent Confidence Interval"

final_model_results_24mo <- cbind(beta_estimates_24mo, CIs_24mo)

rownames(final_model_results_24mo) <- c("Intercept", "Male", "Mental Health Disorder(s)",
                                        "Percent Weight Change")

kable(final_model_results_24mo, linesep = "",
      caption = "Estimates and 95 Percent Confidence Intervals - Change in IWQOL at 24 Months",
      col.names = c("Variable", "Beta Estimate", "95 Percent Confidence Interval")) %>%
  kable_styling(latex_options = "striped")
```

```r
write.csv(final_model_results_24mo,
          "S:/Biostats/BIO-STAT/Brown_Lexie/BIOS898/Olivia/Output Tables/24mo_Estimates.csv")


#final_vars <- c("sex","household_income", "mental_health", "weight_chng_per")

sum_sex_mean <- aggregate(data_24mo_na_rm$iwqol_delta_0to24,
                          list(data_24mo_na_rm$sex), FUN=mean)
sum_sex_sd <- aggregate(data_24mo_na_rm$iwqol_delta_0to24,
                        list(data_24mo_na_rm$sex), FUN=sd)
sum_sex <- merge(sum_sex_mean, sum_sex_sd, by=c("Group.1"))

sum_mental_health_mean <- aggregate(data_24mo_na_rm$iwqol_delta_0to6,
                                    list(data_24mo_na_rm$mental_health), FUN=mean)
sum_mental_health_sd <-aggregate(data_24mo_na_rm$iwqol_delta_0to6,
                                 list(data_24mo_na_rm$mental_health), FUN=sd)
sum_mental_health <- merge(sum_mental_health_mean, sum_mental_health_sd, by=c("Group.1"))

sum_table_24mo <- rbind(sum_sex, sum_mental_health)
colnames(sum_table_24mo) <- c("Variable", "Mean", "Std Deviation")
sum_table_24mo$Variable[3:4] <- c("No Mental Health Disorder", "Mental Health Disorder(s)")

kable(sum_table_24mo, linesep = "", row.names = FALSE,
      caption = "Variable Summary Table - Change in IWQOL at 24 Months") %>%
  kable_styling(latex_options = "striped")
```