

Analysis of Methylprednisolone Pulse Therapy on COVID-19 ICU patients at Thu Duc City Hospital, Vietnam

24-Oct-2021

Context

This RMarkdown file serves as the analysis of the results provided in the manuscript “High dose methylprednisolone pulse therapy as a treatment for severe COVID-19 patients: results from a prospective observational study” of Nghia Thinh Bui et al. (2021).

Setting up with library and dataset import

```
# import necessary libraries
library(BMA)
library(compareGroups)
library(dplyr)
library(epiDisplay)
library(ggplot2)
library(gridExtra)
library(logistf)
library(Matching)
library(pROC)
library(tidyr)
library(table1)
library(knitr)
library(ggplot2)

# import dataset
newPS <- read.csv("./newPS.csv")
```

Descriptive Statistics and Propensity Score

```
# Calculate propensity score
PSlogit <- glm(newPS$death ~ newPS$data.PT + newPS$sex + newPS$age + newPS$BMI + newPS$hypertension + newPS$cardiovascular + newPS$diabetes + newPS$chronic + newPS$obesity + newPS$pregnancy + newPS$stroke + newPS$chronic_liver + newPS$chronic_renal + newPS$cancer_HIV + newPS$SpO2 + newPS$Temp + newPS$Breathing, family = binomial, data = newPS)
summary(PSlogit)

##
## Call:
## glm(formula = newPS$death ~ newPS$data.PT + newPS$sex + newPS$age + newPS$BMI + newPS$hypertension + newPS$cardiovascular + newPS$diabetes + newPS$chronic + newPS$obesity + newPS$pregnancy + newPS$stroke + newPS$chronic_liver + newPS$chronic_renal + newPS$cancer_HIV + newPS$SpO2 + newPS$Temp + newPS$Breathing, family = binomial, data = newPS)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -2.90281 -0.16832 0.08587 0.36732 1.98405
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.83515 6.28115 -0.451 0.651720
## newPS$data.PT1 -2.31231 0.70098 -3.299 0.000971 ***
## newPS$sexM 0.60552 0.72439 0.836 0.403206
## newPS$age 0.14316 0.03360 4.261 2.03e-05 ***
## newPS$BMI 0.14137 0.14762 0.958 0.338219
## newPS$hypertension1 -2.52431 1.06735 -2.365 0.018029 *
## newPS$Cardiovascular1 -1.43646 1.35434 -1.061 0.288854
## newPS$Diabetes1 2.10200 1.33211 1.578 0.114576
## newPS$Chronic1 -2.69542 1.52188 -1.771 0.076542 .
## newPS$Obesity1 -1.40237 1.41000 -0.995 0.319939
## newPS$Pregnancy1 1.74634 1.31512 1.328 0.184212
## newPS$Stroke1 10.67938 1730.74455 0.006 0.995077
## newPS$Chronic_liver1 -7.16071 5594.88416 -0.001 0.998979
## newPS$chronic_renal1 0.00439 1.71731 0.003 0.997960
## newPS$cancer_HIV1 22.12361 3956.18051 0.006 0.995538
## newPS$SpO2 -0.11717 0.03718 -3.151 0.001625 **
## newPS$Temp 0.20585 0.11508 1.789 0.073651 .
## newPS$Breathing -0.11017 0.06658 -1.655 0.097960 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 174.025 on 146 degrees of freedom
## Residual deviance: 75.548 on 129 degrees of freedom
## AIC: 111.55
##
## Number of Fisher Scoring iterations: 16
```

```
logistic.display(PSlogit)
```

```
##
## OR lower95ci upper95ci Pr(>|Z|)
## newPS$data.PT1 9.903175e-02 0.025066671 0.3912481 9.714242e-04
## newPS$sexM 1.832208e+00 0.442971743 7.5783302 4.032055e-01
## newPS$age 1.153919e+00 1.080383458 1.2324597 2.032634e-05
## newPS$BMI 1.151851e+00 0.862472856 1.5383228 3.382186e-01
## newPS$hypertension1 8.011335e-02 0.009889454 0.6489892 1.802904e-02
## newPS$Cardiovascular1 2.377669e-01 0.016723825 3.3803929 2.888542e-01
## newPS$Diabetes1 8.182542e+00 0.601171643 111.3725158 1.145757e-01
## newPS$Chronic1 6.751382e-02 0.003419525 1.3329676 7.654181e-02
## newPS$Obesity1 2.460144e-01 0.015515456 3.9008263 3.199388e-01
## newPS$Pregnancy1 5.733584e+00 0.435507498 75.4843029 1.842123e-01
## newPS$Stroke1 4.345054e+04 0.000000000 Inf 9.950768e-01
## newPS$Chronic_liver1 7.765036e-04 0.000000000 Inf 9.989788e-01
## newPS$chronic_renal1 1.004399e+00 0.034684157 29.0858541 9.979604e-01
## newPS$cancer_HIV1 4.056593e+09 0.000000000 Inf 9.955381e-01
## newPS$SpO2 8.894368e-01 0.826928390 0.9566702 1.624945e-03
## newPS$Temp 1.228566e+00 0.980492900 1.5394029 7.365094e-02
## newPS$Breathing 8.956810e-01 0.786111480 1.0205226 9.796010e-02
```

```
Formula = (newPS$data.PT==1) ~ newPS$sex + newPS$age + newPS$BMI + newPS$hypertension + newPS$Cardiovas
PSlogit1 <- glm(formula = Formula, family=binomial, data = newPS)
summary(PSlogit1)
```

```
##
## Call:
## glm(formula = Formula, family = binomial, data = newPS)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.0093  -0.9526  -0.4765   0.9389   2.1735
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -4.35109     3.85885  -1.128  0.25951
## newPS$sexM       0.46042     0.41127   1.120  0.26292
## newPS$age      -0.04196     0.01622  -2.586  0.00971 **
## newPS$BMI       0.15871     0.08597   1.846  0.06489 .
## newPS$hypertension1 -0.15850     0.62983  -0.252  0.80131
## newPS$Cardiovascular1 1.37157     0.86393   1.588  0.11238
## newPS$Diabetes1  -0.33599     0.64669  -0.520  0.60338
## newPS$Chronic1   -0.47774     1.02972  -0.464  0.64268
## newPS$Obesity1   -0.58079     0.77463  -0.750  0.45340
## newPS$Pregnancy1 -1.16830     1.13561  -1.029  0.30358
## newPS$Stroke1    -14.89267    1064.93152  -0.014  0.98884
## newPS$Chronic_liver1 -32.42211    3393.46875  -0.010  0.99238
## newPS$chronic_renal1 -0.70579     1.35953  -0.519  0.60366
## newPS$cancer_HIV1 16.10080    2399.54479   0.007  0.99465
## newPS$SpO2       0.01948     0.01470   1.325  0.18504
## newPS$Temp       0.04548     0.08199   0.555  0.57908
## newPS$Breathing  -0.02668     0.03218  -0.829  0.40697
## UD              NA          NA      NA      NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 202.25  on 146  degrees of freedom
## Residual deviance: 166.31  on 130  degrees of freedom
## AIC: 200.31
##
## Number of Fisher Scoring iterations: 15
```

```
logistic.display(PSlogit1)
```

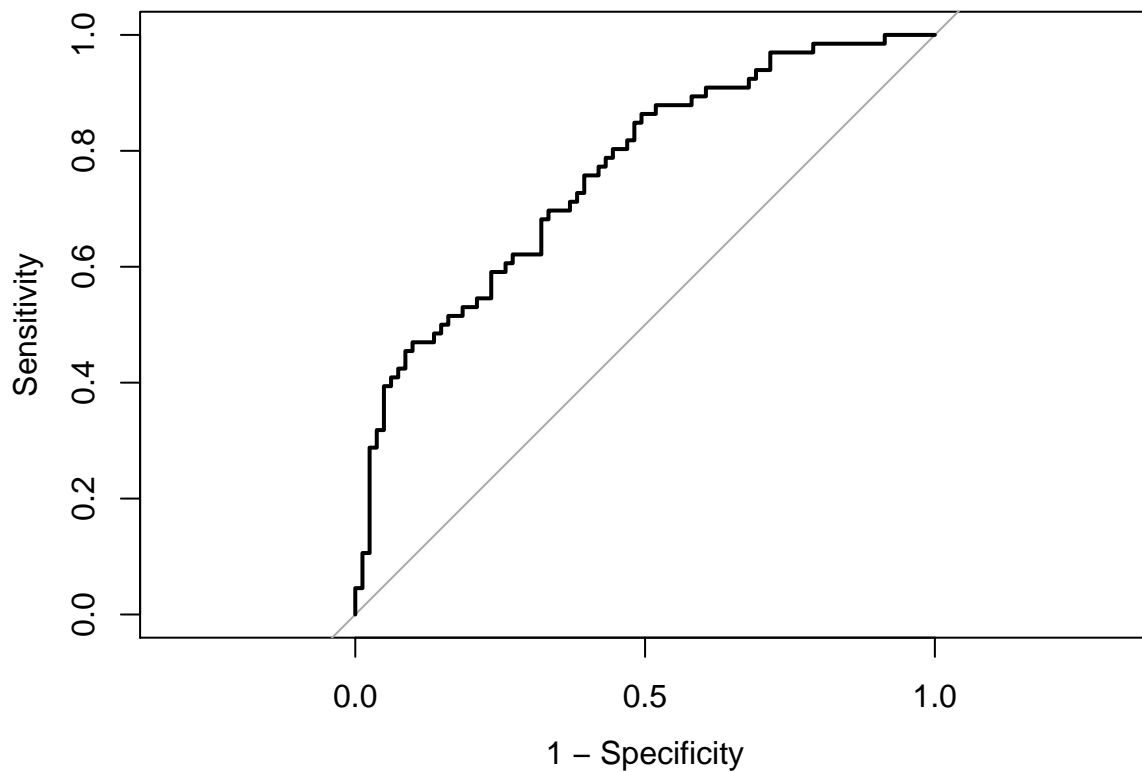
```
##
##              OR  lower95ci  upper95ci  Pr(>|Z|)
## newPS$sexM      1.584744e+00  0.70776338  3.5483815  0.262916883
## newPS$age       9.589107e-01  0.92889817  0.9898929  0.009706883
## newPS$BMI       1.172001e+00  0.99025289  1.3871068  0.064886959
## newPS$hypertension1 8.534260e-01  0.24834586  2.9327484  0.801310734
## newPS$Cardiovascular1 3.941516e+00  0.72491684  21.4308020  0.112377715
## newPS$Diabetes1 7.146334e-01  0.20119690  2.5383142  0.603378706
## newPS$Chronic1 6.201830e-01  0.08241810  4.6667782  0.642681393
```

```
## newPS$Obesity1      5.594587e-01 0.12257384 2.5535144 0.453402824
## newPS$Pregnancy1    3.108936e-01 0.03357240 2.8789974 0.303576497
## newPS$Stroke1       3.405619e-07 0.00000000      Inf 0.988842247
## newPS$Chronic_liver1 8.303388e-15 0.00000000      Inf 0.992376912
## newPS$chronic_renal1 4.937165e-01 0.03437501 7.0910819 0.603659580
## newPS$cancer_HIV1   9.828485e+06 0.00000000      Inf 0.994646285
## newPS$SpO2          1.019676e+00 0.99071445 1.0494837 0.185041681
## newPS$Temp           1.046531e+00 0.89117704 1.2289665 0.579081947
## newPS$Breathing      9.736702e-01 0.91416037 1.0370539 0.406970893
```

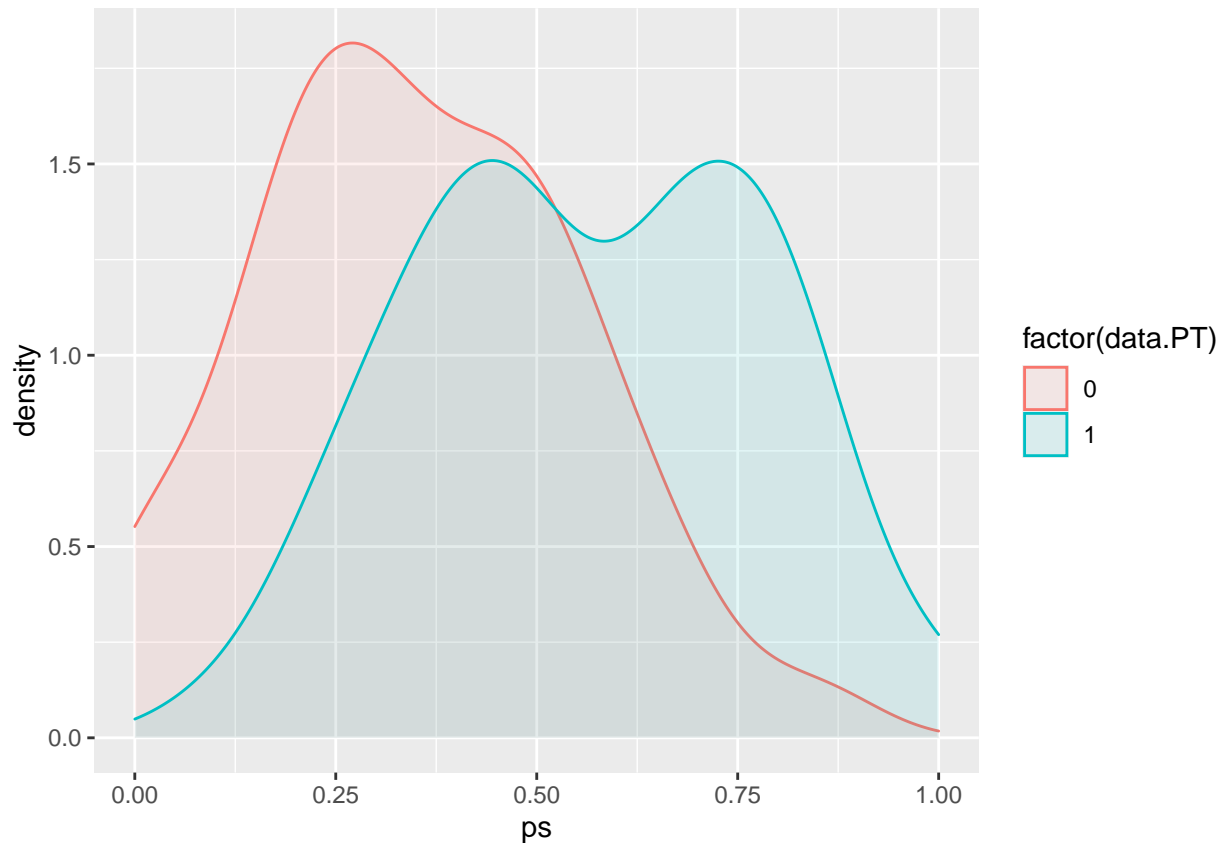
```
newPS$ps = predict(PSlogit1, type="response")
```

```
roc.PSlogit1 = roc(data.PT==1 ~ ps, data = newPS)
```

```
plot(roc.PSlogit1, legacy.axes = T)
```



```
ggplot(data = newPS, aes(x = ps,
  fill = factor(data.PT),
  col = factor(data.PT))) + geom_density(alpha = 0.1)
```



```
# Matching with respect to Propensity Score
listMatch = Match(Tr = (newPS$data.PT==1), X=log(newPS$ps/(1- newPS$ps)), M=1, caliper=0.05, replace =F)

MatchBalance(formul = Formula, data = newPS, match.out=listMatch)
```

```
##
## ***** (V1) newPS$sexM *****
##          Before Matching      After Matching
## mean treatment.....    0.56061          0.5
## mean control.....    0.46914          0.54545
## std mean diff.....    18.29          -8.987
##
## mean raw eQQ diff.....    0.090909          0.045455
## med raw eQQ diff.....    0          0
## max raw eQQ diff.....    1          1
##
## mean eCDF diff.....    0.045735          0.022727
## med eCDF diff.....    0.045735          0.022727
## max eCDF diff.....    0.09147          0.045455
##
## var ratio (Tr/Co).....    0.99189          1.0083
## T-test p-value.....    0.27282          0.59454
##
## ***** (V2) newPS$age *****
##          Before Matching      After Matching
## mean treatment.....    49.758          55.727
```

```

## mean control..... 59.309 56.705
## std mean diff..... -65.73 -7.5615
##
## mean raw eQQ diff..... 9.2424 1.4773
## med raw eQQ diff..... 10 1
## max raw eQQ diff..... 14 7
##
## mean eCDF diff..... 0.15136 0.02531
## med eCDF diff..... 0.14366 0.022727
## max eCDF diff..... 0.30527 0.11364
##
## var ratio (Tr/Co)..... 1.2328 1.1052
## T-test p-value..... 6.0653e-05 0.65352
## KS Bootstrap p-value.. < 2.22e-16 0.88
## KS Naive p-value..... 0.0022763 0.93885
## KS Statistic..... 0.30527 0.11364
##
##
## ***** (V3) newPS$BMI *****
## Before Matching After Matching
## mean treatment..... 25.441 24.595
## mean control..... 23.8 24.657
## std mean diff..... 47.181 -2.1914
##
## mean raw eQQ diff..... 1.9361 1.2239
## med raw eQQ diff..... 1.93 1.04
## max raw eQQ diff..... 7.07 8.29
##
## mean eCDF diff..... 0.11804 0.085664
## med eCDF diff..... 0.10971 0.090909
## max eCDF diff..... 0.27385 0.18182
##
## var ratio (Tr/Co)..... 0.74256 0.44214
## T-test p-value..... 0.0090286 0.93491
## KS Bootstrap p-value.. 0.014 0.408
## KS Naive p-value..... 0.0085529 0.46107
## KS Statistic..... 0.27385 0.18182
##
##
## ***** (V4) newPS$hypertension1 *****
## Before Matching After Matching
## mean treatment..... 0.15152 0.13636
## mean control..... 0.14815 0.15909
## std mean diff..... 0.93192 -6.547
##
## mean raw eQQ diff..... 0.015152 0.022727
## med raw eQQ diff..... 0 0
## max raw eQQ diff..... 1 1
##
## mean eCDF diff..... 0.0016835 0.011364
## med eCDF diff..... 0.0016835 0.011364
## max eCDF diff..... 0.003367 0.022727
##
## var ratio (Tr/Co)..... 1.0216 0.88031

```

```

## T-test p-value.....    0.95505          0.78266
##
##
## ***** (V5) newPS$Cardiovascular1 *****
##               Before Matching      After Matching
## mean treatment.....    0.075758      0.068182
## mean control.....    0.049383      0.068182
## std mean diff.....     9.8917          0
##
## mean raw eQQ diff.....  0.030303          0
## med  raw eQQ diff.....    0          0
## max  raw eQQ diff.....    1          0
##
## mean eCDF diff.....    0.013187          0
## med  eCDF diff.....    0.013187          0
## max  eCDF diff.....    0.026375          0
##
## var ratio (Tr/Co).....  1.4958          1
## T-test p-value.....    0.5191          1
##
##
## ***** (V6) newPS$Diabetes1 *****
##               Before Matching      After Matching
## mean treatment.....    0.12121      0.13636
## mean control.....    0.18519      0.13636
## std mean diff.....   -19.452          0
##
## mean raw eQQ diff.....  0.060606          0
## med  raw eQQ diff.....    0          0
## max  raw eQQ diff.....    1          0
##
## mean eCDF diff.....    0.031987          0
## med  eCDF diff.....    0.031987          0
## max  eCDF diff.....    0.063973          0
##
## var ratio (Tr/Co).....  0.70795          1
## T-test p-value.....    0.28304          1
##
##
## ***** (V7) newPS$Chronic1 *****
##               Before Matching      After Matching
## mean treatment.....    0.045455      0.022727
## mean control.....    0.049383      0.045455
## std mean diff.....   -1.8715      -15.076
##
## mean raw eQQ diff.....    0      0.022727
## med  raw eQQ diff.....    0          0
## max  raw eQQ diff.....    0          1
##
## mean eCDF diff.....    0.0019641      0.011364
## med  eCDF diff.....    0.0019641      0.011364
## max  eCDF diff.....    0.0039282      0.022727
##
## var ratio (Tr/Co).....  0.92689      0.5119

```

```

## T-test p-value.....    0.91184          0.56524
##
##
## ***** (V8) newPS$Obesity1 *****
##               Before Matching          After Matching
## mean treatment.....    0.25758          0.18182
## mean control.....    0.16049          0.15909
## std mean diff.....    22.032           5.8252
##
## mean raw eQQ diff.....    0.10606          0.022727
## med  raw eQQ diff.....    0           0
## max  raw eQQ diff.....    1           1
##
## mean eCDF diff.....    0.048541          0.011364
## med  eCDF diff.....    0.048541          0.011364
## max  eCDF diff.....    0.097082          0.022727
##
## var ratio (Tr/Co).....    1.4233           1.112
## T-test p-value.....    0.15594          0.76424
##
##
## ***** (V9) newPS$Pregnancy1 *****
##               Before Matching          After Matching
## mean treatment.....    0.030303          0.045455
## mean control.....    0.037037          0.045455
## std mean diff.....    -3.8985           0
##
## mean raw eQQ diff.....    0           0
## med  raw eQQ diff.....    0           0
## max  raw eQQ diff.....    0           0
##
## mean eCDF diff.....    0.003367           0
## med  eCDF diff.....    0.003367           0
## max  eCDF diff.....    0.006734           0
##
## var ratio (Tr/Co).....    0.82625           1
## T-test p-value.....    0.82251           1
##
##
## ***** (V10) newPS$Stroke1 *****
##               Before Matching          After Matching
## mean treatment.....    0           0
## mean control.....    0.049383           0
## std mean diff.....    -Inf           0
##
## mean raw eQQ diff.....    0.045455           0
## med  raw eQQ diff.....    0           0
## max  raw eQQ diff.....    1           0
##
## mean eCDF diff.....    0.024691           0
## med  eCDF diff.....    0.024691           0
## max  eCDF diff.....    0.049383           0
##
## var ratio (Tr/Co).....    0           NaN

```



```

## T-test p-value..... 0.044794 1
##
##
## ***** (V11) newPS$Chronic_liver1 *****
## Before Matching After Matching
## mean treatment..... 0 0
## mean control..... 0.012346 0
## std mean diff..... -Inf 0
##
## mean raw eQQ diff..... 0.015152 0
## med raw eQQ diff..... 0 0
## max raw eQQ diff..... 1 0
##
## mean eCDF diff..... 0.0061728 0
## med eCDF diff..... 0.0061728 0
## max eCDF diff..... 0.012346 0
##
## var ratio (Tr/Co)..... 0 NaN
## T-test p-value..... 0.32033 1
##
##
## ***** (V12) newPS$chronic_renal1 *****
## Before Matching After Matching
## mean treatment..... 0.015152 0.022727
## mean control..... 0.037037 0.022727
## std mean diff..... -17.78 0
##
## mean raw eQQ diff..... 0.015152 0
## med raw eQQ diff..... 0 0
## max raw eQQ diff..... 1 0
##
## mean eCDF diff..... 0.010943 0
## med eCDF diff..... 0.010943 0
## max eCDF diff..... 0.021886 0
##
## var ratio (Tr/Co)..... 0.41958 1
## T-test p-value..... 0.40117 1
##
##
## ***** (V13) newPS$cancer_HIV1 *****
## Before Matching After Matching
## mean treatment..... 0.015152 0
## mean control..... 0.012346 0
## std mean diff..... 2.2795 0
##
## mean raw eQQ diff..... 0 0
## med raw eQQ diff..... 0 0
## max raw eQQ diff..... 0 0
##
## mean eCDF diff..... 0.0014029 0
## med eCDF diff..... 0.0014029 0
## max eCDF diff..... 0.0028058 0
##
## var ratio (Tr/Co)..... 1.2273 NaN

```

```

## T-test p-value..... 0.88606 1
##
##
## ***** (V14) newPS$SpO2 *****
## Before Matching After Matching
## mean treatment..... 83.985 82.25
## mean control..... 77.16 81.273
## std mean diff..... 49.288 6.5432
##
## mean raw eQQ diff..... 7.3939 2.3409
## med raw eQQ diff..... 5 2
## max raw eQQ diff..... 25 12
##
## mean eCDF diff..... 0.12022 0.050134
## med eCDF diff..... 0.13805 0.045455
## max eCDF diff..... 0.2138 0.13636
##
## var ratio (Tr/Co)..... 0.66614 1.1691
## T-test p-value..... 0.0080865 0.74119
## KS Bootstrap p-value.. 0.042 0.702
## KS Naive p-value..... 0.07195 0.80792
## KS Statistic..... 0.2138 0.13636
##
##
## ***** (V15) newPS$Temp *****
## Before Matching After Matching
## mean treatment..... 42.174 37.057
## mean control..... 36.716 37.239
## std mean diff..... 13.121 -62.768
##
## mean raw eQQ diff..... 5.6894 0.18182
## med raw eQQ diff..... 0 0
## max raw eQQ diff..... 335 2
##
## mean eCDF diff..... 0.020833 0.054545
## med eCDF diff..... 0.010943 0.022727
## max eCDF diff..... 0.075196 0.13636
##
## var ratio (Tr/Co)..... 99.742 0.26251
## T-test p-value..... 0.29227 0.041853
## KS Bootstrap p-value.. 0.192 0.112
## KS Naive p-value..... 0.98629 0.80792
## KS Statistic..... 0.075196 0.13636
##
##
## ***** (V16) newPS$Breathing *****
## Before Matching After Matching
## mean treatment..... 27.106 28.273
## mean control..... 29.358 27.591
## std mean diff..... -43.25 13.575
##
## mean raw eQQ diff..... 3.6364 3.5455
## med raw eQQ diff..... 3.5 5
## max raw eQQ diff..... 16 10

```

```

##
## mean eCDF diff..... 0.079846      0.15289
## med eCDF diff..... 0.037318      0.20455
## max eCDF diff..... 0.289        0.22727
##
## var ratio (Tr/Co)..... 0.34078      0.43517
## T-test p-value..... 0.05855      0.60218
## KS Bootstrap p-value.. 0.004        0.104
## KS Naive p-value..... 0.0045997    0.20584
## KS Statistic..... 0.289        0.22727
##
##
## ***** (V17) UD *****
##               Before Matching      After Matching
## mean treatment..... 0.71212      0.61364
## mean control..... 0.74074      0.63636
## std mean diff..... -3.2786      -2.7016
##
## mean raw eQQ diff..... 0.090909    0.068182
## med raw eQQ diff..... 0          0
## max raw eQQ diff..... 1          1
##
## mean eCDF diff..... 0.021886    0.013636
## med eCDF diff..... 0.024691    0.022727
## max eCDF diff..... 0.040965    0.022727
##
## var ratio (Tr/Co)..... 0.71252    0.75735
## T-test p-value..... 0.8559      0.91203
## KS Bootstrap p-value.. 0.85        0.998
## KS Naive p-value..... 1          1
## KS Statistic..... 0.040965    0.022727
##
##
## Before Matching Minimum p.value: < 2.22e-16
## Variable Name(s): newPS$age Number(s): 2
##
## After Matching Minimum p.value: 0.041853
## Variable Name(s): newPS$Temp Number(s): 15
psMatch = newPS[unlist(listMatch[c("index.treated", "index.control")]), ]

table1(~ sex + age + BMI + UD + hypertension + Cardiovascular + Diabetes + Chronic + Obesity + Pregnancy

```

	0	1	Overall
	(N=44)	(N=44)	(N=88)
sex			
F	20 (45.5%)	22 (50.0%)	42 (47.7%)
M	24 (54.5%)	22 (50.0%)	46 (52.3%)
age			
Mean (SD)	56.7 (12.3)	55.7 (12.9)	56.2 (12.6)
Median [Min, Max]	60.0 [27.0, 79.0]	58.0 [22.0, 86.0]	59.5 [22.0, 86.0]
BMI			
Mean (SD)	24.7 (4.23)	24.6 (2.81)	24.6 (3.57)
Median [Min, Max]	24.6 [17.6, 41.6]	23.5 [20.2, 33.3]	24.0 [17.6, 41.6]
UD			
Mean (SD)	0.636 (0.967)	0.614 (0.841)	0.625 (0.901)
Median [Min, Max]	0 [0, 4.00]	0 [0, 3.00]	0 [0, 4.00]
hypertension			
0	37 (84.1%)	38 (86.4%)	75 (85.2%)
1	7 (15.9%)	6 (13.6%)	13 (14.8%)
Cardiovascular			
0	41 (93.2%)	41 (93.2%)	82 (93.2%)
1	3 (6.8%)	3 (6.8%)	6 (6.8%)
Diabetes			
0	38 (86.4%)	38 (86.4%)	76 (86.4%)
1	6 (13.6%)	6 (13.6%)	12 (13.6%)
Chronic			
0	42 (95.5%)	43 (97.7%)	85 (96.6%)
1	2 (4.5%)	1 (2.3%)	3 (3.4%)
Obesity			
0	37 (84.1%)	36 (81.8%)	73 (83.0%)
1	7 (15.9%)	8 (18.2%)	15 (17.0%)
Pregnancy			
0	42 (95.5%)	42 (95.5%)	84 (95.5%)
1	2 (4.5%)	2 (4.5%)	4 (4.5%)
Stroke			
0	44 (100%)	44 (100%)	88 (100%)
1	0 (0%)	0 (0%)	0 (0%)
Chronic_liver			
0	44 (100%)	44 (100%)	88 (100%)
1	0 (0%)	0 (0%)	0 (0%)
chronic_renal			
0	43 (97.7%)	43 (97.7%)	86 (97.7%)
1	1 (2.3%)	1 (2.3%)	2 (2.3%)
cancer_HIV			
0	44 (100%)	44 (100%)	88 (100%)
1	0 (0%)	0 (0%)	0 (0%)
SpO2			
Mean (SD)	81.3 (13.8)	82.3 (14.9)	81.8 (14.3)
Median [Min, Max]	85.0 [40.0, 99.0]	86.5 [37.0, 98.0]	85.5 [37.0, 99.0]
Temp			
Mean (SD)	37.2 (0.565)	37.1 (0.290)	37.1 (0.456)
Median [Min, Max]	37.0 [37.0, 40.0]	37.0 [36.0, 38.0]	37.0 [36.0, 40.0]
Breathing		12	
Mean (SD)	27.6 (7.61)	28.3 (5.02)	27.9 (6.42)
Median [Min, Max]	25.0 [18.0, 40.0]	30.0 [18.0, 40.0]	28.0 [18.0, 40.0]

Bayesian Model Averaging and Logistics Regression

```
y = psMatch[,("death")]
x = psMatch[,c("data.PT", "sex", "age", "BMI", "hypertension", "Cardiovascular", "Diabetes", "Chronic",
bma = bicreg(x, y, strict=FALSE, OR=20)
```

```
## Reordering variables and trying again:
```

```
summary(bma)
```

```
##
## Call:
## bicreg(x = x, y = y, strict = FALSE, OR = 20)
##
##
## 115 models were selected
## Best 5 models (cumulative posterior probability = 0.2282 ):
##
##           p!=0    EV      SD      model 1      model 2
## Intercept    100.0  4.7335237  4.226046    7.634092    0.867994
## data.PT1     100.0 -0.3001817  0.077524   -0.313832   -0.278359
## sexM          4.1  0.0022143  0.019062      .          .
## age          100.0  0.0127354  0.003099    0.011888    0.012347
## BMI           5.1 -0.0004390  0.003187      .          .
## hypertension1 32.9 -0.0777786  0.130182      .          .
## Cardiovascular1 9.1 -0.0192951  0.082099      .          .
## Diabetes1     7.3  0.0111800  0.054807      .          .
## Chronic1     10.3 -0.0315189  0.118764      .          .
## Obesity1      5.2 -0.0041962  0.031003      .          .
## Pregnancy1    5.2  0.0091133  0.060300      .          .
## Stroke1       2.8 -0.0011352  0.015966      .          .
## Chronic_liver1 2.8 -0.0011352  0.015966      .          .
## chronic_renal1 5.8 -0.0145650  0.088304      .          .
## cancer_HIV1   2.8 -0.0011352  0.015966      .          .
## SpO2          79.1 -0.0123740  0.057240   -0.006008   -0.007362
## Temp          56.0 -0.1029317  0.356302   -0.183731      .
## Breathing      9.5 -0.0007439  0.003016      .          .
## UD            47.4 -0.0454420  0.577237   -0.108293   -0.095293
##
## nVar          5          4
## r2            0.413      0.379
## BIC           -24.492097 -24.074101
## post prob      0.063      0.051
##
##           model 3      model 4      model 5
## Intercept    8.810379    0.780646    7.200022
## data.PT1     -0.327398   -0.280739   -0.314658
## sexM          .          .          .
## age          0.012681    0.013200    0.012856
## BMI           .          .          .
## hypertension1 .          -0.228881   -0.253751
## Cardiovascular1 .          .          .
## Diabetes1     .          .          .
## Chronic1      .          .          .
## Obesity1      .          .          .
## Pregnancy1    .          .          .
```

```

## Stroke1          .          .          .
## Chronic_liver1   .          .          .
## chronic_renal1   .          .          .
## cancer_HIV1      .          .          .
## SpO2             .          -0.007181  -0.005879
## Temp             -0.229532    .          -0.174598
## Breathing        .          .          .
## UD               -0.114537    .          .
##
## nVar              4          4          5
## r2                0.376      0.375      0.405
## BIC               -23.572144  -23.435485  -23.370437
## post prob         0.040      0.037      0.036
PSlogit5 <- glm(death ~ age, family=binomial, data = newPS)
logistic.display(PSlogit5)

##
## Logistic regression predicting death
##
##                OR(95%CI)        P(Wald's test) P(LR-test)
## age (cont. var.) 1.1 (1.06,1.14) < 0.001      < 0.001
##
## Log-likelihood = -66.2458
## No. of observations = 147
## AIC value = 136.4917
PSlogit6 <- glm(death ~ data.PT, family=binomial, data = newPS)
logistic.display(PSlogit6)

##
## Logistic regression predicting death
##
##                OR(95%CI)        P(Wald's test) P(LR-test)
## data.PT: 1 vs 0 0.13 (0.06,0.31) < 0.001      < 0.001
##
## Log-likelihood = -73.9728
## No. of observations = 147
## AIC value = 151.9456
PSlogit7 <- glm(death ~ sex, family=binomial, data = newPS)
logistic.display(PSlogit7)

##
## Logistic regression predicting death
##
##                OR(95%CI)        P(Wald's test) P(LR-test)
## sex: M vs F 0.86 (0.42,1.78) 0.691      0.691
##
## Log-likelihood = -86.9334
## No. of observations = 147
## AIC value = 177.8667
PSlogit8 <- glm(death ~ SpO2, family=binomial, data = newPS)
logistic.display(PSlogit8)

##

```

```

## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## SpO2 (cont. var.) 0.91 (0.87,0.96) < 0.001      < 0.001
##
## Log-likelihood = -73.8845
## No. of observations = 147
## AIC value = 151.7691
PSlogit9 <- glm(death ~ UD, family=binomial, data = newPS)
logistic.display(PSlogit9)

##
## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## UD (cont. var.) 0.78 (0.54,1.12) 0.174          0.178
##
## Log-likelihood = -86.1051
## No. of observations = 147
## AIC value = 176.2101
PSlogit10 <- glm(death ~ cancer_HIV, family=binomial, data = newPS)
logistic.display(PSlogit10)

##
## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## cancer_HIV: 1 vs 0 2269906.99 (0,Inf) 0.989          0.251
##
## Log-likelihood = -86.3533
## No. of observations = 147
## AIC value = 176.7066
PSlogit11 <- glm(death ~ Chronic, family=binomial, data = newPS)
logistic.display(PSlogit11)

##
## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## Chronic: 1 vs 0 0.27 (0.06,1.26) 0.096          0.096
##
## Log-likelihood = -85.6292
## No. of observations = 147
## AIC value = 175.2585
PSlogit12 <- glm(death ~ BMI, family=binomial, data = newPS)
logistic.display(PSlogit12)

##
## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## BMI (cont. var.) 0.92 (0.84,1.01) 0.072          0.07
##

```

```
## Log-likelihood = -85.3688
## No. of observations = 147
## AIC value = 174.7377
PSlogit14 <- glm(death ~ Temp, family=binomial, data = newPS)
logistic.display(PSlogit14)

##
## Logistic regression predicting death
##
##              OR(95%CI)      P(Wald's test) P(LR-test)
## Temp (cont. var.) 1.09 (0.92,1.3)  0.335      0.12
##
## Log-likelihood = -85.8008
## No. of observations = 147
## AIC value = 175.6017
PSlogit15 <- glm(death ~ Breathing, family=binomial, data = newPS)
logistic.display(PSlogit15)

##
## Logistic regression predicting death
##
##              OR(95%CI)      P(Wald's test) P(LR-test)
## Breathing (cont. var.) 1.05 (1,1.11)  0.046      0.04
##
## Log-likelihood = -84.9059
## No. of observations = 147
## AIC value = 173.8118
PSlogit16 <- glm(death ~ hypertension, family=binomial, data = newPS)
logistic.display(PSlogit16)

##
## Logistic regression predicting death
##
##              OR(95%CI)      P(Wald's test) P(LR-test)
## hypertension: 1 vs 0 0.5 (0.19,1.27)  0.145      0.152
##
## Log-likelihood = -85.9875
## No. of observations = 147
## AIC value = 175.975
PSlogit17 <- glm(death ~ Cardiovascular, family=binomial, data = newPS)
logistic.display(PSlogit17)

##
## Logistic regression predicting death
##
##              OR(95%CI)      P(Wald's test) P(LR-test)
## Cardiovascular: 1 vs 0 0.46 (0.12,1.8)  0.263      0.273
##
## Log-likelihood = -86.4125
## No. of observations = 147
## AIC value = 176.8251
```



```
PSlogit18 <- glm(death ~ Diabetes, family=binomial, data = newPS)
logistic.display(PSlogit18)
```

```
##
## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## Diabetes: 1 vs 0 2.02 (0.64,6.35)  0.229          0.203
##
## Log-likelihood = -86.2038
## No. of observations = 147
## AIC value = 176.4076
```

```
PSlogit19 <- glm(death ~ Obesity, family=binomial, data = newPS)
logistic.display(PSlogit19)
```

```
##
## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## Obesity: 1 vs 0 0.49 (0.21,1.15)  0.101          0.106
##
## Log-likelihood = -85.7075
## No. of observations = 147
## AIC value = 175.415
```

```
PSlogit20 <- glm(death ~ Pregnancy, family=binomial, data = newPS)
logistic.display(PSlogit20)
```

```
##
## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## Pregnancy: 1 vs 0 0.24 (0.04,1.51)  0.13          0.127
##
## Log-likelihood = -85.8476
## No. of observations = 147
## AIC value = 175.6951
```

```
PSlogit21 <- glm(death ~ Stroke, family=binomial, data = newPS)
logistic.display(PSlogit21)
```

```
##
## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## Stroke: 1 vs 0 6291233.26 (0,Inf)  0.99          0.103
##
## Log-likelihood = -85.6831
## No. of observations = 147
## AIC value = 175.3662
```

```
PSlogit22 <- glm(death ~ Chronic_liver, family=binomial, data = newPS)
logistic.display(PSlogit22)
```

```
##
## Logistic regression predicting death
```

```
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## Chronic_liver: 1 vs 0 827098.85 (0,Inf)  0.988      0.418
##
## Log-likelihood = -86.6843
## No. of observations = 147
## AIC value = 177.3686
PSlogit23 <- glm(death ~ chronic_renal, family=binomial, data = newPS)
logistic.display(PSlogit23)

##
## Logistic regression predicting death
##
##              OR(95%CI)          P(Wald's test) P(LR-test)
## chronic_renal: 1 vs 0 1.17 (0.12,11.53)  0.896      0.895
##
## Log-likelihood = -87.0039
## No. of observations = 147
## AIC value = 178.0077
modell1 <- logistf(death ~ Chronic_liver, data = newPS)
summary(modell1)

## logistf(formula = death ~ Chronic_liver, data = newPS)
##
## Model fitted by Penalized ML
## Coefficients:
##              coef se(coef) lower 0.95 upper 0.95      Chisq
## (Intercept)  0.9330175 0.1838614  0.5822457   1.302566 28.8186561
## Chronic_liver1 0.1655948 2.3167085 -2.7859709   5.156952  0.0104251
##              p method
## (Intercept)  7.948181e-08      2
## Chronic_liver1 9.186746e-01      2
##
## Method: 1-Wald, 2-Profile penalized log-likelihood, 3-None
##
## Likelihood ratio test=0.0104251 on 1 df, p=0.9186746, n=147
## Wald test = 0.005109171 on 1 df, p = 0.943017
exp(modell1$coef[2])

## Chronic_liver1
##      1.180095
model <- logistf(death ~ cancer_HIV, data = newPS)
summary(model)

## logistf(formula = death ~ cancer_HIV, data = newPS)
##
## Model fitted by Penalized ML
## Coefficients:
##              coef se(coef) lower 0.95 upper 0.95      Chisq      p
## (Intercept)  0.9234936 0.1841139  0.5721758   1.293473 28.0984956 1.152954e-07
## cancer_HIV1  0.6859460 1.9062797 -1.8504020   5.620961  0.2225323 6.371172e-01
##              method
## (Intercept)      2
```

```
## cancer_HIV1      2
##
## Method: 1-Wald, 2-Profile penalized log-likelihood, 3-None
##
## Likelihood ratio test=0.2225323 on 1 df, p=0.6371172, n=147
## Wald test = 0.1294812 on 1 df, p = 0.7189706
exp(model$coef[2])

## cancer_HIV1
##      1.985649
```

Acknowledgement

We would like to acknowledge Dr. Nguyen Thi Cam Binh and Ms. Tran Thi Thuan Duc for their contribution to this formal analysis of the dataset.