A review of modern methods of estimating the size of health disparities

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Emil Coman¹
Helen Wu²

¹ UConn Health Disparities Institute, ² UConn Health

Health Disparities (HD):
It’s just about comparing two groups

Goals

1. Simplify and reposition common analytic methods
2. Compare methods to estimate HDs
3. Suggest cross-pollinations
4. Encourage disparities investigations
One intuitive model of Health Disparities


Fig. 1. How differential exposure to risk factors (downward arrows) and protective factors (upward arrows) over the life course affect developmental trajectories and contribute to disparities in birth outcomes. The lower reproductive potential of African American women, relative to White women, results from their cumulative exposure to more risk factors and less protective factors across the life span, particularly during sensitive periods of development.

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Another intuitive model of HDs

A Framework for Health Equity

Socio-Ecological Model

Medical Model

UPSTREAM

DISCRIMINATION
- Race
- Class
- Gender
- Immigration Status
- National Origin
- Sexual Orientation
- Disability

INSTITUTIONAL POWER
- Corporations & other businesses
- Gov't agencies
- Schools

SOCIAL INEQUALITIES
- Neighborhood Conditions
- Social Capital
- Residential Segregation
- Worksite Conditions

RISK BEHAVIORS
- Smoking, Nutrition
- Physical activity
- Violence

DISEASE & INJURY
- Infectious diseases
- Chronic diseases
- Injury (intentional & unintentional)

MORTALITY
- Infant mortality
- Life expectancy

HEALTH STATUS

- Adapted by AC/HD from the Bay Area Regional Health Inequities Initiative, Summer 2008


A testable model of HDs

Black vs. White

HD → Anxiety

Caveats:
1. Causality: can race ‘cause’ health?
2. Compare the comparable
3. Control for ‘covariates’


Modeling options for HDs

1. Independent samples t-test
2. Anova
3. Regression
4. Instrumental Variable regression
5. SEM
6. Matching methods
7. +

1. Independent samples T-test is a 2-group model

\[ \sigma^2_{Y_1} \equiv \bar{Y}_1 \]
\[ \sigma^2_{Y_2} \equiv \bar{Y}_2 \]
\[ Y_1 \]
\[ Y_2 \]

eq. (3a.1)

eq. (3a.2)

Figure 3a: The t-test model

Note: The independent samples t-test is testing the hypothesis: \( \bar{Y}_1 = \bar{Y}_2 \); this two-group setup allows for inclusion of group specific covariates; the two equations are simply one variable for each group, but across-group constraints are possible, like \( \sigma^2_{Y_1} = \sigma^2_{Y_2} \).
Modeling options for HDs

1. Independent samples
   T-test is a 2-group model
   \[ ttest\ y, \ by(binary) \]
   \[ pwmean\ y, \ over(binary)\] effects

2. Anova – similar for 2 groups
   \[ anova\ y\ binary \]
   \[ \text{Avoids for covariates though} \]
   \[ anova\ y\ binary\ c.x1\ c.x2 \]

3. Regression
   \[ reg\ y\ binary\ x1\ x2 \]

But: ? Can race cause health?

---


4. IV regression [Cameron]
   - Binary correlated with $u$

   - Need IV-$X$ but not IV-$Y$

```
ivregress 2sls y (binary = x1 x2), first
```

- Tests the IVs:
  ```
estat endogenous
  ```

5. SEM
   - 2-group model, compare intercepts (needs centering)

```
sem y <- x1 x2, group(binary) ginvariant(covex)
```

Can relax the equal $Y$ variances assumption
Modeling options for HDs

6. Matching options

teffects psmatch (y)
(binary x1 x2 )

psmatch2 binary x1 x2 ,
outcome (y) common ate

attnd y binary x1 x2

Stage 1

Stage 2

Match in strata on Binary

Stage 3

Means (+/- 2 SE) of the anxiety baseline
measure for White and Black women (t-test)

1. T-test

2. Anova – identical

➤ Allows for covariates though
anova y binary c.x1 c.x2
Modeling options for HDs

T-test

Anova – with covariates

Means (+/- 2 SE) of the anxiety baseline measure for White and Black women (Anova with covariates)

Means (+/- 2 SE) of the anxiety baseline measure for White and Black women (t-test)

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Modeling options for HDs

Anova – with covariates

SEM with correlates

Means (+/- 2 SE) of the anxiety baseline measure for White and Black women (SEM correlated)

Note: variances assumed equal.
Modeling options for HDs

SEM with *covariates* [0=White; 1=Black]; variances freed

```stata
sem y <- x1 x2, group(binary) ginvariant(covex)

| OIM             | Coef. | Std. Err. | z     | P>|z|    | [95% Conf. Interval] |
|-----------------|-------|-----------|-------|--------|----------------------|
| Structural      | y <-  |           |       |        |                      |
|                 | x1    |           |       |        |                      |
| 0               | 0.0199704 | 2.16228 | 0.01  | 0.993  | -4.21802  4.257961  |
| 1               | 2.61248 | 1.673379 | 1.56  | 0.118  | -6.672832 5.892244  |
| x2              | 0     | 0.164855  | 0.44  | 0.662  | -0.5733159 .9030258 |
| 1               | 0.4905938 | 0.301652 | 1.63  | 0.102  | -0.0977191 1.078907 |
| _cons           | 0     | 13.43964 | 8.259071 | 1.63 | 0.104  | -2.747845 29.62712 |
| 1               | 3.422483 | 6.895766 | 0.50  | 0.620  | -10.09297 16.93794 |

| var(e.y)        |       |           |       |        |                      |
| 0               | 60.78133 | 13.59112 | 39.21351 | 94.21166 |
| 1               | 84.67747 | 14.74046 | 60.19947 | 119.1086 |
```

-----means centered at .050 (X1 neighborhood disorder) and 22.91 (X2=age)------

Modeling options for HDs

tffects psmatch

```
. teffects psmatch (y) (binary x1 x2 )

Treatment-effects estimation Number of obs  =  106
Estimator          : propensity-score matching Matches: requested  =  1
Outcome model      : matching min =  1
Treatment model: logit max =  1

| AI Robust          | Coef. | Std. Err. | z     | P>|z|   | [95% Conf. Interval] |
|--------------------|-------|-----------|-------|--------|----------------------|
| ATE                |       |           |       |        |                      |
| binary             |       |           |       |        |                      |
| (1 vs 0)           | -3.169811 | 2.228166 | -1.42 | 0.155  | -7.536936 1.197313  |
```

---
### Modeling options for HDs

#### psmatch2

**psmatch2 binary x1 x2 , outcome (y) common ate Probit regression**

Number of obs = 106

|                  | Coef.  | Std. Err. | z     | P>|z|  | [95% Conf. Interval] |
|------------------|--------|-----------|-------|-----|---------------------|
| x1               | 0.6428318 | 0.2054421 | 3.13  | 0.002 | 0.2401726 - 1.045491 |
| x2               | 0.0468275 | 0.0366658 | 1.28  | 0.202 | -0.0250361 - 0.1186911 |
| _cons            | -0.7222502 | 0.8205248 | -0.88 | 0.379 | -2.330449 - 0.8859489 |

Chi-square (2) = 12.08

Prob > chi2 = 0.0024

Log likelihood = -64.210562

Pseudo R2 = 0.0860

---

**psmatch2: Common Treatment support assignment**

<table>
<thead>
<tr>
<th></th>
<th>Treated</th>
<th>Controls</th>
<th>Difference</th>
<th>S.E.</th>
<th>T-stat</th>
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<td>15.0757576</td>
<td>17.025</td>
<td>-1.94924242</td>
<td>1.8091337</td>
<td>-1.08</td>
</tr>
<tr>
<td>ATT</td>
<td>13.8</td>
<td>18.9272727</td>
<td>-5.12727273</td>
<td>2.19360704</td>
<td>-2.34</td>
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<tr>
<td>ATU</td>
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<td></td>
<td>.</td>
</tr>
<tr>
<td>ATE</td>
<td></td>
<td>-4.87368421</td>
<td></td>
<td></td>
<td>.</td>
</tr>
</tbody>
</table>

---

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Modeling options for HDs

```
attnd

attnd y binary  x1 x2 , comsup boot reps(100) dots logit detail

Note: the common support option has been selected
The region of common support is [.302525, .89642859]
The distribution of the pscore is

---
Percentiles Smallest
1% .3173758 .302525
5% .3990624 .3173758
10% .4397769 .3197376
25% .4943597 .3332007
50% .6010811 .6028369
75% .7131706 .854728
90% .8165104 .8586264
95% .8644204 .8964286
99% .8644204 .8964286

Obs 141
Sum of Wgt. 141

Largest Mean .6028369

Percentiles Largest Smallest
1% .3173758 .302525
5% .3990624 .3173758
10% .4397769 .3197376
25% .4943597 .3332007
50% .6010811 .6028369
75% .7131706 .854728
90% .8165104 .8586264
95% .8644204 .8964286
99% .8644204 .8964286

Mean .6028369
Std. Dev. .1374292
Variance .0188868
Skewness -.0160976
Kurtosis 2.2178

The program is searching the nearest neighbor of each treated unit.
This operation may take a while.
```

ATT estimation with Nearest Neighbor Matching method
(random draw version)

```
ATT standard errors

<table>
<thead>
<tr>
<th>n. treat.</th>
<th>n. contr.</th>
<th>ATT</th>
<th>Std. Err.</th>
<th>t</th>
</tr>
</thead>
<tbody>
<tr>
<td>85</td>
<td>23</td>
<td>-0.524</td>
<td>0.08</td>
<td>-0.621</td>
</tr>
</tbody>
</table>
```

ivregress 2sls y (binary = x1 x2 ), first

First-stage regressions

| Model | Coef. | Std. Err. | t    | P>|t|  | 95% Conf. Interval |
|-------|-------|-----------|------|------|-------------------|
| binary | 0.2176514 | 0.0672757 | 3.24 | 0.002 | 0.0842259 - 0.3510769 |
| x1    | 0.0148822  | 0.0124655 | 1.19 | 0.235 | -0.0098403 - 0.0396046 |
| x2    | 0.2805711  | 0.281939  | 1.00 | 0.322 | -0.2785883 - 0.8397305 |
| _cons | 0.2805711  | 0.281939  | 0.00 | 0.322 | -0.2785883 - 0.8397305 |

Instrumented: binary
Instruments: x1 x2
Modeling options for HDs

ivregress

estat endogenous

Tests of endogeneity
Ho: variables are exogenous

Durbin (score) chi2(1) = 3.51188 (p = 0.0609)
Wu-Hausman F(1,103) = 3.52942 (p = 0.0631)

“If the test statistic is significant, the variables must be treated as endogenous”

estat overid

Tests of overidentifying restrictions:

Sargan (score) chi2(1) = 0.872447 (p = 0.3503)
Basmann chi2(1) = 0.854791 (p = 0.3552)

“A statistically significant test statistic indicates that the instruments may not be valid”

Modeling options for HDs

Comparisons

Comparison of racial/ethnic (R/E) differences (92 White - 145 Black) in Anxiety baseline scores, by estimation method

All models used age and neighborhood stress as: covariates (regression); propensity predictors (PSM); instruments for R/E (IV).

Some methods are ‘better’ than others in identifying health disparities.

SEM is not shown. the test of HD is a Wald (or chi-squared test).
Conclusions – email for >: comanus@gmail.com

- Some methods are ‘better’ than others in identifying health disparities.

- Comparisons encourage analysts to think about ‘the place’ of the variables in the analytical model.

- One general insight: we can trust estimates when that are somewhat consistent across methods.