NIFB22001U Introduction to Econometrics Exam 2022/2023 - R Code Attachment

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```
#load libaries
library(tidyverse)
library(stargazer)
library(lmtest)
library(car)
library(sandwich)
library(AER)
library(ggrepel)
library(patchwork)
library(corrplot)

#load data
data_01 <- get(load("examdata2023_01.RData"))
data_02 <- get(load("examdata2023_02.RData"))</pre>
```

Part 1: The Returns to Education

1. Below code is used for estimating

```
wage = \alpha + \beta educ + u \tag{1} model\_01\_pred <- lm(data = data\_01, \\ formula = wage ~ education) \#Variance
```

Part 2: Global Food Consumption Patterns

2.1 Data description and preliminary analysis

1. Descriptive statistic of supplied data

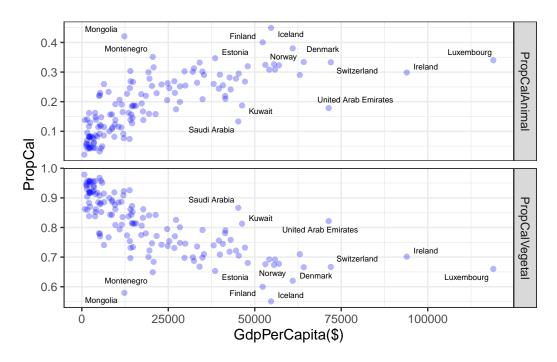
2. Consumption proportion vs GDP Per capita

```
geom_point(color = "blue", alpha = 0.3) +
geom_text_repel(size = 2, verbose = FALSE,
    mapping = aes(label = Country)) +
facet_grid(rows = vars(ConsumType), scales = "free") +
labs(x = "GdpPerCapita($)") +
theme_bw()
```

Warning: Removed 38 rows containing missing values (`geom_point()`).

Warning: Removed 38 rows containing missing values (`geom_text_repel()`).

Warning: ggrepel: 127 unlabeled data points (too many overlaps). Consider increasing max.overggrepel: 127 unlabeled data points (too many overlaps). Consider increasing max.overlaps

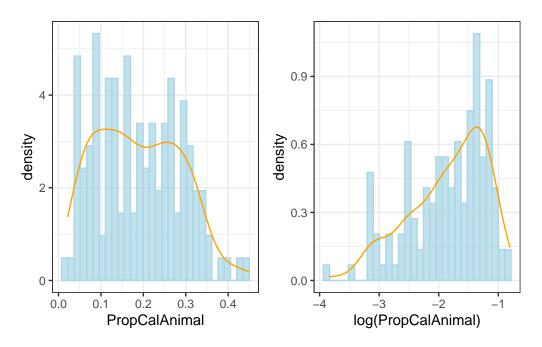


2. PropCalAnimal and log(PropCalAnimal) distribution

```
#|warning : false
#|eval: false
```

Proceeding without missing values

```
data_02 <- data_02 |>
    filter(!is.na(PropCalAnimal))
  PropCalAnimal_dist <- data_02 |>
    select(PropCalAnimal) |>
    mutate("log(PropCalAnimal)" = log(PropCalAnimal))
  p1 <- ggplot(data = PropCalAnimal_dist,</pre>
                mapping = aes(x = PropCalAnimal)) +
    geom_histogram(mapping = aes(y = ..density..),
                    fill = "lightblue", color = "lightblue",
                    alpha = 0.75) +
    geom_density(color = "orange") +
    theme_bw()
  p2 <- ggplot(data = PropCalAnimal_dist,</pre>
               mapping = aes(x = `log(PropCalAnimal)`)) +
    geom_histogram(mapping = aes(y = ..density..),
                    fill = "lightblue", color = "lightblue",
                    alpha = 0.75) +
    geom_density(color = "orange") +
    theme_bw()
  p1+p2
Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
i Please use `after_stat(density)` instead.
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



3. Estimation result, Correlation of explanatory variables, and Homoskedasticity check of model (2):

```
bptest(model_02)
```

3. Estimation result and Homoskedasticity check of model (3):

5. Restricted F-test for model(2) by removing AgLandShare and AgGdpShare

```
model_02_restrict <- lm(data = data_02,</pre>
                         formula = PropCalAnimal ~ ArableLandShare +
                           GdpPerCapita + HCI + LifeExp +
                           PopMiddle + PopOld + PopFemale + PopUrban)
anova(model_02_restrict, model_02)
6. Estimation result of model (4):
model_04 <- lm(data = data_02,</pre>
               formula = PropCalAnimal ~ ArableLandShare +
                → log(GdpPerCapita)
               + HCI + LifeExp + PopMiddle + PopOld + PopFemale +
                → PopUrban)
stargazer(model_04, type = "text", font.size = "footnotesize",
          column.sep.width = "1pt", single.row = TRUE,
          digits=2, no.space = TRUE)
7. Estimation result of model (4) with Quadratic HCI:
model_04_hci_square <- lm(data = data_02,</pre>
               formula = PropCalAnimal ~ ArableLandShare +
                → log(GdpPerCapita)
               + HCI + I(HCI<sup>2</sup>) + LifeExp + PopMiddle + PopOld +
                → PopFemale + PopUrban)
stargazer(model_04_hci_square, type = "text", font.size =
column.sep.width = "1pt", single.row = TRUE,
          digits=4, no.space = TRUE)
8. Complete comparison of models
```

```
bp_test_model_02 <- bptest(model_02)
bp_test2_model_03 <- bptest(model_03)
bp_test2_model_04 <- bptest(model_04)</pre>
```

```
reset_test_model_02 <- resettest(model_02, power=2, type="regressor",</pre>

ycov. = vcovHC(model 02, "HC1"))

reset_test_model_03 <- resettest(model_03, power=2, type="regressor",</pre>

  vcov. = vcovHC(model_03, "HC1"))

reset_test_model_04 <- resettest(model_04, power=2, type="regressor",

  vcov. = vcovHC(model_04, "HC1"))

stargazer(model_02, model_03, model_04, type="text",
          align=TRUE,
          add.lines=list(
            c("BP Test P-value", sprintf("%.3f",

→ bp_test_model_02$p.value),
              sprintf("%.3f", bp_test2_model_03$p.value),
              sprintf("%.3f", bp_test2_model_04$p.value)),
            c("RESET (power=2) Test P-value", sprintf("%.3f",

¬ reset_test_model_02$p.value),

              sprintf("%.3f", reset test model 03$p.value),
              sprintf("%.3f", reset_test_model_04$p.value))
          ),
          column.sep.width = "1pt",
          font.size = "footnotesize"
```

9. Model(3) summary with robust-heteroskedasticity standadrd error