

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

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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$diabetes + newPS$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$diabetes + newPS$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)
```

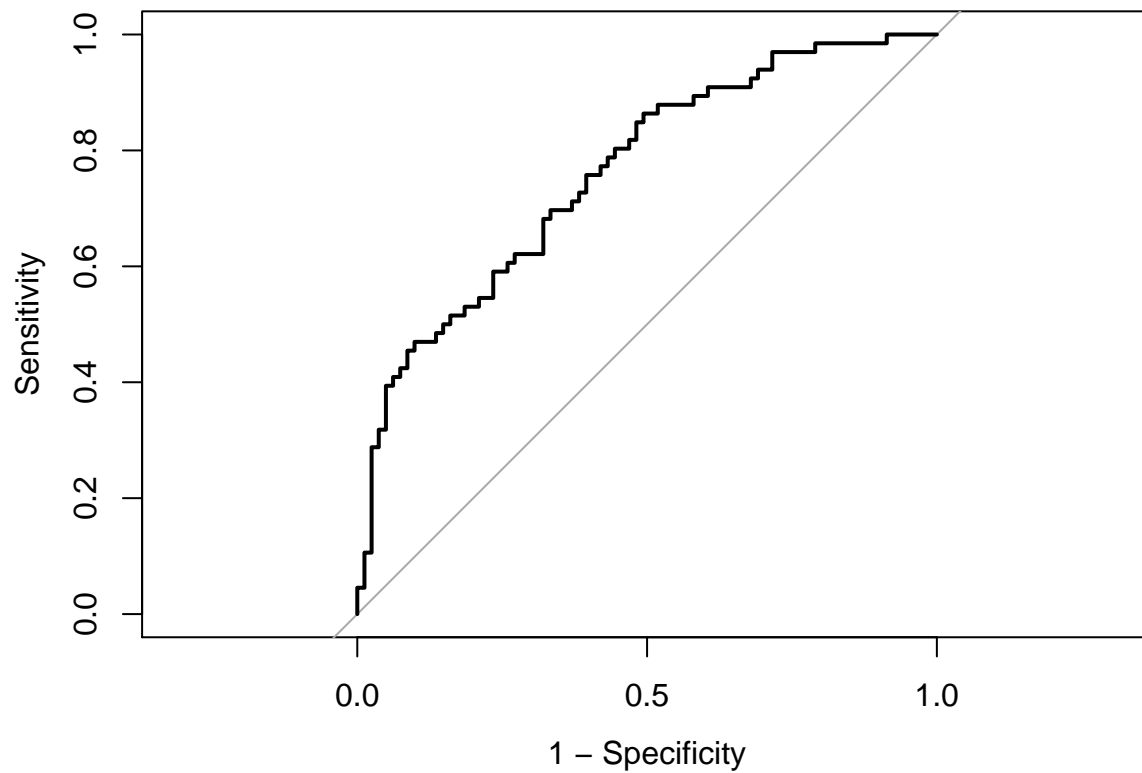
```
##
##              OR  lower95ci  upper95ci  Pr(>|Z|)
## newPS$sexM      1.584744e+00  0.70776338  3.5483815  0.262916883
## newPS$age       9.589107e-01  0.92889817  0.9898929  0.009706883
## newPS$BMI       1.172001e+00  0.99025289  1.3871068  0.064886959
## newPS$hypertension1 8.534260e-01  0.24834586  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
```

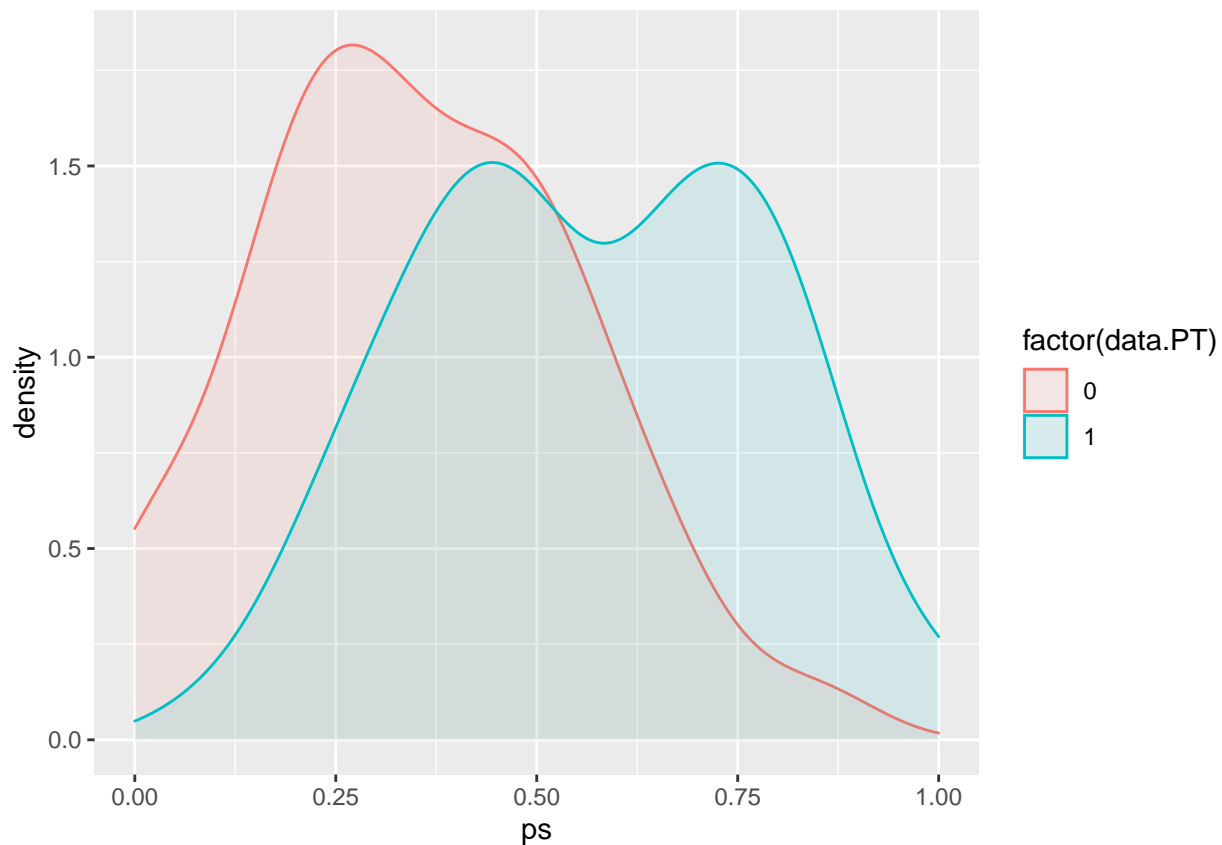
```
newPS$ps = predict(PSlogit1, type="response")
```

```
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$sexM *****
##           Before Matching      After Matching
## mean treatment.....    0.56061          0.5
## mean control.....    0.46914          0.56818
## std mean diff.....    18.29          -13.481
##
## mean raw eQQ diff.....    0.090909          0.068182
## med  raw eQQ diff.....    0          0
## max  raw eQQ diff.....    1          1
##
## mean eCDF diff.....    0.045735          0.034091
## med  eCDF diff.....    0.045735          0.034091
## max  eCDF diff.....    0.09147          0.068182
##
## var ratio (Tr/Co).....    0.99189          1.0189
## T-test p-value.....    0.27282          0.40629
##
## ***** (V2) newPS$age *****
##           Before Matching      After Matching
## mean treatment.....    49.758          55.727
```

```

## mean control..... 59.309 56.432
## std mean diff..... -65.73 -5.4513
##
## mean raw eQQ diff..... 9.2424 1.2955
## med raw eQQ diff..... 10 1
## max raw eQQ diff..... 14 7
##
## mean eCDF diff..... 0.15136 0.021178
## med eCDF diff..... 0.14366 0.022727
## max eCDF diff..... 0.30527 0.090909
##
## var ratio (Tr/Co)..... 1.2328 1.1257
## T-test p-value..... 6.0653e-05 0.74754
## KS Bootstrap p-value.. 0.002 0.974
## KS Naive p-value..... 0.0022763 0.99336
## KS Statistic..... 0.30527 0.090909
##
##
## ***** (V3) newPS$BMI *****
## Before Matching After Matching
## mean treatment..... 25.441 24.595
## mean control..... 23.8 24.515
## std mean diff..... 47.181 2.8383
##
## mean raw eQQ diff..... 1.9361 1.2407
## med raw eQQ diff..... 1.93 1.025
## max raw eQQ diff..... 7.07 8.29
##
## mean eCDF diff..... 0.11804 0.084615
## med eCDF diff..... 0.10971 0.068182
## max eCDF diff..... 0.27385 0.20455
##
## var ratio (Tr/Co)..... 0.74256 0.43197
## T-test p-value..... 0.0090286 0.91519
## KS Bootstrap p-value.. 0.004 0.304
## KS Naive p-value..... 0.0085529 0.31609
## KS Statistic..... 0.27385 0.20455
##
##
## ***** (V4) newPS$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        0.11364
## std mean diff.....   -19.452         6.547
##
## mean raw eQQ diff.....    0.060606        0.022727
## med  raw eQQ diff.....    0          0
## max  raw eQQ diff.....    1          1
##
## mean eCDF diff.....    0.031987        0.011364
## med  eCDF diff.....    0.031987        0.011364
## max  eCDF diff.....    0.063973        0.022727
##
## var ratio (Tr/Co).....    0.70795         1.1692
## T-test p-value.....    0.28304        0.74019
##
##
## ***** (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$Obesity1 *****
##               Before Matching      After Matching
## mean treatment.....    0.25758      0.18182
## mean control.....    0.16049      0.15909
## std mean diff.....    22.032       5.8252
##
## mean raw eQQ diff.....    0.10606      0.022727
## med  raw eQQ diff.....    0          0
## max  raw eQQ diff.....    1          1
##
## mean eCDF diff.....    0.048541     0.011364
## med  eCDF diff.....    0.048541     0.011364
## max  eCDF diff.....    0.097082     0.022727
##
## var ratio (Tr/Co).....    1.4233      1.112
## T-test p-value.....    0.15594      0.74019
##
##
## ***** (V9) newPS$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$SpO2 *****
## Before Matching After Matching
## mean treatment..... 83.985 82.25
## mean control..... 77.16 80.659
## std mean diff..... 49.288 10.652
##
## mean raw eQQ diff..... 7.3939 2.4091
## med raw eQQ diff..... 5 2
## max raw eQQ diff..... 25 9
##
## mean eCDF diff..... 0.12022 0.051471
## med eCDF diff..... 0.13805 0.045455
## max eCDF diff..... 0.2138 0.13636
##
## var ratio (Tr/Co)..... 0.66614 1.0185
## T-test p-value..... 0.0080865 0.59568
## KS Bootstrap p-value.. 0.034 0.678
## KS Naive p-value..... 0.07195 0.80792
## KS Statistic..... 0.2138 0.13636
##
##
## ***** (V15) newPS$Temp *****
## Before Matching After Matching
## mean treatment..... 42.174 37.057
## mean control..... 36.716 37.216
## std mean diff..... 13.121 -54.922
##
## mean raw eQQ diff..... 5.6894 0.15909
## med raw eQQ diff..... 0 0
## max raw eQQ diff..... 335 2
##
## mean eCDF diff..... 0.020833 0.05
## med eCDF diff..... 0.010943 0.022727
## max eCDF diff..... 0.075196 0.13636
##
## var ratio (Tr/Co)..... 99.742 0.23738
## T-test p-value..... 0.29227 0.086167
## KS Bootstrap p-value.. 0.23 0.134
## 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 27.364
## std mean diff..... -43.25 18.1
##
## mean raw eQQ diff..... 3.6364 3.3182
## med raw eQQ diff..... 3.5 5
## max raw eQQ diff..... 16 8

```

```

##
## mean eCDF diff..... 0.079846      0.14669
## med eCDF diff..... 0.037318      0.20455
## max eCDF diff..... 0.289      0.22727
##
## var ratio (Tr/Co)..... 0.34078      0.46313
## T-test p-value..... 0.05855      0.4811
## KS Bootstrap p-value.. < 2.22e-16      0.094
## 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      0.61364
## std mean diff..... -3.2786      0
##
## mean raw eQQ diff..... 0.090909      0.090909
## med raw eQQ diff..... 0      0
## max raw eQQ diff..... 1      1
##
## mean eCDF diff..... 0.021886      0.018182
## med eCDF diff..... 0.024691      0.022727
## max eCDF diff..... 0.040965      0.045455
##
## var ratio (Tr/Co)..... 0.71252      0.75267
## T-test p-value..... 0.8559      1
## KS Bootstrap p-value.. 0.864      0.94
## KS Naive p-value..... 1      1
## KS Statistic..... 0.040965      0.045455
##
##
## Before Matching Minimum p.value: < 2.22e-16
## Variable Name(s): newPS$Breathing Number(s): 16
##
## After Matching Minimum p.value: 0.086167
## Variable Name(s): newPS$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	19 (43.2%)	22 (50.0%)	41 (46.6%)
M	25 (56.8%)	22 (50.0%)	47 (53.4%)
age			
Mean (SD)	56.4 (12.2)	55.7 (12.9)	56.1 (12.5)
Median [Min, Max]	60.0 [27.0, 79.0]	58.0 [22.0, 86.0]	58.5 [22.0, 86.0]
BMI			
Mean (SD)	24.5 (4.28)	24.6 (2.81)	24.6 (3.60)
Median [Min, Max]	24.0 [17.6, 41.6]	23.5 [20.2, 33.3]	23.9 [17.6, 41.6]
UD			
Mean (SD)	0.614 (0.970)	0.614 (0.841)	0.614 (0.903)
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	39 (88.6%)	38 (86.4%)	77 (87.5%)
1	5 (11.4%)	6 (13.6%)	11 (12.5%)
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)	80.7 (14.8)	82.3 (14.9)	81.5 (14.8)
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 (0.595)	37.1 (0.290)	37.1 (0.472)
Median [Min, Max]	37.0 [36.0, 40.0]	37.0 [36.0, 38.0]	37.0 [36.0, 40.0]
Breathing			
Mean (SD)	27.4 (7.38)	28.3 (5.02)	27.8 (6.29)
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)
##
##
## 124 models were selected
## Best 5 models (cumulative posterior probability = 0.2173 ):
##
##           p!=0    EV      SD      model 1      model 2
## Intercept      100.0  4.3645538  3.982901    7.111997    0.823146
## data.PT1       100.0 -0.2964618  0.077183   -0.305185   -0.275759
## sexM           4.5    0.0025827  0.020696      .           .
## age           100.0  0.0128958  0.003131    0.011998    0.012399
## BMI            5.0   -0.0003925  0.003051      .           .
## hypertension1  35.0  -0.0835609  0.133814      .           .
## Cardiovascular1 8.9  -0.0187015  0.080646      .           .
## Diabetes1      8.0    0.0134333  0.061391      .           .
## Chronic1      10.7  -0.0333378  0.122177      .           .
## Obesity1       5.0   -0.0039459  0.030205      .           .
## Pregnancy1     4.9    0.0078002  0.057110      .           .
## Stroke1        3.0  -0.0017002  0.019327      .           .
## Chronic_liver1  3.0  -0.0017002  0.019327      .           .
## chronic_renal1  5.7  -0.0143886  0.087671      .           .
## cancer_HIV1    3.0  -0.0017002  0.019327      .           .
## SpO2           75.6  -0.0108938  0.054828   -0.005658   -0.006889
## Temp           54.9  -0.0935115  0.451778   -0.170876      .
## Breathing       8.0   -0.0005785  0.002691      .           .
## UD             43.9  -0.0412313  0.526231   -0.104876   -0.094611
##
## nVar              5              4
## r2                0.408          0.376
## BIC               -23.683301     -23.546768
## post prob         0.054          0.050
##
##           model 3      model 4      model 5
## Intercept      8.145893    0.737983    6.832615
## data.PT1       -0.320170   -0.280592   -0.309600
## sexM           .           .           .
## age           0.012796    0.013306    0.013002
## BMI            .           .           .
## hypertension1  .          -0.229900   -0.251596
## Cardiovascular1 .           .           .
## Diabetes1      .           .           .
## Chronic1       .           .           .
## Obesity1       .           .           .
## Pregnancy1     .           .           .
```

```

## Stroke1          .          .          .
## Chronic_liver1   .          .          .
## chronic_renal1   .          .          .
## cancer_HIV1      .          .          .
## SpO2             .          -0.006734  -0.005527
## Temp             -0.212022    .          -0.165827
## Breathing        .          .          .
## UD               -0.111350    .          .
##
## nVar             4           4           5
## r2               0.372       0.372       0.402
## BIC              -23.070229  -23.008566  -22.859794
## post prob        0.040       0.038       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
```