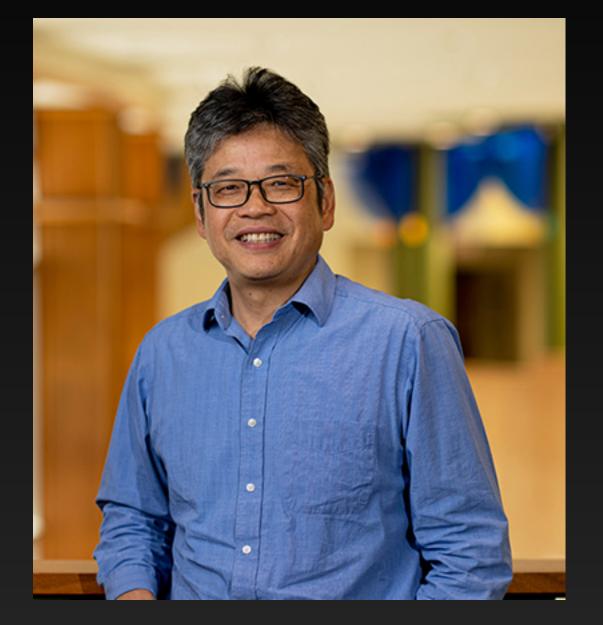
Asymmetric predictability An information theoretic approach to causal inference

Soumik Purkayastha, Department of Biostatistics, University of Michigan.

> 2023 Joint Statistical Meetings, Toronto, Canada.





Dept. of Biostatistics, University of Michigan



Karen E. Peterson, DSc

Acknowledgements





Jackie Goodrich, PhD

Dept. of Environmental Health Sciences, University of Michigan

"Asymmetry mirrors underlying causal structures"

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*Postulates and assumptions apply

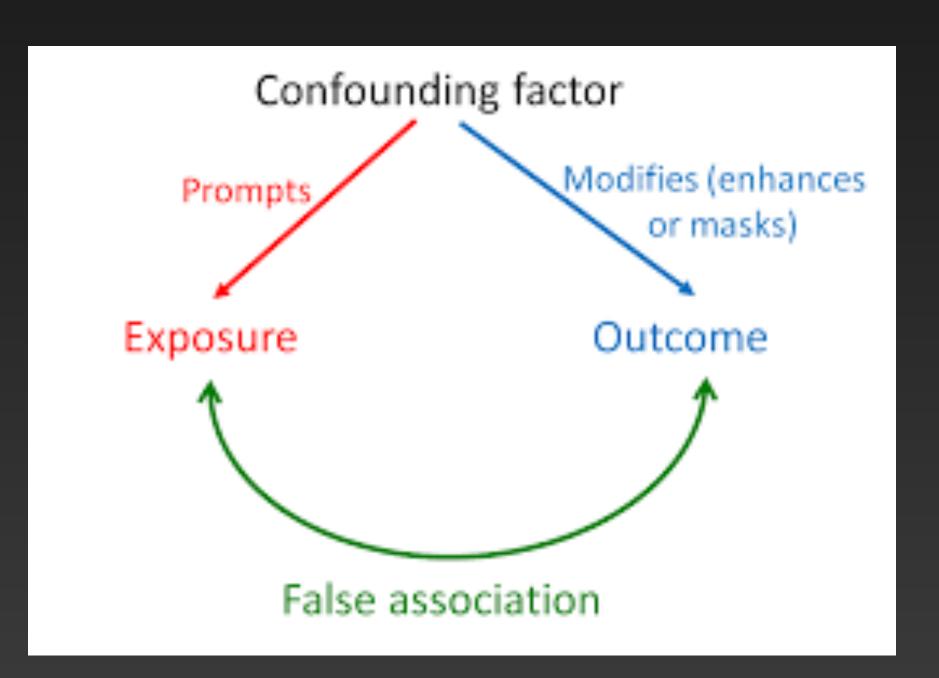
$\frac{\text{Does } X \to Y \text{ or } Y \to X?}{\text{Introduction}}$

• Inferring $X \to Y$ or $Y \to X$ from f_{XY} is challenging.

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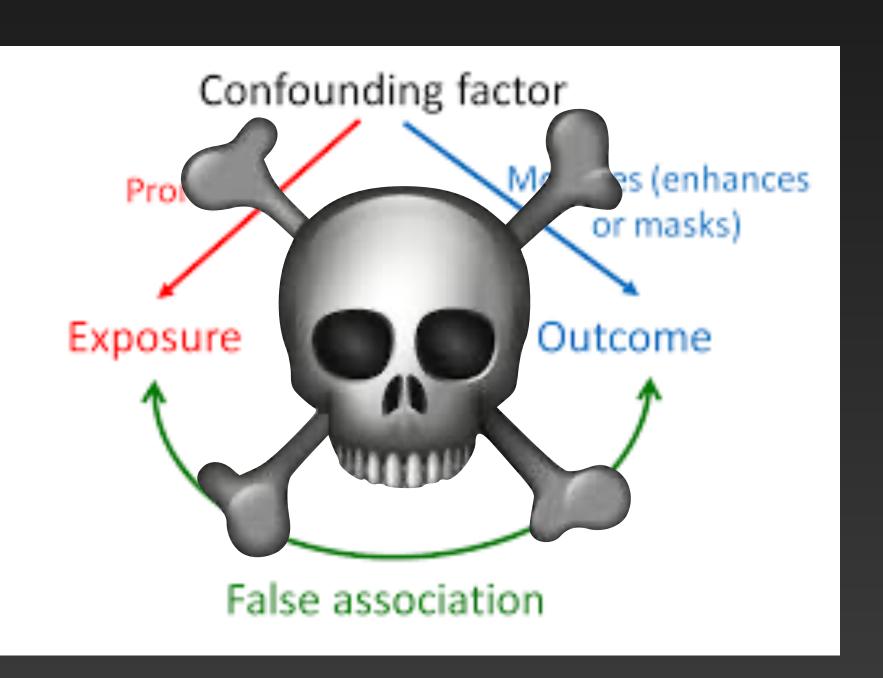
- Simplifying assumptions made:
 - Common confounders:



$\mathsf{Does}\,X\to Y\,\mathsf{or}\,Y\to X?$ Introduction

 f_{XY} is challenging.

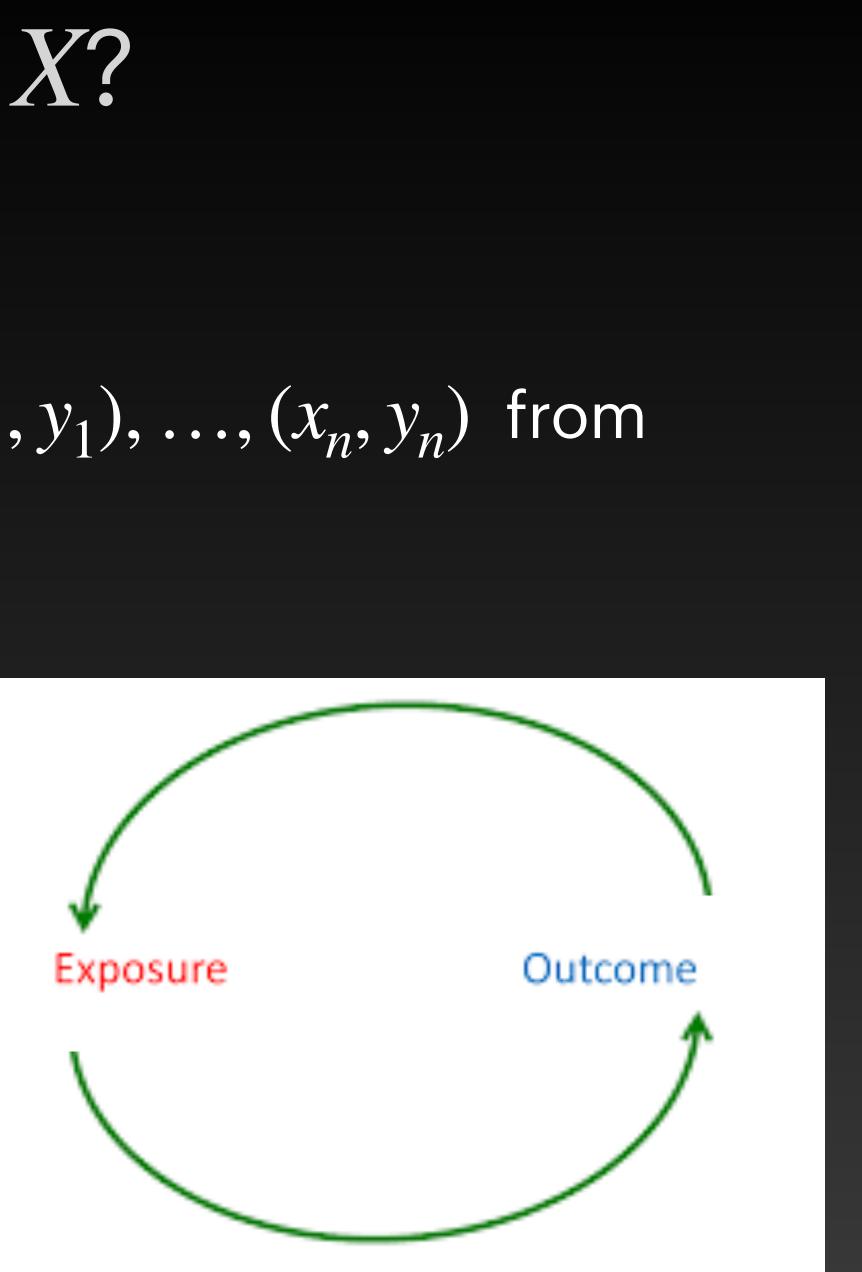
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 - Common confounders: not allowed!
 - Bidirectional influence:



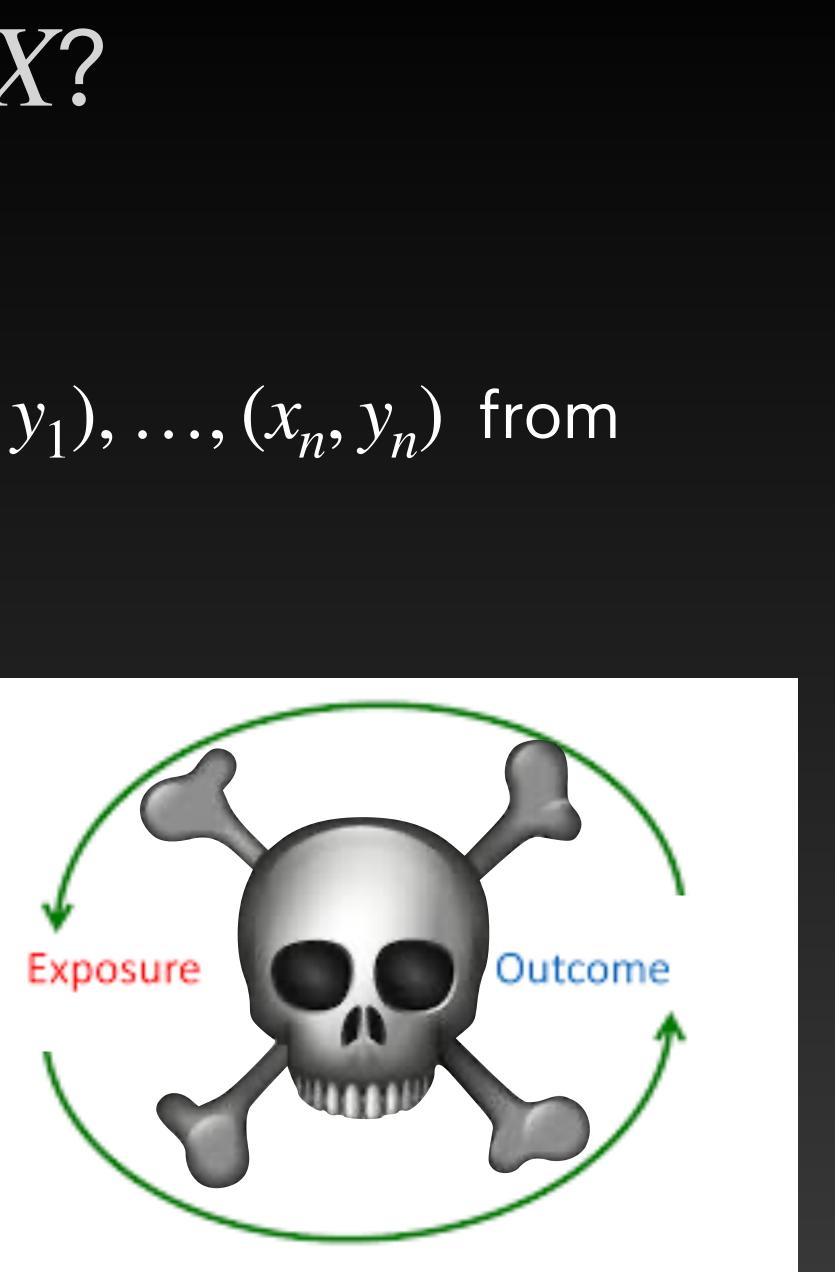
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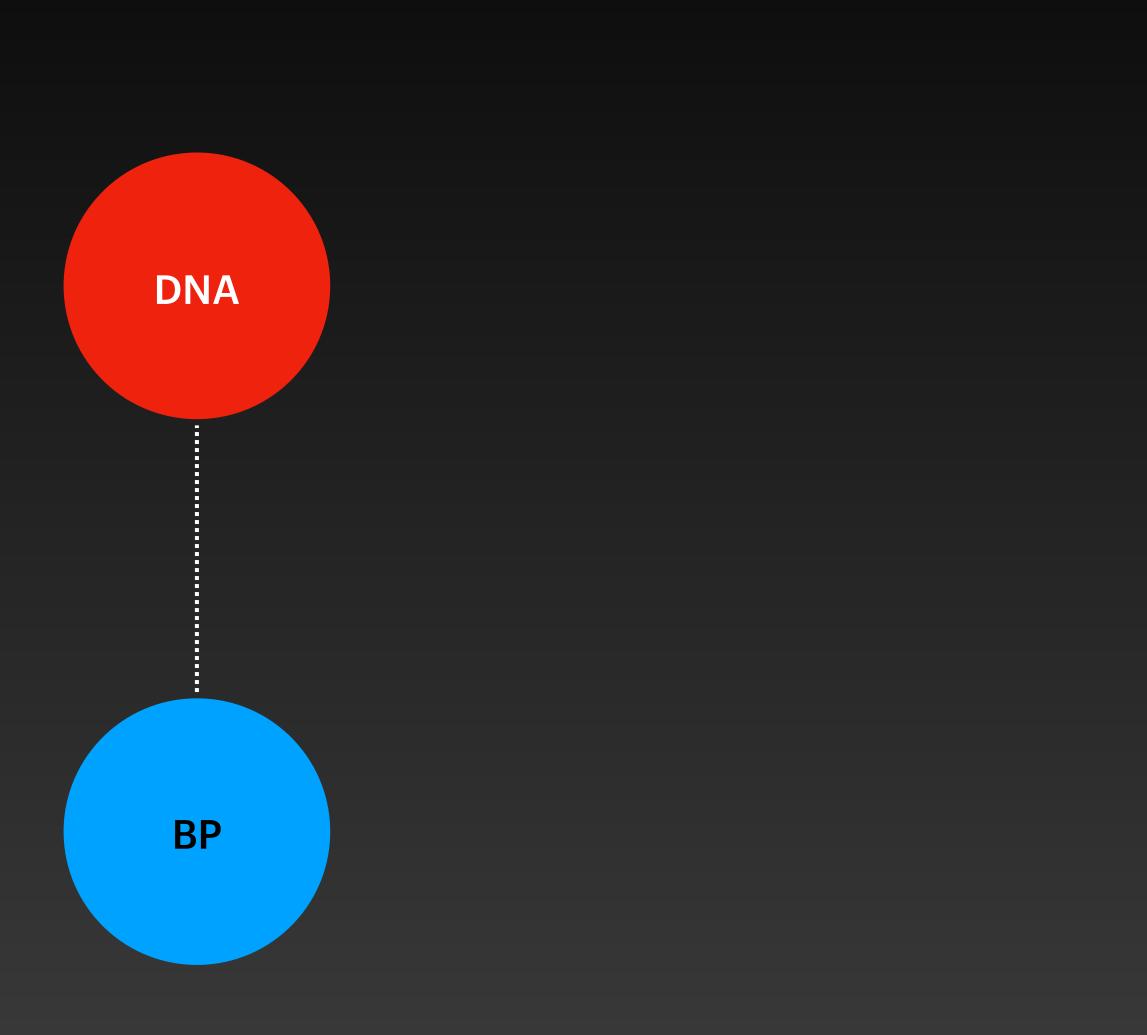
• Inferring $X \to Y$ or $Y \to X$ from observations $(x_1, y_1), \dots, (x_n, y_n)$ from

lowed! lowed!



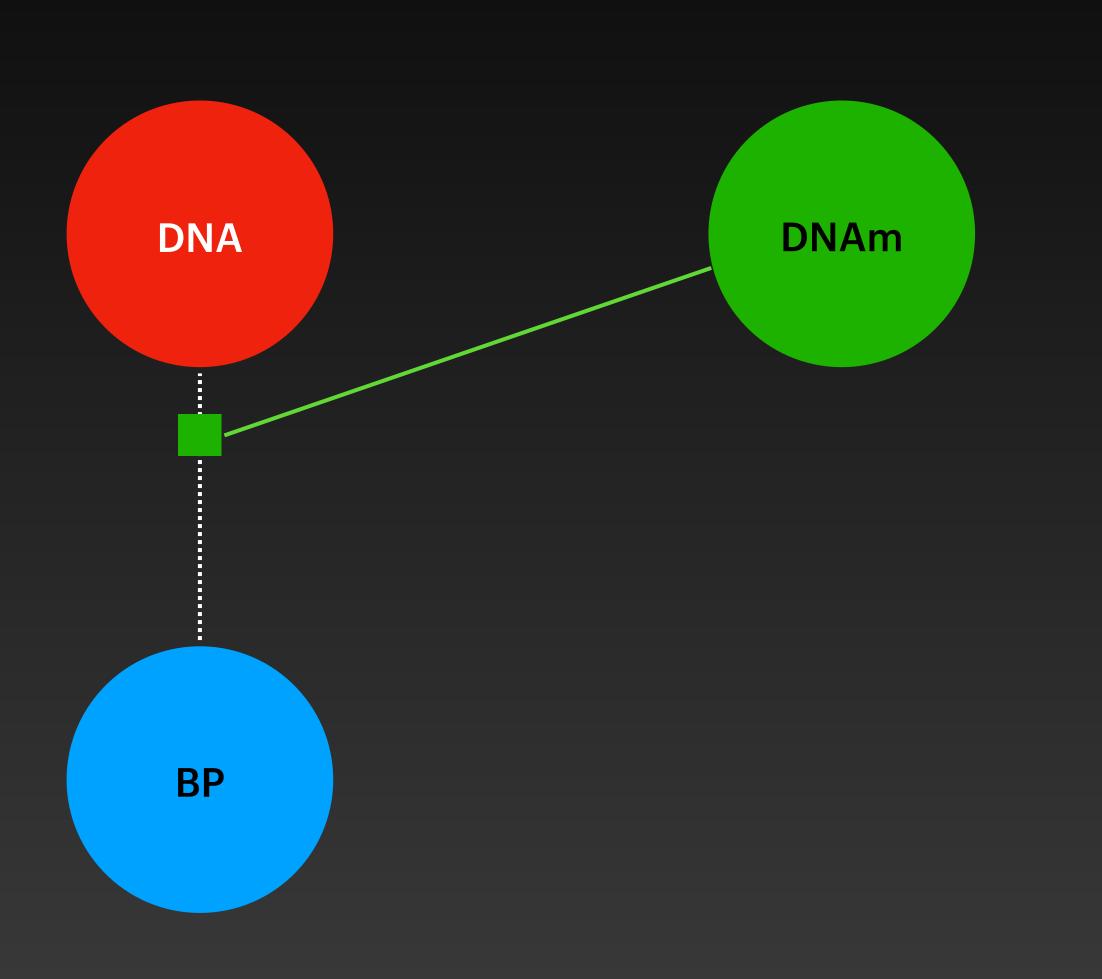
Methodology motivated by an epigenetic question

Early Life Exposures in Mexico to Environmental Toxicants (ELEMENT) cohort study



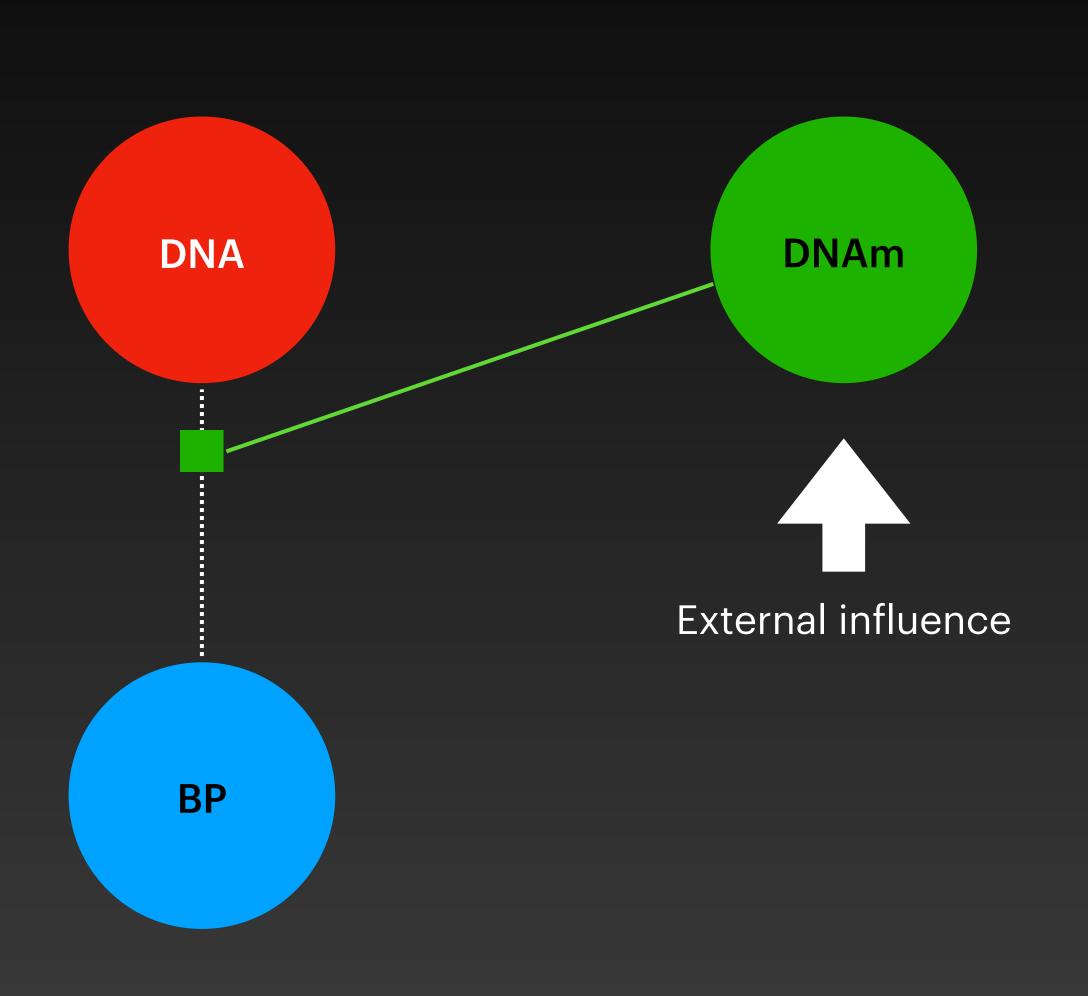
Genes associated with blood pressure:
 ATP2B1, FGF5, and **PRDM8**.

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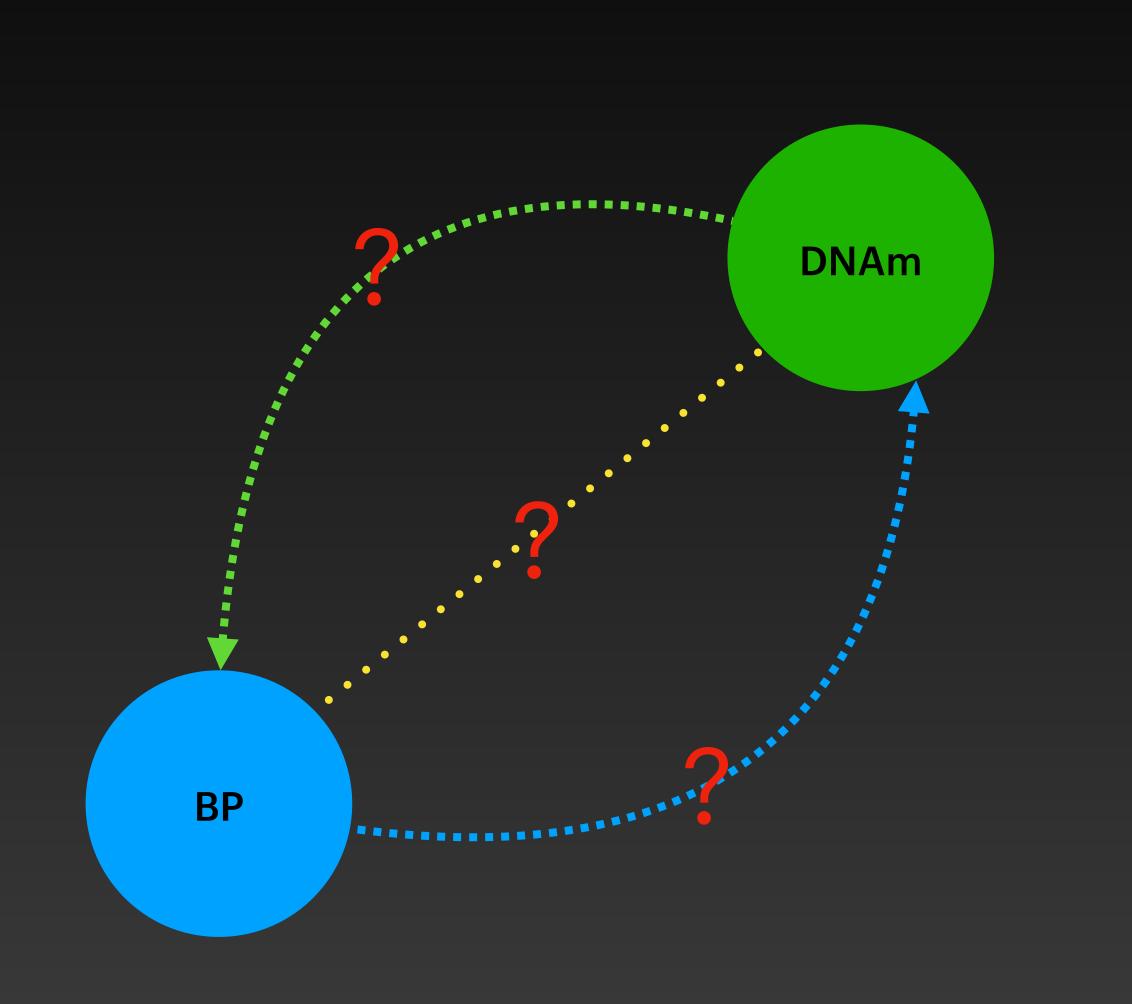
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Early Life Exposures in Mexico to Environmental Toxicants (ELEMENT) cohort study



- Genes associated with blood pressure:
 ATP2B1, FGF5, and PRDM8.
- Gene expression controlled by methylation.
- Methylation influenced by external features.
- Questions:
 - **1. EpiGWAS for BP?**
 - **2. DNAm** \rightarrow **BP** or **BP** \rightarrow **DNAm**?





$\mathsf{Does}\, X \to Y \, \mathsf{or}\, Y \to X?$ **Directed Mutual Information (DMI)**

asymmetries between cause and effect.

1. Asymmetric predictability: well-justified framework for studying statistical

- asymmetries between cause and effect.
- A. DMI can test for independence.

 $\mathsf{Does}\,X\to Y\,\mathsf{or}\,Y\to X?$ **Directed Mutual Information (DMI)**

1. Asymmetric predictability: well-justified framework for studying statistical

2. New information theory-based measure: **Directed Mutual Information** (DMI).

B. DMI can quantify and estimate "asymmetries" between cause and effect.



Asymmetric predictability

Entropy decomposition equation:

H(X, Y) = MI(X, Y) + H(X | Y) + H(Y | X)

Entropy decomposition equation:

Mutual information:

 $MI(X, Y) = E_{XY} \left[\log c_{XY} \right]$

 $MI = 0 \iff X \perp Y$

H(X, Y) = MI(X, Y) + H(X | Y) + H(Y | X)

Symmetric!

Entropy decomposition equation:

Mutual information:

 $MI(X, Y) = E_{XY} \left[\log c_{XY} \right]$

Symmetric!

H(X, Y) = MI(X, Y) + H(X | Y) + H(Y | X)

Study independence with MI. Depends only on copula c_{XY}

$MI = 0 \iff X \perp Y$

Entropy decomposition equation:

Joint entropy: $H(X, Y) = E_{XY} \left[-\log f_{XY} \right]$

Marginal entropies H(X) and H(Y)

Symmetric!

H(X, Y) = M(X, Y) + H(X | Y) + H(Y | X)

Entropy decomposition equation:

Total information in (X, Y)

Joint entropy: $H(X, Y) = E_{XY} \left[-\log f_{XY} \right]$

Marginal entropies H(X) and H(Y)

Symmetric!

H(X, Y) = M(X, Y) + H(X | Y) + H(Y | X)



Entropy decomposition equation:

H(X, Y) = M(X, Y) + H(X | Y) + H(Y | X)

Conditional entropy:

 $H(X \mid Y) = E_{XY} \left[-\log \frac{f_{XY}}{f_Y} \right]$

Asymmetric!



Entropy decomposition equation:

H(X, Y) = M(X, Y) + H(X | Y) + H(Y | X)

Information needed to predict X if we know Y

Conditional entropy:

 $H(X \mid Y) = E_{XY} \left[-\log \frac{f_{XY}}{f_{Y}} \right]$

Asymmetric!





Comparing conditional entropies **Symmetric entropy decomposition**

MI(X, Y)



H(Y|X)



$H(X \mid Y)$

H(X)

Symmetric/balanced

Comparing conditional entropies Asymmetric entropy decomposition



H(Y|X) M(X,Y)

Asymmetry: "Less information needed to predict Y given X''



H(X)

Postulate: If $X \to Y$, the density f_X and the function g are "independent".

- **Step 1:** Consider $Y = g(X) + \epsilon$

Postulate: If $X \to Y$, the density f_X and the function g are "independent".

Step 2: "peaks of f_X do not coincide" with regions of large slope of g''

$$\operatorname{Cov}\left[\log\left(g'\right), f_X\right] = 0$$

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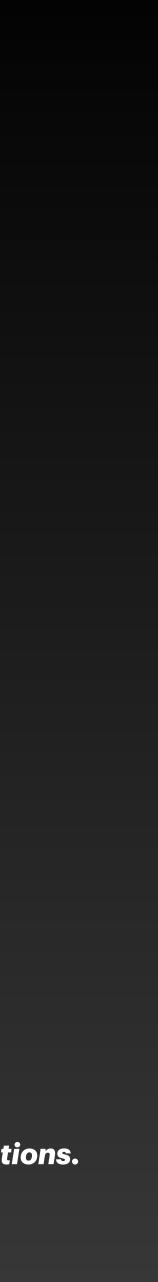
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References:

Janzing, D., et al. (2012). Information-geometric approach to inferring causal directions. Daniusis, P., et al. (2012). Inferring deterministic causal relations.

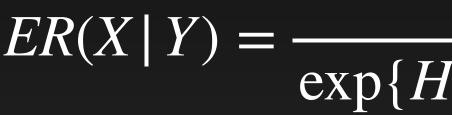




Towards defining DM

Entropy ratio **Definition and properties**

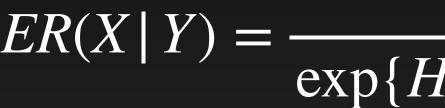
Entropy ratio compares H(X | Y) and $H(Y | \overline{X})$:



 $ER(X | Y) = \frac{\exp\{H(X | Y)\}}{\exp\{H(X | Y)\} + \exp\{H(Y | X)\}}.$

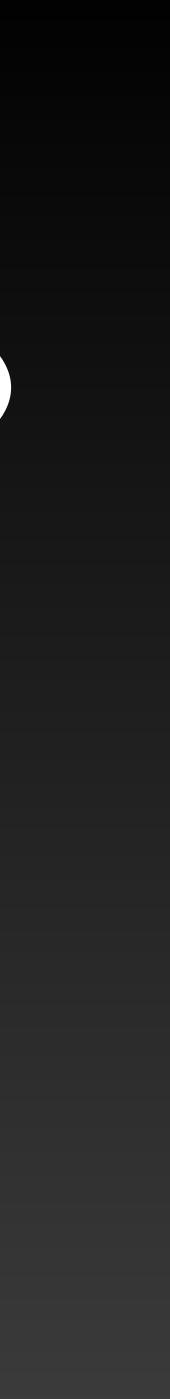
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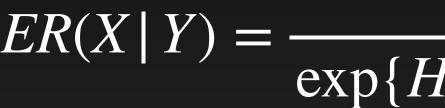
ER > 0

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ER(X|Y) > ER(Y|X) $\iff H(X | Y) > H(Y | X)$

ER > 0



Directed Mutual Information (DMI) Definition and properties

$DMI(X | Y) = MI(X, Y) \times ER(X | Y)$

Directed Mutual Information (DMI) **Definition and properties**

Properties:

- 1. $DMI = 0 \iff MI = 0 \iff X \perp Y$
- 2. $\Delta = DMI(X|Y) DMI(Y|X) > 0 \iff H(X|Y) > H(Y|X) \iff X \to Y$

Test for independence

$DMI(X \mid Y) = MI(X, Y) \times ER(X \mid Y)$

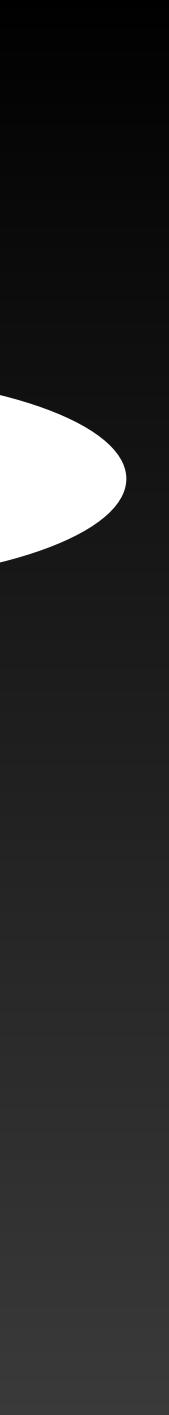
Directed Mutual Information (DMI) **Definition and properties**

$DM(X | Y) = MI(X, Y) \times ER(X | Y)$

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Detect asymmetry



Directed Mutual Information (DMI) **Definition and properties**

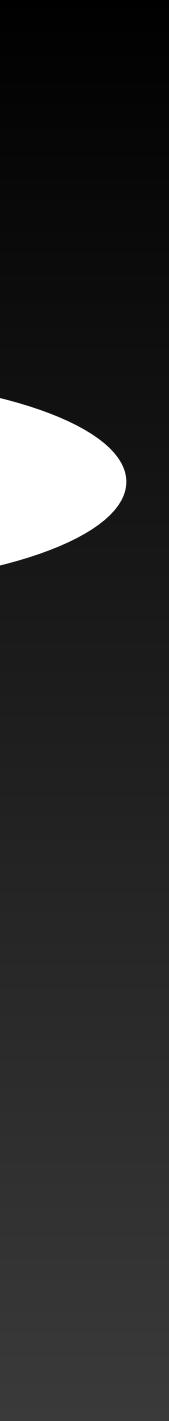
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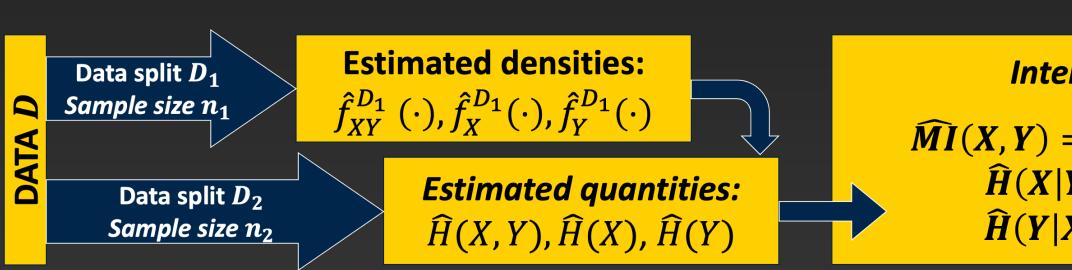
Detect asymmetry



Estimation and inference using DM

Directed Mutual Information (DMI) Estimation and inference

- 1. Estimate density functions ("nuisance parameter") using one split
- 2. Evaluate entropy and mutual information using other split



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Intermediate estimates:

 $\widehat{MI}(X,Y) = \widehat{H}(X) + \widehat{H}(Y) - \widehat{H}(X,Y)$ $\widehat{H}(X|Y) = \widehat{H}(X,Y) - \widehat{H}(Y)$ $\widehat{H}(Y|X) = \widehat{H}(X,Y) - \widehat{H}(X)$



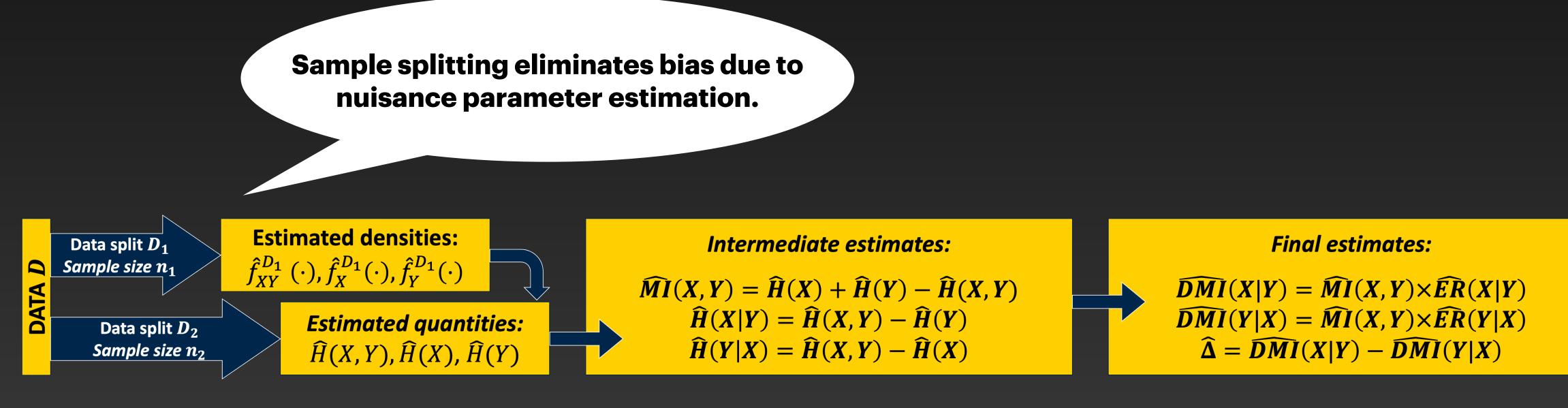
Final estimates:

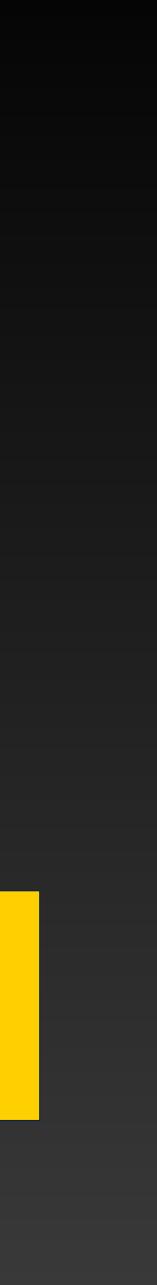
 $\widehat{DMI}(X|Y) = \widehat{MI}(X,Y) \times \widehat{ER}(X|Y)$ $\widehat{DMI}(Y|X) = \widehat{MI}(X,Y) \times \widehat{ER}(Y|X)$ $\widehat{\Delta} = \widehat{DMI}(X|Y) - \widehat{DMI}(Y|X)$



Directed Mutual Information (DMI) Estimation and inference

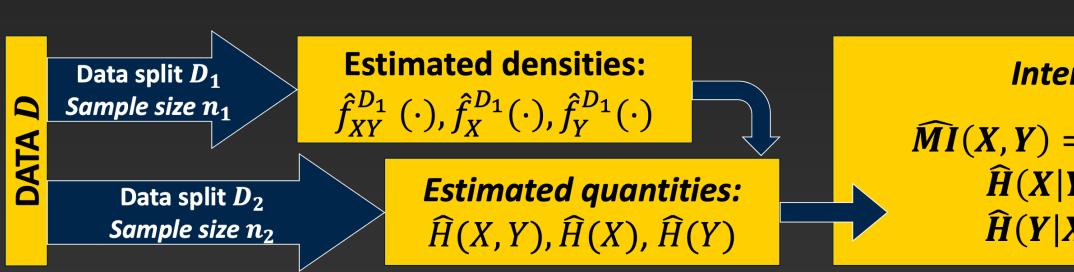
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Directed Mutual Information (DMI) **Estimation and inference**

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- 2. Evaluate entropy and mutual information using other split



Cross-fitting yields improved empirical performance.

Intermediate estimates:

 $\widehat{MI}(X,Y) = \widehat{H}(X) + \widehat{H}(Y) - \widehat{H}(X,Y)$ $\widehat{H}(X|Y) = \widehat{H}(X,Y) - \widehat{H}(Y)$ $\widehat{H}(Y|X) = \widehat{H}(X,Y) - \widehat{H}(X)$

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Directed Mutual Information (DMI) Theoretical guarantees

1. Assuming the density functions are bounded, when $\min(n_1, n_2) \to \infty$, we have $D\hat{M}I(X | Y) \xrightarrow{p} DMI(X | Y)$.

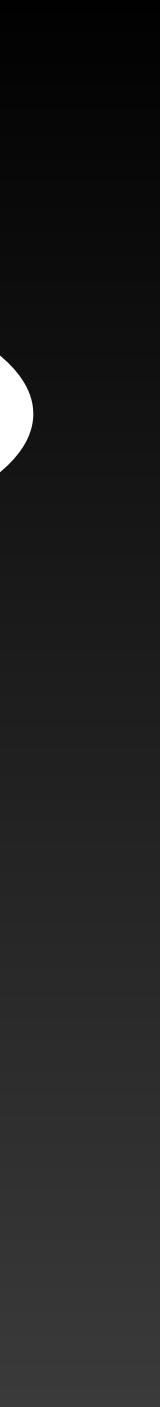
2. Assuming $MI \neq 0$, $\min(n_1, n_2) \rightarrow \infty$, we have $\sqrt{n_2} \left(\hat{\Delta} - \Delta \right) \xrightarrow{D} N(0, \sigma_{\Delta}^2)$.

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Consistent estimates of *DMI* **permit test of independence using permutation.**



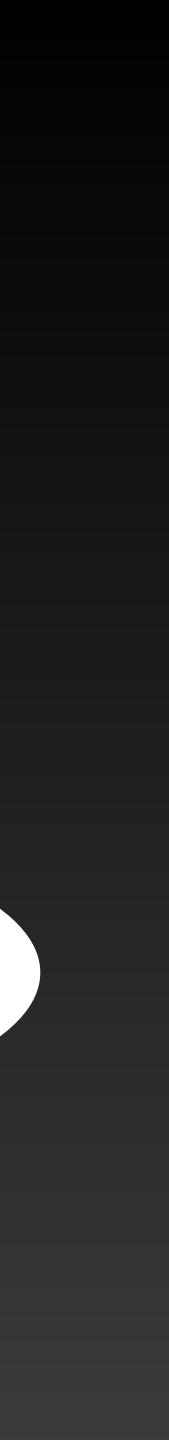
Directed Mutual Information (DMI) **Theoretical guarantees**

have $DM(X | Y) \xrightarrow{p} DM(X | Y)$.

1. Assuming the density functions are bounded, when $\min(n_1, n_2) \rightarrow \infty$, we

Sign of $\hat{\Delta}$ informs $X \to Y$ (95%) CI allows for calibration

2. Assuming $MI \neq 0$, $\min(n_1, n_2) \rightarrow \infty$, we have $\sqrt{n_2} \left(\hat{\Delta} - \Delta \right) \xrightarrow{D} N(0, \sigma_{\Delta}^2)$.



New epigenetic insights using DMI

Does DNAm \rightarrow BP or BP \rightarrow DNAm **Application of DMI to methylation studies**

Cohort of 525 children of age 10 - 18 years in the ELEMENT cohort. ullet

- 3 candidate genes: **ATP2B1, FGF5,** and **PRDM8.**
 - Mildly correlated methylation sites: 21 for ATP2B1, 21 for FGF5, and 51 sites for PRDM8. •

Does DNAm \rightarrow BP or BP \rightarrow DNAm **Application of DMI to methylation studies**

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- 3 candidate genes: **ATP2B1, FGF5,** and **PRDM8.**
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- Test for association between DNAm site and BP for a given gene. 1.
- Aggregate all DNAm-findings using Cauchy combination test for each gene. 2.
- 3. In DNAm sites associated with BP, check if DNAm \rightarrow BP or BP \rightarrow DNAm.

Finding 1: DNAm site #17564205 in ATP2B1

- Strongly associated with **diastolic** BP.
- Strong signal to drive gene-wide association with DBP.
- Next: check $DNAm \rightarrow$ BP or BP $\rightarrow DNAm$?

CCT-based combined p-value for association of ATP2B1 gene with DBP: 0.042

508575 -
729815 -
1505016 -
2904779 -
5379312 -
8975915 -
10501629 -
15721571 -
17455939 -
17564205 -
18542050 -
20641545 -
21712036 -
22043586 -
23204070 -
23392763 -
23461512 -
23525112 -
24171152 -
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Finding 2: DNAm site #125287 in FGF5

- Strongly associated with systolic BP.
- Strong signal to drive gene-wide association with SBP.
- Next: check $DNAm \rightarrow$ BP or BP $\rightarrow DNAm?$

CCT-based combined p-value for association of FGF5 gene with SBP: 0.019

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4401986 -	ŀ
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8409465 -	ŀ
10031614 -	ŀ
10218799 -	
11580948 -	ŀ
12087412 -	ŀ
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12528713 -	ł
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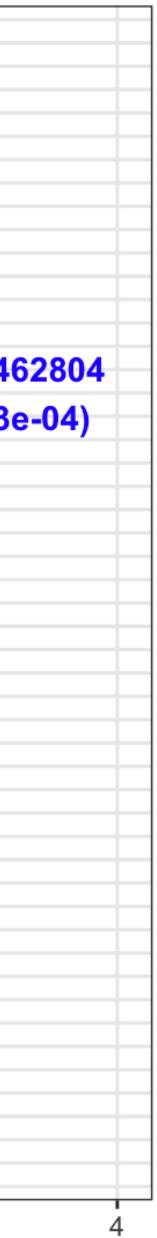
Finding 3: DNAm site #7462804 in PRDM8

- Strongly associated with systolic BP.
- Strong signal to drive gene-wide association with SBP.
- Next: check $DNAm \rightarrow$ BP or BP $\rightarrow DNAm$?

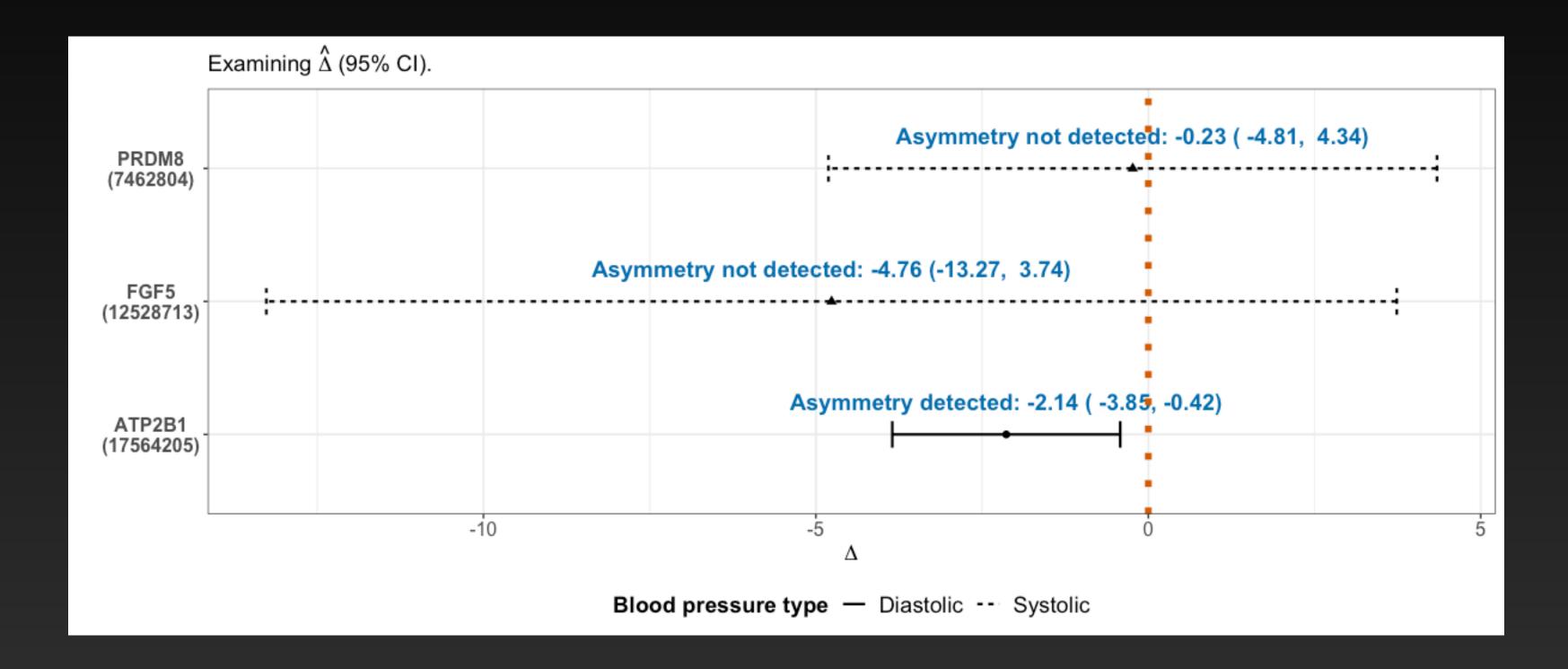
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1304890 1789499 2732915 2941135 3404272 3463411 4214966 4235768 4343891 5059566 5452645 5522011 5974274 6307913 6373870 6440348 7462804 7857469 9560763 9595050 10129063 10694470 10695325 10880006 11388320 11571772 11983124 12572049	
14197071 14326413 14489346 15556886 16117799 18073471 18235100 18624348 18954401 20142271 20817902 21082141 20054918 22186374 22902505 22961278 23874561 26162932 26299084 27018912 26299084 27018912 27242132 27639662	

CCT-based combined p-value for association of PRDM8 gene with SBP: 0.012

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		-	-log ₁₀ (p	– value)			



Finding 4: DBP \rightarrow #17564205 in ATP2B1



- 1. No asymmetry detected: **#7462804** (PRDM8) and **#12528713** (FGF5)
- 2. Asymmetry detected: **Diastolic BP** \rightarrow **#17564205** in **ATP2B1**.

Thank you for your time!

soumikp@umich.edu

• ELEMENT study reference

e030427.

Motivation of entropy ratio

Journal of the Royal Statistical Society. Series A, (Statistics in Society) 179.1 (2016): 1.

Information geometric causal inference

- 31. <u>https://doi.org/10.1016/j.artint.2012.01.002</u>
- Sample splitting and cross-fitting
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