R Practical
Pscore and GenMatch

Case study: Colorado study

- Compare relative cost effectiveness of different reimbursement method for mental health care

- Different reimbursement for Medicaid mental health

- Concern cost/quality of Mental health services

- Capitation lower costs; similar outcomes

- Only partial evaluations, none reported QALY, not applied appropriate statistical method

- Grieve et al. HSR 2008 assessed incremental cost effectiveness

FFS vs CAP in Colorado
see Grieve et al (2008)

- Colorado Medicaid Capitation Pilot Program 1995

- Medicaid services for patients with mental illness

- Counties divided into 3 groups

  - Group 1: Fee for Services (FFS)

  - Group 2: Direct Capitation; not-for-profit providers (CAP_NFP)

  - Group 3: Joint venture between not-for-profit providers and a *for-profit* managed behavioral health organizations (CAP_FP)

- Matched group design compare similar areas across 3 groups

Sites from which Study Subjects are Drawn
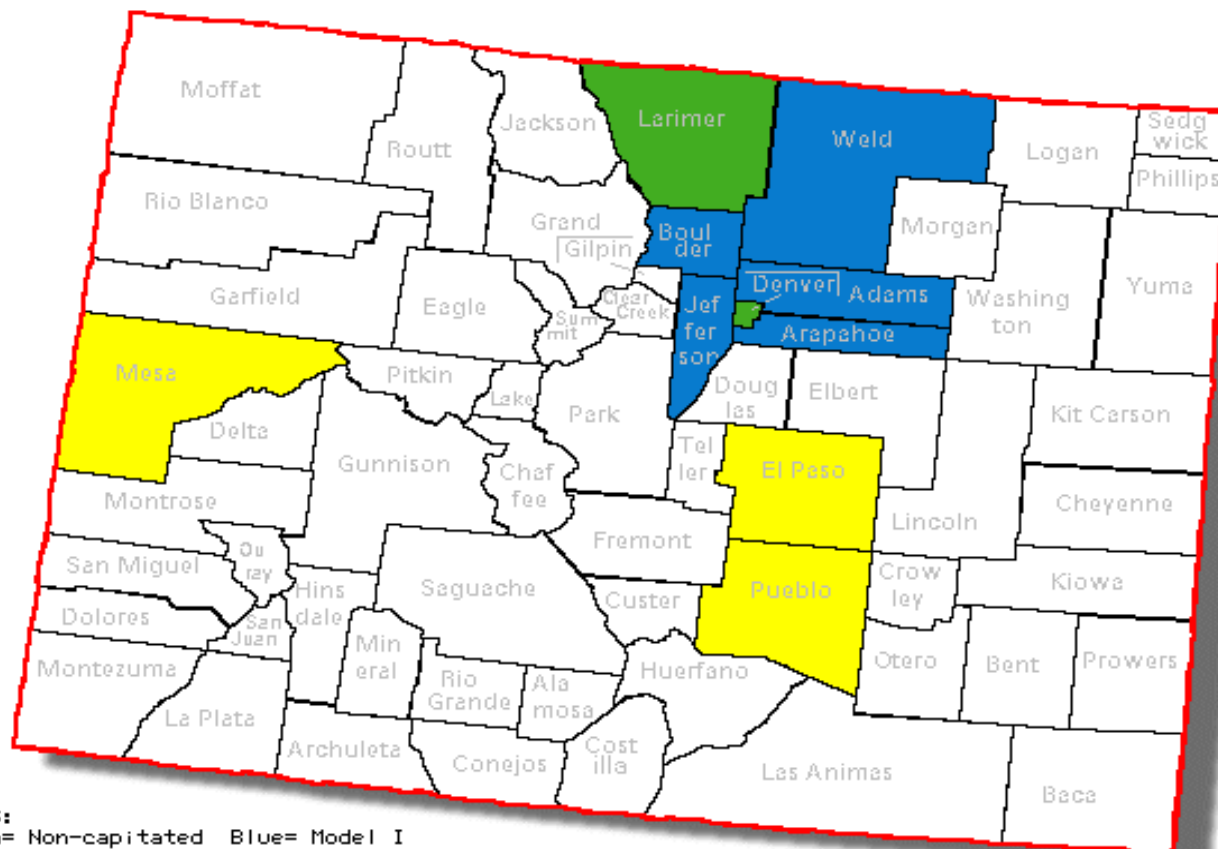
NOTES:
Green= Non-capitated Blue= Model I
(Direct Capitation) Yellow= Model II
(MBHO)

9-24-04

- 🟩 FFS
- 🟦 CAP_NFP
- 🟨 CAP_FP

Data for practical sessions

FFS vs CAP_NFP

Practical based on subset of COLORADO study data

- One treated arm (not for profit capitation) selected

- Control arm comprises of patients under FFS

- Data for analysis for 269 cases across 2 groups

- No missing data

- Costs and outcomes combined over two observation periods

Q: Is CAP_NFP is cost- effective vs FFS for Medicaid patients with severe mental health illness?

Structure of the practical

- Part 1: Propensity score matching in R

- Part 2: Genetic Matching in R

Overall aims:

- Estimate Propensity score, perform matching

- Perform Genetic Matching

- Assess covariate balance before and after matching

- Calculate Average Treatment effect Treated (ATT): cost, QALY

Variables in the dataset

Variable name	Description
Id	Study id
Key Baseline measures	
W1paid	Cost prior to intervention, continuous
W1qaly	QALY prior to intervention, continuous
W1schiz	Schizophrenia, 1=yes; 0=no
W1bipolar	Bipolar, 1=yes; 0=no
W1age	Age (continuous)
W1male	0=women; 1=men
W1highcost	Previously high cost (0=no; 1=yes)
W1lowcost	Previously low cost (0=no; 1=yes)
W1use	Previously used any service (0=no; 1=yes)
W1nonwhite	Ethnicity, 1= white, 0=other
W1phs	Physical health at baseline, continuous
W1mhs	Mental health at baseline, continuous
W1gf	Global functioning at baseline, continuous
age2	Age squared
age3	Age cubed
priorcost2	W1paid squared
priorcost3	W1paid cubed
priorqaly2	W1qaly squared
priorqaly3	W1qaly cubed

Variables in the dataset

Key outcomes	
totalcost	Total discounted cost in first and second follow-up period
totalqaly	Total discounted QALY in first and second follow-up period

Treatment variable	
treated	Treatment indicator =0 for FFS, 1 for DC

Demonstration

Solutions: Propensity score matching

Balance after Propensity score matching
T-tests vs KS tests

```
***** (V2) W1qaly *****
                         Before Matching      After Matching
mean treatment........     0.48518             0.48518
mean control..........     0.47143             0.46888
std mean diff.........     17.416              20.65

mean raw eQQ diff.....     0.015559            0.020918
med  raw eQQ diff.....     0.0105              0.018
max  raw eQQ diff.....     0.04575             0.057

mean eCDF diff........     0.051987            0.071818
med  eCDF diff........     0.028353            0.072727
max  eCDF diff........     0.16367             0.2

var ratio (Tr/Co).....     1.1661              1.3808
T-test p-value........     0.14191             0.051583
KS Bootstrap p-value..     0.042               < 2.22e-16
KS Naive p-value......     0.059248            0.0027207
KS Statistic..........     0.16367             0.2
```

Balance after Propensity score matching
T-tests vs KS tests

```
***** (V1) W1age *****

                        Before Matching      After Matching
mean treatment.......      41.749               41.749
mean control.........      42.713               41.778
std mean diff........      -7.4032              -0.22206

T-test p-value.......      0.54944              0.98426
KS Bootstrap p-value..     0.492                0.302


***** (V3) W1paid *****

                        Before Matching      After Matching
mean treatment.......      4933.3               4933.3
mean control.........      4840.6               5224.5
std mean diff........      1.0001               -3.1402

T-test p-value.......      0.94008              0.79079
KS Bootstrap p-value..     0.166                0.264
```

Balance after Propensity score matching
T-tests vs KS tests

```
***** (V4) W1nonwhite *****
                        Before Matching              After Matching
mean treatment........    0.23226                0.23226
mean control.........     0.42105                 0.2129
std mean diff........     -44.565                 4.5687


var ratio (Tr/Co).....    0.72979                1.0641
T-test p-value.......   0.0012107                0.49167


***** (V5) W1schiz *****
                        Before Matching              After Matching
mean treatment.......     0.61935                0.61935
mean control.........     0.72807                0.64839
std mean diff........     -22.318                  -5.96


var ratio (Tr/Co).....     1.188                  1.0341
T-test p-value.......    0.058908                0.49543
```

Balance after Propensity score matching
T-tests vs KS tests

```
***** (V6) W1bipolar *****
                        Before Matching          After Matching
mean treatment........    0.30968                   0.30968
mean control.........     0.21053                   0.31613
std mean diff........      21.375                   -1.3909


var ratio (Tr/Co).....     1.2832                    0.98883
T-test p-value.......      0.06483                   0.88771


Before Matching Minimum p.value: 0.0012107
Variable Name(s): W1nonwhite  Number(s): 4

After Matching Minimum p.value: < 2.22e-16
Variable Name(s): W1qaly  Number(s): 2
```
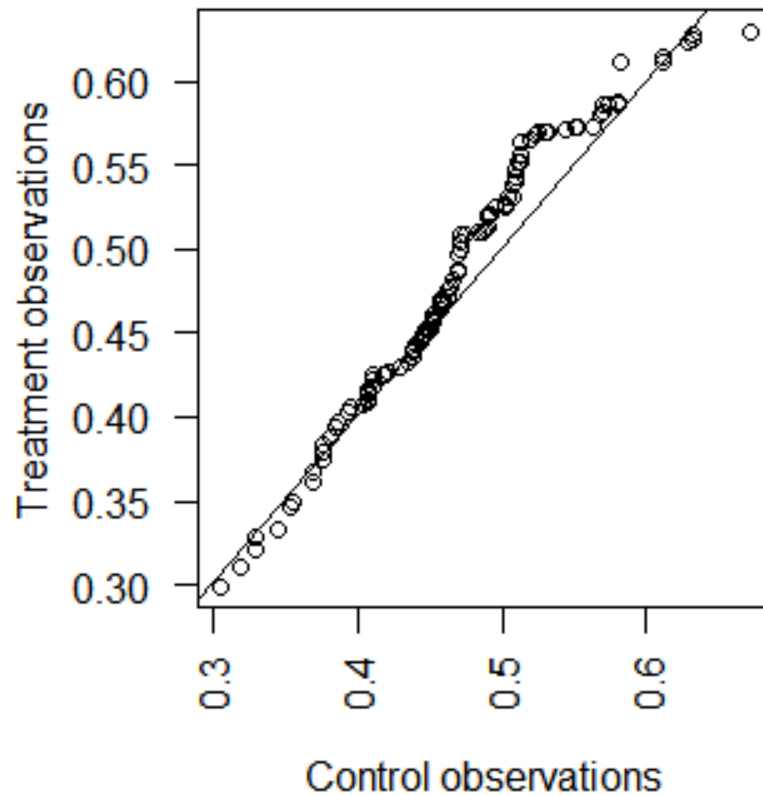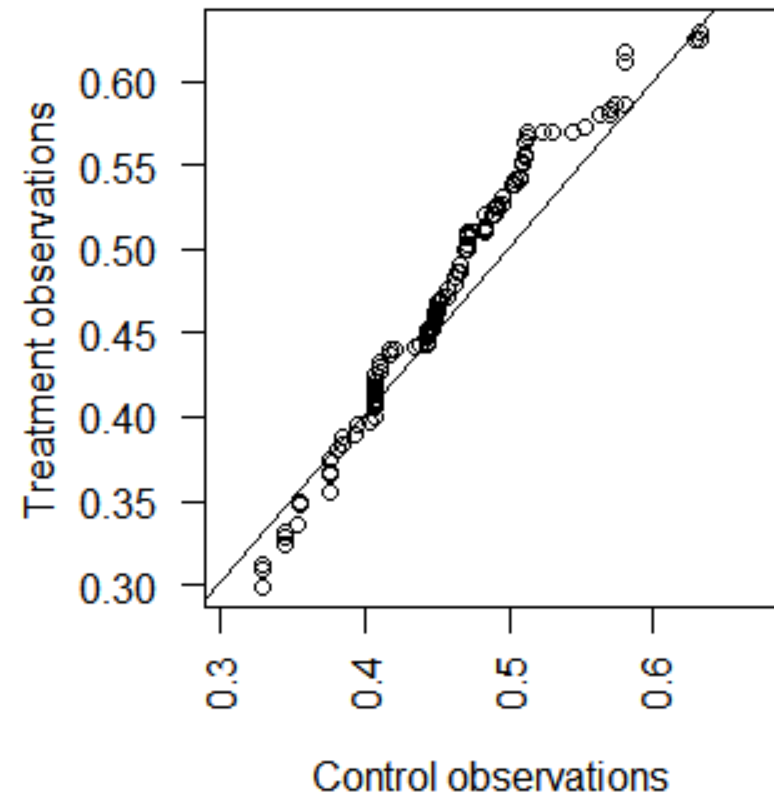
Balance after Propensity score matching
eQQ plots of baseline QALY

Estimated treatment effect after Propensity score matching
QALY

```
> m_ps_qaly  <- Match(Y=totalqaly, Tr=treated, X=pscore_est,
estimand="ATT")


Estimate...   -0.02743
AI SE......    0.027737
T-stat.....   -0.98893
p.val.....     0.3227


Est noAdj..   -0.02743
SE.........    0.016954
T-stat.....   -1.6179
p.val.....     0.10568

Original number of observations..............  269
Original number of treated obs..............  155
Matched number of observations..............  155
Matched number of observations  (unweighted).  165
```

Estimated treatment effect after Propensity score matching
Costs

```
> m_ps_cost  <- Match(Y=totalcost, Tr=treated,  X=pscore_est,
estimand="ATT")
> summary(m_ps_cost, full=TRUE)


Estimate...   970.69
AI SE......   3187.7
T-stat.....   0.30451
p.val......   0.76074

Est noAdj..   970.69
SE.........   1934.8
T-stat.....   0.50169
p.val......   0.61588

Original number of observations..............  269
Original number of treated obs..............  155
Matched number of observations..............  155
Matched number of observations  (unweighted). 165
```

Solutions: Genetic Matching

GenMatch weights

```
Parameters at the Solution:


 X[ 1] :        9.265050e+02
 X[ 2] :        6.271922e+02
 X[ 3] :        3.037749e+02
 X[ 4] :        3.115431e+02
 X[ 5] :        5.836216e+02
 X[ 6] :        5.004798e+02
 X[ 7] :        7.268592e+02
 X[ 8] :        4.184170e+02
 X[ 9] :        7.916147e+02
 X[10] :        5.815102e+02
 X[11] :        1.787976e+02
 X[12] :        7.343106e+02
 X[13] :        7.815934e+02
 X[14] :        1.808917e+02


Solution Found Generation 6
Number of Generations Run 11
```

Balance after GenMatch

```
***** (V1) W1age *****
                        Before Matching          After Matching
mean treatment.......       41.749                  41.749
mean control.........       42.713                  41.354
std mean diff........       -7.4032                  3.032


T-test p-value.......        0.54944                 0.60318
KS Bootstrap p-value..        0.492                   0.272


***** (V2) W1qaly *****
                        Before Matching          After Matching
mean treatment.......        0.48518                 0.48518
mean control.........        0.47143                 0.48058
std mean diff........        17.416                   5.8314


T-test p-value.......         0.14191                 0.23359
KS Bootstrap p-value..         0.042                   0.132
```

Balance after GenMatch

```
***** (V3) W1paid *****

                        Before Matching              After Matching
mean treatment.......      4933.3                       4933.3
mean control.........      4840.6                       3754.1
std mean diff........      1.0001                       12.718


T-test p-value.......      0.94008                      0.099913
KS Bootstrap p-value..      0.166                        0.274


***** (V4) W1nonwhite *****

                        Before Matching              After Matching
mean treatment.......      0.23226                      0.23226
mean control.........      0.42105                      0.2129
std mean diff........      -44.565                      4.5687


var ratio (Tr/Co).....     0.72979                      1.0641
T-test p-value.......      0.0012107                    0.25663
```

Balance after GenMatch

```
***** (V5) W1schiz *****
                        Before Matching              After Matching
mean treatment........     0.61935                      0.61935
mean control.........      0.72807                      0.64516
std mean diff........      -22.318                      -5.2978


var ratio (Tr/Co).....       1.188                       1.0298
T-test p-value.......     0.058908                      0.10155



***** (V6) W1bipolar *****
                        Before Matching              After Matching
mean treatment........     0.30968                      0.30968
mean control.........      0.21053                      0.32258
std mean diff........       21.375                      -2.7817


var ratio (Tr/Co).....      1.2832                      0.97829
T-test p-value.......      0.06483                      0.31732
```

Balance after GenMatch
eQQ plots of baseline QALY
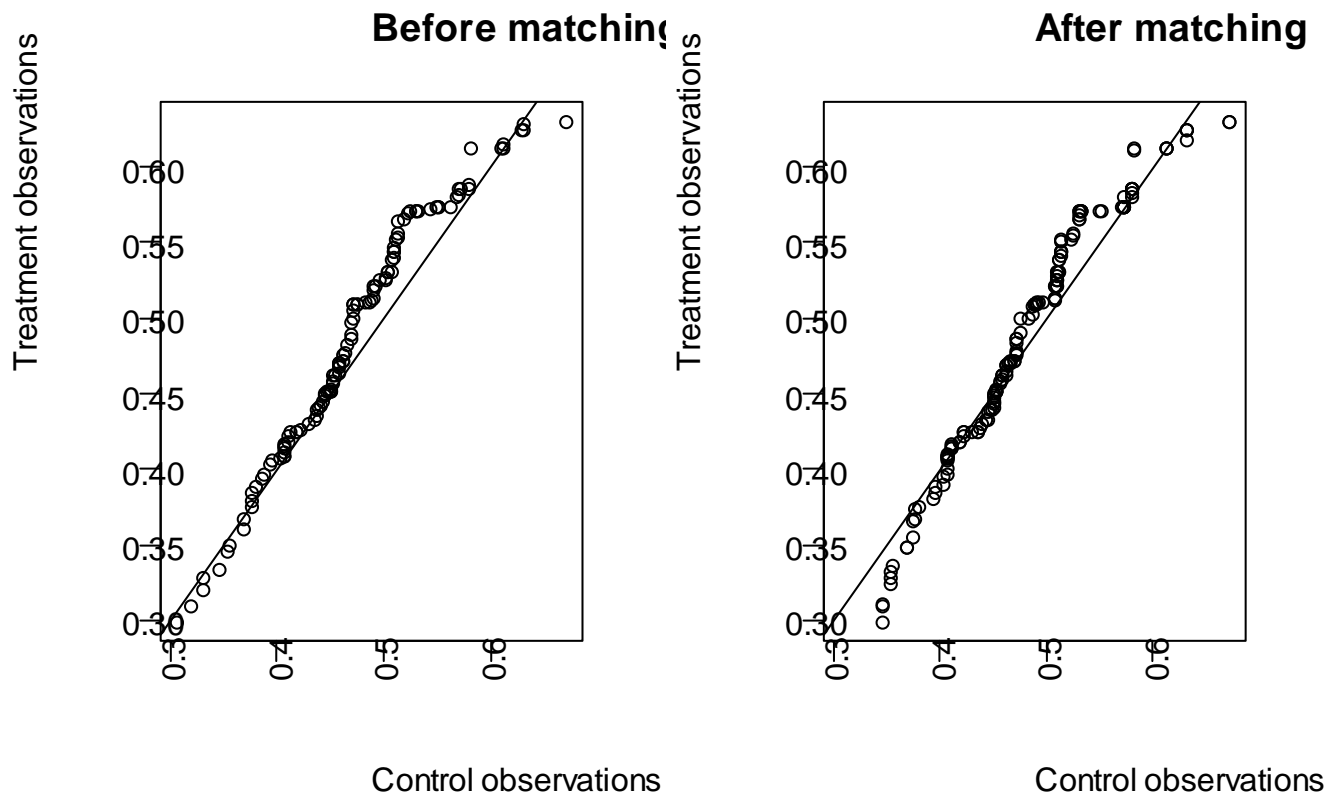
Estimated treatment effects after GenMatch:
Total QALY

```
m.gm1.qaly <- Match(Y=totalqaly, Tr=treated, X=X, Weight.matrix=gen1,
estimand="ATT")


Estimate...   -0.018587
AI SE......    0.018663
T-stat.....   -0.99593
p.val.....     0.31929


Est noAdj..   -0.018587
SE.........    0.013505
T-stat.....   -1.3763
p.val.....     0.16873


Original number of observations..............  269
Original number of treated obs..............  155
Matched number of observations..............  155
Matched number of observations  (unweighted).  155
```

Estimated treatment effects after GenMatch:
Total Costs

```
m_gm1_cost <- Match(Y= totalcost,Tr=treated, X=X, Weight.matrix = gen1,
estimand = "ATT")


Estimate...   2805.1
AI SE......   2018.4
T-stat.....   1.3897
p.val.....   0.16461


Est noAdj..   2805.1
SE.........   1460.6
T-stat.....   1.9205
p.val.....   0.054794


Original number of observations.............  269
Original number of treated obs..............  155
Matched number of observations..............  155
Matched number of observations  (unweighted).  155
```

Summary of results

	Incremental costs	Incremental QALYs
Pscore matching	971 (3188)	0.027 (0.028)
GenMatch	2805 (2018)	-0.019 (0.019)

QUESTIONS?