Stat 209

Week 8 Propensity Scores

Let $z = 1, 0$ T/C $\underset{\sim}{X}$ vector of covariates

propensity score $e(\underset{\sim}{X}) = Pr(z=1 | \underset{\sim}{X})$ scalar $\hat{e}(\underset{\sim}{X})$

cond'l prob unit w vector $\underset{\sim}{X}$ observed cov. assigned to $T(z=1)$

Thm Balancing score $b(\underset{\sim}{X})$ s.t. conditional distrib of $\underset{\sim}{X}$ given $b(\underset{\sim}{X})$ same of treated and control units

$\underset{\sim}{X} \perp\!\!\!\perp z | b(\underset{\sim}{X})$. Coarsest (low dimen) balancing score is propensity score. $Pr(X, z|e) = Pr\{\underset{\sim}{X}|e\} Pr(z|e)$

Thm (result) Approx 90% reduction in bias for subclassifying at quintiles of population propensity score. $B_I = E(f(\underset{\sim}{x})|z=1) - E(f(\underset{\sim}{x})|z=0)$, B_S after strat, treatm percent reduction in bias $100(1 - B_S/B_I) \approx 90\%$

Ros Rubin
1983 Biometrika
1984 JASA

(i) The propensity score is a balancing score.
(ii) Any score that is 'finer' than the propensity score is a balancing score; moreover, x is the finest balancing score and the propensity score is the coarsest.
(iii) If treatment assignment is strongly ignorable given x, then it is strongly ignorable given any balancing score
(iv) At any value of a balancing score, the difference between the treatment and control means is an unbiased estimate of the average treatment effect at that value of the balancing score if treatment assignment is strongly ignorable. Consequently, with strongly ignorable treatment assignment, pair matching on a balancing score, subclassification on a balancing score and covariance adjustment on a balancing score can all produce unbiased estimates of treatment effects.
(v) Using sample estimates of balancing scores can produce sample balance on x.

Applications: Rubin Breast Cancer, Love (RR '84) CAD, Love Aspirin, Hansen SAT coaching, Substance Abuse (UNC), Rosenbaum, Danish downers

Rubin AnnIntMedicine

Table 3: Estimated 5-year Survival Rates for Node-Negative Patients in SEER from Tables 5 and 7 in U.S. GAO Report (1994). AIM pub

Propensity Score

Subclass	Treatment	n	Estimate	n*	Estimate*
1	Breast Conservation	56	85.6%	54	88.8%
	Mastectomy	1,008	86.7%	966	90.5%
2	Breast Conservation	106	82.8%	102	86.0%
	Mastectomy	964	82.8%	917	87.7%
3	Breast Conservation	193	85.2%	184	89.4%
	Mastectomy	866	88.8%	841	91.4%
4	Breast Conservation	289	88.7%	279	92.0%
	Mastectomy	978	87.3%	742	91.5%
5	Breast Conservation	462	89.0%	453	90.7%
	Mastectomy	604	88.5%	589	90.7%

* omitting patients whose deaths were unrelated to cancer.

Lalonde data

Lab 4 stratification

```
> table(propbin, treat)
                 treat
propbin            0   1
  (0,0.0401]     122   1
  (0.0401,0.0872] 116   7
  (0.0872,0.27]  101  21
  (0.27,0.671]    53  71
  (0.671,1]       37  85
> tapply(re78, list(propbin, treat),mean)
                    0    1
(0,0.0401]      10467    0
(0.0401,0.0872]  5797 7919
(0.0872,0.27]    6043 9211
(0.27,0.671]     4977 5819
(0.671,1]        4666 6030
```

counts

means re78

The challenge of matching on the propensity to be coached

Overlap??

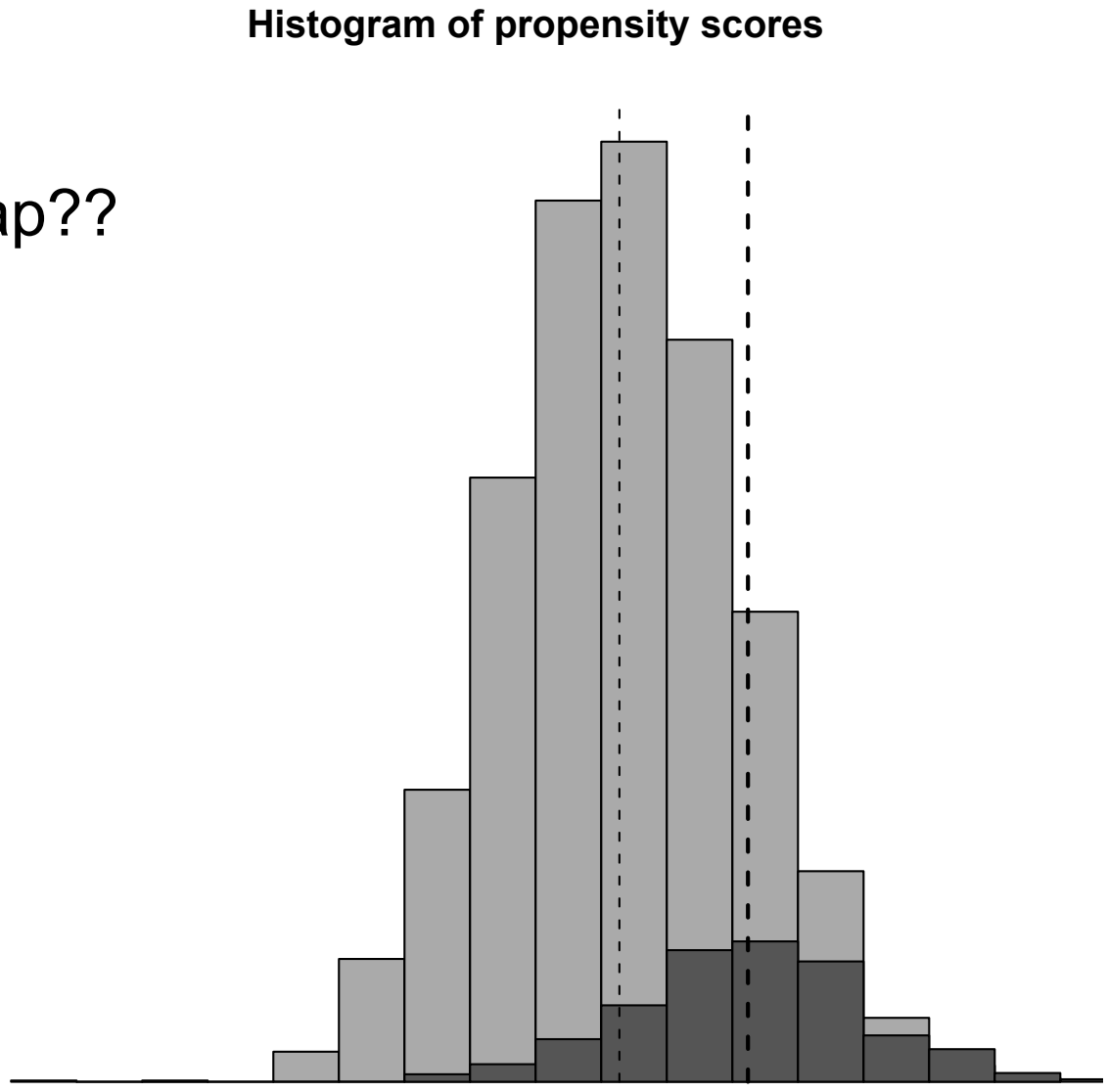


Table 1. Selected Pretreatment Variables

Variable	Range of values	Standardized bias	Percentage of sample
Math section of PSAT	20–43	−.1	18
	45–51	.1	17
	52–57	−.1	16
	58–80	.1	15
	Not taken	.1	34
Mean SAT at respondent's first-choice college	787–987	−.3	16
	988–1,060	−.2	16
	1,061–1,123	.1	16
	1,124–1,336	.3	16
	No response	.0	36
Father's education	High school	−.4	40
	A.A. or B.A.	−.1	26
	Graduate	.4	25
	No response	.2	9
Average math grade	"Excellent"	.1	35
	"Good"–"fail"	−.1	59
	No response	.1	6
Foreign language years taken	0–2	−.3	64
	3–4	.3	27
	No response	.1	9

well as scores on previous SAT–I or PSAT tests and their answers to the Student Descriptive Questionnaire (SDQ), which all SAT–I registrants are asked to complete. By their responses to questions about extracurricular SAT preparation, respondents split into a treated and a control group, and the data describe the results of a classical quasiexperiment (Campbell and Stanley 1966).

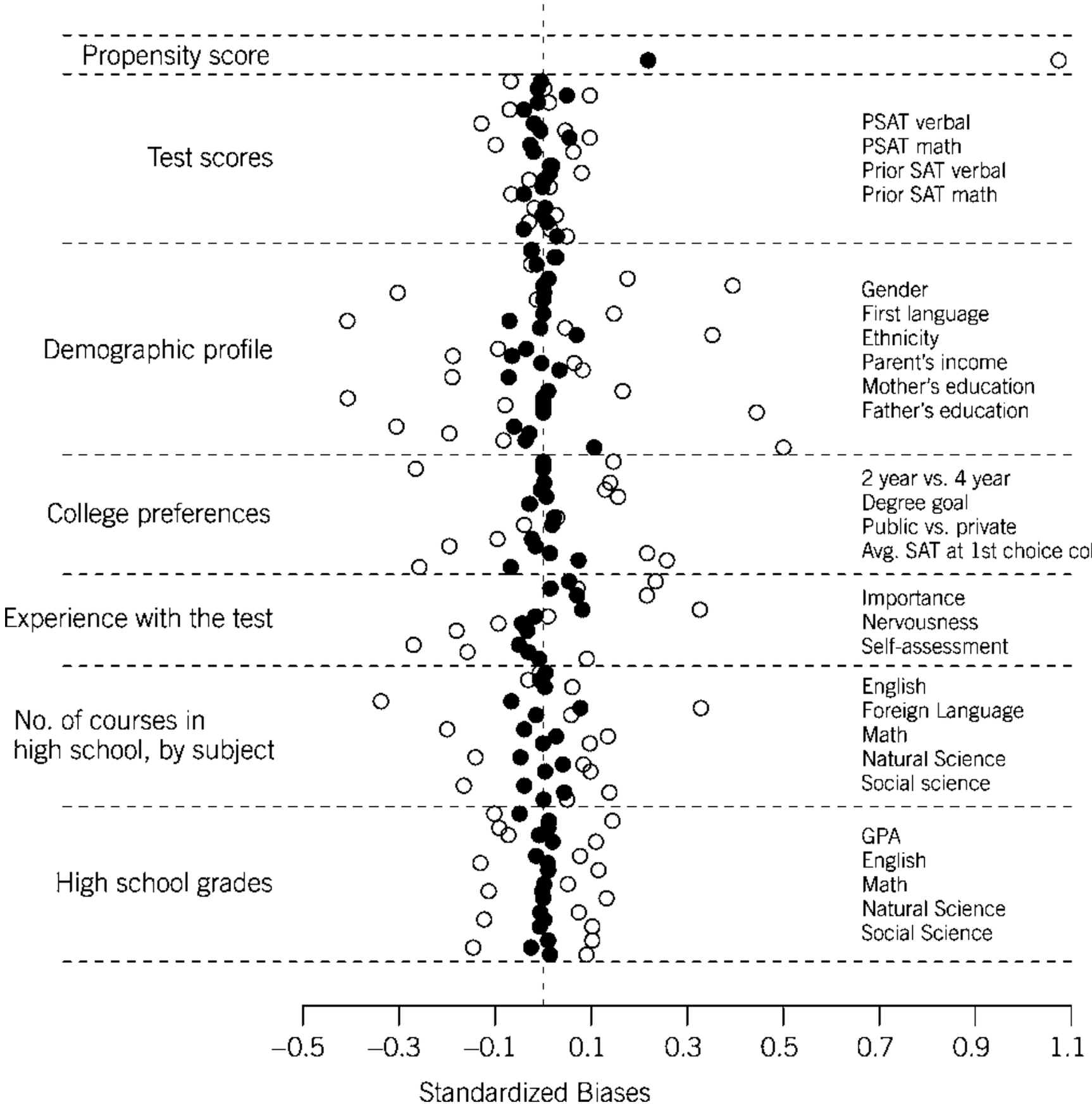
Nineteen in twenty of the survey respondents actually took the spring 1996 or fall 1995 exam for which they had registered. The analysis given below restricts itself to these 3,994 students, using the corresponding SAT scores as outcome measures. Thus the record gives coaching status and SAT outcomes for all students in the sample to be analyzed; among the additional measures, each available for some fraction of the students, are pretest scores, racial and socioeconomic indicators, various data about their academic preparation, and responses to a survey item that, by eliciting students' first choices in colleges, recovered an unusually discriminating measure of students' educational aspirations. In all, there are 27 pretreatment variables.

The coached and uncoached groups differ appreciably in these recorded measures—as do high and low scorers on the SAT. Table 1 offers some illustration of this, giving overall incidences of various covariate attributes and comparing their relative incidences in the coached and uncoached groups. (The statistic here used to effect these comparisons is the *standardized bias*, given for a variable v by $(\bar{v}_t - \bar{v}_c)/s_p$, where $\bar{v}_t$ and $\bar{v}_c$ are the average values of v in the treatment and control groups, respectively, and s_p^2 is the pooled within-group variance in v.) Yet the table shows only five covariates; the analysis must address biases on all 27 of them.

1.2 Missing and Misleading Data in Regression and in Subclassification

In regression-based adjustment, the simplest way to handle missing data on a covariate is to reject cases without complete information. In adjustment based on matching or stratification,

see RItools, PSAgraphics



Multivariate Matching with the Propensity Score

- Match subjects so that they balance on multiple covariates using one scalar score.
- Goal: Emulate a RCT in matching, then use standard analyses to compare matched sets.
- Design: Treated subjects matched to people who didn't receive treatment but who had similar propensity to receive treatment (match the treated to untreated "clones").

Aspirin Use and Mortality

- 6174 consecutive adults at CCF undergoing stress echocardiography for evaluation of known or suspected coronary disease.
- 2310 (37%) were taking aspirin (treatment).
- Main Outcome: all-cause mortality
- Median follow-up: 3.1 years
- Univariate Analysis: 4.5% of aspirin patients died, and 4.5% of non-aspirin patients died…
- Unadjusted Hazard Ratio: 1.08 (0.85, 1.39)

Gum et al. (2001) http://www.ncbi.nlm.nih.gov/pubmed/11559263

JAMA. 2001 Sep 12;286(10):1187-94. http://jama.jamanetwork.com/article.aspx?articleid=194177
Aspirin use and all-cause mortality among patients being evaluated for known or suspected coronary artery disease: A propensity analysis. Gum PA1, Thamilarasan M, Watanabe J, Blackstone EH, Lauer MS.

Propensity Score Model for Aspirin Use

- Logistic Regression predicting aspirin use
- 31 covariates included in the model:
  - Demographics, Clinical history, Medication use
  - Cardiovascular assessment and Exercise capacity
- Estimated propensity scores for aspirin use range from .03 to .98
  - ROC Area shows good discrimination (C = .83)
- But does the propensity score model work?
- Are the covariates balanced?

Baseline Characteristics By Aspirin Use (in %) (before matching)

Variable	Aspirin (n = 2310)	No Aspirin (n = 3864)	P value
Men	77.0	56.1	< .001
Clinical history: diabetes	16.8	11.2	< .001
hypertension	53.0	40.6	< .001
prior coronary artery disease	69.7	20.1	< .001
congestive heart failure	5.5	4.6	.12
Medication use: Beta-blocker	35.1	14.2	< .001
ACE inhibitor	13.0	11.4	< .001

- Baseline characteristics appear very dissimilar: 25 of 31 covariates have $p < .001$, 28 of 31 have $p < .05$.
- Aspirin user covariates indicate higher mortality risk.

Propensity Matcher Results

ID	Treated?	Propensity	Linear Propensity	Match?	Partner ID
1	1	0.2	-1.386	No	-999
2	1	0.3	-0.847	Yes	8
3	1	0.4	-0.405	Yes	10
4	1	0.6	0.405	No	-999
5	1	0.7	0.847	No	-999

logit

SE (Linear Propensity):	0.1829
x % Selected:	0.6
x % of SE:	0.1097

Baseline Characteristics By Aspirin Use [%] (after matching)

Variable	Aspirin (n = 1351)	No Aspirin (n = 1351)	P value
Men	70.4	72.1	.33
Clinical history: diabetes	15.0	15.3	.83
hypertension	50.3	51.7	.46
prior coronary artery disease	48.3	48.8	.79
congestive heart failure	5.8	6.6	.43
Medication use: Beta-blocker	26.1	26.5	.79
ACE inhibitor	15.5	15.8	.79

- Baseline characteristics similar in matched users and non-users.
- 30 of 31 covariates show NS difference between matched users and non-users. [Peak exercise capacity for men is p = .01]

Using Standardized Differences to Measure Covariate Balance

- Standardized Differences are appropriate summaries of Covariate Balance for both Continuous and Categorical Variables

$$d = \frac{100\left(\bar{x}_{Treatment} - \bar{x}_{Control}\right)}{\sqrt{\frac{s^2_{Treatment} + s^2_{Control}}{2}}}$$ for continuous variables

$$d = \frac{100\left(p_{Treatment} - p_{Control}\right)}{\sqrt{\frac{p_T(1-p_T) + p_C(1-p_C)}{2}}}$$ for binary variables

|Standardized Differences| > 10% Indicate Serious Imbalance

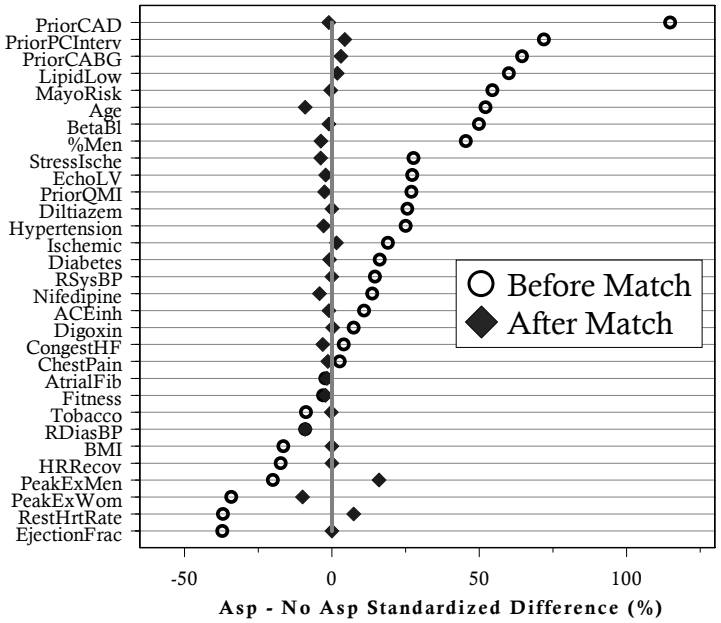
Before Match:

- 811/2310 (35.1%) Aspirin users used β-blockers
- 550/3864 (14.2%) non-Aspirin users used β-blockers
- Standardized Difference is 49.9%
- P value for difference is < .001

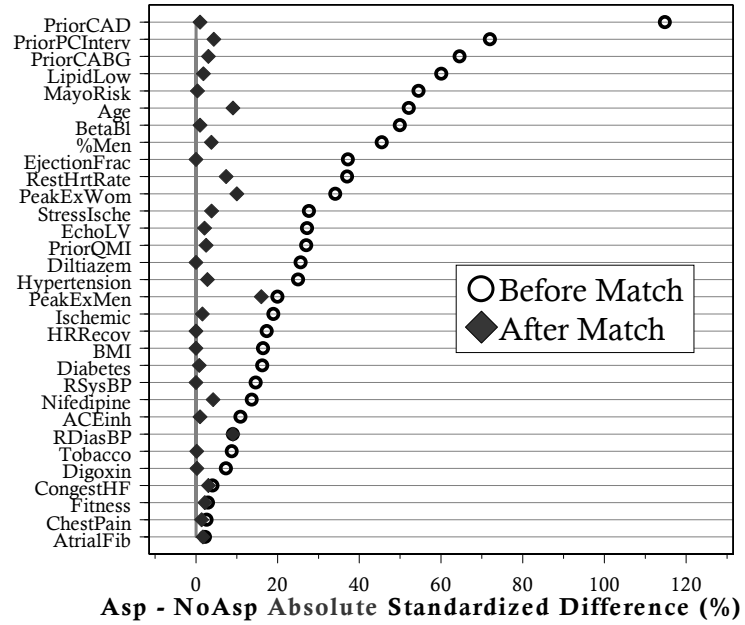
After Match:

- 352/1351 (26.1%) Aspirin users used β-blockers
- 358/1351 (26.5%) non-Aspirin users used β-blockers
- Standardized Difference is –1.0%
- P value for difference is .79

Covariate Balance for Aspirin Study



Absolute Standardized Differences



In other words, *x* and *t* are, necessarily, conditionally independent variables given the propensity score, p = Pr(*t* = 1 | *x*). This is really a very simple theorem in statistics / probability that requires only rather weak assumptions. In fact, the real "problem" in applications is simply that the functional form of the true PS is usually unknown and, thus, needs to be estimated from data!

When the conditional distributions of baseline patient characteristics and treatment choices "fail to factor" as dictated by the fundamental theorem of PS, [2], this is rightfully interpreted as clear evidence that one's estimates of the unknown, true PSs are not even approximately correct.

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4. Case Study Example: Effects of Abciximab use on both Survival and Cardiac Billing.

The (numerical and graphical) output illustrations provided here use the data from Kereiakes et al. (2000). The corresponding command file and data are distributed along with the UPS and SPS "R" functions in the files `ABCIXini.R` and `ABCIX.CSV`. In this prospective study, outcomes variables (survival and cardiac related costs) were collected via follow-up for at least 6 months on 996 PCI patients treated at the Lindner Center, Christ Hospital, Cincinnati. Rather than randomize patients to treatment, the Lindner interventionists practiced "evidence based medicine" in choosing between either augmenting or not augmenting their "usual care" for Percutaneous Coronary Intervention (PCI) with abciximab (Reopro®), a relatively expensive IIb/IIIa cascade inhibitor. Ability-to-pay was not a factor in this treatment choice in the sense that Lindner interventionists had access to "research use" abciximab.

Our objective in this "R user's manual" documentation for the UPS and SPS functions is not to fully discuss and illustrate all aspects of the abciximab case study. Rather, we simply wish to illustrate some example UPS and SPS function invocations as well as the tabular and/or graphical output that results. Readers interested in reading more about UPS and SPS analyses using the abciximab case study are referred to my "white paper," Obenchain(2006a).

Variables in the Kereiakes et al (2000) Abciximab / Lindner Data:

Description	Name	Values
Life Years Preserved = 0 if died within 6 Months or 11.6 Years given Survival for at least 6 Months	`lifepres`	Either 0 or 11.6 Years
Total Cardiac Related Billing within 12 Months of Patient's Initial PCI at Lindner Center	`cardbill`	$2,216 to $178,534 in 1997 US Dollars
Was "Usual PCI Care" augmented with Abciximab?	`abcix`	0 => No, 1 => Yes
Was a Stent (anti-collapse device) Deployed?	`stent`	0 => No, 1 => Yes
Patient Height in Centimeters	`height`	108 cm to 196 cm
Patient Gender	`female`	0 => No, 1 => Yes
Was the patient Diabetic?	`diabetic`	0 => No, 1 => Yes
Had patient suffered an Acute Myocardial Infarction within the Last Seven Days?	`acutemi`	0 => No, 1 => Yes
Left Ventricular Ejection Fraction	`ejecfrac`	0% to 90%
Number of Vessels involved in first PCI procedure	`ves1proc`	0 to 5

without reference to strata.

2. Lindner dataset

We make use of the observational data frame `lindner`, first provided with the R package **USPS**, by Obenchain (2007). The `lindner` data contain data on 996 patients treated at the Lindner Center, Christ Hospital, Cincinnati in 1997. Patients received a Percutaneous Coronary Intervention (PCI). The data consists of 10 variables. Two are outcome: `lifepres` ranges over two values, 11.4 or 0 depending on whether patients survived to six months post treatment or did not survive to six months (respectively), where 11.4 is the mean expected preserved life years for those patients who survive to six months. Secondly, `cardbill` contains the costs in 1998 dollars for the first six months (or less if patient did not survive) after treatment with the drug abciximab. For simplicity we confine our analysis to `cardbill`, focusing on the logarithm of this variate. The treatment variable is `abcix`, where 0 indicates standard PCI treatment and 1 indicates standard PCI treatment and additional treatment in some form with abciximab. Covariates include `acutemi`, 1 indicating a recent acute myocardial infarction and 0 not; `ejecfrac` for the left ventricle ejection fraction, a percentage from 0 to 90; `ves1proc` giving the number of vessels (0 to 5) involved in the initial PCI; `stent` with 1 indicating coronary stent inserted, 0 not; `diabetic` where 1 indicates that the patient has been diagnosed with diabetes, 0 not; `height` in centimeters and `female` coding the sex of the patient, 1 for female, 0 male.

3. Estimation of propensity scores, production of strata

We estimate propensity scores in two ways: via logistic regression and a recursively partitioned tree.

```
R> data("lindner")
R> attach(lindner)
R> lindner.log <- glm(abcix ~ stent + height + female + diabetic +
+    acutemi + ejecfrac + ves1proc, data = lindner, family = binomial)
R> ps <- lindner.log$fitted
R> lindner.s5 <- cut(ps, quantile(ps, seq(0, 1, 1/5)),
+    include.lowest = TRUE, labels = FALSE)
R> lindner.s10 <- cut(ps, quantile(ps, seq(0, 1, 1/10)),
+    include.lowest = TRUE, labels = FALSE)
```

In `lindner.s5` we produced five strata of roughly equal size, ten strata in `lindner.s10`. Alternatively, propensity scores can be estimated and strata defined using a recursively partitioned tree. This generally provides strata that generally differ in their sizes. We use the R function `rpart` from the package of the same name by Therneau and Atkinson (2002) to generate a tree with six bins or strata; the tree is not reproduced here.

```
R> library("rpart")
R> lindner.rpart <- rpart(abcix ~ stent + height + female + diabetic +
```

Examples

```
#Note reordering of columns, binary factor and numeric column are unchanged.
f2 <- factor(sample(c(0, 1), 20, replace = TRUE))
f4 <- factor(sample(c("a", "b", "c", "d"), 20, replace = TRUE))
cv <- rnorm(20)
X <- data.frame(f2, f4, cv)
cv.trans.psa(X)
#
f2 <- factor(sample(c('c', 'C'), 20, replace = TRUE))
f4 <- factor(sample(c("b", "A", "d", "CC"), 20, replace = TRUE))
cv <- rnorm(20)
X <- data.frame(f2, f4, cv)
cv.trans.psa(X)
```

`lindner` *Data on 996 initial Percutaneous Coronary Interventions (PCIs) performed in 1997 at the Lindner Center, Christ Hospital, Cincinnati.*

Description

Data from an observational study of 996 patients receiving a PCI at Ohio Heart Health in 1997 and followed for at least 6 months by the staff of the Lindner Center. This is a landmark dataset in the literature on propensity score adjustment for treatment selection bias due to practice of evidence based medicine; patients receiving abciximab tended to be more severely diseased than those who did not receive a IIb/IIIa cascade blocker.

Usage

```
data(lindner)
```

Format

A data frame with 996 observations on the following 10 variables, no NAs.

`lifepres` Mean life years preserved due to survival for at least 6 months following PCI; numeric value of either 11.4 or 0.

`cardbill` Cardiac related costs incurred within 6 months of patient's initial PCI; numeric value in 1998 dollars; costs were truncated by death for the 26 patients with lifepres == 0.

`abcix` Numeric treatment selection indicator; 0 implies usual PCI care alone; 1 implies usual PCI care deliberately augmented by either planned or rescue treatment with abciximab.

`stent` Coronary stent deployment; numeric, with 1 meaning YES and 0 meaning NO.

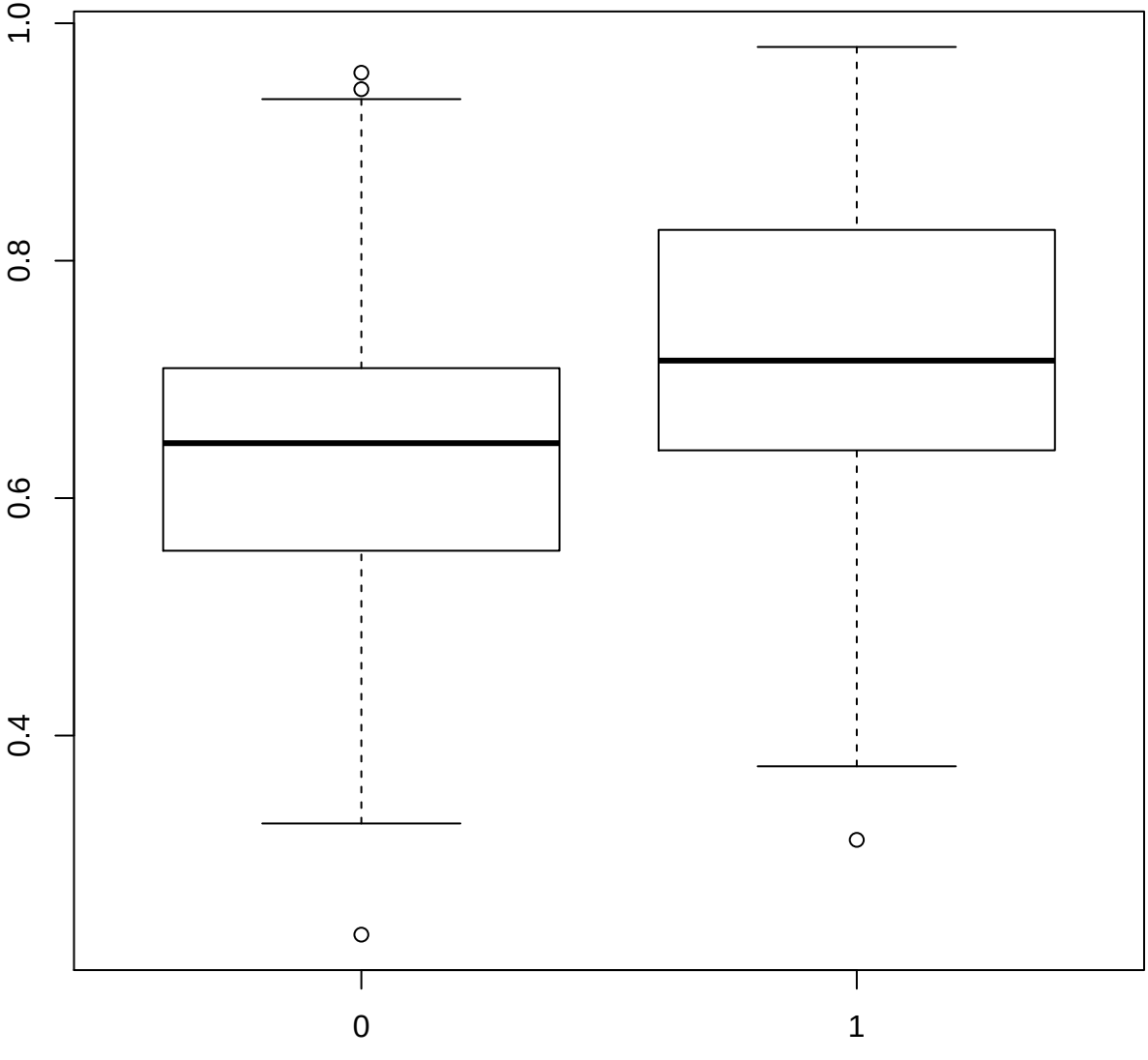
`height` Height in centimeters; numeric integer from 108 to 196.

`female` Female gender; numeric, with 1 meaning YES and 0 meaning NO.

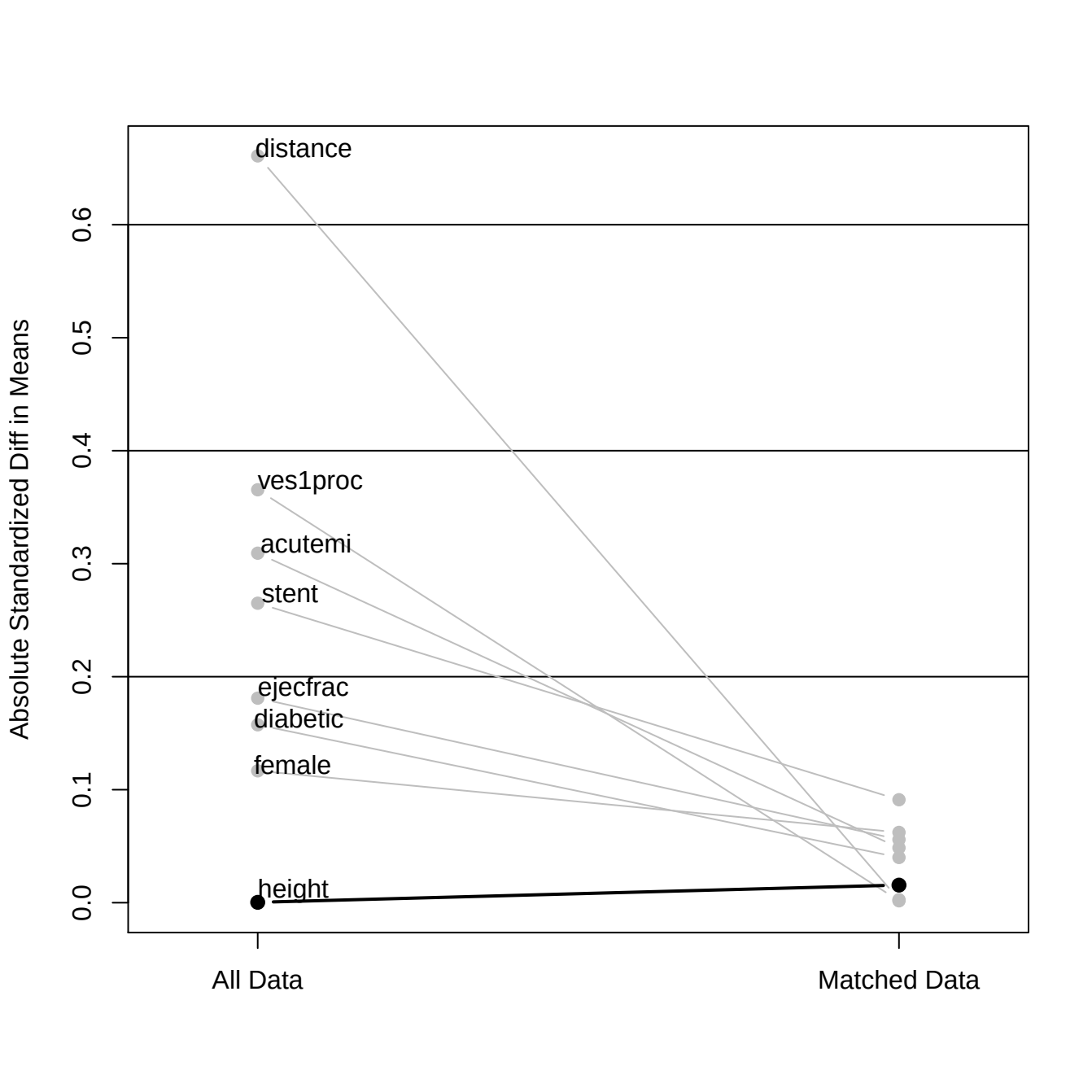
```
###### Week 2 Computing Corner, Rogosa R-session

> library(PSAgraphics)
> data(lindner)
> attach(lindner)
> dim(lindner)
[1] 996  10
> head(lindner)
  lifepres cardbill abcix stent height female diabetic acutemi ejecfrac   ves1proc
1      0.0    14301     1     0    163      1        1       0       56          1
2     11.6     3563     1     0    168      0        0       0       56          1
3     11.6     4694     1     0    188      0        0       0       50          1
4     11.6     7366     1     0    175      0        1       0       50          1
5     11.6     8247     1     0    168      1        0       0       55          1
6     11.6     8319     1     0    178      0        0       0       50          1

> str(lindner)
'data.frame':   996 obs. of  10 variables:
 $ lifepres: num  0 11.6 11.6 11.6 11.6 11.6 11.6 11.6 11.6 11.6 ...
 $ cardbill: int  14301 3563 4694 7366 8247 8319 8410 8517 8763 8823 ...
 $ abcix   : int  1 1 1 1 1 1 1 1 1 1 ...
 $ stent   : int  0 0 0 0 0 0 0 0 0 0 ...
 $ height  : int  163 168 188 175 168 178 185 173 152 180 ...
 $ female  : int  1 0 0 0 1 0 0 1 1 0 ...
 $ diabetic: int  1 0 0 1 0 0 0 0 0 0 ...
 $ acutemi : int  0 0 0 0 0 0 0 0 0 0 ...
 $ ejecfrac: int  56 56 50 50 55 50 58 30 60 60 ...
 $ ves1proc: int  1 1 1 1 1 1 1 1 1 1 ...
> table(abcix)
abcix
  0   1
298 698

                    ####### look at outcomes
> tapply(cardbill, abcix, mean)
       0        1
14614.22 16126.68
> tapply(log(cardbill), abcix, mean) # analyses done in log scale
       0        1
9.398158 9.581579

> t.test(log(cardbill) ~ abcix) # treatment leads to higher bills?

        Welch Two Sample t-test

data:  log(cardbill) by abcix
t = -5.2317, df = 461, p-value = 2.554e-07
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.2523168 -0.1145249
sample estimates:
mean in group 0 mean in group 1
       9.398158        9.581579

> tapply(lifepres, abcix, mean)
       0        1
11.01611 11.41719

> table(lifepres, abcix)
        abcix
lifepres   0   1
    0     15  11
    11.6 283 687
> chisq.test(lifepres, abcix)

        Pearson's Chi-squared test with Yates' continuity correction

data:  lifepres and abcix
```

```
X-squared = 8.5077, df = 1, p-value = 0.003536

> prop.table(table(lifepres, abcix),2) # look at relative risk
        abcix
lifepres          0          1
    0    0.05033557 0.01575931
    11.6 0.94966443 0.98424069

> library(MatchIt)  ## try full matching
> m2full = matchit(abcix ~ stent + height + female + diabetic + acutemi + ejecfrac + ves1proc,
                                                              data = lindner, method = "full")
Loading required package: optmatch
Loading required package: survival

> detach(lindner)
> m2full.dat = match.data(m2full)
> attach(m2full.dat)

> boxplot(distance ~ abcix) # propensity score overlap
> # can also do overlapping histogram as in week 1

> summary(m2full)   # check balance improvement
Call: matchit(formula = abcix ~ stent + height + female + diabetic +
    acutemi + ejecfrac + ves1proc, data = lindner, method = "full")

Summary of balance for all data:
          Means Treated Means Control Mean Diff eQQ Med eQQ Mean eQQ Max
distance         0.7265         0.6406    0.0859  0.0814   0.0852  0.1209
stent            0.7049         0.5839    0.1210  0.0000   0.1208  1.0000
height         171.4427       171.4463   -0.0036  0.0000   0.5638 20.0000
female           0.3309         0.3859   -0.0550  0.0000   0.0537  1.0000
diabetic         0.2049         0.2685   -0.0636  0.0000   0.0638  1.0000
acutemi          0.1791         0.0604    0.1187  0.0000   0.1174  1.0000
ejecfrac        50.4026        52.2886   -1.8860  1.0000   2.0503 20.0000
ves1proc         1.4628         1.2047    0.2581  0.0000   0.2651  1.0000


Summary of balance for matched data:
          Means Treated Means Control Mean Diff eQQ Med eQQ Mean eQQ Max
distance         0.7265         0.7262    0.0003  0.0068   0.0077  0.0798
stent            0.7049         0.7465   -0.0416  0.0000   0.0248  1.0000
height         171.4427       171.6093   -0.1666  0.0000   0.9548 15.0000
female           0.3309         0.3016    0.0293  0.0000   0.0244  1.0000
diabetic         0.2049         0.2210   -0.0162  0.0000   0.0068  1.0000
acutemi          0.1791         0.1605    0.0186  0.0000   0.0300  1.0000
ejecfrac        50.4026        50.9846   -0.5821  0.0000   0.9524 20.0000
ves1proc         1.4628         1.4616    0.0012  0.0000   0.0324  1.0000

Percent Balance Improvement:
          Mean Diff.  eQQ Med  eQQ Mean eQQ Max
distance    99.5977  91.6649   91.0174 33.9503
stent       65.6178   0.0000   79.4711  0.0000
height   -4508.6968   0.0000  -69.3633 25.0000
female      46.6926   0.0000   54.5550  0.0000
diabetic    74.5771   0.0000   89.3347  0.0000
acutemi     84.3069   0.0000   74.4571  0.0000
ejecfrac    69.1376 100.0000   53.5491  0.0000
ves1proc    99.5373   0.0000   87.7782  0.0000

Sample sizes:
          Control Treated
All           298     698
Matched       298     698
Unmatched       0       0
Discarded       0       0
```

Propensity score boxplot



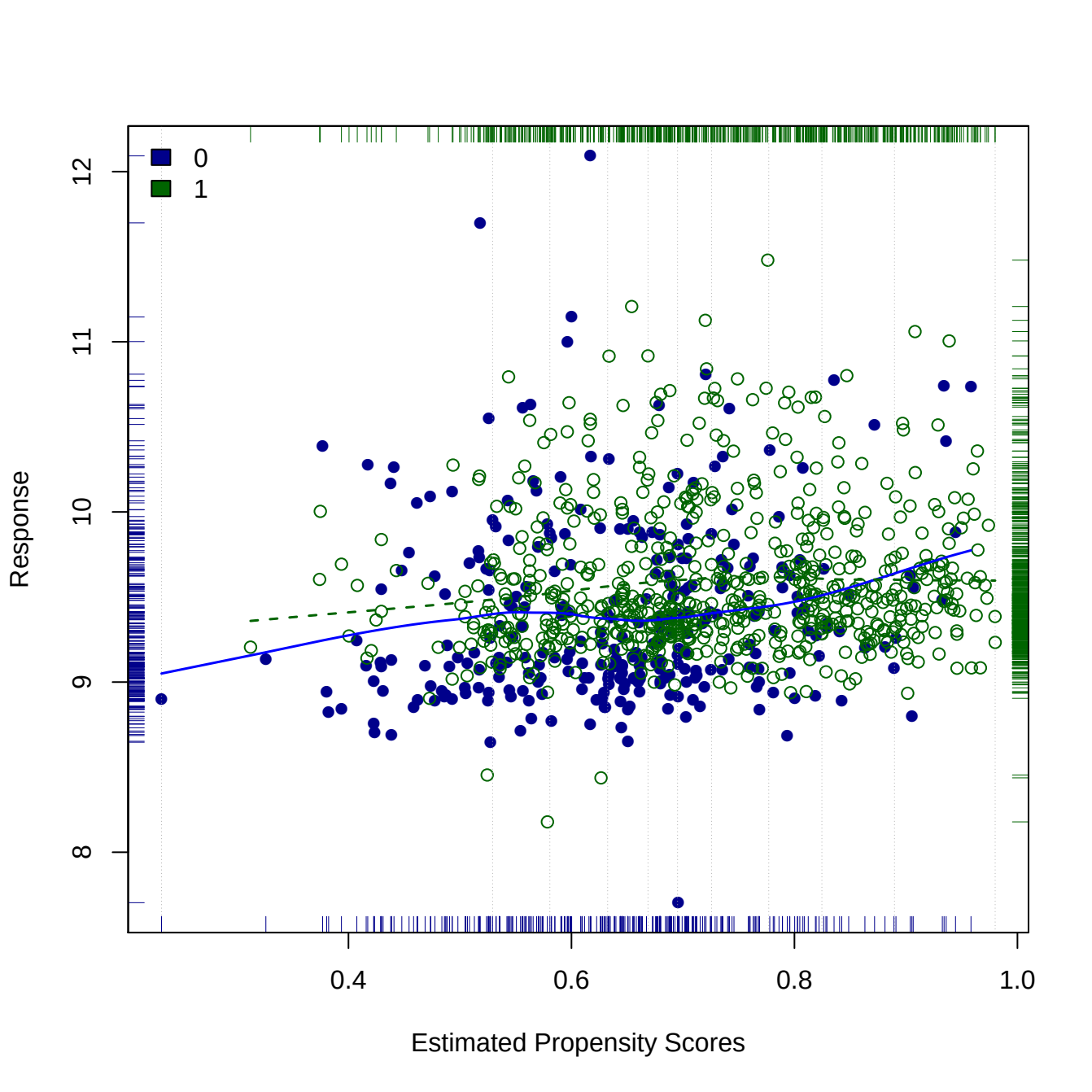
```
> summary(m2full, standardize = T)  # look at standardized mean diffs < .1
Call: matchit(formula = abcix ~ stent + height + female + diabetic +
    acutemi + ejecfrac + ves1proc, data = lindner, method = "full")

Summary of balance for all data:
         Means Treated Means Control Std. Mean Diff. eCDF Med eCDF Mean eCDF Max
distance        0.7265        0.6406          0.6609   0.1777    0.1714   0.2760
stent           0.7049        0.5839          0.2651   0.0605    0.0605   0.1210
height        171.4427      171.4463         -0.0003   0.0060    0.0079   0.0250
female          0.3309        0.3859         -0.1167   0.0275    0.0275   0.0550
diabetic        0.2049        0.2685         -0.1574   0.0318    0.0318   0.0636
acutemi         0.1791        0.0604          0.3093   0.0593    0.0593   0.1187
ejecfrac       50.4026       52.2886         -0.1810   0.0114    0.0356   0.1138
ves1proc        1.4628        1.2047          0.3654   0.0091    0.0433   0.1884


Summary of balance for matched data:
         Means Treated Means Control Std. Mean Diff. eCDF Med eCDF Mean eCDF Max
distance        0.7265        0.7262          0.0027   0.0128    0.0123   0.0300
stent           0.7049        0.7465         -0.0911   0.0240    0.0240   0.0480
height        171.4427      171.6093         -0.0156   0.0128    0.0144   0.0444
female          0.3309        0.3016          0.0622   0.0094    0.0094   0.0188
diabetic        0.2049        0.2210         -0.0400   0.0044    0.0044   0.0088
acutemi         0.1791        0.1605          0.0485   0.0080    0.0080   0.0160
ejecfrac       50.4026       50.9846         -0.0559   0.0080    0.0109   0.0604
ves1proc        1.4628        1.4616          0.0017   0.0044    0.0071   0.0196

Percent Balance Improvement:
         Std. Mean Diff.  eCDF Med eCDF Mean eCDF Max
distance         99.5977   92.7960   92.8062  89.1302
stent            65.6178   60.3235   60.3235  60.3235
height        -4508.6968 -112.9961  -81.7392 -77.8086
female           46.6926   65.7936   65.7936  65.7936
diabetic         74.5771   86.1603   86.1603  86.1603
acutemi          84.3069   86.5184   86.5184  86.5184
ejecfrac         69.1376   29.9650   69.4106  46.9404
ves1proc         99.5373   51.4731   83.5345  89.5977

Sample sizes:
          Control Treated
All           298     698
Matched       298     698
Unmatched       0       0
Discarded       0       0

> plot(summary(m2full, standardize = T))  # see plot, balance improvement

> head(m2full.dat)
  lifepres cardbill abcix stent height female diabetic acutemi ejecfrac ves1proc  distance weights subc
1      0.0    14301     1     0    163      1        1       0       56        1 0.4079170       1
2     11.6     3563     1     0    168      0        0       0       56        1 0.5784602       1
3     11.6     4694     1     0    188      0        0       0       50        1 0.5244469       1
4     11.6     7366     1     0    175      0        1       0       50        1 0.4727311       1
5     11.6     8247     1     0    168      1        0       0       55        1 0.4930466       1
6     11.6     8319     1     0    178      0        0       0       50        1 0.5625524       1

> table(subclass) #267 subclasses (698 treated) mostly small #> table(subclass, abcix) breakdown
subclass
  1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20  21  22  23  24  25  26
  3   4   2   2   5   8   3   2   4  11   5   2   2   2   3   3   5   2   3   4   6   3   3   7   2   9
 33  34  35  36  37  38  39  40  41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58
  8   2   3   6   2   3   5   2   2   3   2   4   2   4   2   6   2   5   4   5   4   2   3   2   2   9
 65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80  81  82  83  84  85  86  87  88  89  90
  2   3   4   2   2   2   3   2   4   2   2   6   2   2   2   2   2   2   5   6   2   5   2   3   2   3
 97  98  99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122
  2   2   2   4   2   2   2   4   3   2   4   2   6   4   3  17   2   3   5   2   3   5   2   5   7  10
```


Absolute Standardized Diff in Means
0.0
0.1
0.2
0.3
0.4
0.5
0.6
distance
ves1proc
acutemi
stent
ejecfrac
diabetic
female
height
All Data
Matched Data

```
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154
 17   4   8   8   4   4   6   2   2   3   3   3   4   5   2   2   6   6   4   7  10   3   2   2   8   2
161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186
  3   2   2   2   4   3   3   2   2   3   3   3   2   2   2   6   2   3   2   3  18   8  17  13  10   5
193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218
  2   2  10   2  15   2   4   9   3   2   7   3   4   4   3   2   5   2   2   4   7   2   2   2   4   2
225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250
  2   2   2   2   2   5   2   4   2   2   2   3   7   2   2   2   2   3   2   2   2   2   2   3   2   2
257 258 259 260 261 262 263 264 265 266 267
  2   2   2   2   2   2   2   2   5   2   2
> fivenum(table(subclass))
subclass
  3 154 266 147 190
  2   2   2   4  18

> library(lme4) compare outcomes over subclasses, log(cardbill) outcome
> mfullL.lmer = lmer(log(cardbill) ~ abcix + (1 + abcix|subclass), data = m2full.dat)
> summary(mfullL.lmer)
Linear mixed model fit by REML ['lmerMod']
Formula: log(cardbill) ~ abcix + (1 + abcix | subclass)   Data: m2full.dat
REML criterion at convergence: 1268.2

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.2325 -0.6183 -0.2411  0.4093  4.2623

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 subclass (Intercept) 0.09744  0.3122
          abcix       0.06809  0.2609   -0.98
 Residual             0.18034  0.4247
Number of obs: 996, groups:  subclass, 267

Fixed effects:
            Estimate Std. Error t value
(Intercept)  9.40576    0.03159  297.71
abcix        0.16440    0.03417    4.81

Correlation of Fixed Effects:
      (Intr)
abcix -0.866

> confint(mfullL.lmer)
Computing profile confidence intervals ...
                  2.5 %     97.5 %
.sig01       0.22608548  0.3882918
.sig02      -1.00000000 -0.8884949
.sig03       0.15108346  0.3579166
.sigma       0.40090446  0.4492170
(Intercept)  9.34378346  9.4678932
abcix        0.09694981  0.2327080
> exp(confint(mfullL.lmer))
Computing profile confidence intervals ...
                   2.5 %       97.5 %
.sig01      1.253683e+00 1.474460e+00
.sig02      3.678794e-01 4.112743e-01
.sig03      1.163094e+00 1.430346e+00
.sigma      1.493175e+00 1.567085e+00
(Intercept) 1.142756e+04 1.293760e+04
abcix       1.101805e+00 1.262013e+00


> # note mfull.lmer = lmer(cardbill ~ abcix + (1 + abcix|subclass), data = m2full.dat)
# gives non-sig result CI: abcix  -497.3218  3009.1425564

##### treat lifepres as a 0,1 outcome
```

```
> mfull.glmer = glmer(as.factor(lifepres) ~ abcix + (1 + abcix|subclass),
                                                  family = binomial, data = m2full.dat)
> summary(mfull.glmer)  # in log-odds metric
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial  ( logit )
Formula: as.factor(lifepres) ~ abcix + (1 + abcix | subclass)   Data: m2full.dat

     AIC      BIC   logLik deviance df.resid
   233.8    258.3   -111.9    223.8      991

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.3416  0.0110  0.0112  0.2300  0.8194

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 subclass (Intercept)  0.003532 0.05943
          abcix       42.902893 6.55003  1.00
Number of obs: 996, groups:  subclass, 267

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   2.9389     0.2659  11.053  < 2e-16 ***
abcix         6.0279     0.8381   7.192 6.39e-13 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:
      (Intr)
abcix -0.305
> exp(fixef(mfull.glmer))  #odds of survival
(Intercept)       abcix
   18.89487   414.82764
```

```
####### alternative, matching by regression interpolation, ancova vs blocking
> # propensity ancova, propensity score (distance) as covariate
> pancL = lm(log(cardbill) ~ abcix + distance, data =m2full.dat)
> summary(pancL)
Call: lm(formula = log(cardbill) ~ abcix + distance, data = m2full.dat)

Residuals:
    Min      1Q  Median      3Q     Max
-1.7137 -0.2979 -0.1257  0.2069  2.7026

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  9.17752    0.07759 118.286  < 2e-16 ***
abcix        0.15384    0.03322   4.630 4.14e-06 ***
distance     0.34443    0.11378   3.027  0.00253 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.4589 on 993 degrees of freedom
Multiple R-squared:  0.04107,   Adjusted R-squared:  0.03914
F-statistic: 21.26 on 2 and 993 DF,  p-value: 9.075e-10

> exp(confint(pancL))  # almost same result as fullmatch lmer
                  2.5 %       97.5 %
(Intercept) 8310.388799 11268.542739
abcix          1.092686     1.244877
distance       1.128783     1.764223

> pLancL = loess.psa(log(cardbill), abcix, distance) # use smoothers rather than straight-line
> pLancL   # similar result; loess.psa from PSAgraphics also generates plot
$ATE
[1] 0.1279487
```


0
1
Response
12
11
10
9
8
0.4
0.6
0.8
1.0
Estimated Propensity Scores

```
$se.wtd
[1] 0.04151743

$CI95
[1] 0.04491388 0.21098361

# compare a smoother ancova package fANCOVA

> install.packages("fANCOVA")
> library(fANCOVA)
> pLanc2L = loess.ancova(distance, log(cardbill), abcix)
> pLanc2L
$linear.fit
                 [,1]
(Intercept) 9.3863321
group1      0.1522632

$smooth.fit
Call:
loess(formula = lm.res ~ x, span = span1, degree = degree, family = family)

Number of Observations: 996
Equivalent Number of Parameters: 5.28
Residual Standard Error: 0.4581


> pLanc2 = loess.ancova(distance, cardbill, abcix) #about same result
> summary(pLanc2)
           Length Class  Mode
linear.fit  2     -none- numeric
smooth.fit 17     loess  list
> pLanc2
$linear.fit
                 [,1]
(Intercept) 14605.635
group1       1127.854

$smooth.fit
Call:
loess(formula = lm.res ~ x, span = span1, degree = degree, family = family)

Number of Observations: 996
Equivalent Number of Parameters: 3.89
Residual Standard Error: 11160
```

lindner {PSAgraphics} R Documentation

Data on 996 initial Percutaneous Coronary Interventions (PCIs) performed in 1997 at the Lindner Center, Christ Hospital, Cincinnati.

Description

Data from an observational study of 996 patients receiving a PCI at Ohio Heart Health in 1997 and followed for at least 6 months by the staff of the Lindner Center. This is a landmark dataset in the literature on propensity score adjustment for treatment selection bias due to practice of evidence based medicine; patients receiving abciximab tended to be more severely diseased than those who did not receive a IIb/IIIa cascade blocker.

Usage data(lindner)

Format
A data frame with 996 observations on the following 10 variables, no NAs.

lifepres

Mean life years preserved due to survival for at least 6 months following PCI; numeric value of either 11.4 or 0. cardbill

Cardiac related costs incurred within 6 months of patient's initial PCI; numeric value in 1998 dollars; costs were truncated by death for the 26 patients with lifepres == 0. abcix

Numeric treatment selection indicator; 0 implies usual PCI care alone; 1 implies usual PCI care deliberately augmented by either planned or rescue treatment with abciximab. stent

Coronary stent deployment; numeric, with 1 meaning YES and 0 meaning NO. height

Height in centimeters; numeric integer from 108 to 196. female

Female gender; numeric, with 1 meaning YES and 0 meaning NO. diabetic

Diabetes mellitus diagnosis; numeric, with 1 meaning YES and 0 meaning NO. acutemi

Acute myocardial infarction within the previous 7 days; numeric, with 1 meaning YES and 0 meaning NO. ejecfrac

Left ejection fraction; numeric value from 0 percent to 90 percent. ves1proc

Number of vessels involved in the patient's initial PCI procedure; numeric integer from 0 to 5.

Source Package USPS, by R. L. Obenchain.

Lindner Data (PCI)

Stat 266 week 2

```
###### Week 2 Computing Corner, Rogosa R-session
> library(PSAgraphics)  > data(lindner)  > attach(lindner)
> dim(lindner)
[1] 996  10
> head(lindner)
  lifepres cardbill abcix stent height female diabetic acutemi ejecfrac vesiproc
1      0.0    14301     1     0    163      1        1       0       56        1
2     11.6     3563     1     0    168      0        0       0       56        1
3     11.6     4694     1     0    188      0        0       0       50        1
4     11.6     7366     1     0    175      0        1       0       50        1
5     11.6     8247     1     0    168      1        0       0       55        1
6     11.6     8319     1     0    178      0        0       0       50        1
> table(abcix)
abcix
  0   1
298 698
```

mostly treated (evidence based medicine)

```
                    ####### look at outcomes
> tapply(cardbill, abcix, mean)  > tapply(log(cardbill), abcix, mean) # analyses done in log scale
       0        1                        0        1
14614.22 16126.68                 9.398158 9.581579
> t.test(log(cardbill) ~ abcix) # treatment leads to higher bills?
        Welch Two Sample t-test
data:  log(cardbill) by abcix
t = -5.2317, df = 461, p-value = 2.554e-07
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:  -0.2523168 -0.1145249
mean in group 0 mean in group 1
       9.398158        9.581579

> table(lifepres, abcix)
        abcix
lifepres   0   1
    0     15  11
    11.6 283 687
> chisq.test(lifepres, abcix)
        Pearson's Chi-squared test with Yates' continuity correction
data:  lifepres and abcix
X-squared = 8.5077, df = 1, p-value = 0.003536
> prop.table(table(lifepres, abcix),2) # look at relative risk
        abcix
lifepres          0          1
    0    0.05033557 0.01575931
    11.6 0.94966443 0.98424069
```

describe outcomes then set aside

on association

```
> library(MatchIt)  ## try full matching
> m2full = matchit(abcix ~ stent + height + female + diabetic + acutemi + ejecfrac + vesiproc,
                                                    data = lindner, method = "full")
> m2full.dat = match.data(m2full) > attach(m2full.dat) # get matched data (distance, subclass)

> boxplot(distance ~ abcix) # propensity score overlap; also overlapping histogram as in week 1
```

see figure

```
> summary(m2full)   # check balance improvement
Call: matchit(formula = abcix ~ stent + height + female + diabetic +
    acutemi + ejecfrac + vesiproc, data = lindner, method = "full")
Summary of balance for all data:
         Means Treated Means Control Mean Diff eQQ Med eQQ Mean eQQ Max
distance        0.7265        0.6406    0.0859  0.0814   0.0852  0.1209
stent           0.7049        0.5839    0.1210  0.0000   0.1208  1.0000
height        171.4427      171.4463   -0.0036  0.0000   0.5638 20.0000
female          0.3309        0.3859   -0.0550  0.0000   0.0537  1.0000
diabetic        0.2049        0.2685   -0.0636  0.0000   0.0638  1.0000
acutemi         0.1791        0.0604    0.1187  0.0000   0.1174  1.0000
ejecfrac       50.4026       52.2886   -1.8860  1.0000   2.0503 20.0000
vesiproc        1.4628        1.2047    0.2581  0.0000   0.2651  1.0000
Summary of balance for matched data:
         Means Treated Means Control Mean Diff eQQ Med eQQ Mean eQQ Max
distance        0.7265        0.7262    0.0003  0.0068   0.0077  0.0798
```

```
stent           0.7049        0.7465   -0.0416  0.0000   0.0248  1.0000
height        171.4427      171.6093   -0.1666  0.0000   0.9548 15.0000
female          0.3309        0.3016    0.0293  0.0000   0.0244  1.0000
diabetic        0.2049        0.2210   -0.0162  0.0000   0.0068  1.0000
acutemi         0.1791        0.1605    0.0186  0.0000   0.0300  1.0000
ejecfrac       50.4026       50.9846   -0.5821  0.0000   0.9524 20.0000
ves1proc        1.4628        1.4616    0.0012  0.0000   0.0324  1.0000
Percent Balance Improvement:
           Mean Diff.  eQQ Med eQQ Mean eQQ Max
distance      99.5977  91.6649  91.0174 33.9503
stent         65.6178   0.0000  79.4711  0.0000
height     -4508.6968   0.0000 -69.3633 25.0000
female        46.6926   0.0000  54.5550  0.0000
diabetic      74.5771   0.0000  89.3347  0.0000
acutemi       84.3069   0.0000  74.4571  0.0000
ejecfrac      69.1376 100.0000  53.5491  0.0000
ves1proc      99.5373   0.0000  87.7782  0.0000
           Control Treated
All            298     698
Matched        298     698
Unmatched        0       0
Discarded        0       0

> summary(m2full, standardize = T)  # look at standardized mean diffs < .1
Summary of balance for matched data:
           Means Treated Means Control Std. Mean Diff. eCDF Med eCDF Mean eCDF Max
distance          0.7265         0.7262          0.0027   0.0128    0.0123   0.0300
stent             0.7049         0.7465         -0.0911   0.0240    0.0240   0.0480
height          171.4427       171.6093         -0.0156   0.0128    0.0144   0.0444
female            0.3309         0.3016          0.0622   0.0094    0.0094   0.0188
diabetic          0.2049         0.2210         -0.0400   0.0044    0.0044   0.0088
acutemi           0.1791         0.1605          0.0485   0.0080    0.0080   0.0160
ejecfrac         50.4026        50.9846         -0.0559   0.0080    0.0109   0.0604
ves1proc          1.4628         1.4616          0.0017   0.0044    0.0071   0.0196

> plot(summary(m2full, standardize = T))  # see plot, balance improvement

> head(m2full.dat)
> table(subclass) #267 subclasses (698 treated) mostly small #> table(subclass, abcix) breakdown
> fivenum(table(subclass))
subclass
  3 154 266 147 190
  2   2   2   4  18

> library(lme4) compare outcomes over subclasses, log(cardbill) outcome
> mfullL.lmer = lmer(log(cardbill) ~ abcix + (1 + abcix|subclass), data = m2full.dat)
> summary(mfullL.lmer)
Formula: log(cardbill) ~ abcix + (1 + abcix | subclass)   Data: m2full.dat
Random effects:
 Groups   Name        Variance Std.Dev. Corr
 subclass (Intercept) 0.09744  0.3122
          abcix       0.06809  0.2609   -0.98
 Residual             0.18034  0.4247
Number of obs: 996, groups:  subclass, 267

Fixed effects:
            Estimate Std. Error t value
(Intercept)  9.40576    0.03159  297.71
abcix        0.16440    0.03417    4.81
> confint(mfullL.lmer)
Computing profile confidence intervals ...
                2.5 %     97.5 %
.sig01      0.22608548  0.3882918
.sig02     -1.00000000 -0.8884949
.sig03      0.15108346  0.3579166
.sigma      0.40090446  0.4492170
(Intercept) 9.34378346  9.4678932
```

see picture

```
abcix         0.09694981  0.2327080
> exp(confint(mfullL.lmer))
(Intercept) 1.142756e+04 1.293760e+04
abcix       1.101805e+00 1.262013e+00
```

in $ < vending machine

```
> # note mfull.lmer = lmer(cardbill ~ abcix + (1 + abcix|subclass), data = m2full.dat)
# gives non-sig result CI: abcix  -497.3218  3009.1425564

##### treat lifepres as a 0,1 outcome
> mfull.glmer = glmer(as.factor(lifepres) ~ abcix + (1 + abcix|subclass),
                                                    family = binomial, data = m2full.dat)
> summary(mfull.glmer)  # in log-odds metric
Generalized linear mixed model  Family: binomial  ( logit )
Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 subclass (Intercept)  0.003532 0.05943
          abcix       42.902893 6.55003  1.00
Number of obs: 996, groups:  subclass, 267

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   2.9389     0.2659  11.053  < 2e-16 ***
abcix         6.0279     0.8381   7.192 6.39e-13 ***
```

log odds

```
> exp(fixef(mfull.glmer))  #odds of survival
(Intercept)       abcix
   18.89487   414.82764

####### alternative, matching by regression interpolation, ancova vs blocking
> # propensity ancova, propensity score (distance) as covariate
> pancL = lm(log(cardbill) ~ abcix + distance, data =m2full.dat)
> summary(pancL)
Call: lm(formula = log(cardbill) ~ abcix + distance, data = m2full.dat)
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  9.17752    0.07759 118.286  < 2e-16 ***
abcix        0.15384    0.03322   4.630 4.14e-06 ***
distance     0.34443    0.11378   3.027  0.00253 **
---
> exp(confint(pancL))  # almost same result as fullmatch lmer
                 2.5 %       97.5 %
(Intercept) 8310.388799 11268.542739
abcix          1.092686     1.244877
distance       1.128783     1.764223

> pLancL = loess.psa(log(cardbill), abcix, distance) # use smoothers rather than straight-line
> pLancL   # similar result; loess.psa from PSAgraphics also generates plot
$ATE            $se.wtd           $CI95
[1] 0.1279487   [1] 0.04151743    [1] 0.04491388 0.21098361

# compare a smoother ancova package fANCOVA
> install.packages("fANCOVA") > library(fANCOVA)
> pLanc2L = loess.ancova(distance, log(cardbill), abcix) #about same result
> pLanc2L
$linear.fit
                [,1]
(Intercept) 9.3863321
group1      0.1522632

$smooth.fit
Call: loess(formula = lm.res ~ x, span = span1, degree = degree, family = family)
```

ancova
straight-line

see picture
loess
ancova

full session posted.
move in RQ