

# 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 veslproc
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

*describe outcomes*  
*men set aside*

```
> 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

*an association*

```
> 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 + veslproc,
                  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 + veslproc, 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
veslproc	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
veslproc	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
veslproc	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
veslproc	1.4628	1.4616	0.0017	0.0044	0.0071	0.0196

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

see picture

```
> 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

```

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 **
---

```

*ancova  
straight-line*

```

> 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

```

*see picture  
loess*

```

# 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

```

*ancova*

```

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

```

*full session posted.  
more in RQ*