Full matching in a study of coaching for the SAT (condensed treatment)

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This is a condensed, ever-so-slightly simplified session culminating in a full match discussed and recommended in my paper "Propensity score matching to extract latent experiments from nonexperimental data: A case study" (Hansen, 2011). The longer, unsimplfied session is available in a similar format.

The match this script leads to combines propensity and prognostic scores in a way that I've found reliably and effectively to reduce bias while limiting the losses of sample size and precision that can sometimes accompany matching-based analysis.

```
> load("satcoach.RData")
> library(optmatch)
> library(RItools)
> library(xtable)
> library(splines)
> options(digits = 3)
> sessionInfo()

R version 2.11.1 (2010-05-31)
x86_64-apple-darwin9.8.0

locale:
[1] C

attached base packages:
[1] splines   stats     graphics  grDevices utils     datasets  methods
[8] base

other attached packages:
[1] Design_2.3-0       Hmisc_3.8-2        survival_2.36-2    brglm_0.5-5
[5] profileModel_0.5-7 RItools_0.1-11     xtable_1.5-6       optmatch_0.7-1

loaded via a namespace (and not attached):
[1] SparseM_0.86    cluster_1.13.2  grid_2.11.1     lattice_0.19-17
[5] tools_2.11.1
```

1 Preliminaries to matching

1.1 the Race× SES subclassification

The reasons to subclassify prior to matching are that large matching problems can take a lot of time, more time than several smaller matching problems taken to gether, at the same time that subclassifying is more intuitive than propensity score matching.

As noted by Hansen and Klopfer (2006), the matching algorithm `optmatch` is based on uses roughly $O(n^3 \log n)$ floating point operations, where n is the sample size. Comparing this estimate for the problem of matching without subclasses to that of matching withing Race× SES subclasses gives:

```
> nrow(satcoach)

[1] 3994

> table(satcoach$ethn3levels, satcoach$dadsed)

        (0,5] (5,7] (7,9]   na
  Asian   149   102   103   16
  White  1026   794   786  273
  URM     435   136   120   54

> matchflops <- function(n) n^3 * log(n)
> sum(matchflops(table(satcoach$ethn3levels, satcoach$dadsed)))/matchflops(nrow(satcoach))

[1] 0.0279
```

Preceding matching by the Race×SES subclassification is the same as to match exactly (on propensity scores, Mahalanobis distances, prognostics scores or whatever) within Race× SES subclasses, which seems a sensible thing to do.

The Race × SES subclassification does improves balance, as the following calculations show. Matching will bring more satisfying improvements to balance, however, as will be seen below. Significance calculations here are permutation-based, as discussed in (Hansen and Bowers, 2008).

```
> xbs <- xtabs <- printtabs <- list()
> xbs$sc.big <- xBalance(Coach ~ psatv + pmin(psatv, 40) + pmax(psatv,
+     60) + psatm + pmin(psatm, 40) + pmax(psatm, 60) + psat.NA +
+     presatv + pmin(presatv, 400) + pmax(presatv, 600) + presatm +
+     pmin(presatm, 400) + pmax(presatm, 600) + presat.NA + gpa +
+     avgeng + avgmath + avgnatsci + avgssci + nyrseng + nyrsfl +
+     nyrsmath + nyrsnatsci + nyrsssci + parentsincome + dadsed +
+     momsed + full.1stlang + gender + ethn3levels + Coll1mean +
+     Coll1mean.NA + I23 + I24 + I25 + yearpref + deggoal + pubpripref,
+     strata = list(no.stratification = NULL, racebyses = ~ethn3levels +
+         dadsed), data = satcoach, report = c("adj.mean.diffs",
+         "chisquare.test"))
> xbs$sc.big

                     strata no.stratification          racebyses
                     stat            adj.diff           adj.diff
vars
psatv                                -1.1e-01           -5.0e-01
pmin(psatv, 40)                      9.5e-02            1.8e-01
pmax(psatv, 60)                      -2.1e-01 .         -3.7e-01 **
psatm                                9.1e-01  *         1.2e-01
pmin(psatm, 40)                      2.2e-01  *         2.0e-01  *
pmax(psatm, 60)                      1.5e-01            -5.6e-02
psat.NATRUE                          4.6e-02  *         5.6e-02  *
presatv                              -1.7e+00 .         -2.4e+00 *
pmin(presatv, 400)                   -2.2e-01           -3.7e-01
pmax(presatv, 600)                   -1.6e-01           -2.8e-01
presatm                              9.4e-01            5.3e-01
pmin(presatm, 400)                   1.8e-02            -1.8e-02
```

```
pmax(presatm, 600)                   2.2e-01            2.1e-01
presat.NATRUE                        -5.9e-03           -5.7e-03
gpa(0,1]                             -2.6e-02 *         -3.6e-02 **
gpa(1,3]                             6.7e-02  **        5.3e-02  *
gpa(3,6]                             -4.5e-02 .         -1.0e-02
gpa(6,12]                            -2.2e-02           -9.0e-03
gpana                                2.6e-02  *         2.3e-03
avgeng(0,1]                          3.8e-02            1.8e-02
avgeng(1,5]                          -6.5e-02 **        -2.1e-02
avgengna                             2.7e-02  *         3.4e-03
avgmath(0,1]                         2.5e-02            8.6e-03
avgmath(1,5]                         -5.6e-02 *         -1.4e-02
avgmathna                            3.1e-02  **        5.6e-03
avgnatsci(0,1]                       3.6e-02            1.8e-02
avgnatsci(1,5]                       -6.1e-02 *         -2.1e-02
avgnatscina                          2.5e-02  *         2.9e-03
avgssci(0,1]                         5.1e-02  *         2.9e-02
avgssci(1,5]                         -7.3e-02 **        -2.9e-02
avgsscina                            2.2e-02  .         -4.7e-04
nyrseng(0,4]                         -2.6e-03           8.4e-03
nyrseng(4,6]                         -1.4e-02           -9.4e-05
nyrsengna                            1.6e-02            -8.3e-03
nyrsfl(0,4]                          -1.6e-01 ***       -1.2e-01 ***
nyrsfl(4,6]                          1.4e-01  ***       1.3e-01  ***
nyrsflna                             1.7e-02            -4.6e-03
nyrsmath(0,4]                        -9.0e-02 ***       -5.7e-02 **
nyrsmath(4,6]                        6.4e-02  **        5.9e-02  **
nyrsmathna                           2.5e-02  *         -2.6e-03
nyrsnatsci(0,4]                      -7.0e-02 **        -3.0e-02
nyrsnatsci(4,6]                      4.2e-02  .         2.7e-02
nyrsnatscina                         2.8e-02  *         3.0e-03
nyrsssci(0,4]                        -8.2e-02 ***       -6.7e-02 **
nyrsssci(4,6]                        6.9e-02  **        7.8e-02  ***
nyrsssscina                          1.4e-02            -1.1e-02
parentsincome[1,6]                   -1.3e-01 ***       -9.6e-02 ***
parentsincome(6,9]                   -8.7e-02 ***       -4.8e-02 *
parentsincome(9,11]                  -2.9e-02 .         -3.2e-02 .
parentsincome(11,13]                 1.9e-01  ***       1.5e-01  ***
parentsincomena                      5.9e-02  ***       3.1e-02  *
dadsed(0,5]                          -2.0e-01 ***       -6.6e-17
dadsed(5,7]                          -3.5e-02 .         -1.3e-16
dadsed(7,9]                          1.9e-01  ***       -1.5e-16
dadsedna                             4.1e-02  **        3.2e-17
momsed(0,5]                          -2.0e-01 ***       -9.9e-02 ***
momsed(5,7]                          2.0e-02            9.1e-03
momsed(7,9]                          1.3e-01  ***       7.4e-02  ***
momsedna                             4.7e-02  ***       1.5e-02  *
full.1stlang1                        -1.1e-01 ***       -7.7e-03
full.1stlang2                        3.9e-02  **        6.5e-03
full.1stlang3                        3.5e-02  **        -7.7e-03
full.1stlangna                       3.5e-02  **        8.9e-03
genderB                              -1.1e-02           -3.1e-02
genderG                              1.1e-02            3.1e-02
ethn3levelsAsian                     1.1e-01  ***       -1.6e-17
```

```
ethn3levelsWhite                     -1.1e-01 ***      -5.3e-16
ethn3levelsURM                       -5.2e-03          -3.3e-17
Coll1mean                            3.9e+01  ***      3.0e+01  ***
Coll1mean.NATRUE                     4.8e-03           1.0e-02
I230                                 -4.3e-02 .        -3.1e-02
I231                                 -7.3e-02 ***      -7.1e-02 ***
I232                                 1.2e-01  ***      1.0e-01  ***
I240                                 2.9e-02           3.5e-02  .
I241                                 8.5e-02  ***      8.0e-02  ***
I242                                 -4.6e-02 *        -5.0e-02 *
I243                                 -6.8e-02 ***      -6.5e-02 ***
I250                                 2.7e-02           3.3e-02
I251                                 3.9e-02  .        2.7e-02
I252                                 -6.6e-02 ***      -5.9e-02 ***
yearpref0                            -9.0e-03          -2.7e-02 *
yearpref1                            9.0e-03           2.7e-02  *
deggoal0                             -1.7e-02          -2.4e-02
deggoal1                             -1.4e-02 *        -9.2e-03
deggoal2                             -7.7e-02 ***      -5.1e-02 **
deggoal3                             1.1e-01  ***      8.4e-02  ***
pubpripref0                          1.2e-01  ***      8.6e-02  ***
pubpripref1                          -1.2e-01 ***      -8.6e-02 ***
---Overall Test---
                  chisquare df p.value
no.stratification       486 66 3.2e-65
racebyses               287 61 5.3e-31
---
Signif. codes:  0 '***' 0.001 '** ' 0.01 '*  ' 0.05 '.  ' 0.1 '   ' 1
```

So the stratification helps, mostly, but observed balance is still far worse than it would have been under random assignment.

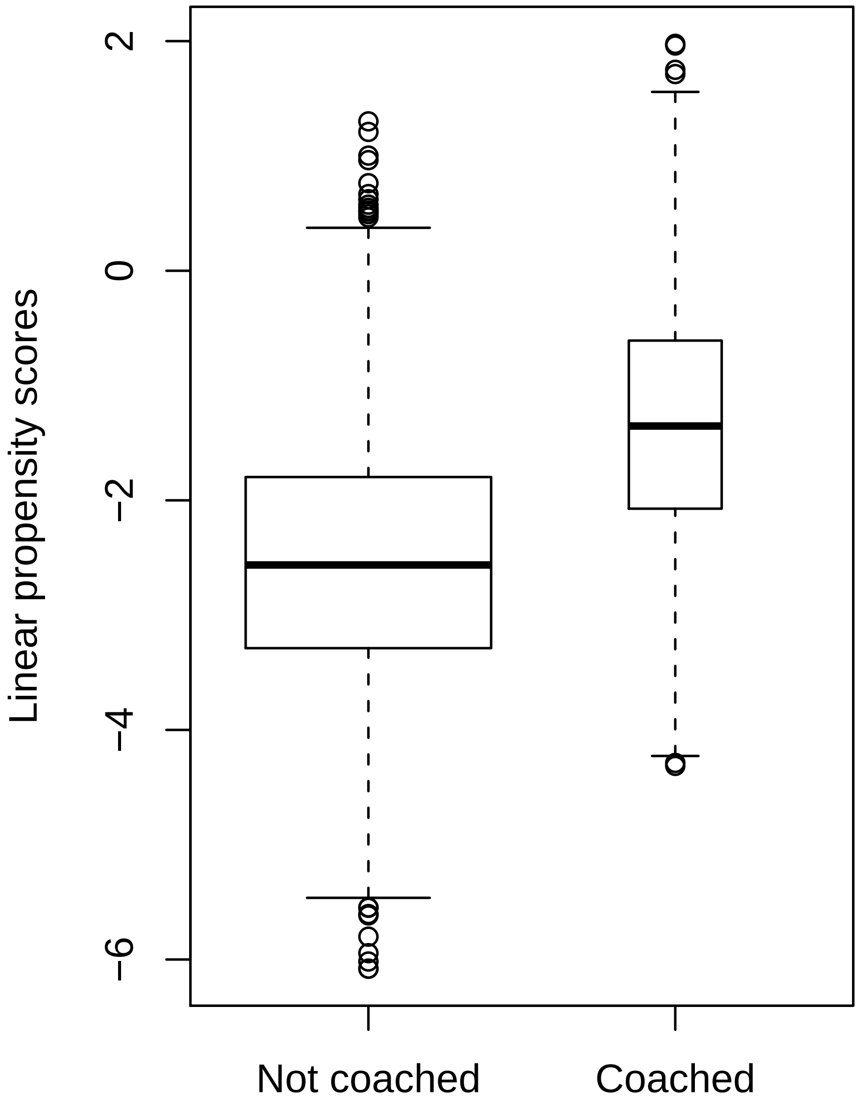
1.2 Estimating the propensity score

Here is an estimated propensity score. To somewhat relax the assumption of linearity of the propensity score in the 5 measurement variables, we expand each of them in natural splines.

```
> ppty <- list()
> ppty$fmla <- Coach ~ ns(psatv, df = 4) + ns(psatm, df = 4) +
+     ns(presatv, df = 4) + ns(presatm, df = 4) + ns(Coll1mean,
+     df = 4) + I23 + I24 + I25 + parentsincome + dadsed + momsed +
+     clpsed.ethn + full.1stlang + yearpref + deggoal + pubpripref +
+     gpa + avgeng + avgmath + avgnatsci + avgssci + nyrseng +
+     nyrsfl + nyrsmath + nyrsnatsci + nyrsssci + gender + ethn3levels +
+     psat.NA + presat.NA + Coll1mean.NA
> ppty$model <- glm(ppty$fmla, data = satcoach, family = binomial)
> ppty$score <- ppty$model$linear.predictors
> all.equal(names(ppty$score), row.names(satcoach))
```

```
[1] TRUE
```

```
> boxplot(ppty$score ~ factor(satcoach$Coach, labels = c("Not coached",
+     "Coached")), ylab = "Linear propensity scores", xlab = "",
+     varwidth = TRUE)
```



2 Full matching on the propensity score

To match within Race×SES subclasses, we only need to calculate discrepancies on the propensity score (and/or on whatever else we may decided to match on) within these subclasses.

```
> ppty$dist <- mdist(ppty$model, structure.fmla = ~ethn3levels +
+     dadsed)
```

This incidentally reduces the burden of the problem on memory: matching within subclasses involves storing 12 distance matrices, with 230000 entries in total, whereas matching without subclasses requires us to store one large 500 × 3494 matrix, with 1750000 entries.

2.1 Propensity score full matching

Plain-vanilla full matching on the propensity score (within Race×SES subclasses).

```
> fm.ppty <- fullmatch(ppty$dist)
> summary(fm.ppty, ppty$model)
```

```
Structure of matched sets:
5+:1  4:1  3:1  2:1  1:1  1:2  1:3  1:4 1:5+
   3    3    4   15  102   47   43   42  192
Effective Sample Size:  679
(equivalent number of matched pairs).

sum(matched.distances)=328
(within 2.22 of optimum).
Percentiles of matched distances:
   0%   50%   95%  100%
0.000 0.026 0.404 2.380
Balance test overall result:
  chisquare df p.value
       16.6 69       1
```

Balance looks good, but there are outliers in terms of matched distances on the propensity score. This is something to avoid (Hansen, 2009). Calipers are the natural remedy:

```
> fm.ppty.clpr050 <- fullmatch(ppty$dist + caliper(ppty$dist, width = 0.5))
> summary(fm.ppty.clpr050, ppty$model)
```

```
Structure of matched sets:
 1:0 5+:1  4:1  3:1  2:1  1:1  1:2  1:3  1:4 1:5+  0:1
  10    2    4    3   15   97   51   43   39  194  140
Effective Sample Size:  676
(equivalent number of matched pairs).

sum(matched.distances)=199
(within 2.23 of optimum).
Percentiles of matched distances:
    0%    50%    95%   100%
0.0000 0.0238 0.2330 0.4990
Balance test overall result:
  chisquare df p.value
       10.5 69       1
```

Note that the addition of this caliper has caused some treatment group members to go unmatched — these are the "1:0" matched sets noted in the summary. (`fullmatch(<...>)` and `pairmatch(<...>, remove.unmatchables=T)` automatically remove subjects without permissible matches before they begin to match. That's what's happened to these treatment group members, as well as to the controls falling in 0:1 "matched sets.")

3 Full matching with prognostic and propensity scores

Here's another way to manage the tradeoff between bias reduction and effective sample size, one that can be operationally simpler and might offer some additional bias protection as well: matching one propensity score within calipers of another, constructing the first propensity score in such a way as to keep to a minimum separation between coached and uncoached kids while constructing the second in such a way as to promote balance on as many covariates as possible. A natural way to get less-separation propensity scores is to permit in them only covariates or functions of the covariate that are most predictive of the response.

3.1 A focused propensity score

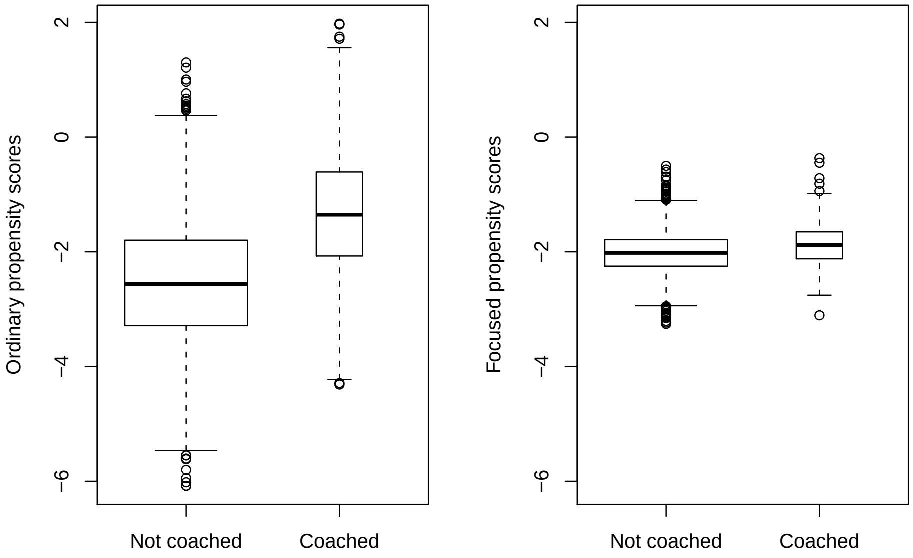
Extracting summaries of the part of the covariate other than pretests, as it relates to pretest score. Because these summaries are inherently one-dimensional, because OLS is not necessarily the best approach, and because we're skipping any diagnostics, they are potentially rather crude. I have set to 'NA' early SAT scores or PSAT scores from test sittings after a student was coached, as well as prior test scores of uncoached students from sittings close in time to their sitting for the posttest, as discussed in (Hansen, 2004, § 1.2). This helps to ensure that the pretest genuinely anteceded the treatment, and improves motivation of models in which assignment to treatment occurs strictly after (what we are considering to be) pretests.

```
> pg.mod <- list()
> (pg.mod$m.fmla <- update.formula(ppty$fmla, postsatmath ~ . -
+     ethn3levels))

postsatmath ~ ns(psatv, df = 4) + ns(psatm, df = 4) + ns(presatv,
    df = 4) + ns(presatm, df = 4) + ns(Coll1mean, df = 4) + I23 +
    I24 + I25 + parentsincome + dadsed + momsed + clpsed.ethn +
    full.1stlang + yearpref + deggoal + pubpripref + gpa + avgeng +
    avgmath + avgnatsci + avgssci + nyrseng + nyrsfl + nyrsmath +
    nyrsnatsci + nyrsssci + gender + psat.NA + presat.NA + Coll1mean.NA

> (pg.mod$v.fmla <- update.formula(ppty$fmla, postsatverb ~ . -
+     ethn3levels))

postsatverb ~ ns(psatv, df = 4) + ns(psatm, df = 4) + ns(presatv,
    df = 4) + ns(presatm, df = 4) + ns(Coll1mean, df = 4) + I23 +
    I24 + I25 + parentsincome + dadsed + momsed + clpsed.ethn +
    full.1stlang + yearpref + deggoal + pubpripref + gpa + avgeng +
    avgmath + avgnatsci + avgssci + nyrseng + nyrsfl + nyrsmath +
    nyrsnatsci + nyrsssci + gender + psat.NA + presat.NA + Coll1mean.NA

> pg.mod$v <- lm(pg.mod$v.fmla, data = satcoach, subset = !Coach)
> pg.mod$m <- lm(pg.mod$m.fmla, data = satcoach, subset = !Coach)
> pg.mod$scorenames <- c("psatv", "psatm", "presatv", "presatm",
+     "psat.NA", "presat.NA")
> pg.mod$scores <- data.frame(satcoach[c("Coach", pg.mod$scorenames)],
+     pg.v = predict(pg.mod$v, satcoach), pg.m = predict(pg.mod$m,
+         satcoach), check.rows = T)
> pg.ppty <- list()
> pg.ppty$fmla <- Coach ~ psatv + psatm + presatv + presatm + psat.NA +
+     presat.NA + pg.v + pg.m
> (pg.ppty$model <- glm(pg.ppty$fmla, data = pg.mod$scores, family = binomial))

Call:  glm(formula = pg.ppty$fmla, family = binomial, data = pg.mod$scores)

Coefficients:
  (Intercept)          psatv          psatm        presatv        presatm
      0.10274       -0.06651       -0.01100       -0.01103        0.00339
  psat.NATRUE  presat.NATRUE           pg.v           pg.m
```

```
      0.68817        0.55884        0.00559        0.00359

Degrees of Freedom: 3993 Total (i.e. Null);  3985 Residual
Null Deviance:            3010
Residual Deviance: 2950         AIC: 2970
```

Here's how the ordinary propensity and the prognostic propensity differ in terms of how they separate treatment and control groups.

```
> pg.ppty$score <- pg.ppty$model$linear.predictor
> all.equal(names(pg.ppty$score), row.names(satcoach))

[1] TRUE

> par(mfrow = c(1, 2))
> boxplot(ppty$score ~ factor(satcoach$Coach, labels = c("Not coached",
+     "Coached")), ylab = "Ordinary propensity scores", xlab = "",
+     varwidth = TRUE, ylim = range(ppty$score))
> boxplot(pg.ppty$score ~ factor(satcoach$Coach, labels = c("Not coached",
+     "Coached")), ylab = "Focused propensity scores", xlab = "",
+     varwidth = TRUE, ylim = range(ppty$score))
> par(mfrow = c(1, 1))
> lm1 <- lm(ppty$score ~ Coach, data = satcoach)
> (ppty$meansep <- coef(lm1)["Coach"]/sqrt(mean(residuals(lm1)^2)))

Coach
 1.11

> lm1 <- lm(pg.ppty$score ~ Coach, data = satcoach)
> (pg.ppty$meansep <- coef(lm1)["Coach"]/sqrt(mean(residuals(lm1)^2)))

Coach
0.376

> rm(lm1)
```



3.2 Full matching on propensity and prognostic propensity scores

Distance on the prognostic score (to begin with, without calipers). Note the complaint from the distance-making functions about the stratifying variables not being in the propensity specification. Given that they are included in the ordinary propensity score, and we'll putting in a caliper on that, it's nothing to worry about. However, we do have to take a special step to tell `mdist()` where to find the variables `ethn3levels` and `dadsed`, since they weren't used in the model we're feeding to `mdist()` as a basis for constructing this propensity score.

```
> pg.ppty$dist <- mdist(pg.ppty$model, structure.fmla = ~satcoach$ethn3levels +
+     satcoach$dadsed)
```

```
> pg.ppty$dist.with.ppty.calipers <- pg.ppty$dist + caliper(ppty$dist,
+     width = 0.5)
> fm.pgppty.pptyclpr <- fullmatch(pg.ppty$dist.with.ppty.calipers)
```

3.3 Assessing the match

Summary, including summary of balance on all variables contributing to the (ordinary) propensity score.

```
> summary(fm.pgppty.pptyclpr, ppty$model)
```

```
Structure of matched sets:
 1:0  4:1  3:1  2:1  1:1  1:2  1:3  1:4 1:5+  0:1
  10    2    5    8  123   47   42   29  210  140
Effective Sample Size:  696
(equivalent number of matched pairs).

sum(matched.distances)=837
(within 2.22 of optimum).
Percentiles of matched distances:
    0%    50%    95%   100%
0.0000 0.0809 1.0800 4.3800
Balance test overall result:
  chisquare df p.value
       48.2 69   0.973
```

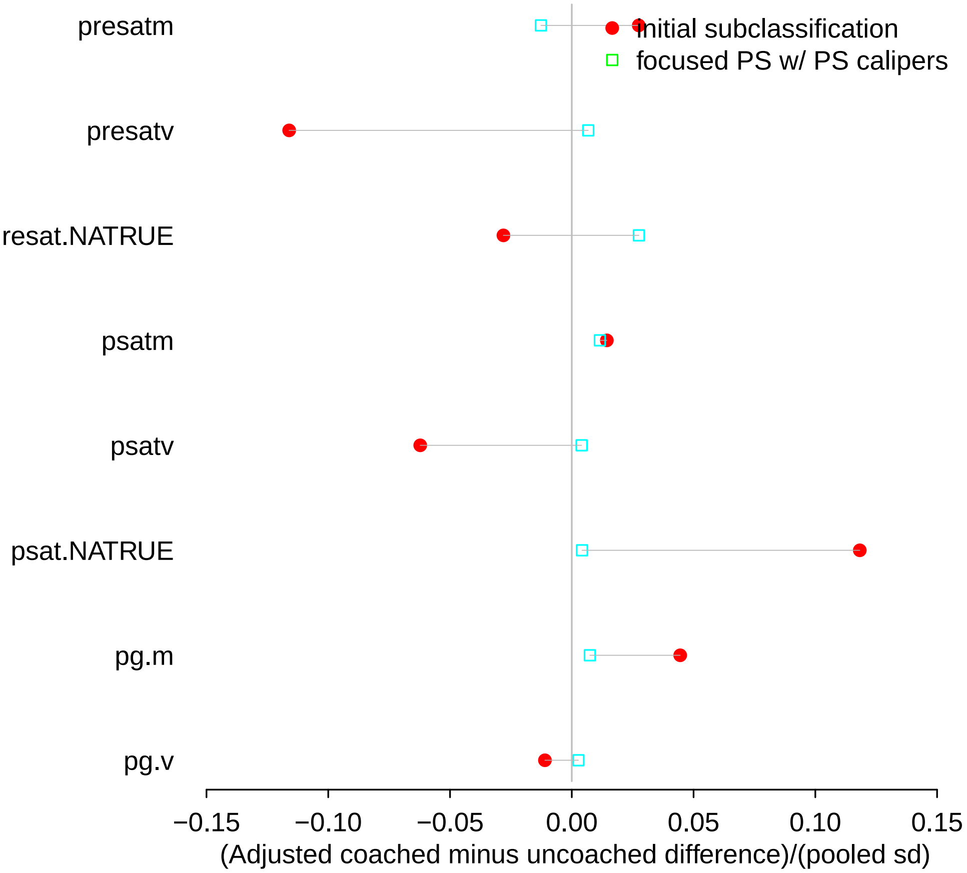
Plot of balance on variables contributing to focused/prognostic propensity score.

```
> (xb <- xBalance(Coach ~ pg.v + pg.m + psat.NA + psatv + psatm +
+     presat.NA + presatv + presatm, strata = list(racebySES = ~interaction(satcoach$dadsed,
+     satcoach$ethn3levels), matched = ~fm.pgppty.pptyclpr), report = c("std.diffs",
+     "p.values", "chisquare.test"), data = pg.mod$scores))
```

```
              strata racebySES          matched
              stat    std.diff         std.diff
vars
pg.v                   -0.0110          0.0027
pg.m                   0.0445           0.0074
psat.NATRUE            0.1183  *        0.0042
psatv                  -0.0622          0.0040
psatm                  0.0144           0.0115
presat.NATRUE          -0.0281          0.0276
presatv                -0.1161 *        0.0068
presatm                0.0275          -0.0127
---Overall Test---
```

```
           chisquare df p.value
racebySES      47.28  8 1.4e-07
matched         0.73  8 1.0e+00
---
Signif. codes:  0 '***' 0.001 '** ' 0.01 '*  ' 0.05 '.  ' 0.1 '   ' 1
```

```
> plot(xb, legend = FALSE, thexlab = "(Adjusted coached minus uncoached difference)/(pooled sd)")
> legend(x = "topright", legend = c("initial subclassification",
+     "focused PS w/ PS calipers"), col = rainbow(3), pch = c(19,
+     22, 23), bty = "n")
```



4 Outcome Analysis

4.1 Matched permutation tests without covariance adjustment

Here is a formula that will be used to adjust the outcome vector for various hypothesized treatment effects.

```
> verbfmla <- paste("Coach ~", paste(paste("I(postsatverb -", -15:35,
+     "*Coach)"), collapse = "+"))
> verbfmla <- as.formula(verbfmla)
```

p-values, a Hodges-Lehmann point estimate and confidence intervals.

```
> pvals.verb <- xBalance(verbfmla, strata = fm.pgppty.pptyclpr,
+     data = satcoach, report = c("p.values"))$results[, "p", 1]
> names(pvals.verb) <- -15:35
> (-15:35)[pvals.verb == max(pvals.verb)]

[1] 0

> range((-15:35)[pvals.verb >= 0.05])

[1] -9  9
```

Similarly for math effects:

```
> mathfmla <- paste("Coach ~", paste(paste("I(postsatmath -", -5:45,
+     "*Coach)"), collapse = "+"))
> mathfmla <- as.formula(mathfmla)
> pvals.math <- xBalance(mathfmla, strata = fm.pgppty.pptyclpr,
+     data = satcoach, report = c("p.values"))$results[, "p", 1]
> names(pvals.math) <- -5:45
> (-5:45)[pvals.math == max(pvals.math)]

[1] 21

> range((-5:45)[pvals.math >= 0.05])

[1] 12 30
```

4.2 Matched permutation tests with Rosenbaum-type covariance adjustment

Here is a data frame consisting of sat-verbal responses adjusted, first, for one of 51 hypothesised treatment effects; and, second, adjusted for covariance with pretests. From the perspective of any of the 51 null hypotheses, after the two adjustments residuals ought to be permutable within matched sets, and a permutation test is appropriate. The RItools function xBalance() is used to provide Normal approximations to these permutation tests.

Because we first introduce offsets for hypothesized treatment effects and then perform covariance adjustment, on the entire data set, I call this Rosenbaum (2002) type covariance adjustment.

```
> fmla.lhs <- ~psatv + psatm + psat.NA + presatv + presatm + presat.NA
> adj.vresp <- lapply(-15:35, function(tau) {
+     fmla <- as.formula(paste("I(postsatverb -", tau, "*Coach)~.",
+         collapse = ""))
+     fmla <- update.formula(fmla.lhs, fmla)
+     residuals(lm(fmla, data = satcoach))
+ })
> adj.vresp <- as.data.frame(adj.vresp)
> names(adj.vresp) <- paste("e", 1:length(adj.vresp), sep = "")
```

Now to compute and extract the confidence interval.

```
> xbfmla.rhs <- paste("e", 1:length(adj.vresp), sep = "")
> xbfmla.rhs <- as.formula(paste("~", paste(xbfmla.rhs, collapse = "+")))
> adj.vresp$Coach <- satcoach$Coach
> pvals.verb <- xBalance(update.formula(xbfmla.rhs, Coach ~ .),
+     strata = fm.pgppty.pptyclpr, data = adj.vresp, report = c("p.values"))$results[,
+     "p", 1]
> names(pvals.verb) <- -15:35
> (-15:35)[pvals.verb == max(pvals.verb)]
```

```
[1] 0
```

```
> range((-15:35)[pvals.verb >= 0.05])
```

```
[1] -7  7
```

Now to do the same for math.

```
> adj.mresp <- lapply(-5:45, function(tau) {
+     fmla <- as.formula(paste("I(postsatmath -", tau, "*Coach)~.",
+         collapse = ""))
+     fmla <- update.formula(fmla.lhs, fmla)
+     residuals(lm(fmla, data = satcoach))
+ })
> adj.mresp <- as.data.frame(adj.mresp)
> names(adj.mresp) <- paste("e", 1:length(adj.mresp), sep = "")
> adj.mresp$Coach <- satcoach$Coach
> pvals.math <- xBalance(update.formula(xbfmla.rhs, Coach ~ .),
+     strata = fm.pgppty.pptyclpr, data = adj.mresp, report = c("p.values"))$results[,
+     "p", 1]
> names(pvals.math) <- -5:45
> (-5:45)[pvals.math == max(pvals.math)]
```

```
[1] 21
```

```
> range((-5:45)[pvals.math >= 0.05])
```

```
[1] 14 27
```

References

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