

*How to Peel Oranges into Apples:  
Finding Causes and Effects of Health Disparities  
with Difference Scores Built by 1-on-1 Matching*

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**[** HDs with *1-on-1 Matching* **]**

Goals

Introduce a new method to estimate HDs

Interpret results

Suggest uses/extensions

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## HDs with 1-on-1 Matching

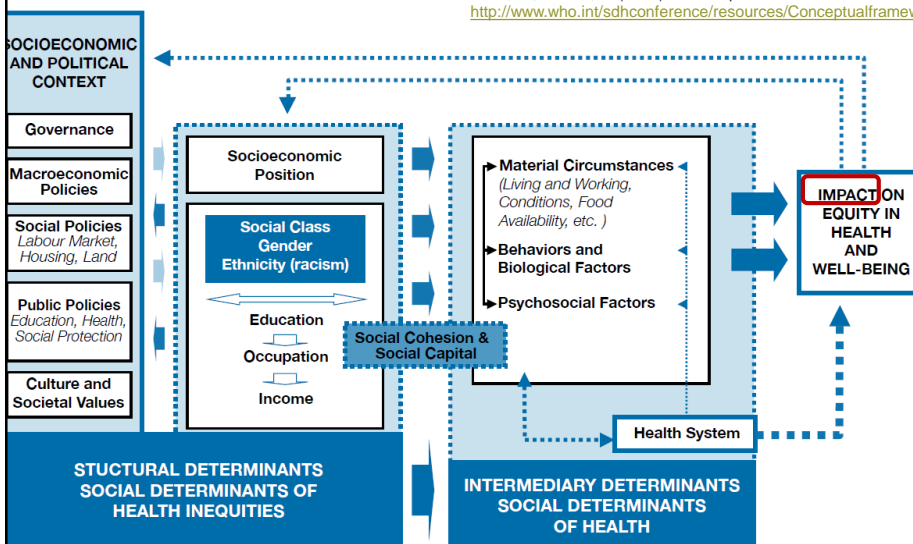
- Understanding the underlying causes of health disparities (HD) is a major public health objective
- HDs are defined as differences in health resulting from avoidable 'social forces', not due to unavoidable biological (or genetic) differences
- Challenge: compare the comparable to confidently reach causal inference

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## HDs and causes - example

Figure 5. Final form of the CSDH conceptual framework

Solar, O., & Irwin, A. (2007). A conceptual framework for action on the social determinants of health. from [http://www.who.int/sdhconference/resources/ConceptualframeworkforactiononSDH\\_eng.pdf](http://www.who.int/sdhconference/resources/ConceptualframeworkforactiononSDH_eng.pdf)



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## HDs with 1-on-1 Matching on what

	White (%)	N	Black (%)	N	All (%)	N	
<b>Total</b>		92		145		237	
<b>Employment</b>							
Unemployed	38.64	34	45.83	66	43.1	100	0.165
Homemaker	13.64	12	7.64	11	9.91	23	
Part-time	20.45	18	13.19	19	15.95	37	
Fulltime	27.27	24	33.33	48	31.03	72	
<b>Education</b>							
0 < Grade < 12	33.79	30	33.33	49	33.33	79	0.523
Grade = 12	48.28	40	46.41	70	46.41	110	
Grade > 12	17.93	22	20.25	26	20.25	48	
<b>Marital status</b>							
Married	20.65	19	7.59	11	12.66	30	<.001
Co-habiting	32.61	30	16.55	24	22.78	54	
Not married w/ boyfriend	21.74	20	51.03	74	39.66	94	
Not married w/o boyfriend	25	23	24.83	36	24.89	59	
<b>Means</b>	White	SDs	Black	SDs	All	SDs	P <sub>t</sub> test
Age	22.59	3.66	23.11	3.63	22.91	3.64	0.282

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## 1-on-1 matching approach

Deceptively simple:

1. Get probabilities/propensities for all in logistic e.g. model  
Black vs. white regressed on SES = Match on SES factors
2. Apply a rule for matching 1-on-1
3. Create dyads
  1. One has now 4 groups: B/W matched, and B/W unmatched
4. Analyze as 'repeated measures'
5. Build difference (latent, why not) scores, and find its predictors
6. Matching can be done in clusters/strata too.

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# 1-on-1 matching approach

dyads4c	match61	m2b1wh2	dyads4c	yhat4v	blvswh	clust13
.	0	Unmatched white	1	.0987048671	0	1
2	1	Matched Black	1	.1613160819	1	1
.	0	Unmatched white	.	.228888303	0	1
3	1	Matched white	.	.228888303	0	1
.	0	Unmatched white	2	.2410351187	0	1
9	1	Matched Black	2	.2429085672	1	1
.	0	Unmatched white	.	.2457663268	0	1
7	1	Matched white	3	.2457663268	0	1
1	1	Matched Black	3	.2605578601	1	2
.	0	Unmatched white	.	.2678673267	0	2
.	0	Unmatched white	.	.2678673267	0	2
.	0	Unmatched white	.	.2678673267	0	2
.	0	Unmatched white	.	.2723173499	0	2
.	0	Unmatched white	4	.2880042493	0	2
.	0	Unmatched white	.	.2880042493	0	2
4	1	Matched Black	4	.2889622152	1	2
9	1	Matched white	.	.2958693802	0	2
8	1	Matched white	5	.2991040349	0	2
8	1	Matched Black	6	.2991040349	1	2
7	1	Matched Black	5	.2991040349	1	2
1	1	Matched white	6	.2999676168	0	2
2	1	Matched white	.	.3110224009	0	3
.	0	Unmatched white	.	.3170807958	0	3

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# 1-on-1 matching approach – AMOS version

NPreg run 5/18/2017, ChiSq=\cmin  
 Df=ldf, Params=\npar, Chi/Df=\cmin/df, P=\p, NFI=\nfi, TLI = \TLI, CFI=\cfi  
 RMSEA=\rmsea, [rmsealo,rmseahj], PClose=\pclose, AIC = \AIC  
 N[.5]=\hfive, N[.1]= \hone

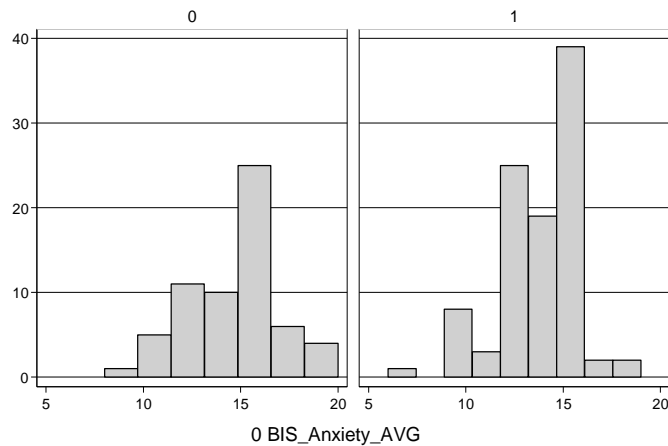
Labels in diagram:  
 BMa\_MAnx, BMa\_VAnx  
 disomean, anx0, BMa\_MpSS, BMa\_VpSS  
 BMa\_MNDIS, BMa\_VNDis, pss\_0  
 age, BMa\_MAge, BMa\_VAge

Manage Models dialog box:  
 Model Name: Lin\_Test\_Anx  
 Parameter Constraints: B[Ln\_MAnx]=W[Ln\_MAnx]

➤ There are then 4 groups:  
 matched (comparison and reference) and unmatched (comparison and reference)

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## Anxiety scores



Graphs by blvsw

The distribution of Y scores in the 2 groups (initial, unmatched).

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## 1-on-1 matching approach

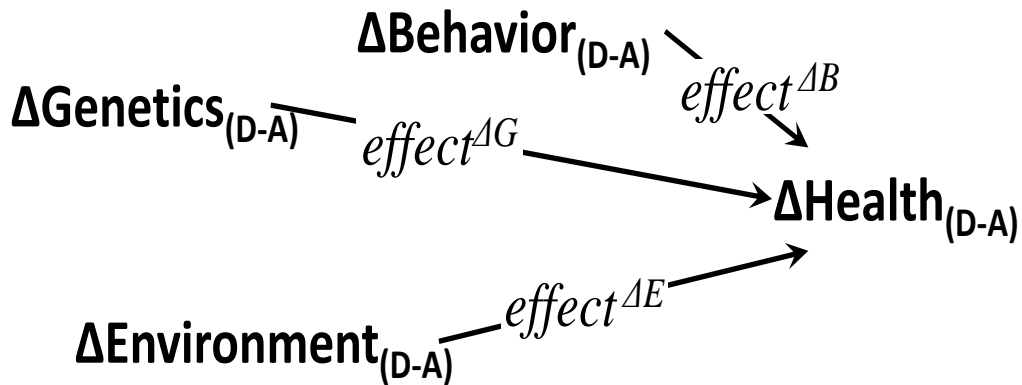
	Mean	SE	$P_{SEM}$ B vs. W	$P_{LDS}$	'Dyadic' correlations
Anxiety - whites	14.269	0.345	0.213		0.128 <sup>NS</sup>
Anxiety - Blacks	13.692	0.323			
HD-Anxiety <sub>LDS</sub>	-0.512	0.408		0.209	

We can compare 'before' matching (92 white, 145 Black women) and then 'after' matching – 61 dyads. Black women report lower BIS anxiety than white women, indicating a HD favoring Blacks, by about .40 standard deviation of the combined measure.

Unmatched sample (n = 115)	Mean	SE	$P_{SEM}$ B vs. W
Anxiety - whites	15.066	0.414	0.019
Anxiety - Blacks	13.853	0.26	

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## Simplified model of HD causes



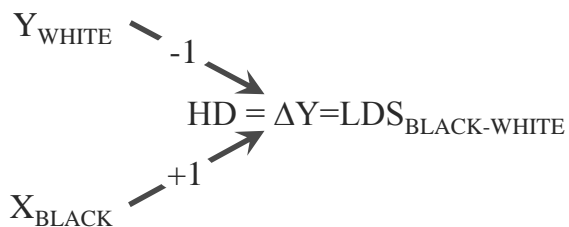
D=Disadvantaged group; A= advantaged.

$\Delta G$ ,  $\Delta E$ , and  $\Delta B$  are the effects of the *differences* in genetics, environment, and behavior on health disparities (HD, differences in health).

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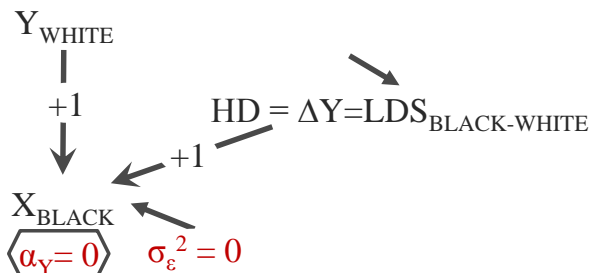
## 1-on-1 matching approach

### Intuitive model



Computing the difference:  
possible in the raw data

### LDS/LCS McArdle's



LDS is a DV now: we estimate intercepts, hence centering is crucial: the tests should be done at the predictors values set to 0.

## 1-on-1 matching approach - intuition

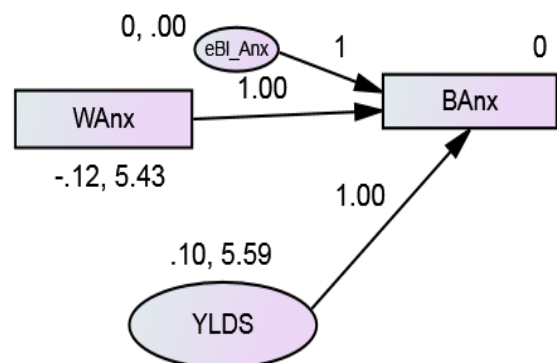
- ❑ One gets 2 variables out of any Y:  $Y_{\text{group 1}}$  &  $Y_{\text{group 2}}$
- ❑ It turns the data from 'independent groups' to 'repeated' tests one can run change in nature: t-test and others
- ❑ It changes the logic:  
 'Being in group 2 (vs reference group 1) leads to a difference between Y averages:  $\bar{Y}_2 - \bar{Y}_1$ '  
 to:  
 'There are varying differences between similar group 2 and group 1 *pairs* of cases.' ( $\Delta Y_j$ , j are dyads), hence we get  $\overline{\Delta Y}$

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## 1-on-1 matching HDs

AMOS [setup and] results

YLDS has a mean and a variance.  
 WANx was centered (not needed unless  
 it points to YLDS).



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## Cluster matching in HD

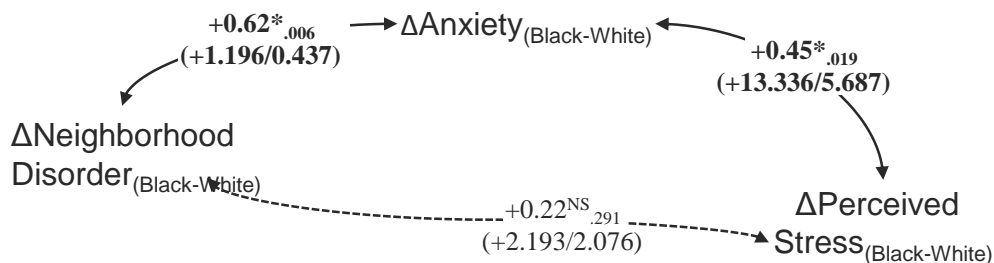
```
mixed y binary || clust13:
```

y	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
binary	<u><b>-.9425</b></u> 287	<u><b>.361</b></u> 2864	-2.61	0.009	-1.650637 - .2344204

We can also compare the 2 groups (binary) in terms of the matched clusters Y averages in comparable Black and white clusters (13 here).

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## Correlations between three disparity measures



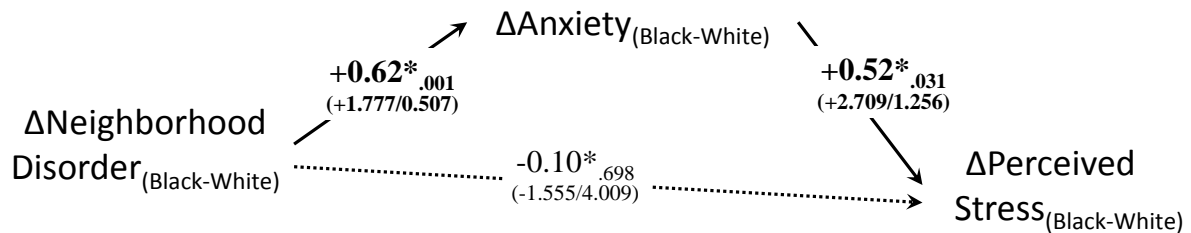
Larger Neighborhood pairwise differences translate into larger Anxiety pairwise differences.

Notes: Correlation<sub>p value</sub> (covariance/standard error); \* :  $p < .05$ ; NS = non-significant ( $p > .05$ ).

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## Effects among three disparity measures



Notes: Correlation<sub>p\_value</sub>(covariance/standard error); \* :  $p < .05$ ; NS = non-significant ( $p > .05$ ).

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## Conclusions – email for >: [comanus@gmail.com](mailto:comanus@gmail.com)

1. Capturing causal processes responsible for health disparities (by any groupings) may be served by models explaining actual such disparities.
2. The latent difference score (LCS) method of J. McArdle is uniquely qualified
3. Extensions can be envisioned: combinations of difference and change scores, partialling out group specific unreliabilities, etc.

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