Antiparasitic Drugs and Birth Weight

2025-04-09

Setup

Install packages and data

Installing important packages for the project and downloading the dataset

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(srvyr)
```

```
##
## Attaching package: 'srvyr'
##
## The following object is masked from 'package:stats':
##
##     filter
```

```
library(gt)
library(tinytex)
library(naniar)
library(ggthemes)
library(glmnet)
```

```
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
##
## Loaded glmnet 4.1-8
```

```
library(olsrr)
```

```
##
## Attaching package: 'olsrr'
```

```
##
## The following object is masked from 'package:datasets':
##
##     rivers
```

```r
library(car)
```

```
## Loading required package: carData
##
## Attaching package: 'car'
##
## The following object is masked from 'package:dplyr':
##
##     recode
##
## The following object is masked from 'package:purrr':
##
##     some
```

```r
library(survey)
```

```
## Loading required package: grid
## Loading required package: survival
##
## Attaching package: 'survey'
##
## The following object is masked from 'package:graphics':
##
##     dotchart
```

```r
library(gt)
library(tidyr)
library(caret)
```

```
## Loading required package: lattice
##
## Attaching package: 'caret'
##
## The following object is masked from 'package:survival':
##
##     cluster
##
## The following object is masked from 'package:purrr':
##
##     lift
```

```r
library(qqplotr)
```

```
##
## Attaching package: 'qqplotr'
##
## The following objects are masked from 'package:ggplot2':
##
##     stat_qq_line, StatQqLine
```

```r
dhs <- read_csv("~/Documents/GitHub/bios/453/bios453/IAIR7EFL.csv")
```

```
## Warning: One or more parsing issues, call `problems()` on your data frame for details,
## e.g.:
##   dat <- vroom(...)
##   problems(dat)

## Rows: 724115 Columns: 423
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr   (1): caseid
## dbl (277): v001, v002, v003, v004, v005, v012, v015, v020, v021, v022, v023,...
## lgl (145): midx_4, midx_5, midx_6, m3a_4, m3a_5, m3a_6, m2n_2, m2n_3, m2n_4,...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Description of data management utilized and cleaning

As part of the data management process fo this project, I significantly reduced its size to include only variables that I believe are relevant for my research question. This includes all of the relevant variables, in addition to each confounder listed in my concept map (both primary and secondary). Once I had each of these variables selected, In went through and ensured that they were all formatted correctly for the types of regression I wanted to run during my analysis. I also made sure that certain items were filtered out. For example, some continuous reportings like birth weight in kg clearly contained severe misinputs. Since I am also only concerned with it as a numerical variable, I removed some of the categorical sections on the upper end like not weighed at birth, dont know, or missing. Additionally, I chose to adhere to UNICEF's validity threshold: 250g <= birthweight <=5,500g for a more realistic analysis. I also chose to keep variables like time pregnant and age numeric because that makes sense given what I am interested in exploring. Binary variables like whether or not someone took antiparasitics) were limited to only response values, as I am not interested in those who couldnt answer the question. This leaves us with a hefty 153,582 observations for analysis. Finally, I included a scaled weight column for womens sample weights due to the neture of my analysis (centering around womens reproductive health). I scaled it by 1,000,000 because DHS weights are stored as six digit strings, and scaling is necesary to prevent serious distortions, getting the weights into their correct format.

```
dhs_clean <- dhs %>%
  select(v005, m60_1, v481, m18_1, m19_1, m17_1, v457, m15_1, v228, v208, v190a, v190, v149, v131, v024
  rename(
    ids = v021,
    strata = v023,
    wsweight = v005,
    paradrug = m60_1,
    insured = v481,
    sizechild = m18_1,
    bwg = m19_1,
    csect = m17_1,
    anemia = v457,
    delivplace = m15_1,
    termpreg = v228,
    bpast5 = v208,
    wind_urbrur = v190a,
    wind = v190,
    educ = v149,
    ethnic = v131,
    state = v024,
    smokes = v463aa,
    married = v501,
    age = v447a,
  ) %>%
  filter(
    paradrug!=8,
    paradrug!=9,
    bwg <5501,
    bwg > 249,
    bwg != 9996,
    bwg != 9998,
    bwg != 9999,
    sizechild!=8,
    insured != 9,
    sizechild != 9,
    csect != 9,
    anemia != 9,
    termpreg != 9,
    educ != 9,
    smokes != 9,
    married != 9,
    age != 99,
  ) %>%
  mutate(
    wsweight = wsweight/1000000,
    paradrug = as.factor(paradrug),
    insured = as.factor(insured),
    sizechild = factor(sizechild,
                          levels = c("very large" = "1",
                                     "larger than average" = "2",
                                     "average" = "3",
                                     "smaller than average" = "4",
                                     "very small" = "5")),
    csect = factor(csect),
    anemia = factor(anemia,
                    levels = c("severe" = "1",
                               "moderate" = "2",
                               "mild" = "3",
                               "not anemic" = "4")),
    delivplace = factor(delivplace),
    termpreg = factor(termpreg),
    bpast5 = factor(bpast5),
    wind = factor(wind,
                  levels = c("poorest" = "1",
                             "poorer" = "2",
                             "middle" = "3",
                             "richer" = "4",
                             "richest" = "5")),
    educ = factor(educ,
                  levels = c("none" = "0",
                             "incomplete primary" = "1",
                             "complete primary" = "2",
                             "incomplete secondary" = "3",
                             "complete secondary" = "4",
                             "higher" = "5")),
    ethnic = factor(ethnic,
                    levels = c("caste" = "991",
                               "tribe" = "992",
                               "no caste/tribe" = "993",
                               "dont know" = "998")),
    smokes = factor(smokes)
  )
```

Missing data report

According to a missing data summary, there are no missing observations within the cleaned dataset. After removing “dont know” values from majority of the variables of interest (due to their being irrelevent) we no longer have any data that are not available and a final cleaned dataset of 153582 observations.

```
miss_var_summary(dhs_clean) %>%
  arrange(desc(pct_miss))
```

```
## # A tibble: 20 x 3
##    variable    n_miss pct_miss
##    <chr>        <int>    <num>
##  1 wsweight         0        0
##  2 paradrug         0        0
##  3 insured          0        0
##  4 sizechild        0        0
##  5 bwg              0        0
##  6 csect            0        0
##  7 anemia           0        0
##  8 delivplace       0        0
##  9 termpreg         0        0
## 10 bpast5           0        0
## 11 wind_urbrur      0        0
## 12 wind             0        0
## 13 educ             0        0
## 14 ethnic           0        0
## 15 state            0        0
## 16 smokes           0        0
## 17 married          0        0
## 18 age              0        0
## 19 ids              0        0
## 20 strata           0        0
```

Concept map

Summary table of characteristics

```
# categorical summary
cat_summary <- dhs_clean %>%
  select(paradrug, insured, educ) %>%
  pivot_longer(everything(), names_to = "variable", values_to = "category") %>%
  group_by(variable) %>%
  mutate(total = n()) %>%
  group_by(variable, category) %>%
  summarise(
    count = n(),
    percent = paste0(round(100 * count / first(total), 1), "%"),
```

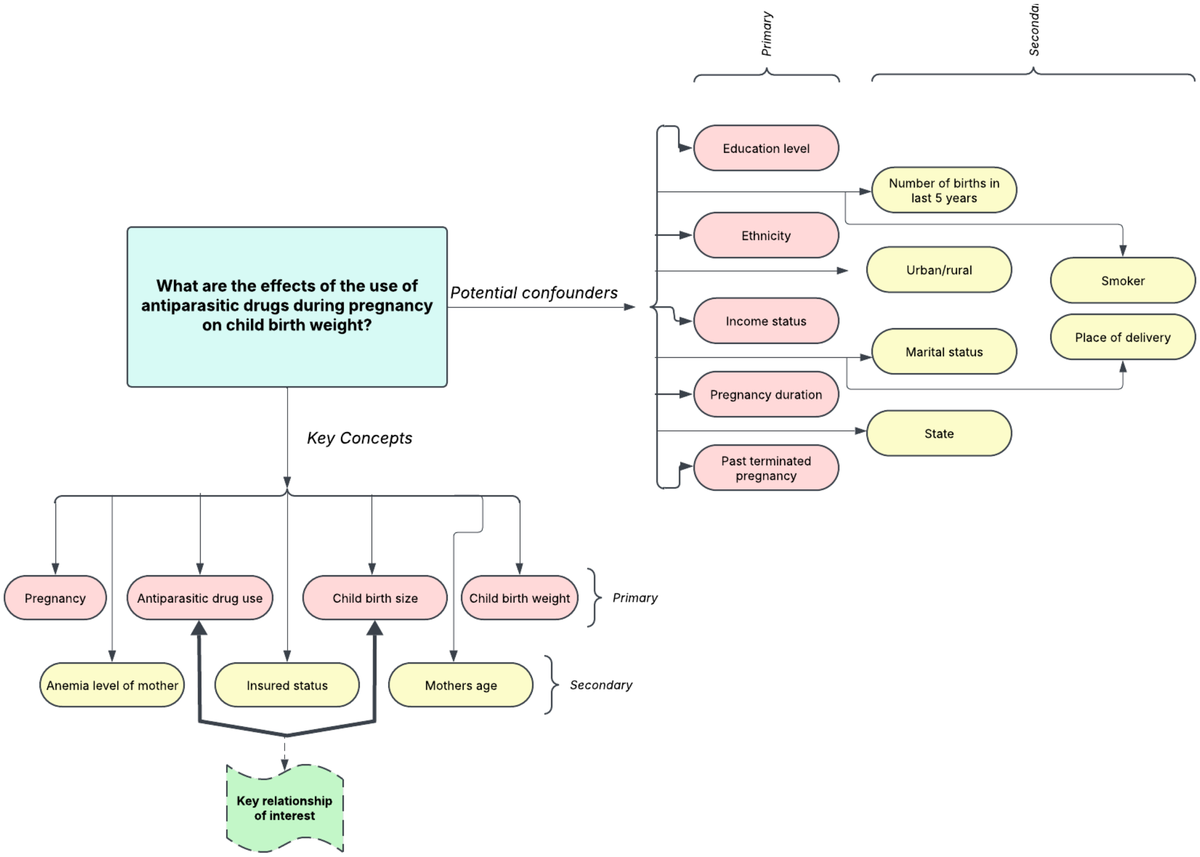


Figure 1: Concept Map

```
    .groups = "drop"
  ) %>%
  arrange(variable, category) %>%
  group_by(variable) %>%
  mutate(row_id = row_number()) %>%
  ungroup()

# summary for numerical variables
num_summary <- dhs_clean %>%
  summarise(across(c(age, bwg),
    list(mean = ~round(mean(., na.rm = TRUE), 2),
         median = ~round(median(., na.rm = TRUE), 2),
         sd = ~round(sd(., na.rm = TRUE), 2)),
    .names = "{.col}_{.fn}")) %>%
  pivot_longer(everything(), names_to = c("variable", "statistic"), names_sep = "_") %>%
  pivot_wider(names_from = statistic, values_from = value) %>%
  mutate(row_id = 1)

# merge and gt table
bind_rows(
  cat_summary,
  num_summary %>% mutate(category = NA, count = NA, percent = NA)
) %>%
  arrange(factor(variable, levels = c("paradrug", "insured", "educ", "age", "bwg"))) %>%
  gt(groupname_col = "variable") %>%
  tab_header(
    title = "Summary Statistics for DHS Dataset",
  ) %>%
  cols_label(
    category = "Category",
    count = "Count",
    percent = "Percentage",
    mean = "Mean",
    median = "Median",
    sd = "Std Dev"
  ) %>%
  fmt_number(
    columns = c(mean, median, sd),
    decimals = 2
  ) %>%
  cols_align(
    align = "center",
    columns = c(category, count, percent, mean, median, sd)
  ) %>%
  tab_style(
    style = cell_text(weight = "bold"),
    locations = cells_column_labels()
  ) %>%
  tab_style(
    style = cell_fill(color = "#C5DECD"),
    locations = cells_body(
      rows = variable %in% c("paradrug", "insured", "educ")
    )
```

Summary Statistics for DHS Dataset

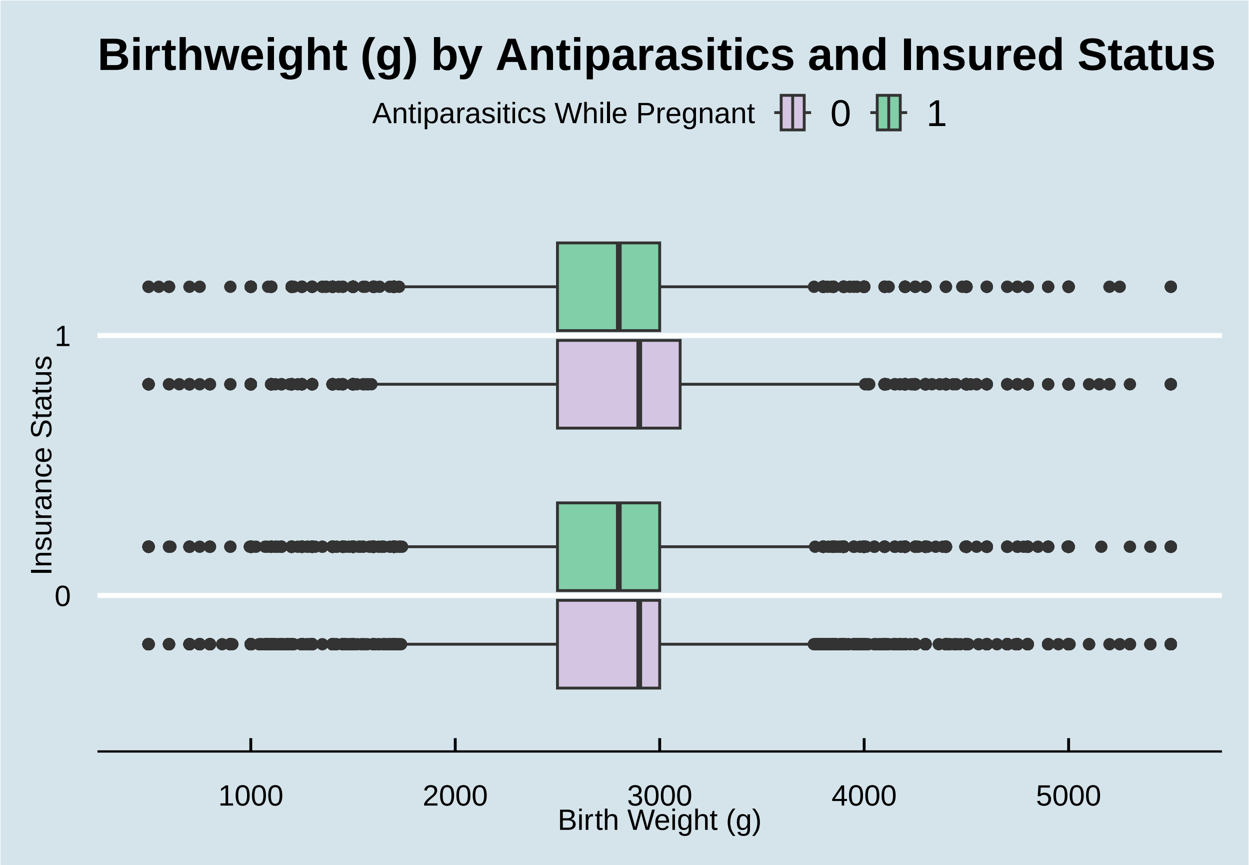
Category	Count	Percentage	Mean	Median	Std Dev
paradrug					
0	104771	68.2%	-	-	-
1	48811	31.8%	-	-	-
insured					
0	109570	71.3%	-	-	-
1	44012	28.7%	-	-	-
educ					
0	28084	18.3%	-	-	-
1	18238	11.9%	-	-	-
3	80116	52.2%	-	-	-
4	3000	2%	-	-	-
5	24144	15.7%	-	-	-
age					
-	-	-	27.38	27.00	5.12
bwg					
-	-	-	2,816.83	2,900.00	554.07

```
  ) %>%
  fmt_missing(columns = everything(), missing_text = "-") %>%
  cols_hide(columns = c(row_id))%>%
  tab_options(table.background.color = "#F1F7ED")
```

```
## Warning: Since gt v0.6.0 `fmt_missing()` is deprecated and will soon be removed.
## i Use `sub_missing()` instead.
## This warning is displayed once every 8 hours.
```

Graphical representation of characteristics

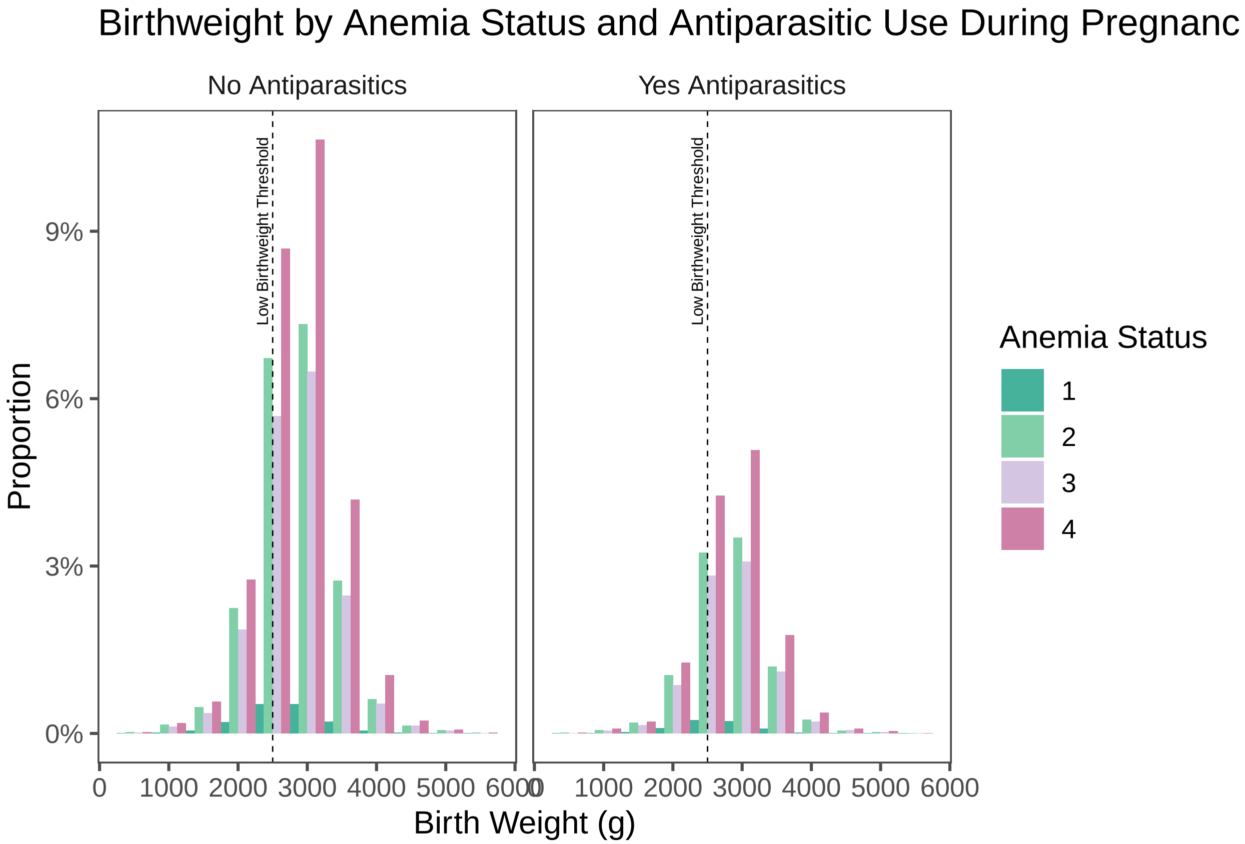
```
# boxplot comparing birthweights by antiparasitic use and insurance status
ggplot(data = dhs_clean, mapping = aes(y = insured, x = bwg, fill = paradrug)) +
  geom_boxplot() +
  theme_economist() +
  scale_fill_manual(values = c("#D4C5E2", "#80CFA9")) +
  labs(title = "Birthweight (g) by Antiparasitics and Insured Status",
       y = "Insurance Status",
       x = "Birth Weight (g)",
       fill = "Antiparasitics While Pregnant")
```



```
# make labels for facetwrap
paradrug_labels <- c("0" = "No Antiparasitics", "1" = "Yes Antiparasitics")

# barplot comparing birthweight by anemia status and antiparasitic use
ggplot(dhs_clean, aes(x = bwg, fill = factor(anemia))) +
  geom_histogram(aes(y=after_stat(count/sum(count))),
                 position = "dodge",
                 binwidth = 500) +
  facet_wrap(~paradrug, labeller = as_labeller(paradrug_labels)) +
  scale_fill_manual(
    values = c("#46B29B", "#80CFA9", "#D4C5E2", "#CF80A6"),
    name = "Anemia Status") +
  labs( title = "Birthweight by Anemia Status and Antiparasitic Use During Pregnancy", x = "Birth Weigh
  theme_few() +
  scale_y_continuous(labels = scales::percent) +
  geom_vline(
    xintercept = 2500,
    linetype = "dashed",
    size = .25,
  ) +
  annotate(
    "text",
    x = 2350, y = .09,  # Label position
    label = "Low Birthweight Threshold",
    angle = 90,
    color = "black",
    size = 2
  )
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



Summary and interpretation of characteristics

Based on the characteristics obseved in the table and graphic, a few things stand out. To start, given the fact that the core questions involves antiparasitic drug use, its important to point out that majority of people to not use antiparasitics during pregnancy. Additionally, less than 30% of people have some form of health insurance which may act as a major confounder when trying to predict birth weight. Majority of people surveyed have completed primary school (around 52.2%) but only 2% have some form of higher education. As for age, most of those who participated in the survey were in their late 20s, with a median age of 27 (SD of 5.12). The median birth weight was 2900g, which is less than the international average of roughly 3300g. Based on the graphic, it is evident that on average, children born to mothers who received antiparasitics during pregnancy weighed less at birth than those of mothers who did not. There is also a much larger interquartile range of birthweights for children born to mothers who were insured but did not receive antiparasitics during pregnancy than any other combined category. The Lowest average birth weights were among children born to mothers who were both insured and received antiparasitics during pregnancy. It is possible that due to the large discrepancy between number of insured vs uninsured, this relationship is due to noise, but it is interesting nonetheless. Overall, the spread is relatively consistent across categories.

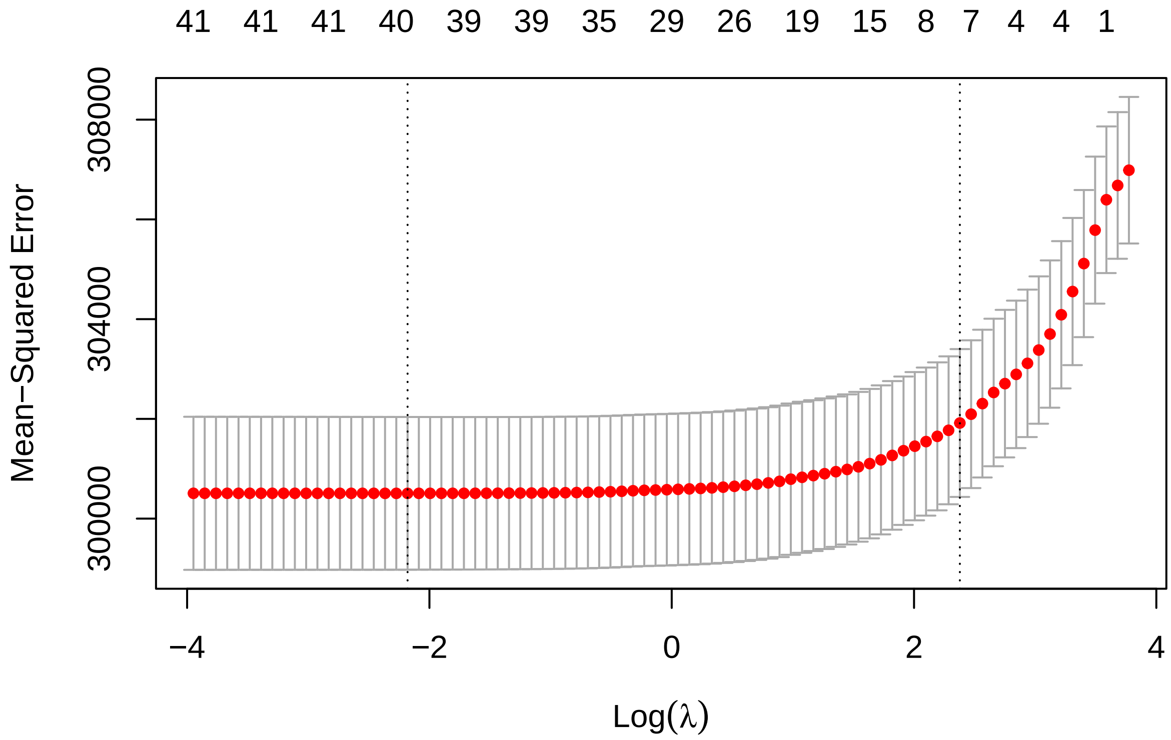
Variable selection for statistical analysis and assumption testing

```
## LASSO
# Create predictor matrix (exclude intercept and outcome variable)
x <- model.matrix(bwg ~ paradrug + insured + csect + anemia + delivplace +
                  termpreg + bpast5 + wind_urbrur + wind + educ + ethnic +
                  state + smokes + married + age,
                data = dhs_clean)[, -1]  # Remove intercept column

# Outcome variable
y <- dhs_clean$bwg

# Cross-validate to find optimal lambda (penalty parameter)
set.seed(123)  # For reproducibility
lasso_model <- cv.glmnet(x, y, alpha = 1)  # alpha=1 for LASSO

# Plot cross-validation error
plot(lasso_model)
```



```
# Coefficients at lambda.min (retains more variables)
coef(lasso_model, s = "lambda.min")
```

```
## 43 x 1 sparse Matrix of class "dgCMatrix"
##                           s1
## (Intercept)  2453.62676242
## paradrug1     -14.45031861
## insured1        2.78115360
## csect1         21.22229514
## anemia2        41.52196936
## anemia3        54.15828788
## anemia4        67.69394321
## delivplace12   13.82230763
## delivplace13    9.22314701
## delivplace21   20.12884041
## delivplace22   15.89831366
## delivplace23   16.29798578
## delivplace24   17.10129444
## delivplace25   22.08062354
## delivplace26   11.11465591
## delivplace27   35.16148399
## delivplace31    7.73316354
## delivplace32    .
## delivplace33   51.52247256
## delivplace96   31.79118017
## termpreg1       0.11128850
## bpast52        -3.94368315
## bpast53       -37.73086027
## bpast54       -60.13109914
## bpast55       109.30143226
## wind_urbrur     6.00574549
## wind2          35.31232295
## wind3          53.38908578
## wind4          56.56319494
## wind5          50.18093174
## educ1          16.57187002
## educ2           .
## educ3          55.58945073
## educ4          69.44232237
## educ5         110.24243606
## ethnic992     144.45099655
## ethnic993      34.87722706
## ethnic998       3.89257727
## state           0.04242206
## smokes1       179.61847673
## smokes2        49.37416028
## married        -5.29778897
## age             6.28193847
```

```
# Coefficients at lambda.1se (simpler model)
coef(lasso_model, s = "lambda.1se")
```

```
## 43 x 1 sparse Matrix of class "dgCMatrix"
##                        s1
## (Intercept)  2630.793251
## paradrug1       .
## insured1        .
## csect1          7.575041
## anemia2         .
## anemia3         .
## anemia4         6.461215
## delivplace12    .
## delivplace13    .
## delivplace21    .
## delivplace22    .
## delivplace23    .
## delivplace24    .
## delivplace25    .
## delivplace26    .
## delivplace27    .
## delivplace31    .
## delivplace32    .
## delivplace33    .
## delivplace96    .
## termpreg1       .
## bpast52         .
## bpast53         .
## bpast54         .
## bpast55         .
## wind_urbrur    15.024979
## wind2           .
## wind3           .
## wind4           .
## wind5           .
## educ1           .
## educ2           .
## educ3          11.549754
## educ4           .
## educ5          56.124309
## ethnic992     105.435788
## ethnic993       .
## ethnic998       .
## state           .
## smokes1         .
## smokes2         .
## married         .
## age             3.925296
```

```
## Predictors with non-zero coefficients are deemed important for explaining bwkg. It appears as though

## Check for multicolinearity
vifmod <- lm(data = dhs_clean, bwg~paradrug+age+ethnic+educ+bpast5+csect+anemia)
vif_values <- vif(vifmod)  # Calculate VIF values
print(vif_values)         # Display VIF values
```

```
##              GVIF Df GVIF^(1/(2*Df))
## paradrug 1.003222  1        1.001609
## age      1.070778  1        1.034784
## ethnic   1.030956  3        1.005094
## educ     1.139842  4        1.016496
## bpast5   1.034103  4        1.004201
## csect    1.070456  1        1.034628
## anemia   1.010921  3        1.001812
```

```
## VIF are all aprox =1 implying low to no nulticolinearity
```

Regressions and interpretation

```
## several single stratas, merge singles for comparison
options(survey.lonely.psu = "adjust")

single_strata <- c(1023, 3241, 3261, 57221, 57222, 62921, 83823, 84022, 84122, 84223, 84421, 84621, 846

dhs_clean <- dhs_clean %>%
  mutate(strata = ifelse(strata %in% single_strata, 1024, strata))

# Count PSUs per stratum
psu_counts <- dhs_clean %>%
  group_by(strata) %>%
  summarize(n_psu = n_distinct(ids))  # Replace 'ids' with your PSU variable name

# List strata with 1 PSU
single_strata <- psu_counts %>% filter(n_psu == 1)
print(single_strata)
```

```
## # A tibble: 0 x 2
## # i 2 variables: strata <dbl>, n_psu <int>
```

```
single_strata <- c(1023, 3241, 3261, 57221, 57222, 62921, 83823, 84022, 84122, 84223, 84421, 84621, 846

#mutate
dhs_clean <- dhs_clean %>%
  mutate(
    strata = ifelse(strata %in% single_strata, 1024, strata)
  )

## Weighting and survey design specification
sdesign <- as_survey_design(
  .data = dhs_clean,
  ids = ids,
  strata = strata,
  weights = wsweight
)
## Run main regression. Included interraction terms for age*paradrug and educ*bpast5 due to suspected i
unrefined_coremodel <- sdesign %>%
  svyglm(
    formula = bwg~paradrug+age+ethnic+educ+bpast5+csect+anemia+anemia*paradrug+educ*bpast5,
    family = gaussian())
summary(unrefined_coremodel)
```

```
##
## Call:
## svyglm(formula = bwg ~ paradrug + age + ethnic + educ + bpast5 +
##     csect + anemia + anemia * paradrug + educ * bpast5, design = .,
##     family = gaussian())
##
## Survey design:
## Called via srvyr
##
## Coefficients: (3 not defined because of singularities)
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)       2533.8332    21.6209 117.194  < 2e-16 ***
## paradrug1           32.1070    33.5970   0.956 0.339258    
## age                  5.2230     0.4251  12.287  < 2e-16 ***
## ethnic992           -4.5421     7.1061  -0.639 0.522707    
## ethnic993           31.7584     9.3892   3.382 0.000719 ***
## ethnic998           -9.1008    25.7122  -0.354 0.723380    
## educ1               -3.2216     9.2330  -0.349 0.727150    
## educ3               55.6727     6.8716   8.102 5.64e-16 ***
## educ4               50.8085    17.2959   2.938 0.003310 ** 
## educ5              130.4074     8.0575  16.185  < 2e-16 ***
## bpast52             -6.0065    10.0405  -0.598 0.549697    
## bpast53            -43.5147    20.7325  -2.099 0.035838 *  
## bpast54            -78.0202    69.9704  -1.115 0.264841    
## bpast55            248.6160    10.0055  24.848  < 2e-16 ***
## csect1              14.8893     5.1067   2.916 0.003552 ** 
## anemia2             60.8170    17.4858   3.478 0.000506 ***
## anemia3             67.5114    17.6470   3.826 0.000131 ***
## anemia4             70.8712    17.4808   4.054 5.04e-05 ***
## paradrug1:anemia2  -26.0589    34.3415  -0.759 0.447969    
## paradrug1:anemia3  -23.4416    34.4628  -0.680 0.496383    
## paradrug1:anemia4  -26.4609    34.1033  -0.776 0.437813    
## educ1:bpast52        9.0219    17.1192   0.527 0.598195    
## educ3:bpast52       -5.5710    11.7924  -0.472 0.636628    
## educ4:bpast52       16.7582    37.0742   0.452 0.651260    
## educ5:bpast52      -28.5304    15.7938  -1.806 0.070862 .  
## educ1:bpast53      -36.0340    36.9172  -0.976 0.329037    
## educ3:bpast53       33.4801    29.0108   1.154 0.248488    
## educ4:bpast53       -9.0230    84.8786  -0.106 0.915341    
## educ5:bpast53     -114.5483    52.5950  -2.178 0.029420 *  
## educ1:bpast54      212.1435   144.9045   1.464 0.143200    
## educ3:bpast54      -27.8951   118.9913  -0.234 0.814653    
## educ4:bpast54      334.3582    77.5989   4.309 1.65e-05 ***
## educ5:bpast54     -615.4513   232.7468  -2.644 0.008191 ** 
## educ3:bpast55     -419.0672    11.6558 -35.954  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for gaussian family taken to be 305744.5)
## 
## Number of Fisher Scoring iterations: 2
```

```r
## Refined core model
coremodel <- sdesign %>%
  svyglm(
    formula = bwg ~ paradrug + age + ethnic + educ +
               bpast5 + csect + anemia + educ*bpast5,
    family = gaussian()
  )
summary(coremodel)
```

```
## 
## Call:
## svyglm(formula = bwg ~ paradrug + age + ethnic + educ + bpast5 + 
##     csect + anemia + educ * bpast5, design = ., family = gaussian())
## 
```

```
## Survey design:
## Called via srvyr
##
## Coefficients: (3 not defined because of singularities)
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2541.542     19.683 129.127  < 2e-16 ***
## paradrug1         7.101      4.027   1.763 0.077898 .
## age               5.223      0.425  12.288  < 2e-16 ***
## ethnic992        -4.523      7.103  -0.637 0.524288
## ethnic993        31.744      9.393   3.380 0.000727 ***
## ethnic998        -9.165     25.717  -0.356 0.721570
## educ1            -3.216      9.235  -0.348 0.727684
## educ3            55.682      6.871   8.104 5.56e-16 ***
## educ4            50.813     17.289   2.939 0.003295 **
## educ5           130.412      8.062  16.176  < 2e-16 ***
## bpast52          -5.962     10.040  -0.594 0.552635
## bpast53         -43.519     20.719  -2.100 0.035703 *
## bpast54         -77.284     70.043  -1.103 0.269871
## bpast55         248.109      9.698  25.583  < 2e-16 ***
## csect1           14.895      5.107   2.917 0.003542 **
## anemia2          52.759     14.992   3.519 0.000434 ***
## anemia3          60.308     15.355   3.928 8.60e-05 ***
## anemia4          62.672     15.026   4.171 3.04e-05 ***
## educ1:bpast52     8.913     17.117   0.521 0.602567
## educ3:bpast52    -5.600     11.791  -0.475 0.634867
## educ4:bpast52    16.669     37.067   0.450 0.652933
## educ5:bpast52   -28.559     15.794  -1.808 0.070585 .
## educ1:bpast53   -35.988     36.905  -0.975 0.329488
## educ3:bpast53    33.447     28.999   1.153 0.248773
## educ4:bpast53    -8.949     84.865  -0.105 0.916024
## educ5:bpast53  -114.414     52.596  -2.175 0.029614 *
## educ1:bpast54   211.021    144.945   1.456 0.145442
## educ3:bpast54   -28.485    119.076  -0.239 0.810936
## educ4:bpast54   333.853     77.610   4.302 1.70e-05 ***
## educ5:bpast54  -617.194    233.008  -2.649 0.008082 **
## educ3:bpast55  -418.220     10.975 -38.108  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 305747.7)
##
## Number of Fisher Scoring iterations: 2
```

```
# Drop unused levels for all factor variables
dhs_clean <- dhs_clean %>%
  mutate(across(where(is.factor), droplevels))

# Then recreate your survey design and model


## Unweighted coremodel
coremodelunw <- lm(data = dhs_clean, bwg~paradrug+age+ethnic+educ+bpast5+csect+anemia+educ*bpast5)
summary(coremodelunw)
```

```
##
```

```
## Call:
## lm(formula = bwg ~ paradrug + age + ethnic + educ + bpast5 +
##     csect + anemia + educ * bpast5, data = dhs_clean)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2490.58  -311.38    28.83   271.42  2840.04
##
## Coefficients: (3 not defined because of singularities)
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2474.9705    13.1998 187.500  < 2e-16 ***
## paradrug1      -14.5371     3.0116  -4.827 1.39e-06 ***
## age              6.6920     0.2832  23.629  < 2e-16 ***
## ethnic992      132.3587     4.0425  32.741  < 2e-16 ***
## ethnic993       28.4006     6.4062   4.433 9.29e-06 ***
## ethnic998        6.1665    19.1284   0.322 0.747171
## educ1           29.5576     6.4468   4.585 4.55e-06 ***
## educ3           82.0725     4.7711  17.202  < 2e-16 ***
## educ4          103.1462    12.2017   8.453  < 2e-16 ***
## educ5          153.5773     5.7867  26.540  < 2e-16 ***
## bpast52          0.2704     7.2425   0.037 0.970213
## bpast53        -46.4182    15.0623  -3.082 0.002058 **
## bpast54        -10.5414    65.7140  -0.160 0.872556
## bpast55        268.3289   387.9885   0.692 0.489196
## csect1          27.3449     3.4637   7.895 2.93e-15 ***
## anemia2         52.0177     9.6717   5.378 7.53e-08 ***
## anemia3         65.6903     9.7257   6.754 1.44e-11 ***
## anemia4         81.4989     9.5852   8.503  < 2e-16 ***
## educ1:bpast52   -4.9443    11.5648  -0.428 0.668994
## educ3:bpast52   -3.7783     8.5412  -0.442 0.658231
## educ4:bpast52   -8.1080    25.7163  -0.315 0.752545
## educ5:bpast52  -31.4146    11.6976  -2.686 0.007242 **
## educ1:bpast53  -13.3432    25.9963  -0.513 0.607760
## educ3:bpast53   21.2279    19.8308   1.070 0.284420
## educ4:bpast53   -8.4797    73.3097  -0.116 0.907914
## educ5:bpast53  -77.5505    40.1294  -1.933 0.053298 .
## educ1:bpast54  -12.7683   111.7083  -0.114 0.909000
## educ3:bpast54  -91.8172    92.8624  -0.989 0.322790
## educ4:bpast54  471.6026   323.7171   1.457 0.145164
## educ5:bpast54 -793.8416   217.5708  -3.649 0.000264 ***
## educ1:bpast55        NA         NA      NA       NA
## educ3:bpast55 -431.3054   671.9877  -0.642 0.520981
## educ4:bpast55        NA         NA      NA       NA
## educ5:bpast55        NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 548.7 on 153551 degrees of freedom
## Multiple R-squared:  0.01967,    Adjusted R-squared:  0.01948
## F-statistic: 102.7 on 30 and 153551 DF,  p-value: < 2.2e-16
```

```
## Finding $R^2$
weighted_r2 <- function(model) {
  y <- model.response(model.frame(model))
```

```r
  w <- weights(model, type = "prior")
  pred <- predict(model)

  # NA handling
  valid <- complete.cases(y, pred, w)
  y <- y[valid]
  pred <- pred[valid]
  w <- w[valid]

  ss_res <- sum(w * (y - pred)^2)
  ss_tot <- sum(w * (y - weighted.mean(y, w))^2)

  1 - (ss_res / ss_tot)
}

# Usage with survey model
coremodel <- svyglm(bwg ~ paradrug + age,
                   design = sdesign,
                   family = gaussian())

weighted_r2(coremodel)
```

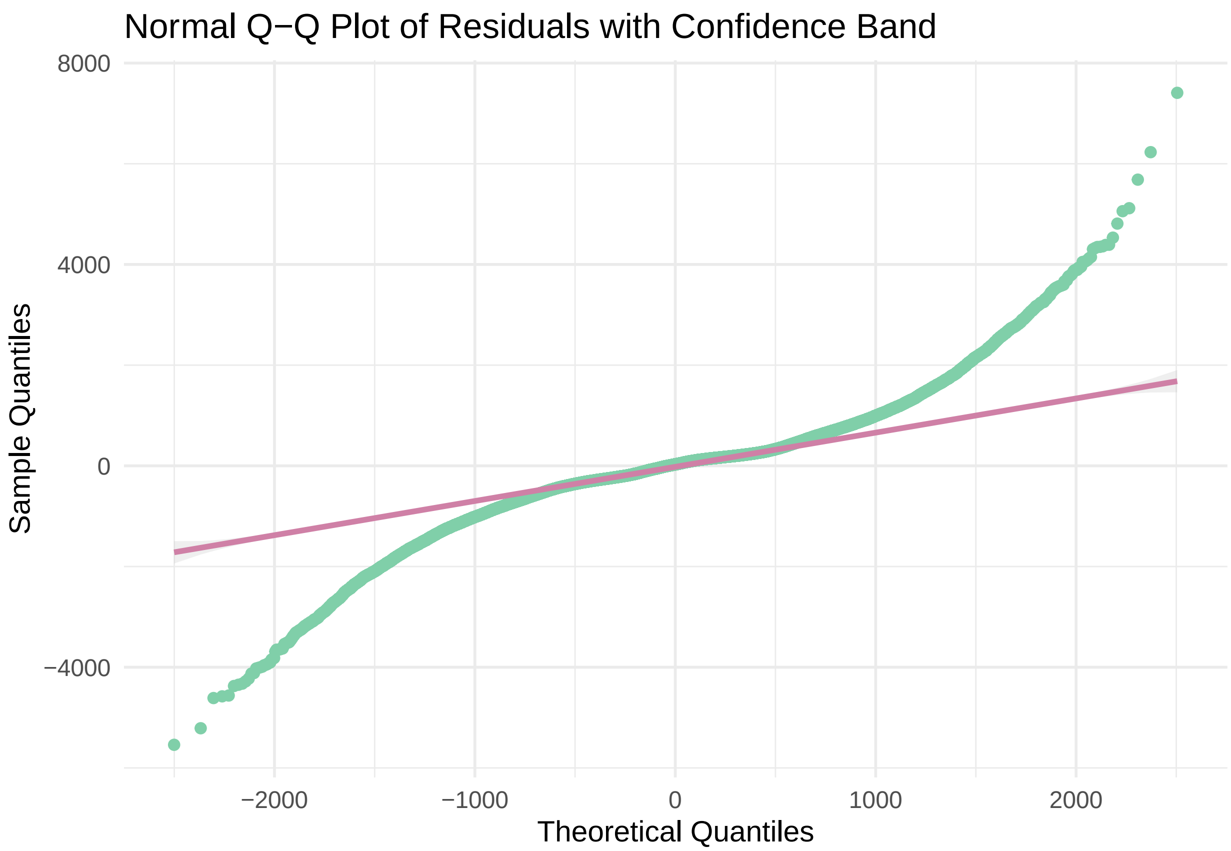
```
## [1] 0.002233451
```

```r
## This implies that the variabce observed in the model can only explain about 0.22% of that observed i
```

Residual analysis, multicolinearity, and validation

```r
residuals <- residuals(coremodel)

ggplot(data.frame(residuals = residuals), aes(sample = residuals)) +
  stat_qq_band(distribution = "norm", alpha = 0.2, fill = "grey70") + # Adds confidence band
  stat_qq_point(color = "#80CFA9") +
  stat_qq_line(color = "#CF80A6", linewidth = 1) +
  theme_minimal() +
  labs(x = "Theoretical Quantiles", y = "Sample Quantiles",
       title = "Normal Q-Q Plot of Residuals with Confidence Band")
```



```r
## The residuals generally follow the diagonal line, suggesting that the residuals are approximately no

# Perform Durbin-Watson test
durbinWatsonTest(coremodel)
```

```
##  lag Autocorrelation D-W Statistic p-value
##    1      0.04293297      1.914134       0
##  Alternative hypothesis: rho != 0
```

```r
## D-W Statistic = 1.914134: This value is reasonably close to 2 (which indicates no autocorrelation), 

## Validation K-Fold
# Define cross-validation method
ctrl <- trainControl(method = "cv", number = 5)

# Train model with k-fold CV
model_cv <- train(
  bwg ~ paradrug+age+ethnic+educ+bpast5+csect+anemia+age*paradrug+educ*bpast5,  # Include all predictor
  data = dhs_clean,
  method = "lm",
  trControl = ctrl
)
```

```
## Warning in predict.lm(modelFit, newdata): prediction from rank-deficient fit;
## attr(*, "non-estim") has doubtful cases
```

```r
# View average RMSE and R² across folds
print(model_cv$results)
```

```
##   intercept     RMSE   Rsquared     MAE   RMSESD  RsquaredSD    MAESD
## 1      TRUE 548.7155 0.01923701 419.986 3.654693 0.001421575 2.479597
```

The validation results suggest poor model preformance across the board.An RMSE (Root Mean Squared Error, A measure of the average distance between predicted and actual values. Lower values indicate better fit) of ~548.7 kg means that the models predictions are super inacurate. The R2 of 0.22% indicated that paradrug and other predictors have very minimal explanatory power for bwkg. Low standard deviations (SD) in RMSE/R^2 across folds indicate the model isn’t overfitting, but it’s consistently underperforming.