Standardized Mean Differences (SMD)

Shawn Garbett

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Purpose

To create a SMD statistic in the style of tableone inside of tangram. See 'Using standardized mean differences' by Kazuki Yoshida for original work and description of method. This is a reproduction of the original document using `tangram`.

Load Packages and Data

The right heart catheterization dataset is available at http://biostat.mc.vanderbilt.edu/wiki/Main/DataSets . This dataset was originally used in Connors et al. JAMA 1996;276:889-897, and has been made publicly available.

```
library(Matching)
```

```
## Loading required package: MASS
```

```
## ##
## ##  Matching (Version 4.9-3, Build Date: 2018-05-03)
## ##  See http://sekhon.berkeley.edu/matching for additional documentation.
## ##  Please cite software as:
## ##   Jasjeet S. Sekhon. 2011. ``Multivariate and Propensity Score Matching
## ##   Software with Automated Balance Optimization: The Matching package for R.''
## ##   Journal of Statistical Software, 42(7): 1-52.
## ##
```

```
library(tangram)
```

```
## Loading required package: R6
```

```
## Loading required package: magrittr
```

```
## Loading required package: knitr
```

```
## Right heart cath dataset
rhc <- read.csv("http://biostat.mc.vanderbilt.edu/wiki/pub/Main/DataSets/rhc.csv")
```

Unmatched table

```
vars <- c("age","sex","race","edu","income","ninsclas","cat1","das2d3pc","dnr1",
          "ca","surv2md1","aps1","scoma1","wtkilo1","temp1","meanbp1","resp1",
          "hrt1","pafi1","paco21","ph1","wblc1","hema1","sod1","pot1","crea1",
          "bili1","alb1","resp","card","neuro","gastr","renal","meta","hema",
          "seps","trauma","ortho","cardiohx","chfhx","dementhx","psychhx",
          "chrpulhx","renalhx","liverhx","gibledhx","malighx","immunhx",
          "transhx","amihx")
```

```
formula <- paste0("swang1~", paste0(vars, collapse="+"))
```

```
tangram(formula, rhc, "unmatched", smd, "Unmatched", style="nejm", pct_width=0.5)
```

Unmatched

	N	No RHC	RHC	SMD
		(N=3551)	(N=2184)	
age	5735	61.76 (17.29)	60.75 (15.63)	0.061
sex : Male	5735	1914 (53.90)	1278 (58.52)	0.093
race	5735			0.036
black		585 (16.47)	335 (15.34)	
other		213 (6.00)	142 (6.50)	
white		2753 (77.53)	1707 (78.16)	
edu	5735	11.57 (3.13)	11.86 (3.16)	0.091
income	5735			0.142
> 50k		257 (7.24)	194 (8.88)	
11-25k		713 (20.08)	452 (20.70)	
25-50k		500 (14.08)	393 (17.99)	
Under 11k		2081 (58.60)	1145 (52.43)	
ninsclas	5735			0.194
Medicaid		454 (12.79)	193 (8.84)	
Medicare		947 (26.67)	511 (23.40)	
Medicare & Medicaid		251 (7.07)	123 (5.63)	
No insurance		186 (5.24)	136 (6.23)	
Private		967 (27.23)	731 (33.47)	
Private & Medicare		746 (21.01)	490 (22.44)	
cat1	5735			0.583
ARF		1581 (44.52)	909 (41.62)	
CHF		247 (6.96)	209 (9.57)	
Cirrhosis		175 (4.93)	49 (2.24)	
Colon Cancer		6 (0.17)	1 (0.05)	
Coma		341 (9.60)	95 (4.35)	
COPD		399 (11.24)	58 (2.66)	
Lung Cancer		34 (0.96)	5 (0.23)	
MOSF w/Malignancy		241 (6.79)	158 (7.23)	
MOSF w/Sepsis		527 (14.84)	700 (32.05)	
das2d3pc	5735	20.37 (5.48)	20.70 (5.03)	0.063
dnr1 : Yes	5735	499 (14.05)	155 (7.10)	0.228
ca	5735			0.107
Metastatic		261 (7.35)	123 (5.63)	
No		2652 (74.68)	1727 (79.08)	
Yes		638 (17.97)	334 (15.29)	
surv2md1	5735	0.61 (0.19)	0.57 (0.20)	0.198
aps1	5735	50.93 (18.81)	60.74 (20.27)	0.501
scoma1	5735	22.25 (31.37)	18.97 (28.26)	0.110
wtkilo1	5735	65.04 (29.50)	72.36 (27.73)	0.256
temp1	5735	37.63 (1.74)	37.59 (1.83)	0.021
meanbp1	5735	84.87 (38.87)	68.20 (34.24)	0.455
resp1	5735	28.98 (13.95)	26.65 (14.17)	0.165
hrt1	5735	112.87 (40.94)	118.93 (41.47)	0.147
pafi1	5735	240.63 (116.66)	192.43 (105.54)	0.433
paco21	5735	39.95 (14.24)	36.79 (10.97)	0.249
ph1	5735	7.39 (0.11)	7.38 (0.11)	0.120
wblc1	5735	15.26 (11.41)	16.27 (12.55)	0.084
hema1	5735	32.70 (8.79)	30.51 (7.42)	0.269
sod1	5735	137.04 (7.68)	136.33 (7.60)	0.092
pot1	5735	4.08 (1.04)	4.05 (1.01)	0.027
crea1	5735	1.92 (2.03)	2.47 (2.05)	0.270
bili1	5735	2.00 (4.43)	2.71 (5.33)	0.145
alb1	5735	3.16 (0.67)	2.98 (0.93)	0.230
resp : Yes	5735	1481 (41.71)	632 (28.94)	0.270
card : Yes	5735	1007 (28.36)	924 (42.31)	0.295
neuro : Yes	5735	575 (16.19)	118 (5.40)	0.353
gastr : Yes	5735	522 (14.70)	420 (19.23)	0.121
renal : Yes	5735	147 (4.14)	148 (6.78)	0.116
meta : Yes	5735	172 (4.84)	93 (4.26)	0.028
hema : Yes	5735	239 (6.73)	115 (5.27)	0.062
seps : Yes	5735	515 (14.50)	516 (23.63)	0.234
trauma : Yes	5735	18 (0.51)	34 (1.56)	0.104
ortho : Yes	5735	3 (0.08)	4 (0.18)	0.027
cardiohx	5735	0.16 (0.37)	0.20 (0.40)	0.116
chfhx	5735	0.17 (0.37)	0.19 (0.40)	0.070
dementhx	5735	0.12 (0.32)	0.07 (0.25)	0.163
psychhx	5735	0.08 (0.27)	0.05 (0.21)	0.143
chrpulhx	5735	0.22 (0.41)	0.14 (0.35)	0.192
renalhx	5735	0.04 (0.20)	0.05 (0.21)	0.032
liverhx	5735	0.07 (0.26)	0.06 (0.24)	0.049
gibledhx	5735	0.04 (0.19)	0.02 (0.16)	0.070
malighx	5735	0.25 (0.43)	0.20 (0.40)	0.101
immunhx	5735	0.26 (0.44)	0.29 (0.45)	0.080
transhx	5735	0.09 (0.29)	0.15 (0.36)	0.170
amihx	5735	0.03 (0.17)	0.04 (0.20)	0.074

Table 1: Unmatched

Numerical summary is mean (sd). Categorical is N(%)

Propensity Score Matching

```
## Fit model
psModel <- glm(formula = formula,
               family  = binomial(link = "logit"),
               data    = rhc)

## Predicted probability of being assigned to RHC
rhc$pRhc <- predict(psModel, type = "response")
## Predicted probability of being assigned to no RHC
rhc$pNoRhc <- 1 - rhc$pRhc

## Predicted probability of being assigned to the
## treatment actually assigned (either RHC or no RHC)
rhc$pAssign <- NA
rhc$pAssign[rhc$swang1 == "RHC"]    <- rhc$pRhc[rhc$swang1   == "RHC"]
rhc$pAssign[rhc$swang1 == "No RHC"] <- rhc$pNoRhc[rhc$swang1 == "No RHC"]
## Smaller of pRhc vs pNoRhc for matching weight
rhc$pMin <- pmin(rhc$pRhc, rhc$pNoRhc)

listMatch <- Match(Tr       = (rhc$swang1 == "RHC"),      # Need to be in 0,1
                   ## logit of PS,i.e., log(PS/(1-PS)) as matching scale
                   X        = log(rhc$pRhc / rhc$pNoRhc),
                   ## 1:1 matching
                   M        = 1,
                   ## caliper = 0.2 * SD(logit(PS))
                   caliper  = 0.2,
                   replace  = FALSE,
                   ties     = TRUE,
                   version  = "fast")
## Extract matched data
rhcMatched <- rhc[unlist(listMatch[c("index.treated","index.control")]), ]

tangram(formula, rhcMatched, "matched", smd, "Propesnity Score Matched", style="nejm", pct_width=0.5)
```

Propesnity Score Matched	N	No RHC	RHC	SMD
		(N=1563)	(N=1563)	
age	3126	60.88 (17.21)	60.55 (15.71)	0.020
sex : Male	3126	887 (56.75)	891 (57.01)	0.005
race	3126			0.033
black		239 (15.29)	248 (15.87)	
other		89 (5.69)	99 (6.33)	
white		1235 (79.01)	1216 (77.80)	
edu	3126	11.79 (3.19)	11.78 (3.16)	0.003
income	3126			0.024
> 50k		129 (8.25)	124 (7.93)	
11-25k		322 (20.60)	336 (21.50)	
25-50k		262 (16.76)	262 (16.76)	
Under 11k		850 (54.38)	841 (53.81)	
ninsclas	3126			0.028
Medicaid		155 (9.92)	152 (9.72)	
Medicare		371 (23.74)	370 (23.67)	
Medicare & Medicaid		92 (5.89)	94 (6.01)	
No insurance		81 (5.18)	90 (5.76)	
Private		506 (32.37)	498 (31.86)	
Private & Medicare		358 (22.90)	359 (22.97)	
cat1	3126			0.040
ARF		702 (44.91)	680 (43.51)	
CHF		170 (10.88)	175 (11.20)	
Cirrhosis		48 (3.07)	47 (3.01)	
Colon Cancer		1 (0.06)	1 (0.06)	
Coma		81 (5.18)	76 (4.86)	
COPD		53 (3.39)	57 (3.65)	
Lung Cancer		4 (0.26)	5 (0.32)	
MOSF w/Malignancy		127 (8.13)	128 (8.19)	
MOSF w/Sepsis		377 (24.12)	394 (25.21)	
das2d3pc	3126	20.51 (5.48)	20.58 (5.08)	0.015
dnr1 : Yes	3126	135 (8.64)	130 (8.32)	0.011
ca	3126			0.005
Metastatic		96 (6.14)	98 (6.27)	
No		1196 (76.52)	1194 (76.39)	
Yes		271 (17.34)	271 (17.34)	
surv2md1	3126	0.58 (0.20)	0.59 (0.20)	0.021
aps1	3126	57.30 (19.66)	57.26 (19.65)	0.002
scoma1	3126	19.04 (28.92)	18.87 (28.25)	0.006
wtkilo1	3126	70.41 (26.79)	70.73 (27.19)	0.012
temp1	3126	37.65 (1.90)	37.62 (1.74)	0.016
meanbp1	3126	73.16 (35.27)	73.09 (35.73)	0.002
resp1	3126	28.33 (13.80)	28.07 (14.17)	0.019
hrt1	3126	117.58 (42.40)	117.77 (40.24)	0.005
pafi1	3126	209.59 (108.29)	211.26 (107.98)	0.015
paco21	3126	37.63 (10.84)	37.46 (11.56)	0.015
ph1	3126	7.39 (0.11)	7.39 (0.11)	0.005
wblc1	3126	15.59 (11.54)	15.93 (13.00)	0.028
hema1	3126	30.86 (7.94)	30.89 (7.53)	0.004
sod1	3126	136.55 (7.92)	136.64 (7.42)	0.011
pot1	3126	4.02 (1.01)	4.04 (0.99)	0.029
crea1	3126	2.27 (2.40)	2.28 (1.97)	0.003
bili1	3126	2.54 (5.64)	2.55 (5.09)	0.002
alb1	3126	3.05 (0.70)	3.04 (0.96)	0.010
resp : Yes	3126	547 (35.00)	519 (33.21)	0.038
card : Yes	3126	591 (37.81)	598 (38.26)	0.009
neuro : Yes	3126	108 (6.91)	109 (6.97)	0.003
gastr : Yes	3126	274 (17.53)	291 (18.62)	0.028
renal : Yes	3126	85 (5.44)	94 (6.01)	0.025
meta : Yes	3126	70 (4.48)	74 (4.73)	0.012
hema : Yes	3126	93 (5.95)	97 (6.21)	0.011
seps : Yes	3126	339 (21.69)	332 (21.24)	0.011
trauma : Yes	3126	14 (0.90)	13 (0.83)	0.007
ortho : Yes	3126	1 (0.06)	1 (0.06)	<0.001
cardiohx	3126	0.20 (0.40)	0.20 (0.40)	0.010
chfhx	3126	0.20 (0.40)	0.20 (0.40)	0.003
dementhx	3126	0.08 (0.27)	0.07 (0.26)	0.007
psychhx	3126	0.06 (0.23)	0.05 (0.23)	0.011
chrpulhx	3126	0.16 (0.36)	0.15 (0.36)	0.009
renalhx	3126	0.05 (0.22)	0.05 (0.22)	0.003
liverhx	3126	0.06 (0.24)	0.07 (0.26)	0.031
gibledhx	3126	0.03 (0.16)	0.03 (0.17)	0.023
malighx	3126	0.23 (0.42)	0.23 (0.42)	0.006
immunhx	3126	0.28 (0.45)	0.28 (0.45)	0.010
transhx	3126	0.12 (0.33)	0.12 (0.33)	0.004
amihx	3126	0.04 (0.19)	0.03 (0.17)	0.032

Table 2: Propesnity Score Matched

Numerical summary is mean (sd). Categorical is N(%)

Propensity Score Matching Weight

```
tangram(formula, rhc, "weighted", smd,
        "Propensity Score Weighted",
        style="nejm",
        weight=rhc$pMin/rhc$pAssign, pct_width=0.5)
```

Propensity Score Weighted	N	No RHC (N=3551)	RHC (N=2184)	SMD
age	5735	61.76 (17.29)	60.75 (15.63)	0.003
sex : Male	5735	1914 (53.90)	1278 (58.52)	0.003
race	5735			0.009
black		585 (16.47)	335 (15.34)	
other		213 (6.00)	142 (6.50)	
white		2753 (77.53)	1707 (78.16)	
edu	5735	11.57 (3.13)	11.86 (3.16)	0.002
income	5735			0.004
> 50k		257 (7.24)	194 (8.88)	
11-25k		713 (20.08)	452 (20.70)	
25-50k		500 (14.08)	393 (17.99)	
Under 11k		2081 (58.60)	1145 (52.43)	
ninsclas	5735			0.014
Medicaid		454 (12.79)	193 (8.84)	
Medicare		947 (26.67)	511 (23.40)	
Medicare & Medicaid		251 (7.07)	123 (5.63)	
No insurance		186 (5.24)	136 (6.23)	
Private		967 (27.23)	731 (33.47)	
Private & Medicare		746 (21.01)	490 (22.44)	
cat1	5735			0.017
ARF		1581 (44.52)	909 (41.62)	
CHF		247 (6.96)	209 (9.57)	
Cirrhosis		175 (4.93)	49 (2.24)	
Colon Cancer		6 (0.17)	1 (0.05)	
Coma		341 (9.60)	95 (4.35)	
COPD		399 (11.24)	58 (2.66)	
Lung Cancer		34 (0.96)	5 (0.23)	
MOSF w/Malignancy		241 (6.79)	158 (7.23)	
MOSF w/Sepsis		527 (14.84)	700 (32.05)	
das2d3pc	5735	20.37 (5.48)	20.70 (5.03)	0.005
dnr1 : Yes	5735	499 (14.05)	155 (7.10)	0.005
ca	5735			0.006
Metastatic		261 (7.35)	123 (5.63)	
No		2652 (74.68)	1727 (79.08)	
Yes		638 (17.97)	334 (15.29)	
surv2md1	5735	0.61 (0.19)	0.57 (0.20)	0.011
aps1	5735	50.93 (18.81)	60.74 (20.27)	0.008
scoma1	5735	22.25 (31.37)	18.97 (28.26)	0.001
wtkilo1	5735	65.04 (29.50)	72.36 (27.73)	<0.001
temp1	5735	37.63 (1.74)	37.59 (1.83)	<0.001
meanbp1	5735	84.87 (38.87)	68.20 (34.24)	0.001
resp1	5735	28.98 (13.95)	26.65 (14.17)	0.004
hrt1	5735	112.87 (40.94)	118.93 (41.47)	0.006
pafi1	5735	240.63 (116.66)	192.43 (105.54)	0.003
paco21	5735	39.95 (14.24)	36.79 (10.97)	0.004
ph1	5735	7.39 (0.11)	7.38 (0.11)	0.003
wblc1	5735	15.26 (11.41)	16.27 (12.55)	0.011
hema1	5735	32.70 (8.79)	30.51 (7.42)	0.007
sod1	5735	137.04 (7.68)	136.33 (7.60)	0.005
pot1	5735	4.08 (1.04)	4.05 (1.01)	0.004
crea1	5735	1.92 (2.03)	2.47 (2.05)	<0.001
bili1	5735	2.00 (4.43)	2.71 (5.33)	0.009
alb1	5735	3.16 (0.67)	2.98 (0.93)	<0.001
resp : Yes	5735	1481 (41.71)	632 (28.94)	0.004
card : Yes	5735	1007 (28.36)	924 (42.31)	0.006
neuro : Yes	5735	575 (16.19)	118 (5.40)	0.001
gastr : Yes	5735	522 (14.70)	420 (19.23)	0.005
renal : Yes	5735	147 (4.14)	148 (6.78)	0.004
meta : Yes	5735	172 (4.84)	93 (4.26)	0.001
hema : Yes	5735	239 (6.73)	115 (5.27)	0.004
seps : Yes	5735	515 (14.50)	516 (23.63)	0.005
trauma : Yes	5735	18 (0.51)	34 (1.56)	0.003
ortho : Yes	5735	3 (0.08)	4 (0.18)	0.003
cardiohx	5735	0.16 (0.37)	0.20 (0.40)	<0.001
chfhx	5735	0.17 (0.37)	0.19 (0.40)	0.004
dementhx	5735	0.12 (0.32)	0.07 (0.25)	0.003
psychhx	5735	0.08 (0.27)	0.05 (0.21)	0.004
chrpulhx	5735	0.22 (0.41)	0.14 (0.35)	0.001
renalhx	5735	0.04 (0.20)	0.05 (0.21)	0.001
liverhx	5735	0.07 (0.26)	0.06 (0.24)	0.003
gibledhx	5735	0.04 (0.19)	0.02 (0.16)	0.007
malighx	5735	0.25 (0.43)	0.20 (0.40)	0.007
immunhx	5735	0.26 (0.44)	0.29 (0.45)	<0.001
transhx	5735	0.09 (0.29)	0.15 (0.36)	0.004
amihx	5735	0.03 (0.17)	0.04 (0.20)	0.006

Table 3: Propensity Score Weighted

Numerical summary is mean (sd). Categorical is N(%)