ECMA 31360, PSet 2: Solutions

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Carry-over from PSet2

([ ] out of 50p) PART I: Test Balance in the Observed Predetermined Variables (OPVs)

([ ] out of 15p) Q1: Read and Understand the NSW Application's Companion Document

Done!

([ ] out of 23p) Q2: Implement Procedure 4 (SUR Estimation followed by Joint Testing)

([ ] out of 10p) Q2.a: SUR Estimation

```
# Load packages
library(systemfit)
```

```
## Loading required package: Matrix

## Loading required package: car

## Loading required package: carData

## Loading required package: lmtest

## Loading required package: zoo

##
## Attaching package: 'zoo'

## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric

##
## Please cite the 'systemfit' package as:
## Arne Henningsen and Jeff D. Hamann (2007). systemfit: A Package for Estimating Systems of Simultaneous Equati
##
## If you have questions, suggestions, or comments regarding the 'systemfit' package, please use a forum or 'tra
## https://r-forge.r-project.org/projects/systemfit/
```

```r
# Load data and create treatment indicator
treated <- read.csv("nswre74_treated.csv")
control <- read.csv("nswre74_control.csv")
treated$treat <- 1
control$treat <- 0
df <- rbind(treated, control)

# OPVs
opvs <- c("age","edu","nodegree","black","hisp",
          "married","u74","u75","re74","re75")

# SUR system: one equation per OPV
sur_system <- setNames(
  lapply(opvs, function(v) as.formula(paste(v, "~ treat"))),
  opvs
)

# Estimate SUR (FGLS)
sur_fit <- systemfit(sur_system, data = df, method = "SUR")

summary(sur_fit)
```

```
##
## systemfit results
## method: SUR
##
##             N   DF         SSR      detRCov   OLS-R2 McElroy-R2
## system   4450 4430 17173687963 15749397122 0.000443   0.004599
##
##             N  DF         SSR         MSE         RMSE       R2     Adj R2
## age       445 443 2.23210e+04 5.03860e+01     7.098310 0.002807   0.000556
## edu       445 443 1.41882e+03 3.20276e+00     1.789627 0.005025   0.002779
## nodegree  445 443 7.41263e+01 1.67328e-01     0.409057 0.022805   0.020599
## black     445 443 6.16656e+01 1.39200e-01     0.373095 0.000467  -0.001790
## hisp      445 443 3.53306e+01 7.97530e-02     0.282406 0.007067   0.004826
## married   445 443 6.22245e+01 1.40462e-01     0.374782 0.002165  -0.000087
## u74       445 443 8.69878e+01 1.96361e-01     0.443126 0.002176  -0.000077
## u75       445 443 1.00538e+02 2.26949e-01     0.476392 0.007639   0.005399
## re74      445 443 1.27730e+10 2.88329e+07  5369.629678 0.000001  -0.002256
## re75      445 443 4.40068e+09 9.93381e+06  3151.795133 0.001724  -0.000530
##
## The covariance matrix of the residuals used for estimation
##                   age          edu      nodegree          black          hisp
## age         50.385999    0.2449745 -3.08372e-01    0.22820169 -1.72655e-01
## edu          0.244974    3.2027649 -4.63917e-01    0.02937517 -7.06147e-02
## nodegree    -0.308372   -0.4639166  1.67328e-01    0.00698155  8.67174e-03
## black        0.228202    0.0293752  6.98155e-03    0.13919998 -7.32043e-02
## hisp        -0.172655   -0.0706147  8.67174e-03   -0.07320434  7.97530e-02
## married      0.553676    0.0527165 -4.89481e-03    0.00318186  1.37974e-03
## u74          0.330871   -0.0712617  7.87322e-03    0.00515832 -6.29614e-03
## u75          0.272721   -0.1041674  1.31794e-02    0.00724084  5.20924e-04
## re74       -44.770874  397.5322464 -1.51065e+02   10.95804850 -4.34831e+01
## re75      1130.716679  129.6734756  3.53185e+01  -67.43711762  3.96010e+01
##               married          u74          u75          re74          re75
## age        0.55367627  3.30871e-01  2.72721e-01 -4.47709e+01  1.13072e+03
## edu        0.05271655 -7.12617e-02 -1.04167e-01  3.97532e+02  1.29673e+02
## nodegree  -0.00489481  7.87322e-03  1.31794e-02 -1.51065e+02  3.53185e+01
## black      0.00318186  5.15832e-03  7.24084e-03  1.09580e+01 -6.74371e+01
## hisp       0.00137974 -6.29614e-03  5.20924e-04 -4.34831e+01  3.96010e+01
```

```
## married      0.14046170 -1.30559e-02 -1.66696e-02  2.87226e+02  3.14799e+02
## u74         -0.01305595  1.96361e-01  1.53273e-01 -1.54716e+03 -7.87361e+02
## u75         -0.01666956  1.53273e-01  2.26949e-01 -1.24249e+03 -8.92930e+02
## re74       287.22640387 -1.54716e+03 -1.24249e+03  2.88329e+07  1.10989e+07
## re75       314.79930993 -7.87361e+02 -8.92930e+02  1.10989e+07  9.93381e+06
##
## The covariance matrix of the residuals
##                   age          edu      nodegree         black          hisp
## age         50.385999    0.2449745 -3.08372e-01   0.22820169 -1.72655e-01
## edu          0.244974    3.2027649 -4.63917e-01   0.02937517 -7.06147e-02
## nodegree    -0.308372   -0.4639166  1.67328e-01   0.00698155  8.67174e-03
## black        0.228202    0.0293752  6.98155e-03   0.13919998 -7.32043e-02
## hisp        -0.172655   -0.0706147  8.67174e-03  -0.07320434  7.97530e-02
## married      0.553676    0.0527165 -4.89481e-03   0.00318186  1.37974e-03
## u74          0.330871   -0.0712617  7.87322e-03   0.00515832 -6.29614e-03
## u75          0.272721   -0.1041674  1.31794e-02   0.00724084  5.20924e-04
## re74       -44.770874  397.5322464 -1.51065e+02  10.95804850 -4.34831e+01
## re75      1130.716679  129.6734756  3.53185e+01 -67.43711762  3.96010e+01
##               married          u74          u75         re74         re75
## age         0.55367627  3.30871e-01  2.72721e-01 -4.47709e+01  1.13072e+03
## edu         0.05271655 -7.12617e-02 -1.04167e-01  3.97532e+02  1.29673e+02
## nodegree   -0.00489481  7.87322e-03  1.31794e-02 -1.51065e+02  3.53185e+01
## black       0.00318186  5.15832e-03  7.24084e-03  1.09580e+01 -6.74371e+01
## hisp        0.00137974 -6.29614e-03  5.20924e-04 -4.34831e+01  3.96010e+01
## married     0.14046170 -1.30559e-02 -1.66696e-02  2.87226e+02  3.14799e+02
## u74        -0.01305595  1.96361e-01  1.53273e-01 -1.54716e+03 -7.87361e+02
## u75        -0.01666956  1.53273e-01  2.26949e-01 -1.24249e+03 -8.92930e+02
## re74      287.22640387 -1.54716e+03 -1.24249e+03  2.88329e+07  1.10989e+07
## re75      314.79930993 -7.87361e+02 -8.92930e+02  1.10989e+07  9.93381e+06
##
## The correlations of the residuals
##                   age          edu    nodegree         black          hisp      married
## age         1.00000000   0.0192843 -0.1062028   0.08616766 -0.08612917   0.2081239
## edu         0.01928428   1.0000000 -0.6337137   0.04399449 -0.13972027   0.0785969
## nodegree   -0.10620285  -0.6337137  1.0000000   0.04574547  0.07506690  -0.0319280
## black       0.08616766   0.0439945  0.0457455   1.00000000 -0.69477442   0.0227553
## hisp       -0.08612917  -0.1397203  0.0750669  -0.69477442  1.00000000   0.0130361
## married     0.20812393   0.0785969 -0.0319280   0.02275529  0.01303605   1.0000000
## u74         0.10519033  -0.0898599  0.0434351   0.03120047 -0.05031221  -0.0786144
## u75         0.08064906  -0.1221814  0.0676311   0.04073851  0.00387201  -0.0933643
## re74       -0.00117462   0.0413681 -0.0687759   0.00546977 -0.02867497   0.1427253
## re75        0.05054066   0.0229896  0.0273943  -0.05734842  0.04449124   0.2664998
##                  u74          u75         re74         re75
## age         0.1051903   0.08064906 -0.00117462   0.0505407
## edu        -0.0898599  -0.12218137  0.04136809   0.0229896
## nodegree    0.0434351   0.06763105 -0.06877588   0.0273943
## black       0.0312005   0.04073851  0.00546977  -0.0573484
## hisp       -0.0503122   0.00387201 -0.02867497   0.0444912
## married    -0.0786144  -0.09336432  0.14272533   0.2664998
## u74         1.0000000   0.72606314 -0.65022329  -0.5637523
## u75         0.7260631   1.00000000 -0.48571844  -0.5946962
## re74       -0.6502233  -0.48571844  1.00000000   0.6558102
## re75       -0.5637523  -0.59469615  0.65581024   1.0000000
##
##
## SUR estimates for 'age' (equation 1)
## Model Formula: age ~ treat
## <environment: 0x117865e40>
##
##               Estimate Std. Error  t value Pr(>|t|)
```

```
## (Intercept) 25.053846    0.440218 56.91230  < 2e-16 ***
## treat          0.762370    0.682751  1.11661  0.26476
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.09831 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 22320.997505 MSE: 50.385999 Root MSE: 7.09831
## Multiple R-Squared: 0.002807 Adjusted R-Squared: 0.000556
##
##
## SUR estimates for 'edu' (equation 2)
## Model Formula: edu ~ treat
## <environment: 0x11786b820>
##
##              Estimate Std. Error  t value Pr(>|t|)
## (Intercept) 10.088462    0.110988 90.89690  < 2e-16 ***
## treat          0.257484    0.172135  1.49583  0.13541
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.789627 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 1418.824844 MSE: 3.202765 Root MSE: 1.789627
## Multiple R-Squared: 0.005025 Adjusted R-Squared: 0.002779
##
##
## SUR estimates for 'nodegree' (equation 3)
## Model Formula: nodegree ~ treat
## <environment: 0x1179217e8>
##
##               Estimate Std. Error  t value   Pr(>|t|)
## (Intercept)  0.8346154  0.0253687 32.89946 < 2.22e-16 ***
## treat       -0.1265073  0.0393452 -3.21532  0.0013984 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.409057 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 74.126299 MSE: 0.167328 Root MSE: 0.409057
## Multiple R-Squared: 0.022805 Adjusted R-Squared: 0.020599
##
##
## SUR estimates for 'black' (equation 4)
## Model Formula: black ~ treat
## <environment: 0x117923f58>
##
##              Estimate Std. Error  t value Pr(>|t|)
## (Intercept) 0.8269231  0.0231384 35.73816  < 2e-16 ***
## treat       0.0163202  0.0358862  0.45478  0.64949
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.373095 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 61.665593 MSE: 0.1392 Root MSE: 0.373095
## Multiple R-Squared: 0.000467 Adjusted R-Squared: -0.00179
##
##
## SUR estimates for 'hisp' (equation 5)
```

```
## Model Formula: hisp ~ treat
## <environment: 0x1179227b8>
##
##                Estimate Std. Error  t value   Pr(>|t|)
## (Intercept)  0.1076923  0.0175141  6.14891 1.7434e-09 ***
## treat       -0.0482328  0.0271632 -1.77567   0.076474 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.282406 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 35.330561 MSE: 0.079753 Root MSE: 0.282406
## Multiple R-Squared: 0.007067 Adjusted R-Squared: 0.004826
##
##
## SUR estimates for 'married' (equation 6)
## Model Formula: married ~ treat
## <environment: 0x117924f28>
##
##                Estimate Std. Error t value   Pr(>|t|)
## (Intercept) 0.1538462  0.0232430 6.61903 1.0471e-10 ***
## treat       0.0353430  0.0360484 0.98043    0.32741
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.374782 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 62.224532 MSE: 0.140462 Root MSE: 0.374782
## Multiple R-Squared: 0.002165 Adjusted R-Squared: -8.7e-05
##
##
## SUR estimates for 'u74' (equation 7)
## Model Formula: u74 ~ treat
## <environment: 0x117927698>
##
##                Estimate Std. Error  t value Pr(>|t|)
## (Intercept)  0.7500000  0.0274815 27.29107  < 2e-16 ***
## treat       -0.0418919  0.0426221 -0.98287  0.32621
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.443126 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 86.987838 MSE: 0.196361 Root MSE: 0.443126
## Multiple R-Squared: 0.002176 Adjusted R-Squared: -7.7e-05
##
##
## SUR estimates for 'u75' (equation 8)
## Model Formula: u75 ~ treat
## <environment: 0x117929e08>
##
##                Estimate Std. Error  t value Pr(>|t|)
## (Intercept)  0.6846154  0.0295446 23.17230  < 2e-16 ***
## treat       -0.0846154  0.0458218 -1.84662 0.065469 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.476392 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 100.538462 MSE: 0.226949 Root MSE: 0.476392
```

```
## Multiple R-Squared: 0.007639 Adjusted R-Squared: 0.005399
##
##
## SUR estimates for 're74' (equation 9)
## Model Formula: re74 ~ treat
## <environment: 0x117928668>
##
##             Estimate Std. Error  t value    Pr(>|t|)
## (Intercept) 2107.027    333.010  6.32721 6.1166e-10 ***
## treat        -11.453    516.478 -0.02218    0.98232
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5369.629678 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 12772984837.6605 MSE: 28832922.884109 Root MSE: 5369.629678
## Multiple R-Squared: 1e-06 Adjusted R-Squared: -0.002256
##
##
## SUR estimates for 're75' (equation 10)
## Model Formula: re75 ~ treat
## <environment: 0x11792add8>
##
##             Estimate Std. Error t value    Pr(>|t|)
## (Intercept) 1266.909    195.466 6.48148 2.4248e-10 ***
## treat        265.146    303.155 0.87462    0.38225
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3151.795133 on 443 degrees of freedom
## Number of observations: 445 Degrees of Freedom: 443
## SSR: 4400678965.09339 MSE: 9933812.562288 Root MSE: 3151.795133
## Multiple R-Squared: 0.001724 Adjusted R-Squared: -0.00053
```

Script and Output

We estimate a 10-equation SUR system where each OPV is regressed on the treatment indicator. The intercept in each equation equals the control-group mean of that OPV, and the coefficient on treat equals the treated–control difference in means. The estimated residual covariance/correlation matrices show substantial cross-equation dependence for economically related OPVs (e.g., u74–u75, re74–re75, edu–nodegree), which motivates using SUR and is required for the joint balance test in subsequent questions.

([ ] out of 1p) Q2.b: Compare FGLS to OLS equation-by-equation

```r
# Q2.b: OLS equation-by-equation (for comparison)
ols_fits <- lapply(opvs, function(v) lm(as.formula(paste0(v, " ~ treat")), data = df))
names(ols_fits) <- opvs

# Compare treat coefficients
sapply(ols_fits, function(m) coef(m)["treat"])
```

```
##       age.treat       edu.treat nodegree.treat     black.treat      hisp.treat
##      0.76237006      0.25748441    -0.12650728      0.01632017     -0.04823285
##   married.treat       u74.treat       u75.treat      re74.treat      re75.treat
##      0.03534304     -0.04189189    -0.08461538    -11.45295788    265.14629853
```

```
coef(sur_fit)[grep("treat", names(coef(sur_fit)))]
```

```
##      age_treat        edu_treat nodegree_treat      black_treat       hisp_treat
##     0.76237006       0.25748441    -0.12650728       0.01632017      -0.04823285
##  married_treat        u74_treat       u75_treat       re74_treat       re75_treat
##     0.03534304      -0.04189189    -0.08461538     -11.45295788     265.14629853
```

Since each equation has the same regressors (an intercept term and a common treatment indicator), the point estimates from SUR/FGLS are the same as those from OLS for each equation (i.e., the estimated mean differences between the treatment and control groups are the same). The key advantage of SUR is that it can estimate the full cross-equation variance-covariance structure, which is necessary for conducting joint balance tests across different OPVs (and may lead to different systematic standard errors for linear combinations of the coefficients).

([   ] out of 3p) Q2.c: Take a closer look at the variance-covariance matrix

Script and Output

```
V_hat <- vcov(sur_fit)
nm <- names(coef(sur_fit))
nm[1:4]   # should look like: age_(Intercept), age_treat, edu_(Intercept), edu_treat
```

```
## [1] "age_(Intercept)" "age_treat"       "edu_(Intercept)" "edu_treat"
```

```
i01 <- 1   # pi0,1
i11 <- 2   # pi1,1
i02 <- 3   # pi0,2
i12 <- 4   # pi1,2

# (i) should be ~ 0
V_hat[i01, i11] + V_hat[i01, i01]
```

```
## [1] 0
```

```
# (ii) should be ~ 0
V_hat[i01, i12] + V_hat[i01, i02]
```

```
## [1] 2.732189e-17
```

```
# (iii) should be ~ 0
V_hat[i01, i12] - V_hat[i11, i02]
```

```
## [1] 4.466913e-17
```

We estimate, for each OPV $j = 1, \ldots, 10$, the regression

$$X_{ij} = \pi_{0,j} + \pi_{1,j} D_i + u_{ij},$$

where $D_i \in \{0, 1\}$ is the treatment indicator. Because the regressor is only an intercept and a binary variable, the OLS (and hence the equation-by-equation component of the SUR estimator) admits a simple "group-mean" representation:

$$\widehat{\pi}_{0,j} = \bar{X}_{j,0}, \qquad \widehat{\pi}_{1,j} = \bar{X}_{j,1} - \bar{X}_{j,0},$$

where

$$\bar{X}_{j,0} := \frac{1}{n_0} \sum_{i:D_i=0} X_{ij}, \qquad \bar{X}_{j,1} := \frac{1}{n_1} \sum_{i:D_i=1} X_{ij}.$$

Thus, $\widehat{\pi}_{0,j}$ is the control-group mean of OPV j, and $\widehat{\pi}_{1,j}$ is the treated–control difference in means for OPV j.

Expression (1) is the top-left 4×4 block of $\widehat{\mathrm{Var}}(\widehat{\pi})$ for the parameter vector

$$(\widehat{\pi}_{0,1}, \widehat{\pi}_{1,1}, \widehat{\pi}_{0,2}, \widehat{\pi}_{1,2})'.$$

The following equalities follow directly from the above identities and the (approximate) independence between the treated and control subsamples implied by unconditional random assignment (URA).

(i) Why is $\widehat{\mathrm{Cov}}[\widehat{\pi}_{0,1}, \widehat{\pi}_{1,1}] = -\widehat{\mathrm{Var}}[\widehat{\pi}_{0,1}]$? Using $\widehat{\pi}_{0,1} = \bar{X}_{1,0}$ and $\widehat{\pi}_{1,1} = \bar{X}_{1,1} - \bar{X}_{1,0}$,

$$\widehat{\mathrm{Cov}}(\widehat{\pi}_{0,1}, \widehat{\pi}_{1,1}) = \widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{1,1} - \bar{X}_{1,0}) = \widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{1,1}) - \widehat{\mathrm{Var}}(\bar{X}_{1,0}).$$

Under URA, $\bar{X}_{1,0}$ and $\bar{X}_{1,1}$ are based on non-overlapping subsamples and are approximately independent, hence $\widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{1,1}) \approx 0$. Therefore,

$$\widehat{\mathrm{Cov}}(\widehat{\pi}_{0,1}, \widehat{\pi}_{1,1}) = -\widehat{\mathrm{Var}}(\bar{X}_{1,0}) = -\widehat{\mathrm{Var}}(\widehat{\pi}_{0,1}).$$

(ii) Why is $\widehat{\mathrm{Cov}}[\widehat{\pi}_{0,1}, \widehat{\pi}_{1,2}] = -\widehat{\mathrm{Cov}}[\widehat{\pi}_{0,1}, \widehat{\pi}_{0,2}]$? Using $\widehat{\pi}_{0,1} = \bar{X}_{1,0}$ and $\widehat{\pi}_{1,2} = \bar{X}_{2,1} - \bar{X}_{2,0}$,

$$\widehat{\mathrm{Cov}}(\widehat{\pi}_{0,1}, \widehat{\pi}_{1,2}) = \widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{2,1} - \bar{X}_{2,0}) = \widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{2,1}) - \widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{2,0}).$$

Again, URA implies $\widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{2,1}) \approx 0$, so

$$\widehat{\mathrm{Cov}}(\widehat{\pi}_{0,1}, \widehat{\pi}_{1,2}) = -\widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{2,0}) = -\widehat{\mathrm{Cov}}(\widehat{\pi}_{0,1}, \widehat{\pi}_{0,2}),$$

since $\widehat{\pi}_{0,2} = \bar{X}_{2,0}$.

(iii) Why is $\widehat{\mathrm{Cov}}[\widehat{\pi}_{0,1}, \widehat{\pi}_{1,2}] = \widehat{\mathrm{Cov}}[\widehat{\pi}_{1,1}, \widehat{\pi}_{0,2}]$? Compute

$$\widehat{\mathrm{Cov}}(\widehat{\pi}_{1,1}, \widehat{\pi}_{0,2}) = \widehat{\mathrm{Cov}}(\bar{X}_{1,1} - \bar{X}_{1,0}, \bar{X}_{2,0}) = \widehat{\mathrm{Cov}}(\bar{X}_{1,1}, \bar{X}_{2,0}) - \widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{2,0}).$$

Under URA, $\widehat{\mathrm{Cov}}(\bar{X}_{1,1}, \bar{X}_{2,0}) \approx 0$, hence

$$\widehat{\mathrm{Cov}}(\widehat{\pi}_{1,1}, \widehat{\pi}_{0,2}) = -\widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{2,0}).$$

But part (ii) showed

$$\widehat{\mathrm{Cov}}(\widehat{\pi}_{0,1}, \widehat{\pi}_{1,2}) = -\widehat{\mathrm{Cov}}(\bar{X}_{1,0}, \bar{X}_{2,0}),$$

so

$$\widehat{\mathrm{Cov}}(\widehat{\pi}_{0,1}, \widehat{\pi}_{1,2}) = \widehat{\mathrm{Cov}}(\widehat{\pi}_{1,1}, \widehat{\pi}_{0,2}).$$

Commentary

Because each equation includes only an intercept and a binary treatment indicator, $\widehat{\pi}_{0,j}$ equals the control-group mean and $\widehat{\pi}_{1,j}$ equals the treated–control difference in means. Under unconditional random assignment, treated and control subsamples are (approximately) independent. These two facts jointly imply the sign and symmetry restrictions in the top-left 4×4 block of $\widehat{\mathrm{Var}}(\widehat{\pi})$, and the implied equalities are verified numerically up to machine precision.

([ ] out of 4p) Q2.d: Implement Joint Test Manually

```r
# coef and vcov from SUR
b_hat <- coef(sur_fit)
V_hat <- vcov(sur_fit)
nm <- names(b_hat)

# 1) pick the J=10 treat coefficients
treat_idx <- grep("_treat$", nm)
J <- length(treat_idx)          # should be 10
K <- length(b_hat)              # should be 20

# 2) build R matrix selecting treat coefficients: R b = (pi_1,1,...,pi_1,J)'
R <- matrix(0, nrow = J, ncol = K)
for (j in 1:J) R[j, treat_idx[j]] <- 1
r0 <- rep(0, J)

# 3) compute quadratic form Q = (R b - r)' (R V R')^{-1} (R b - r)
d <- as.vector(R %*% b_hat - r0)
Q <- as.numeric(t(d) %*% solve(R %*% V_hat %*% t(R)) %*% d)

# 4) F statistic and p-value using F_{J, Jn-K}
F_stat <- Q / J
df1 <- J
n <- 445
df2 <- J*n - K                          # should be 4430
p_F <- 1 - pf(F_stat, df1 = df1, df2 = df2)

# 5) S (Wald) statistic and p-value using Chi-square_J
S_stat <- J * F_stat    # equals Q
p_S <- 1 - pchisq(S_stat, df = J)


c(J=J, K=K, n=n, df2=df2,
  F_stat=F_stat, p_value_F=p_F,
  S_stat=S_stat, p_value_S=p_S)
```

```
##             J            K            n           df2       F_stat     p_value_F
## 1.000000e+01 2.000000e+01 4.450000e+02 4.430000e+03 2.046563e+00 2.538070e-02
##        S_stat     p_value_S
## 2.046563e+01 2.514383e-02
```

Script and Output

We test the joint null hypothesis that the coefficients on `treat` are zero in all $J = 10$ equations:

$$H_0: \ \pi_{1,1} = \pi_{1,2} = \cdots = \pi_{1,10} = 0.$$

Using the companion document's expressions for Procedure 4, we compute the F statistic and the Wald (S) statistic. With $n = 445$ observations per equation and $K = 2J = 20$ parameters in the stacked system, the denominator degrees of freedom are

$$Jn - K = 10 \times 445 - 20 = 4430.$$

Our manual calculations yield

$$F = 2.0466 \quad \text{with} \quad p\text{-value} = 0.0254 \ \text{ using } F_{10,4430},$$

and equivalently

$$S = J \cdot F = 20.4656 \quad \text{with} \quad p\text{-value} = 0.0251 \ \text{ using } \chi^2_{10}.$$

At the 5% level, we reject H_0, indicating that the OPVs are not jointly balanced across treatment and control.

([ ] out of 4p) Q2.e: Implement Joint Test Automatically

Script and Output

```r
library(car)

# Names of coefficients
names(coef(sur_fit))
```

```
##  [1] "age_(Intercept)"     "age_treat"            "edu_(Intercept)"
##  [4] "edu_treat"           "nodegree_(Intercept)" "nodegree_treat"
##  [7] "black_(Intercept)"   "black_treat"          "hisp_(Intercept)"
## [10] "hisp_treat"          "married_(Intercept)"  "married_treat"
## [13] "u74_(Intercept)"     "u74_treat"            "u75_(Intercept)"
## [16] "u75_treat"           "re74_(Intercept)"     "re74_treat"
## [19] "re75_(Intercept)"    "re75_treat"
```

```r
# Joint null: all treat coefficients equal zero
# We write one restriction per equation
lh <- linearHypothesis(
  sur_fit,
  c(
    "age_treat = 0",
    "edu_treat = 0",
    "nodegree_treat = 0",
    "black_treat = 0",
    "hisp_treat = 0",
    "married_treat = 0",
    "u74_treat = 0",
    "u75_treat = 0",
    "re74_treat = 0",
    "re75_treat = 0"
  ),
  test = "F"
)

lh
```

```
## Linear hypothesis test (F statistic of a Wald test)
##
## Hypothesis:
## age_treat = 0
## edu_treat = 0
## nodegree_treat = 0
## black_treat = 0
## hisp_treat = 0
## married_treat = 0
## u74_treat = 0
## u75_treat = 0
## re74_treat = 0
## re75_treat = 0
##
## Model 1: restricted model
## Model 2: sur_fit
##
##   Res.Df Df      F  Pr(>F)
## 1   4440
## 2   4430 10 2.0466 0.02538 *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

F_auto <- lh[2, "F"]
S_auto <- 10 * F_auto

c(F_auto = F_auto, S_auto = S_auto)
```

```
##     F_auto     S_auto
##   2.046563 20.465626
```

Commentary

The automatic joint test implemented via `car::linearHypothesis()` yields an F statistic of 2.0466 with a p-value of 0.02538. These values coincide exactly with those obtained from the manual construction of the Wald test in Q2.d, as both procedures rely on the same linear restrictions and the same estimated variance–covariance matrix from the SUR estimator.

([   ] out of 1p) Q2.f: Decision

At the 5% significance level, we reject the joint null hypothesis that all coefficients on `treat` are equal to zero across the system of equations. —

([   ] out of 3p) Q3: Implement Procedure 5 (Hotelling's T2 Test)

Script and Output

```
opvs <- c("age","edu","nodegree","black","hisp",
          "married","u74","u75","re74","re75")

X1 <- df[df$treat == 1, opvs]
X0 <- df[df$treat == 0, opvs]

# Use DescTools::HotellingsT2Test()
if (!requireNamespace("DescTools", quietly = TRUE)) install.packages("DescTools")
library(DescTools)
```

```
##
## Attaching package: 'DescTools'
```

```
## The following object is masked from 'package:car':
##
##     Recode
```

```
ht <- DescTools::HotellingsT2Test(X1, X0)
ht
```

```
##
##  Hotelling's two sample T2-test
##
## data:  X1 and X0
## T.2 = 2.005, df1 = 10, df2 = 434, p-value = 0.0314
## alternative hypothesis: true location difference is not equal to c(0,0,0,0,0,0,0,0,0,0)
```

```r
# Extract T2 and p-value (in case you want to print neatly)
T2 <- as.numeric(ht$statistic)
p_T2 <- as.numeric(ht$p.value)

c(T2 = T2, p_value = p_T2)
```

```
##        T2    p_value
## 2.00498455 0.03140293
```

Commentary

We implement Procedure 5 using Hotelling's two-sample T^2 test via `DescTools::HotellingsT2Test()` to assess joint balance in the $J = 10$ observed predetermined variables (OPVs). The null hypothesis is

$$H_0 : \ \mathbb{E}[X \mid D = 1] = \mathbb{E}[X \mid D = 0],$$

against the alternative that at least one component differs.

The test yields a Hotelling's statistic of $T^2 = 2.005$. Using the finite-sample F-approximation with degrees of freedom $(10, 434)$, the associated p-value is 0.0314. At the 5% significance level, we therefore reject the null hypothesis of joint balance in the OPVs.

This result is consistent with the joint SUR-based Wald test in Procedure~4 and with the treatment-assignment regression test in Procedure~6. Differences in numerical values across procedures reflect different finite-sample approximations (chi-square versus F), not differences in the underlying hypothesis being tested. —

([   ] out of 4p) Q4: Implement Procedure 6 (OPV do not predict treatment assignment)

Script and Output

```r
opvs <- c("age","edu","nodegree","black","hisp",
          "married","u74","u75","re74","re75")

lm_fit <- lm(treat ~ age + edu + nodegree + black + hisp +
               married + u74 + u75 + re74 + re75,
             data = df)

summary(lm_fit)$r.squared
```

```
## [1] 0.04415781
```

```r
summary(lm_fit)$fstatistic   # (value, numdf, dendf)
```

```
##     value      numdf      dendf
##   2.004985  10.000000 434.000000
```

```r
R2 <- summary(lm_fit)$r.squared
n  <- nobs(lm_fit)
M  <- length(opvs)  # number of slope parameters (10)

F_manual <- (R2 / M) / ((1 - R2) / (n - (M + 1)))
p_manual <- 1 - pf(F_manual, df1 = M, df2 = n - (M + 1))

c(R2 = R2, n = n, M = M, F_manual = F_manual, p_manual = p_manual)
```

```
##          R2            n            M     F_manual     p_manual
##   0.04415781 445.00000000  10.00000000   2.00498455   0.03140293
```

Commentary

We implement Procedure 6 by regressing the treatment indicator on a constant and the $J = 10$ observed predetermined variables using a linear probability model. Let R^2 denote the coefficient of determination from this regression and let $M = 10$ be the number of slope parameters. Following the companion document, we compute the overall significance test statistic

$$F = \frac{R^2/M}{(1 - R^2)/(n - (M + 1))},$$

and obtain the corresponding p-value from an $F_{M,\,n-(M+1)}$ distribution. Using $n = 445$, we obtain $F = 2.005$ with a p-value of 0.0314. We reject the null hypothesis. —

([ ] out of 5p) Q5: Implement Procedures 7 and 8 (control for FWER)

Script and Output

```
# Q5: Procedures 7 (Bonferroni) and 8 (Holm-Bonferroni)
# We use the one-at-a-time p-values for H0,j: pi_{1,j}=0 (treat coefficient = 0) for each OPV.

opvs <- c("age","edu","nodegree","black","hisp","married","u74","u75","re74","re75")

# If you already created ols_fits in Q2.b, you can reuse it.
# Otherwise:
ols_fits <- lapply(opvs, function(v) lm(as.formula(paste0(v, " ~ treat")), data = df))
names(ols_fits) <- opvs

# Extract unadjusted p-values for treat in each equation
p_raw <- sapply(ols_fits, function(m) summary(m)$coefficients["treat","Pr(>|t|)"])

# Procedure 7: Bonferroni adjusted p-values = p_adj_j = min(1, J * p_j)
# (implemented by p.adjust(method="bonferroni"))
p_bonf <- p.adjust(p_raw, method = "bonferroni")

# Procedure 8: Holm-Bonferroni adjusted p-values (implemented by p.adjust(method="holm"))
p_holm <- p.adjust(p_raw, method = "holm")

# Collect results
res_q5 <- data.frame(
  OPV = opvs,
  p_raw = as.numeric(p_raw),
  p_bonf = as.numeric(p_bonf),
  p_holm = as.numeric(p_holm),
  reject_bonf_5pct = (p_bonf <= 0.05),
  reject_holm_5pct = (p_holm <= 0.05)
)

# Show table sorted by raw p-values (helpful for interpretation)
res_q5[order(res_q5$p_raw), ]
```

```
##                   OPV       p_raw      p_bonf      p_holm reject_bonf_5pct
## nodegree nodegree 0.001398352 0.01398352 0.01398352             TRUE
## u75           u75 0.065468962 0.65468962 0.58922066             FALSE
## hisp         hisp 0.076473893 0.76473893 0.61179115             FALSE
## edu           edu 0.135411167 1.00000000 0.94787817             FALSE
## age           age 0.264764269 1.00000000 1.00000000             FALSE
## u74           u74 0.326208987 1.00000000 1.00000000             FALSE
## married   married 0.327408105 1.00000000 1.00000000             FALSE
## re75         re75 0.382253831 1.00000000 1.00000000             FALSE
```

13

```
## black            black 0.649493182 1.00000000 1.00000000                    FALSE
## re74              re74 0.982318253 1.00000000 1.00000000                    FALSE
##             reject_holm_5pct
## nodegree                TRUE
## u75                    FALSE
## hisp                   FALSE
## edu                    FALSE
## age                    FALSE
## u74                    FALSE
## married                FALSE
## re75                   FALSE
## black                  FALSE
## re74                   FALSE
```

Commentary

Q5 controls the family-wise error rate (FWER) when testing balance in the $J = 10$ OPVs using one-at-a-time tests of $H_{0,j} : \pi_{1,j} = 0$ for each OPV j. Following the programming guidance, we implement:

- **Procedure 7 (Bonferroni)**, which adjusts p-values as $p_j^{(B)} = \min\{1, Jp_j\}$; and
- **Procedure 8 (Holm–Bonferroni)**, a step-down procedure that is weakly less conservative than Bonferroni.

Both procedures are implemented using `stats::p.adjust()`. At the 5% significance level, only `nodegree` remains statistically significant after controlling the FWER under both Bonferroni and Holm–Bonferroni adjustments. All other OPVs have adjusted p-values well above 0.05.

Therefore, we reject the joint null hypothesis of perfect balance across the OPVs, but the evidence for imbalance is driven entirely by the `nodegree` variable. This result is consistent with the earlier joint balance tests (Procedures 4 and 5) and the treatment-assignment test (Procedure 6). —

([   ] out of 50p) PART II: Review of OLS for Causal Analysis

([   ] out of 3p) Q6: Two ways of obtaining the DM estimator

Script and Output

Commentary

([   ] out of 4p) Q7: Fully-saturated specification in Nodegree

Script and Output

([   ] out of 2p) Q8: Get $\widehat{ATE}$ in one step

Script and Output

([   ] out of 22p) Q9: Implications of estimating a not-fully saturated specification in an OPV that takes M distinct values

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([   ] out of 14p) Q10: Implement the DM estimator with Regression Adjustment (various specifications)

([   ] out of 3p) Q10.a: Estimate Specifications 2, 3 and 4

([   ] out of 1p) Q10.a.i: Estimate Specification 2

Script and Output

Commentary

([   ] out of 1p) Q10.a.ii: Estimate Specification 3

Script and Output

Commentary

([   ] out of 1p) Q10.a.iii: Estimate Specification 4

Script and Output

Commentary

([   ] out of 5p) Q10.b: Reasons to include OPVs when they are balanced

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([   ] out of 1p) Q10.c: Is it problematic to regression-adjust for OPVs that are lagged outcomes?

([   ] out of 5p) Q10.d: Interactions of OPV with Treatment Indicator and Two Hypothesis Testing Problems

Script and Output

Commentary

([   ] out of 5p) Q11: Mechanisms for NSW intervention to impact post-intervention earnings