

# 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$hypertension + newPS$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 + UD
```

```
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)
```

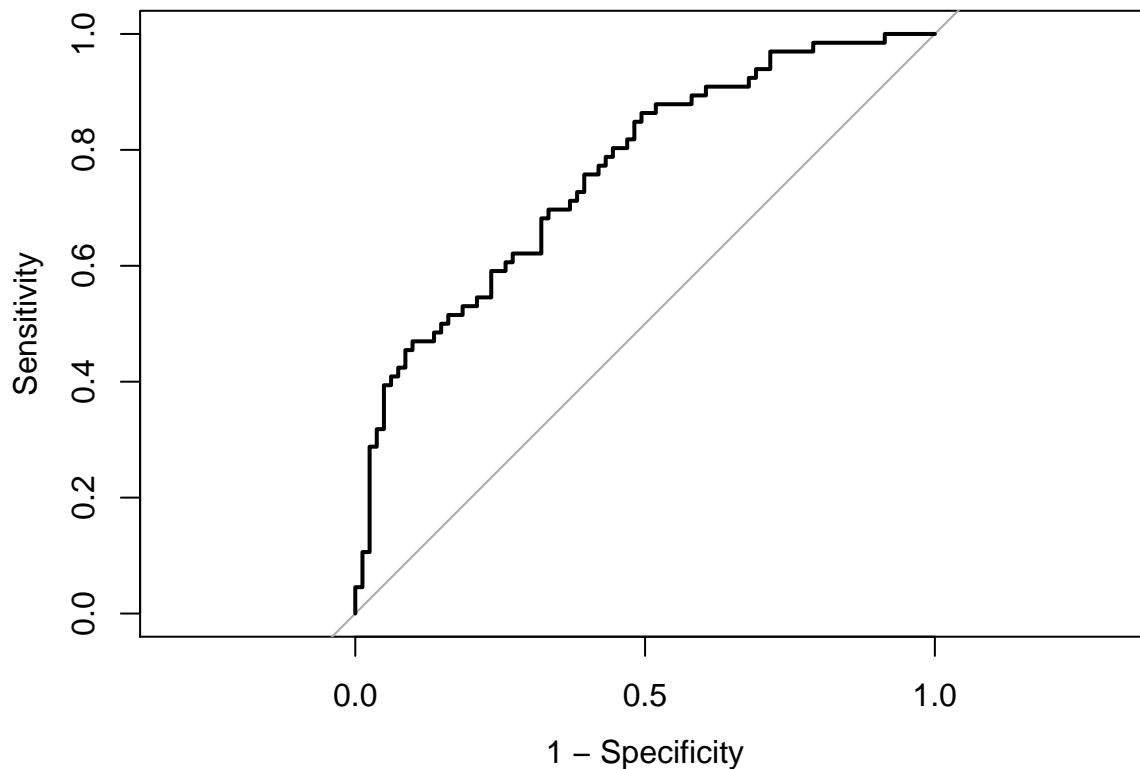
```
##
```

```
##               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
```

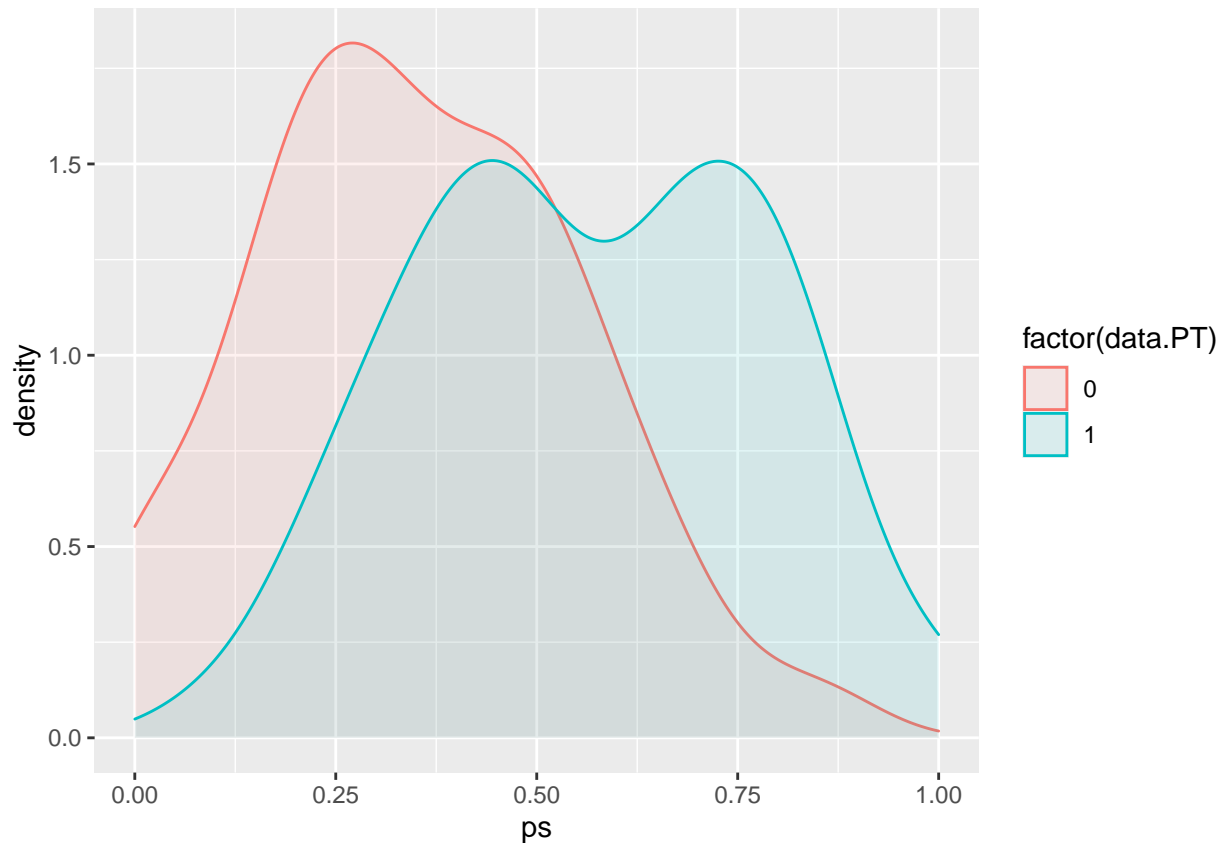
```
newPS$ps = predict(PSlogit1, type="response")
```

```
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 =FALSE, ties=TRUE, version="fast")

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      57.114
## std mean diff..... -65.73      -10.727
##
## mean raw eQQ diff..... 9.2424      1.7955
## med raw eQQ diff..... 10      1.5
## max raw eQQ diff..... 14      7
##
## mean eCDF diff..... 0.15136      0.032025
## med eCDF diff..... 0.14366      0.022727
## max eCDF diff..... 0.30527      0.11364
##
## var ratio (Tr/Co)..... 1.2328      1.1357
## T-test p-value..... 6.0653e-05      0.52347
## KS Bootstrap p-value.. < 2.22e-16      0.882
## KS Naive p-value..... 0.0022763      0.93885
## KS Statistic..... 0.30527      0.11364
##
##
## ***** (V3) newPS$BMI *****
##               Before Matching      After Matching
## mean treatment..... 25.441      24.595
## mean control..... 23.8      24.555
## std mean diff..... 47.181      1.407
##
## mean raw eQQ diff..... 1.9361      1.2423
## med raw eQQ diff..... 1.93      1.025
## max raw eQQ diff..... 7.07      8.29
##
## mean eCDF diff..... 0.11804      0.084872
## med eCDF diff..... 0.10971      0.079545
## max eCDF diff..... 0.27385      0.20455
##
## var ratio (Tr/Co)..... 0.74256      0.4336
## T-test p-value..... 0.0090286      0.95297
## KS Bootstrap p-value.. 0.008      0.256
## KS Naive p-value..... 0.0085529      0.31609
## KS Statistic..... 0.27385      0.20455
##
##
## ***** (V4) newPS$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$Obesity1 *****
##                               Before Matching      After Matching
## mean treatment.....        0.25758          0.18182
## mean control.....          0.16049          0.15909
## std mean diff.....         22.032           5.8252
##
## mean raw eQQ diff.....      0.10606          0.022727
## med  raw eQQ diff.....        0              0
## max  raw eQQ diff.....        1              1
##
## mean eCDF diff.....         0.048541         0.011364
## med  eCDF diff.....         0.048541         0.011364
## max  eCDF diff.....         0.097082         0.022727
##
## var ratio (Tr/Co).....        1.4233          1.112
## T-test p-value.....         0.15594          0.70686
##
##
## ***** (V9) newPS$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$SpO2 *****
##                               Before Matching      After Matching
## mean treatment.....      83.985      82.25
## mean control.....      77.16      81.795
## std mean diff.....      49.288      3.0433
##
## mean raw eQQ diff.....      7.3939      1.9545
## med raw eQQ diff.....      5      1
## max raw eQQ diff.....      25      12
##
## mean eCDF diff.....      0.12022      0.038567
## med eCDF diff.....      0.13805      0.022727
## max eCDF diff.....      0.2138      0.11364
##
## var ratio (Tr/Co).....      0.66614      1.1564
## T-test p-value.....      0.0080865      0.88061
## KS Bootstrap p-value..      0.04      0.83
## KS Naive p-value.....      0.07195      0.93885
## KS Statistic.....      0.2138      0.11364
##
##
## ***** (V15) newPS$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      0.059091
## med eCDF diff.....      0.010943      0.022727
## max eCDF diff.....      0.075196      0.15909
##
## var ratio (Tr/Co).....      99.742      0.22916
## T-test p-value.....      0.29227      0.070071
## KS Bootstrap p-value..      0.236      0.086
## KS Naive p-value.....      0.98629      0.63356
## KS Statistic.....      0.075196      0.15909
##
##
## ***** (V16) newPS$Breathing *****
##                               Before Matching      After Matching
## mean treatment.....      27.106      28.273
## mean control.....      29.358      26.727
## std mean diff.....      -43.25      30.77
##
## mean raw eQQ diff.....      3.6364      3.5909
## med raw eQQ diff.....      3.5      5

```

```

## max raw eQQ diff.....      16          8
##
## mean eCDF diff.....      0.079846      0.175
## med eCDF diff.....      0.037318      0.25
## max eCDF diff.....      0.289      0.27273
##
## var ratio (Tr/Co).....      0.34078      0.46903
## T-test p-value.....      0.05855      0.21465
## KS Bootstrap p-value..      0.002      0.028
## KS Naive p-value.....      0.0045997      0.075802
## KS Statistic.....      0.289      0.27273
##
##
## ***** (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      0.90607
## KS Bootstrap p-value..      0.872      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$age Number(s): 2
##
## After Matching Minimum p.value: 0.028
## Variable Name(s): newPS$Breathing Number(s): 16
psMatch = newPS[unlist(listMatch[c("index.treated", "index.control")]), ]

table1(~ sex + age + BMI + UD + hypertension + Cardiovascular + Diabetes + Chronic +
  Obesity + Pregnancy + Stroke + Chronic_liver + chronic_renal + cancer_HIV +
  SpO2 + Temp + Breathing + UD|data.PT, data = psMatch)

```

	0	1	Overall
	(N=44)	(N=44)	(N=88)
<b>sex</b>			
F	20 (45.5%)	22 (50.0%)	42 (47.7%)
M	24 (54.5%)	22 (50.0%)	46 (52.3%)
<b>age</b>			
Mean (SD)	57.1 (12.1)	55.7 (12.9)	56.4 (12.5)
Median [Min, Max]	60.0 [27.0, 79.0]	58.0 [22.0, 86.0]	59.5 [22.0, 86.0]
<b>BMI</b>			
Mean (SD)	24.6 (4.27)	24.6 (2.81)	24.6 (3.59)
Median [Min, Max]	24.3 [17.6, 41.6]	23.5 [20.2, 33.3]	23.9 [17.6, 41.6]
<b>UD</b>			
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]
<b>hypertension</b>			
0	37 (84.1%)	38 (86.4%)	75 (85.2%)
1	7 (15.9%)	6 (13.6%)	13 (14.8%)
<b>Cardiovascular</b>			
0	41 (93.2%)	41 (93.2%)	82 (93.2%)
1	3 (6.8%)	3 (6.8%)	6 (6.8%)
<b>Diabetes</b>			
0	38 (86.4%)	38 (86.4%)	76 (86.4%)
1	6 (13.6%)	6 (13.6%)	12 (13.6%)
<b>Chronic</b>			
0	42 (95.5%)	43 (97.7%)	85 (96.6%)
1	2 (4.5%)	1 (2.3%)	3 (3.4%)
<b>Obesity</b>			
0	37 (84.1%)	36 (81.8%)	73 (83.0%)
1	7 (15.9%)	8 (18.2%)	15 (17.0%)
<b>Pregnancy</b>			
0	42 (95.5%)	42 (95.5%)	84 (95.5%)
1	2 (4.5%)	2 (4.5%)	4 (4.5%)
<b>Stroke</b>			
0	44 (100%)	44 (100%)	88 (100%)
1	0 (0%)	0 (0%)	0 (0%)
<b>Chronic_liver</b>			
0	44 (100%)	44 (100%)	88 (100%)
1	0 (0%)	0 (0%)	0 (0%)
<b>chronic_renal</b>			
0	43 (97.7%)	43 (97.7%)	86 (97.7%)
1	1 (2.3%)	1 (2.3%)	2 (2.3%)
<b>cancer_HIV</b>			
0	44 (100%)	44 (100%)	88 (100%)
1	0 (0%)	0 (0%)	0 (0%)
<b>SpO2</b>			
Mean (SD)	81.8 (13.9)	82.3 (14.9)	82.0 (14.3)
Median [Min, Max]	85.0 [40.0, 99.0]	86.5 [37.0, 98.0]	86.0 [37.0, 99.0]
<b>Temp</b>			
Mean (SD)	37.2 (0.605)	37.1 (0.290)	37.1 (0.480)
Median [Min, Max]	37.0 [36.0, 40.0]	37.0 [36.0, 38.0]	37.0 [36.0, 40.0]
<b>Breathing</b>		12	
Mean (SD)	26.7 (7.33)	28.3 (5.02)	27.5 (6.30)
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", "Obesity", "Pregnancy", "Stroke", "Chronic_liver",
               "chronic_renal", "cancer_HIV", "SpO2", "Temp", "Breathing", "UD")]
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)
##
##
## 123 models were selected
## Best 5 models (cumulative posterior probability = 0.218 ):
##
##           p!=0    EV      SD      model 1      model 2
## Intercept      100.0  3.7324594  3.718257    0.849964    6.836623
## data.PT1        100.0 -0.2910622  0.076791   -0.276775   -0.307719
## sexM             4.1  0.0021996  0.019091      .          .
## age             100.0  0.0131483  0.003117    0.012623    0.012245
## BMI              4.8 -0.0003957  0.003040      .          .
## hypertension1    33.0 -0.0764920  0.128115      .          .
## Cardiovascular1  10.6 -0.0237023  0.089874      .          .
## Diabetes1         7.1  0.0105664  0.053357      .          .
## Chronic1         11.9 -0.0375175  0.128951      .          .
## Obesity1          4.6 -0.0034539  0.028536      .          .
## Pregnancy1        5.7  0.0104486  0.064305      .          .
## Stroke1           2.6 -0.0008233  0.012591      .          .
## Chronic_liver1    2.6 -0.0008233  0.012591      .          .
## chronic_renal1     6.0 -0.0151643  0.089727      .          .
## cancer_HIV1        2.6 -0.0008233  0.012591      .          .
## SpO2             82.6 -0.0115054  0.056163   -0.007351   -0.006094
## Temp             47.4 -0.0773902  0.316723      .          -0.162753
## Breathing        12.2 -0.0010461  0.003606      .          .
## UD              44.1 -0.0411977  0.489897   -0.095156   -0.106463
##
## nVar              4          5
## r2                0.383      0.412
## BIC               -24.551845 -24.388718
## post prob         0.057      0.053
##
##           model 3      model 4      model 5
## Intercept      0.756628    0.794053    6.462145
## data.PT1       -0.278682   -0.274472   -0.308368
## sexM            .          .          .
## age            0.013519    0.012691    0.013245
## BMI            .          .          .
## hypertension1  -0.229244      .          -0.251304
## Cardiovascular1 .          .          .
## Diabetes1       .          .          .
## Chronic1        .          .          .
```

```
## Obesity1          .          .          .
## Pregnancy1        .          .          .
## Stroke1           .          .          .
## Chronic_liver1    .          .          .
## chronic_renal1    .          .          .
## cancer_HIV1       .          .          .
## SpO2              -0.007130   -0.007455   -0.005910
## Temp              .          .          -0.155381
## Breathing         .          .          .
## UD                .          .          .
##
## nVar               4          3          5
## r2                 0.379      0.343      0.406
## BIC                -23.952237 -23.507476 -23.398564
## post prob          0.042      0.034      0.032
```

```
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)
## Sp02 (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.