

Comobidities of Iraqi children with ASD: Reproducible Report

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1 Settings

1.1 Clear working environment

```
rm(list = ls())
```

1.2 Set a random seed

```
set.seed(123)
```

1.3 Required packages

rcompanion : Compute effect sizes following nonparametric tests

ggplot2 : Create jitter and median plots

scales : Format percents

```
packages <- c("rcompanion", "ggplot2", "scales")

for (package in packages) {

  if (!requireNamespace(package, quietly = TRUE))
    install.packages(package)

  suppressPackageStartupMessages(library(package, character.only = TRUE))
}

## Warning: package 'rcompanion' was built under R version 4.4.3

## Warning: package 'ggplot2' was built under R version 4.4.3

## Warning: package 'scales' was built under R version 4.4.3
```

1.4 Import and inspect data attributes

```
df <- read.csv("ASD_comobidity_dataset.csv")

attributes(df)[names(attributes(df)) != "row.names"]

## $names
## [1] "ID"                  "source"              "age"
## [4] "gender"               "dx_age"              "asd_fhx"
## [7] "epilepsy"             "sleep_disorder"      "sleep_duration"
## [10] "bmi"                  "calorie"             "chronic_condition"
## [13] "family_hx"            "daytime_activity"    "family_lifestyle"
## [16] "daily_screentime"     "excessive_screentime" "resperidone"
##
## $class
## [1] "data.frame"
```

2 Difference in sample characteristics across healthcare centers

2.1 Define Variables and result objects

```
#Specify continuous and grouping variables
scales <- c("age", "dx_age", "bmi")
centre <- "source"
cat_vars <- c("gender", "asd_fhx", "epilepsy", "sleep_disorder")

#Prepare an empty data frame for Kruskal-Wallis test results
results_char1 <- data.frame(scale      = character(),
                             H_value     = numeric(),
                             df          = integer(),
                             p_value     = numeric(),
                             eps_sq      = numeric(),
                             CI_lower_95 = numeric(),
                             CI_upper_95 = numeric(),
                             stringsAsFactors = FALSE
                            )

#Prepare an empty data frame for chi-square test results
results_char2 <- data.frame(variable   = character(),
                             chisq_stat = numeric(),
                             df         = integer(),
                             p_value    = numeric(),
                             cramers_V = numeric(),
                             CI_lower_95 = numeric(),
                             CI_upper_95 = numeric(),
                             stringsAsFactors = FALSE
                            )
```

2.2 Epsilon-squared effect size for continuous characteristics

```
#Loop over continuous variables
for (y in scales){

  # Subset and clean the data
  sub      <- df[, c(y, centre)]
  names(sub) <- c("y", "g")
  sub       <- na.omit(sub)
  sub$y     <- as.numeric(sub$y)
  sub$g     <- factor(sub$g, levels = c("al_subtайн", "al_хусайн", "baghdad"))

  # Kruskal-Wallis test
  kw <- kruskal.test(y ~ g, data = sub)

  # Epsilon-squared effect size:
  eps <- epsilonSquared(x          = sub$y,
                         g           = sub$g,
                         ci          = TRUE,
                         conf.level = 0.95,
                         type        = "bca",
                         R            = 10000
                       )

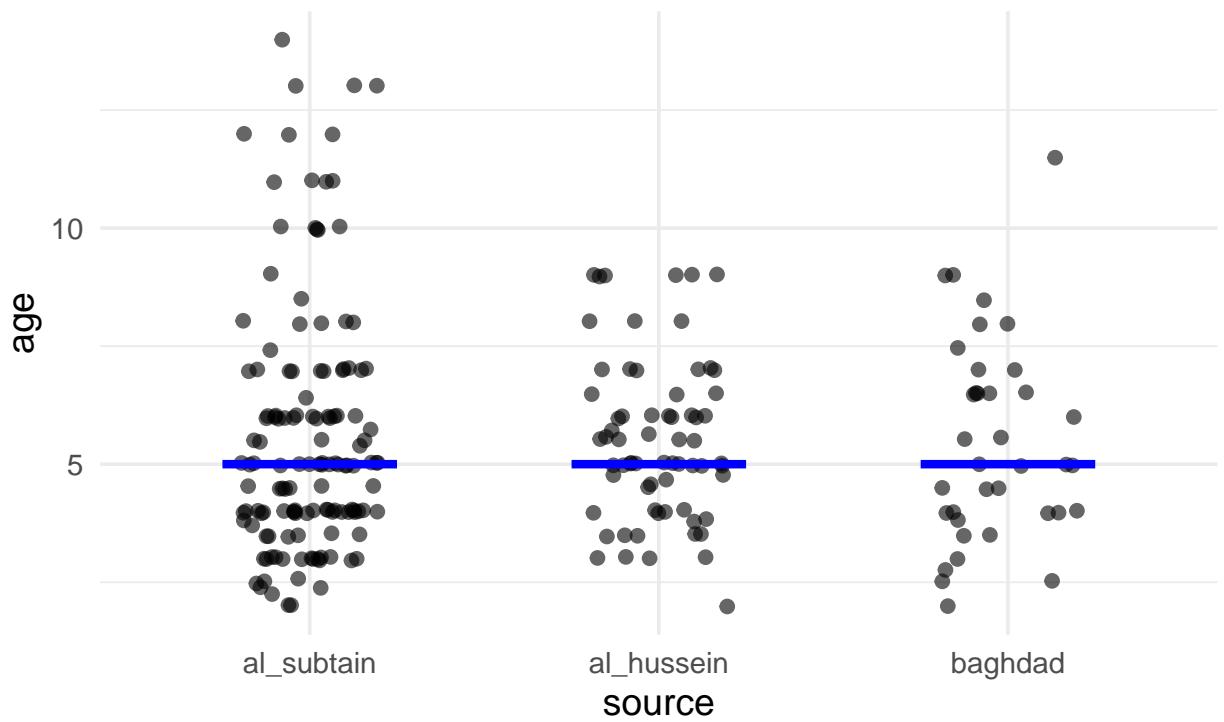
  # Jitter and median crossbar plot
  p <- ggplot(sub, aes(x = g, y = y)) +
    geom_jitter(width = 0.2, alpha = 0.6) +
    stat_summary(fun = median,
                 geom = "crossbar",
                 width = 0.5,
                 color = "blue",
                 linewidth = 0.6
               ) +
    labs(title   = paste0("Scatter of ", y, " by ", centre),
         subtitle = paste0("Epsilon-squared = ", round(eps, 3)),
         x        = centre,
         y        = y
       ) +
    theme_minimal(base_size = 14)
  print(p)

  # Append results
  results_char1 <- rbind(results_char1,
                           data.frame(scale      = y,
                                      H_value    = as.numeric(kw$statistic),
                                      df         = kw$parameter,
                                      p_value    = kw$p.value,
                                      eps_sq    = eps,
                                      stringsAsFactors = FALSE
                                    )
                         )
}

}
```

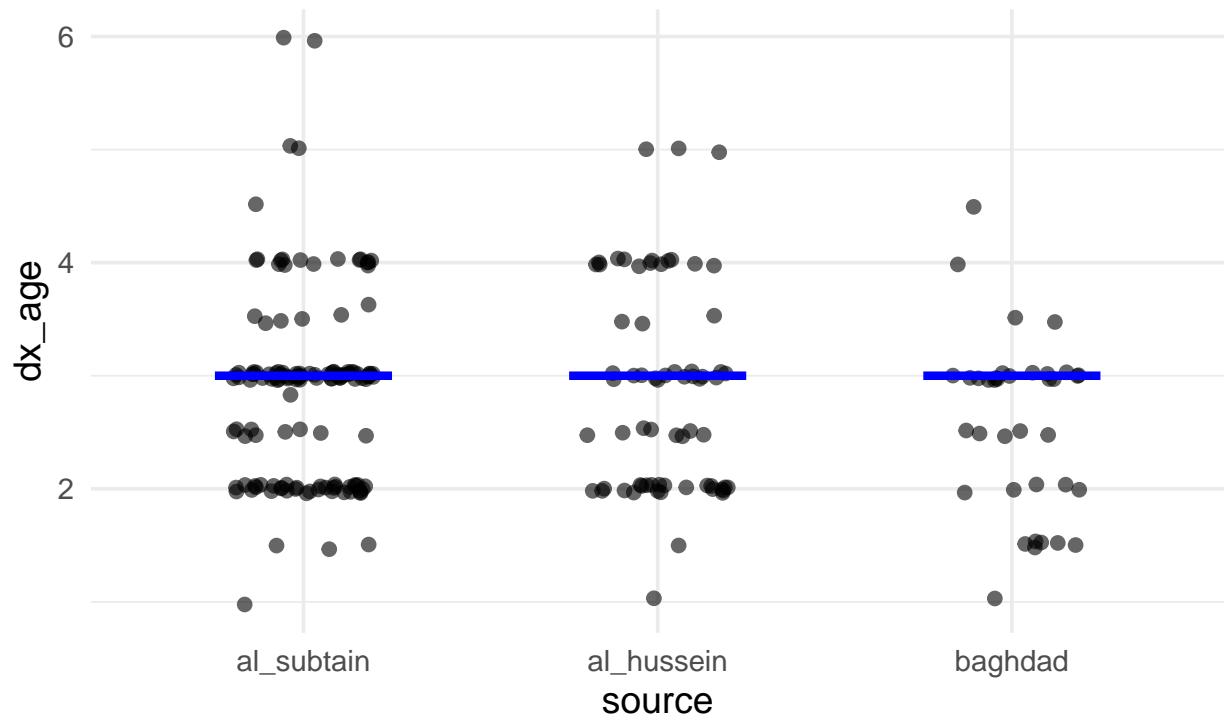
Scatter of age by source

Epsilon-squared = 0.004



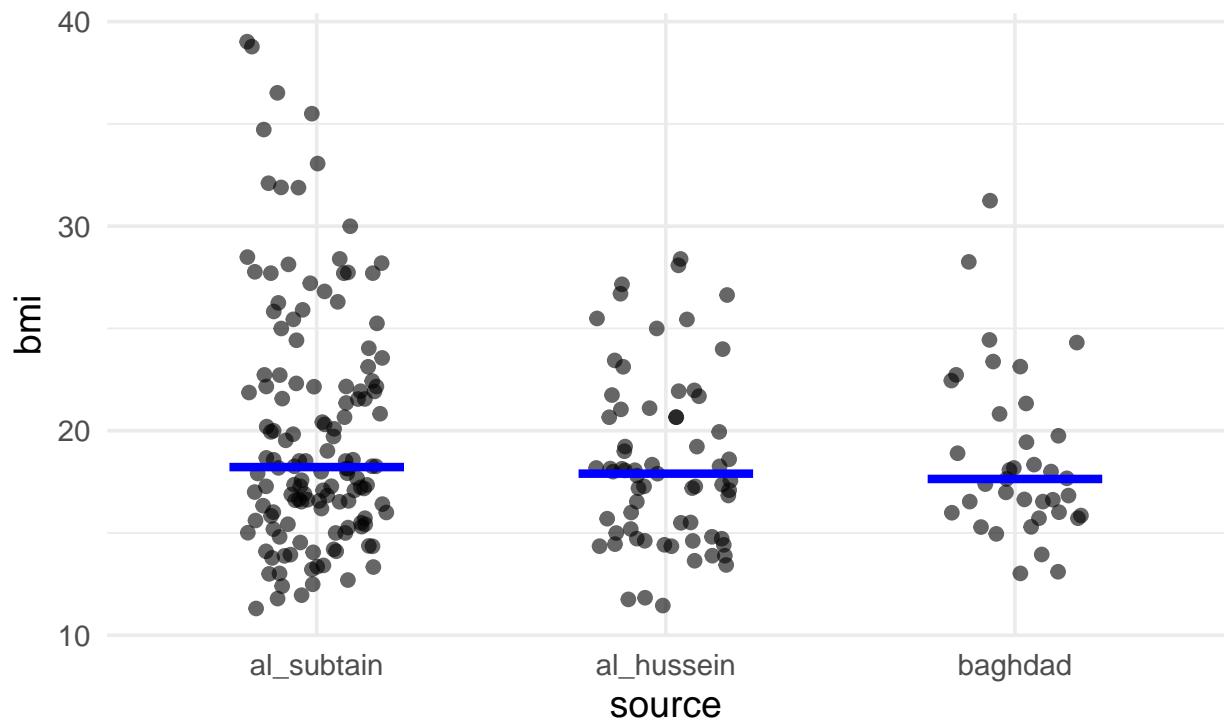
Scatter of dx_age by source

Epsilon-squared = 0.011



Scatter of bmi by source

Epsilon-squared = 0.008



```
# Print results
print(results_char1)
```

```
##      scale   H_value df   p_value eps_sq.epsilon.squared eps_sq.lower.ci
## df     age 0.8462549  2 0.6549952                      0.00354    3.22e-06
## df1 dx_age 2.5953899  2 0.2731607                      0.01090    7.97e-05
## df2   bmi 1.9653671  2 0.3743053                      0.00822    6.91e-05
##      eps_sq.upper.ci
## df          0.0146
## df1         0.0390
## df2         0.0335
```

2.3 Cramer's V effect size for categorical characteristics

```
# Loop over categorical variables
for (v in cat_vars) {

  # Subset and clean the data
  sub <- df[, c(v, centre)]
  names(sub) <- c("y", "g")
  sub <- na.omit(sub)
  sub$y <- factor(sub$y)
  sub$g <- factor(sub$g, levels = c("al_subtайн", "al_хусайн", "багдад"))

  tbl <- table(sub$y, sub$g)

  # Chi-square test
  chi <- chisq.test(tbl, correct = FALSE)

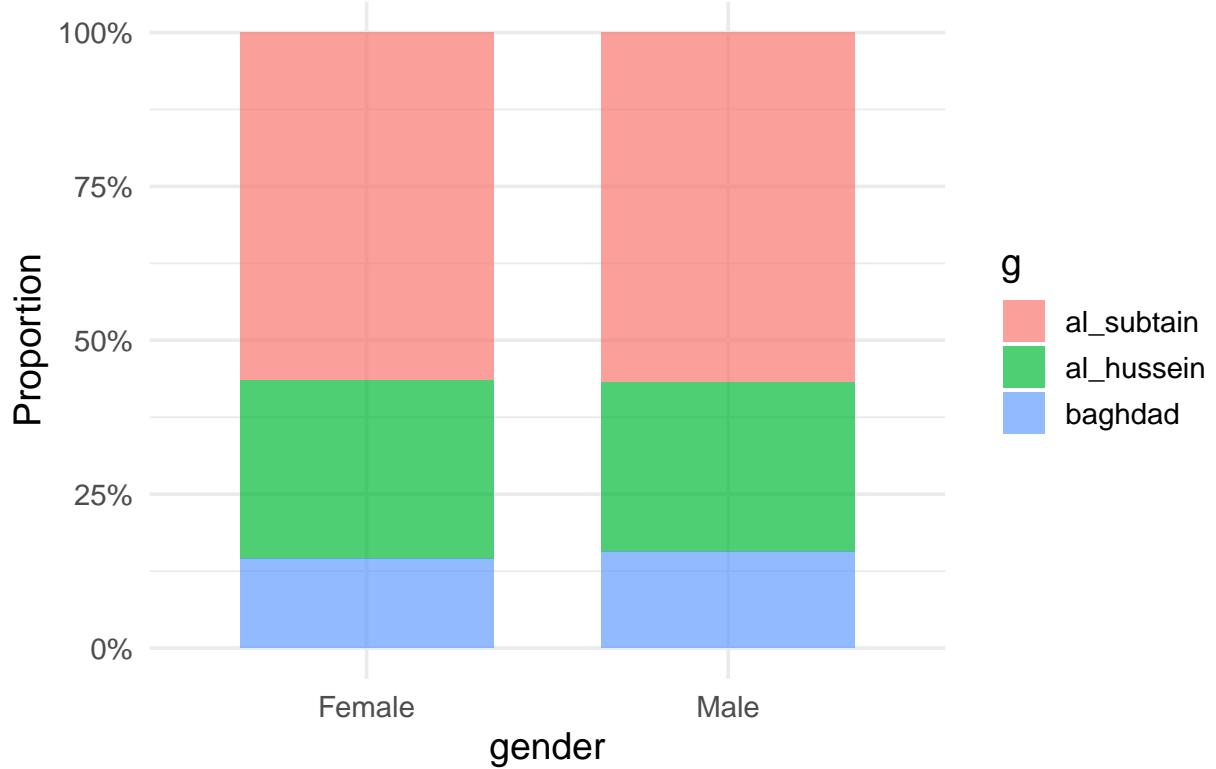
  # Cramer's V effect size
  cv <- cramerV(tbl,
                  ci      = TRUE,
                  conf    = 0.95,
                  type    = "bca",
                  R       = 10000
  )

  # Stacked bar chart
  p <- ggplot(sub, aes(x = y, fill = g)) +
    geom_bar(position = "fill", width = 0.7, alpha = 0.7) +
    scale_y_continuous(labels = percent_format()) +
    labs(title    = sprintf("Distribution of %s by %s", v, centre),
         x        = v,
         y        = "Proportion"
    ) +
    theme_minimal(base_size = 14)
  print(p)

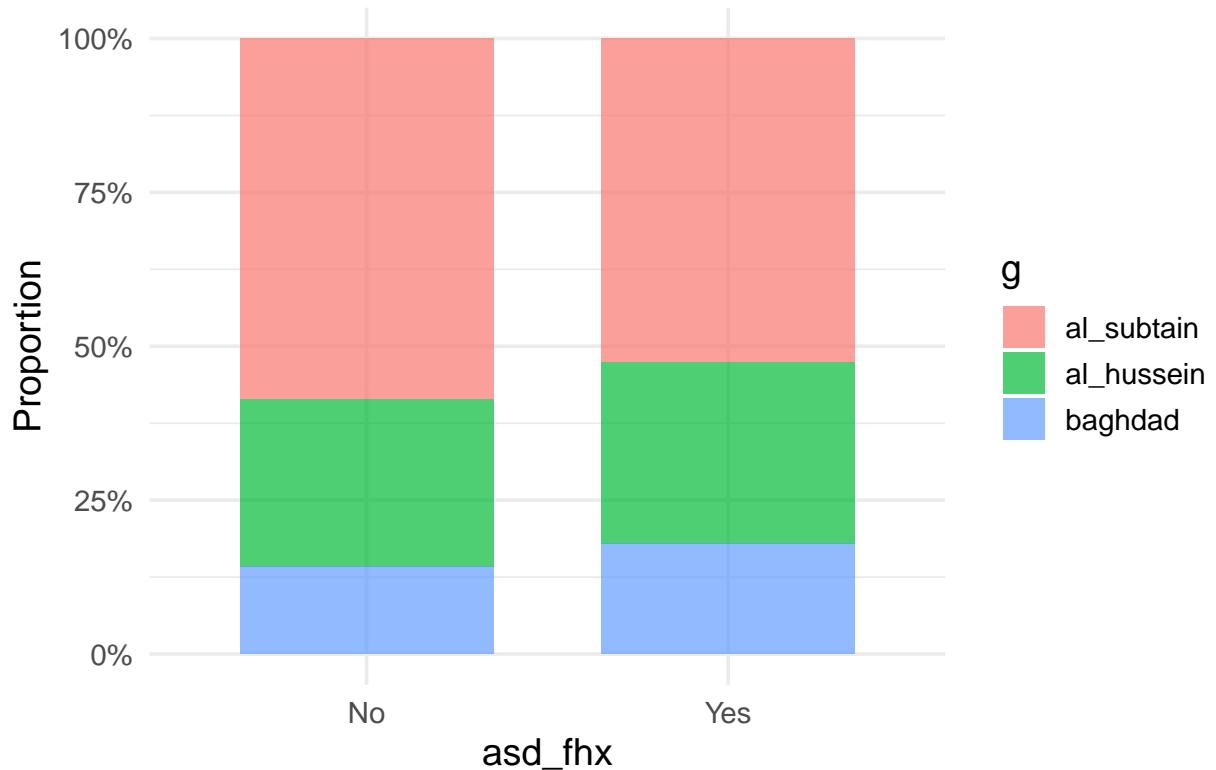
  # Append results
  results_char2 <- rbind(results_char2,
                           data.frame(variable      = v,
                                      chisq_stat   = as.numeric(chi$statistic),
                                      df           = as.integer(chi$parameter),
                                      p_value     = chi$p.value,
                                      cramers_V   = cv,
                                      stringsAsFactors = FALSE
                           )
  )
}

## Warning in norm.inter(t, adj.alpha): extreme order statistics used as endpoints
```

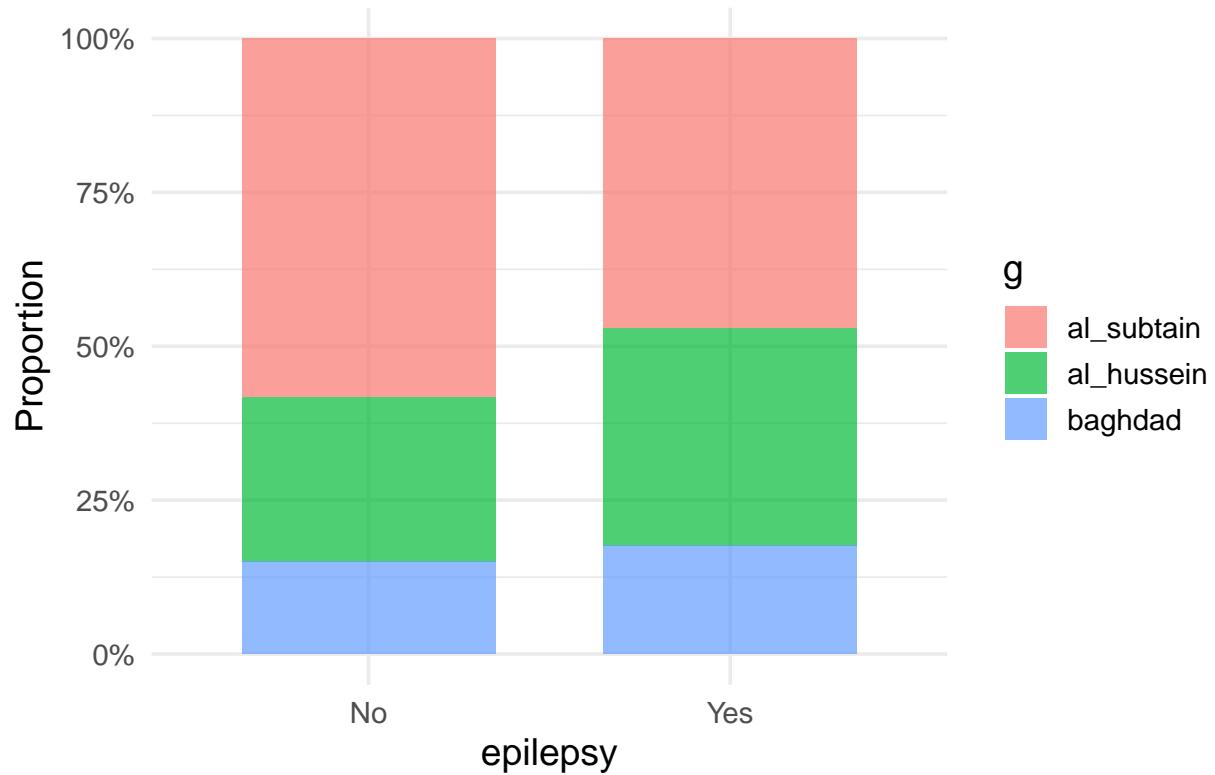
Distribution of gender by source

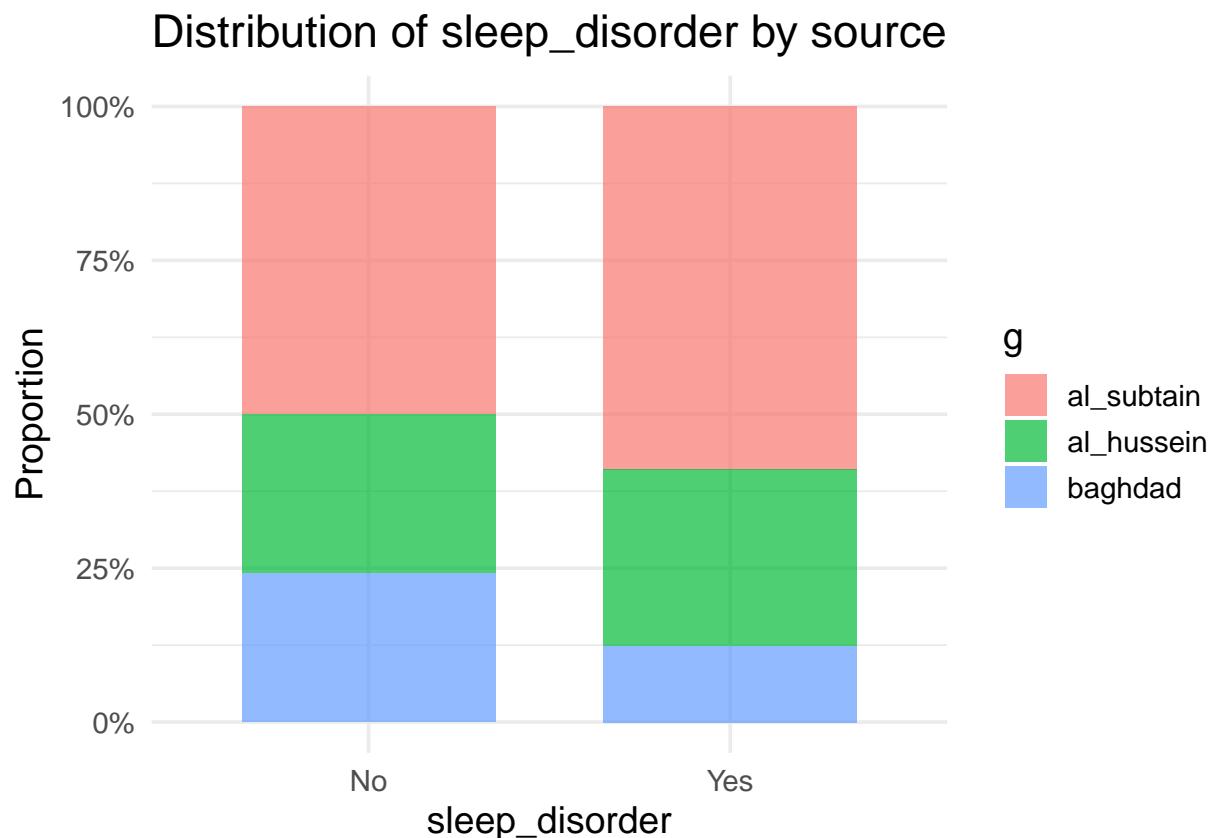


Distribution of asd_fhx by source



Distribution of epilepsy by source





```
# Print results
print(results_char2)
```

```
##          variable chisq_stat df      p_value cramers_V.Cramer.V cramers_V.lower.ci
## 1        gender  0.08192373  2  0.95986573          0.01848          0.000000
## 2       asd_fhx  0.92587489  2  0.62943201          0.06211          0.003493
## 3      epilepsy 1.54537230  2  0.46177101          0.08024          0.005074
## 4 sleep_disorder 4.96607621  2  0.08348919          0.14380          0.025680
##   cramers_V.upper.ci
## 1             0.0217
## 2             0.1321
## 3             0.1649
## 4             0.2693
```

3 Difference in BMI across potentially-associated factors

3.1 Define Variables and result objects

```
#Specify continuous and grouping variables
y_var           <- "bmi"
binary_groups   <- c("chronic_condition", "family_hx", "excessive_screentime", "resperidone")
multi_groups    <- c("calorie", "daytime_activity", "family_lifestyle")

#Prepare an empty data frame for Man-Whitney U test results
results_binary <- data.frame(group      = character(),
                               U_stat      = numeric(),
                               p_value     = numeric(),
                               r_value    = numeric(),
                               CI_lower_95 = numeric(),
                               CI_upper_95 = numeric(),
                               stringsAsFactors = FALSE
                             )

#Prepare an empty data frame for Kruskal-Wallis test results
results_multi <- data.frame(group      = character(),
                             H_value     = numeric(),
                             df          = integer(),
                             p_value     = numeric(),
                             eps_sq      = numeric(),
                             CI_lower_95 = numeric(),
                             CI_upper_95 = numeric(),
                             stringsAsFactors = FALSE
                           )
```

3.2 Wilixicon R effect size for binary grouping variables

```
# Loop over binary grouping variables
for (g in binary_groups) {

  # Subset and clean the data
  sub <- df[, c(y_var, g)]
  names(sub) <- c("y", "g")
  sub <- na.omit(sub)
  sub$g <- factor(sub$g, levels = c("No", "Yes"))

  # Mann-Whitney test
  wt <- wilcox.test(y ~ g, data = sub, exact = FALSE)

  # R-values effect size
  r <- -1*wilcoxonR(x = sub$y,
                      g = sub$g,
                      ci = TRUE,
                      conf.level = 0.95,
                      type = "bca",
                      R = 10000
                     )
  r[c(2, 3)] <- r[c(3, 2)]

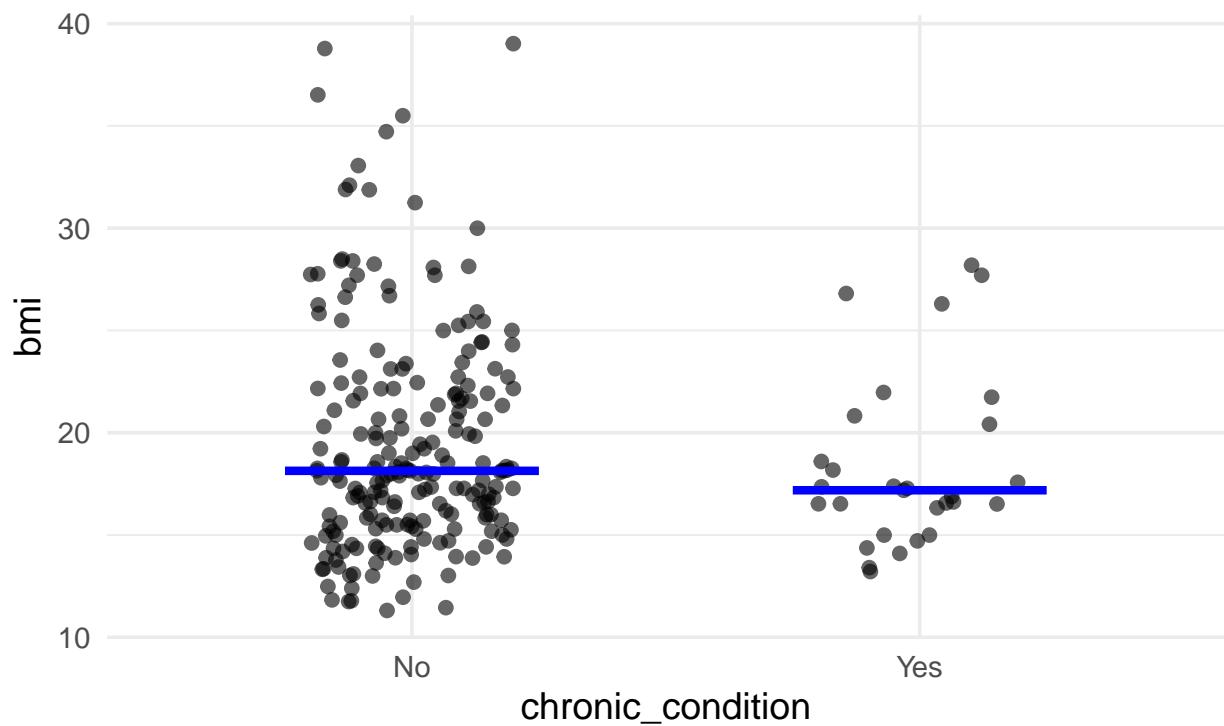
  # Jitter and median crossbar plot
  p <- ggplot(sub, aes(x = g, y = y)) +
    geom_jitter(width = 0.2, alpha = 0.6) +
    stat_summary(fun = median,
                 geom = "crossbar",
                 width = 0.5,
                 color = "blue",
                 linewidth = 0.6
                ) +
    labs(title = paste0("Scatter of ", y_var, " by ", g),
         subtitle = paste0("r = ", round(r, 3)),
         x = g,
         y = y_var
        ) +
    theme_minimal(base_size = 14)
  print(p)

  #Append result
  results_binary <- rbind(results_binary,
                           data.frame(group = g,
                                      U_stat = as.numeric(wt$statistic),
                                      p_value = wt$p.value,
                                      r_value = r,
                                      stringsAsFactors = FALSE
                                     )
                          )
}

}
```

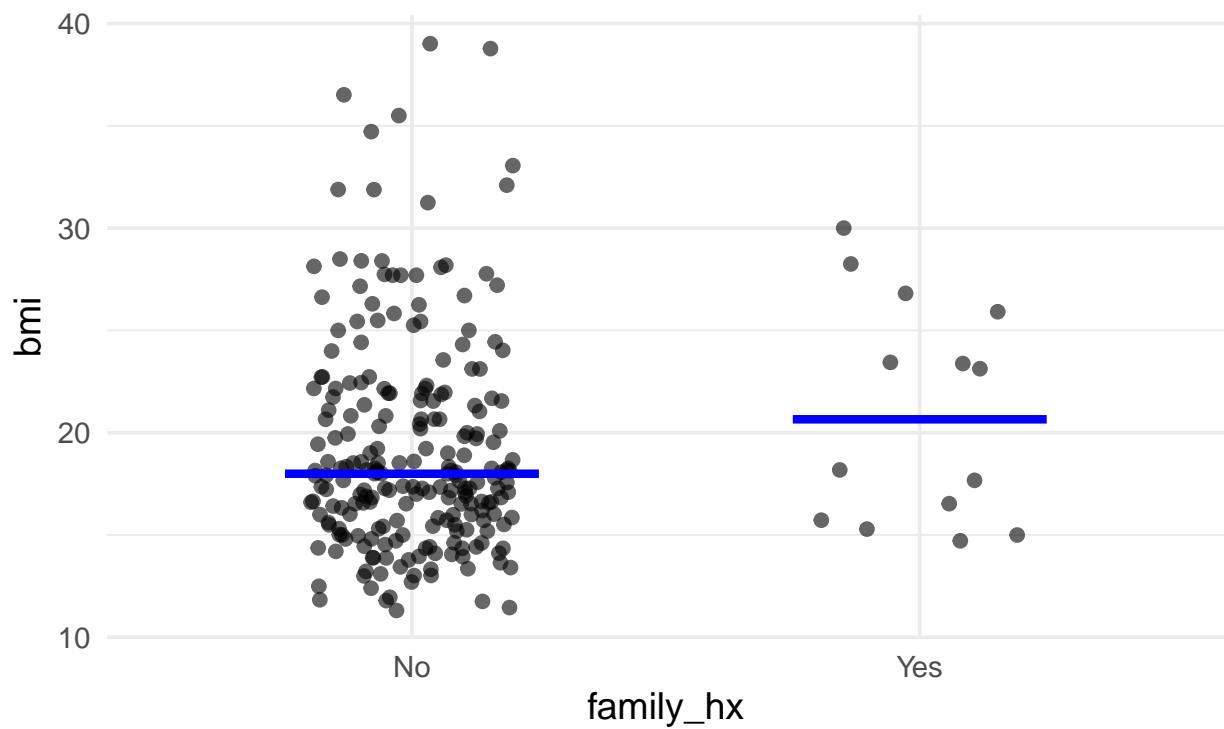
Scatter of bmi by chronic_condition

$r = -0.066$



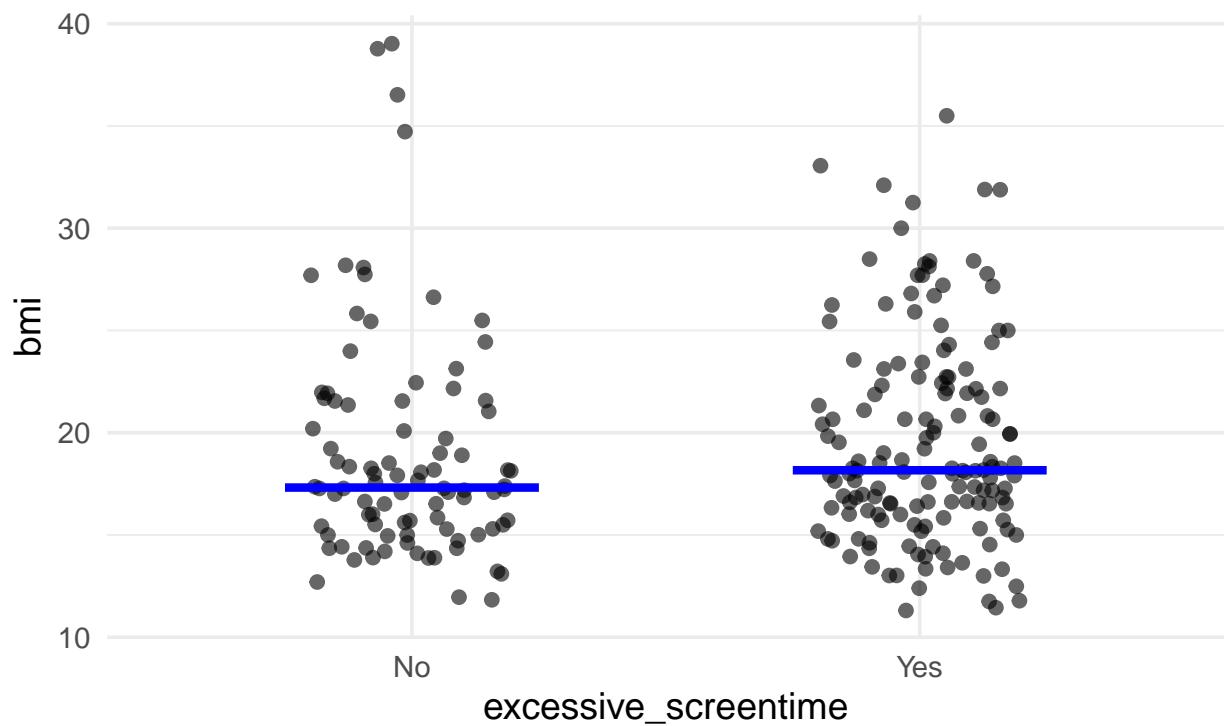
Scatter of bmi by family_hx

$r = 0.078$



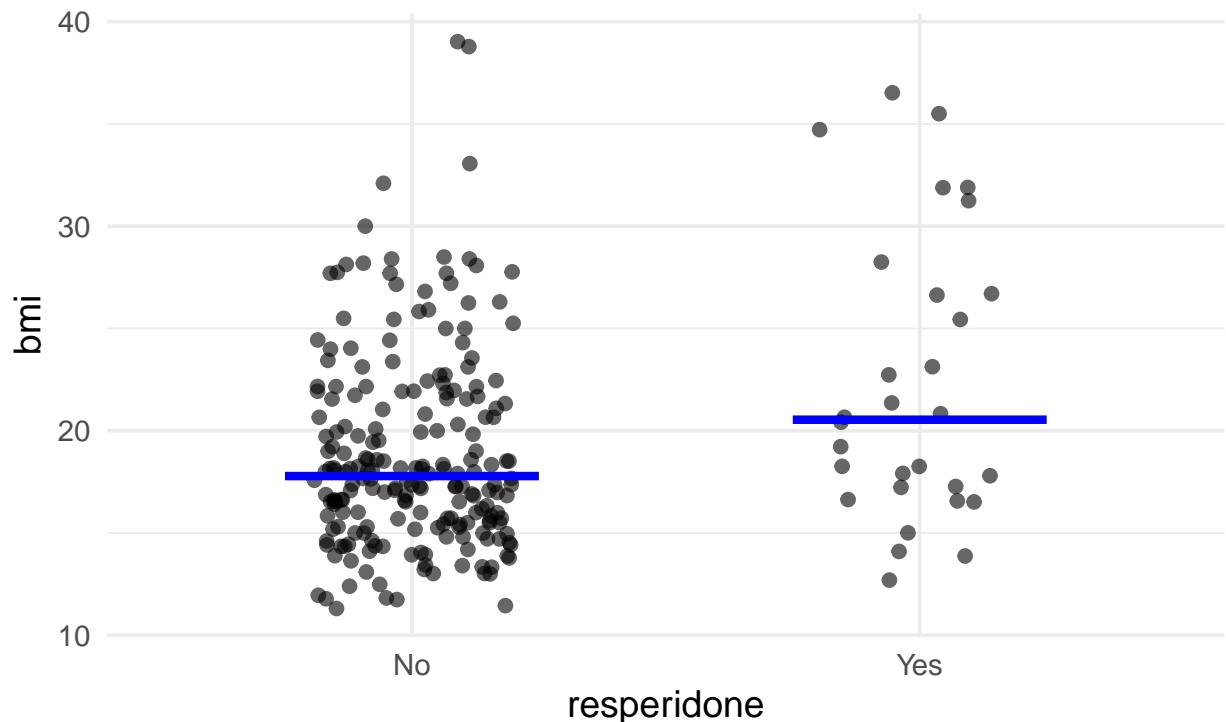
Scatter of bmi by excessive_screentime

$r = 0.087$



Scatter of bmi by resperidone

r = 0.163



```
# Print results
print(results_binary)
```

```
##          group U_stat   p_value r_value.r r_value.lower.ci
## 1    chronic_condition 3415.5 0.3105225 -0.0658      -0.1800
## 2           family_hx 1280.5 0.2324386  0.0775      -0.0566
## 3 excessive_screentime 6045.5 0.1763537  0.0871      -0.0422
## 4        resperidone 2254.0 0.0118155  0.1630      0.0308
##   r_value.upper.ci
## 1          0.0553
## 2          0.2110
## 3          0.2110
## 4          0.2880
```

3.3 Epsilon-squared effect size for multi-level grouping variables

```
#Loop over non-binary grouping variables
for (g in multi_groups) {

  # Subset and clean the data
  sub      <- df[, c(y_var, g)]
  names(sub) <- c("y", "g")
  sub       <- na.omit(sub)
  sub$y     <- as.numeric(sub$y)
  sub$g     <- factor(sub$g, levels = c("Low", "Moderate", "High"))

  # Kruskal-Wallis test
  kw <- kruskal.test(y ~ g, data = sub)

  # Epsilon-squared effect size:
  eps <- epsilonSquared(x          = sub$y,
                        g           = sub$g,
                        ci          = TRUE,
                        conf.level = 0.95,
                        type        = "bca",
                        R           = 10000
                      )

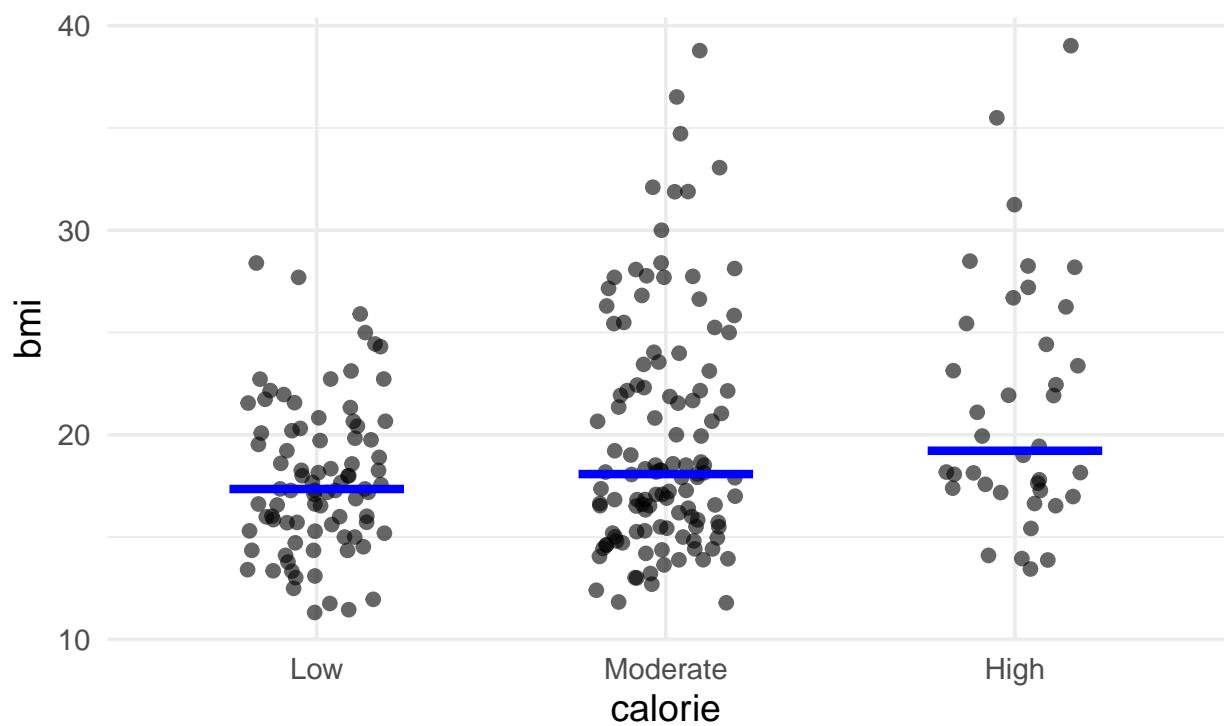
  # Jitter and median crossbar plot
  p <- ggplot(sub, aes(x = g, y = y)) +
    geom_jitter(width = 0.2, alpha = 0.6) +
    stat_summary(fun = median,
                 geom = "crossbar",
                 width = 0.5,
                 color = "blue",
                 linewidth = 0.6
               ) +
    labs(title   = paste0("Scatter of ", y_var, " by ", g),
         subtitle = paste0("Epsilon-squared = ", round(eps, 3)),
         x        = g,
         y        = y_var
       ) +
    theme_minimal(base_size = 14)
  print(p)

  # Append results
  results_multi <- rbind(results_multi,
                         data.frame(group      = g,
                                     H_value    = as.numeric(kw$statistic),
                                     df         = kw$parameter,
                                     p_value    = kw$p.value,
                                     eps_sq    = eps,
                                     stringsAsFactors = FALSE
                                   )
                        )
}

}
```

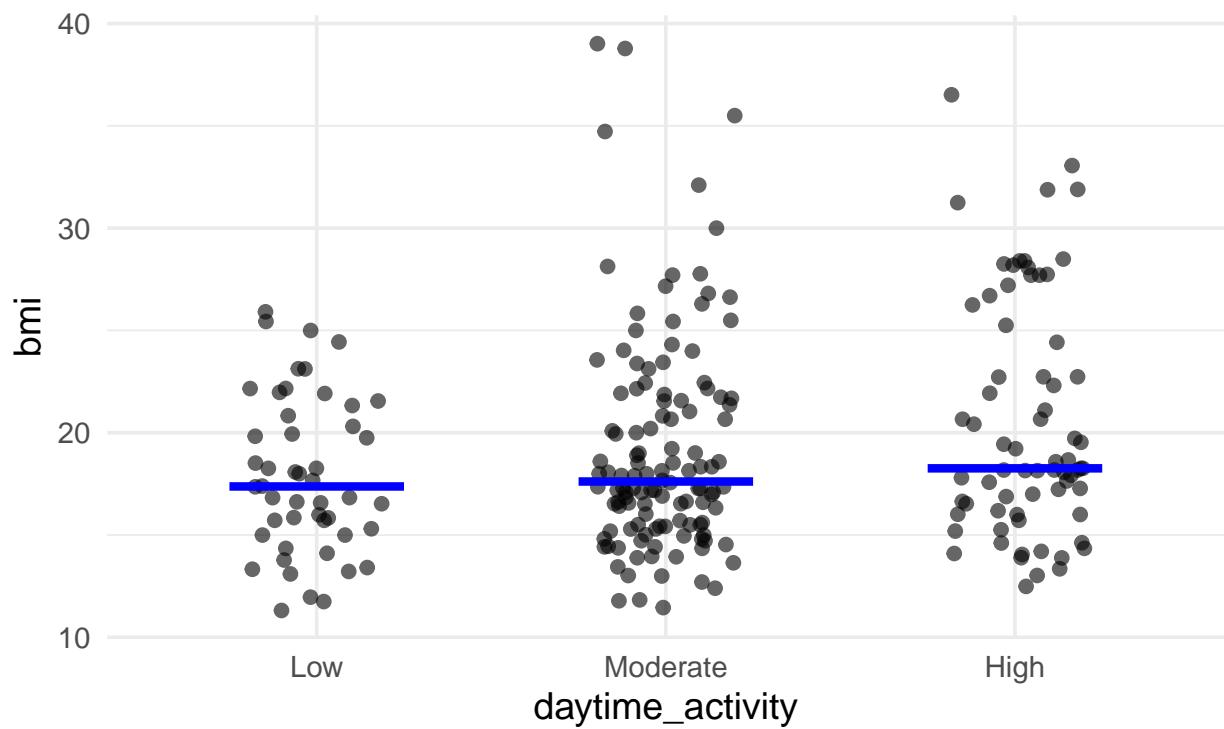
Scatter of bmi by calorie

Epsilon-squared = 0.038



Scatter of bmi by daytime_activity

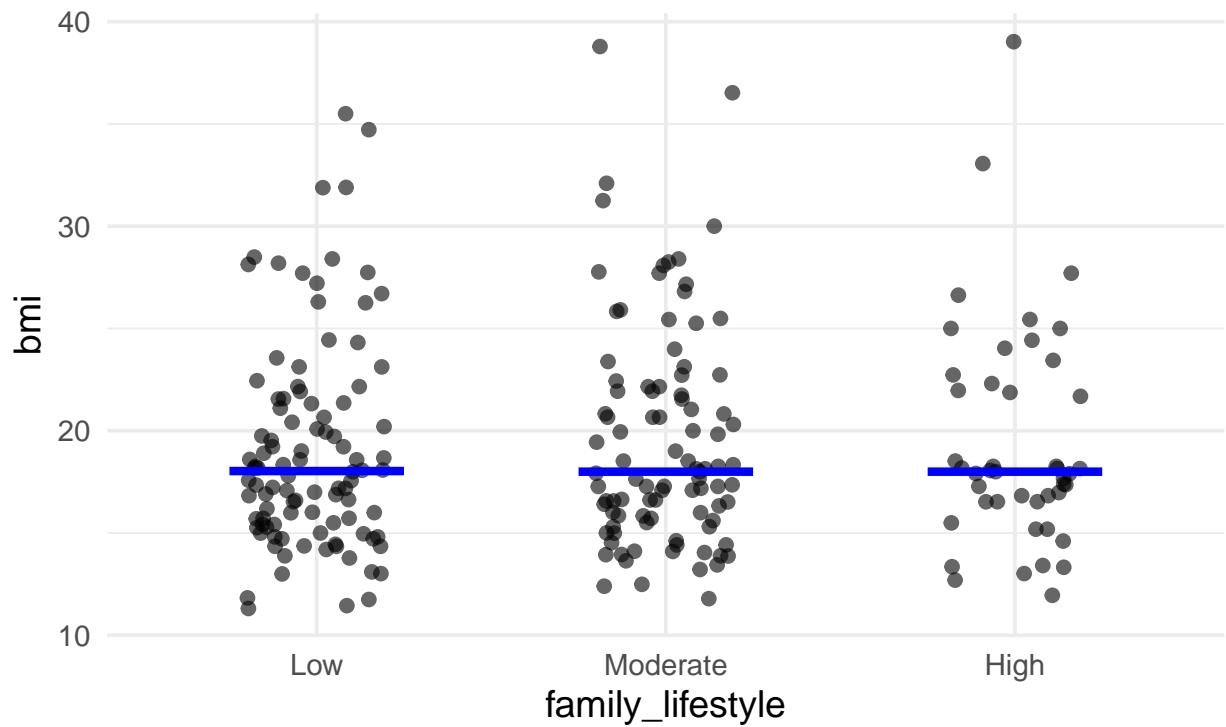
Epsilon-squared = 0.023



```
## Warning in norm.inter(t, adj.alpha): extreme order statistics used as endpoints
```

Scatter of bmi by family_lifestyle

Epsilon-squared = 0.001



```
# Print results
print(results_multi)
```

```
##          group H_value df   p_value eps_sq.epsilon.squared
## df      calorie 8.9746725 2 0.01125057               0.03760
## df1 daytime_activity 5.4465608 2 0.06565901               0.02280
## df2 family_lifestyle 0.2686765 2 0.87429430               0.00112
##   eps_sq.lower.ci eps_sq.upper.ci
## df      5.25e-03       0.08720
## df1    9.60e-04       0.06800
## df2    2.94e-08       0.00362
```