

# Asymmetric predictability

An information theoretic approach to  
causal inference

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# Acknowledgements

**“Asymmetry mirrors underlying  
causal structures\*”**

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\*Postulates and assumptions apply

Does  $X \rightarrow Y$  or  $Y \rightarrow X$ ?

## Introduction

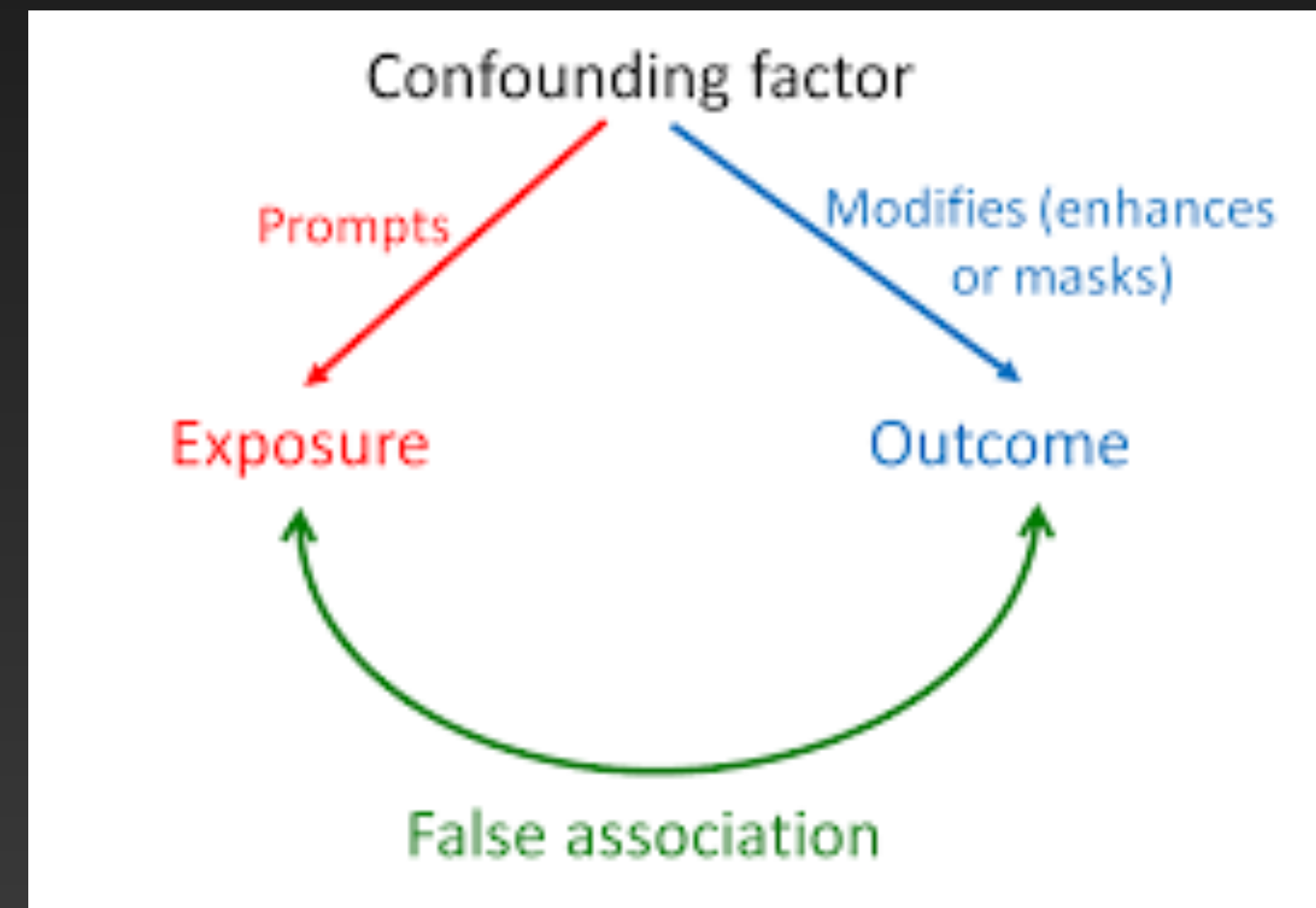
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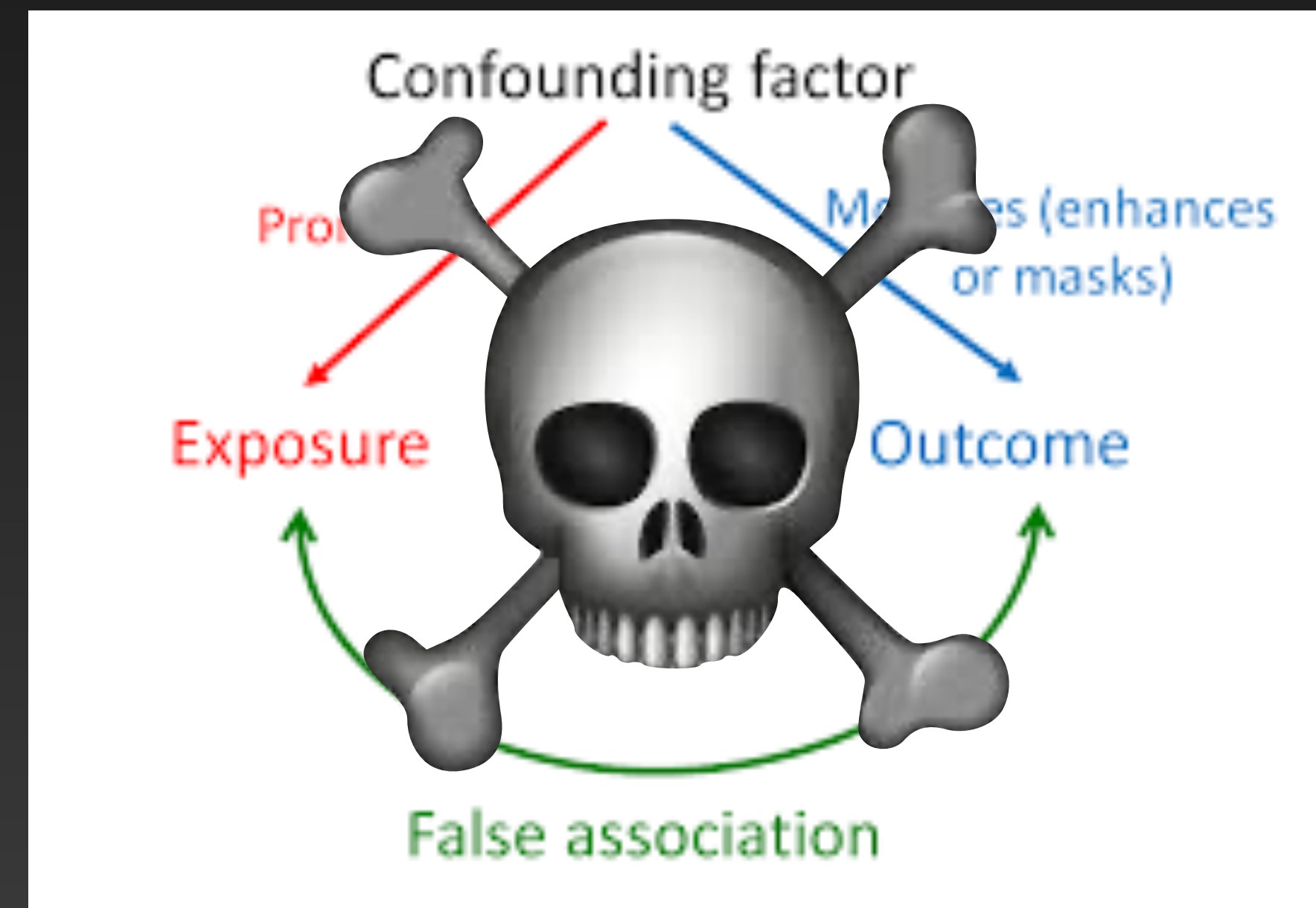


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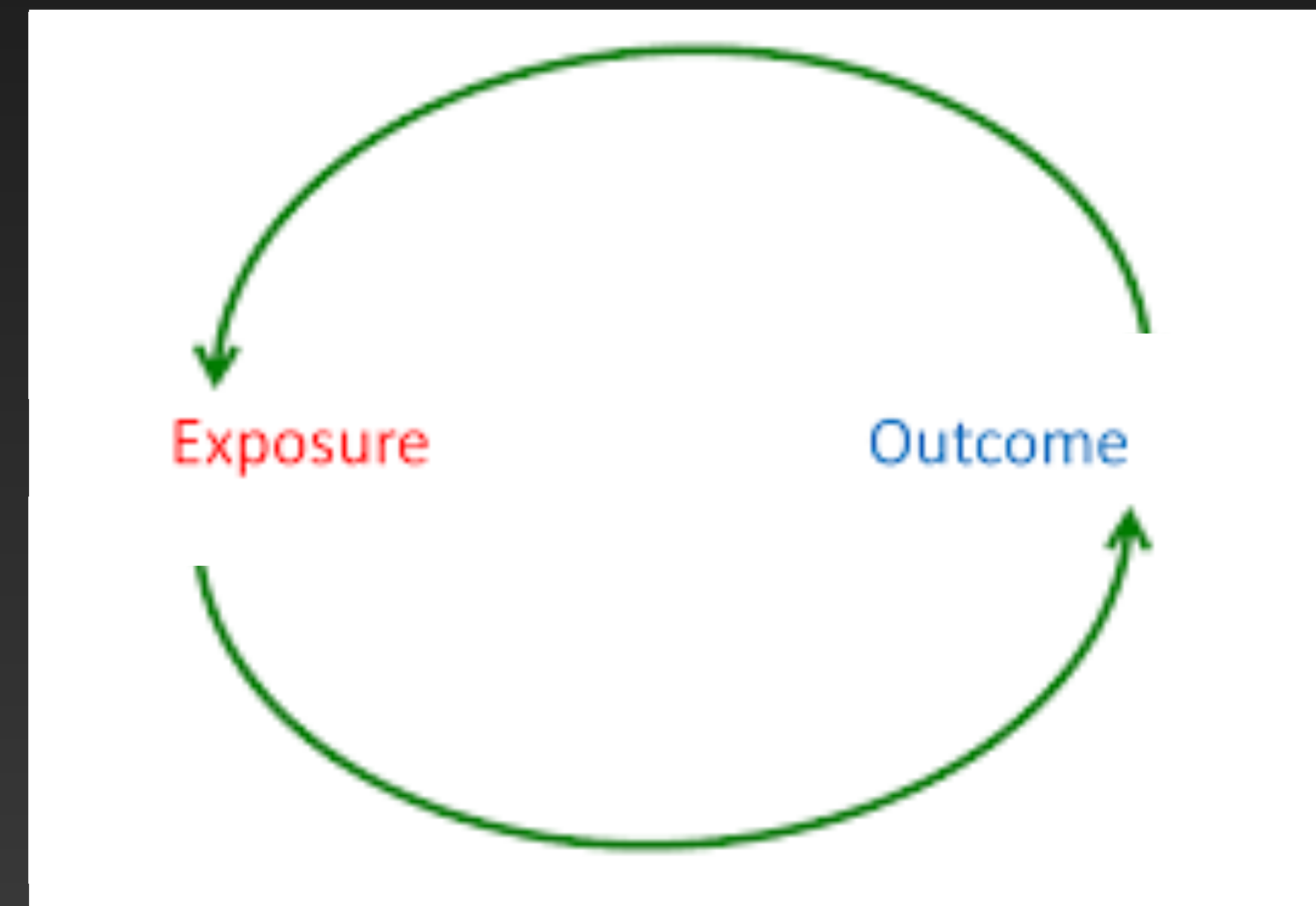
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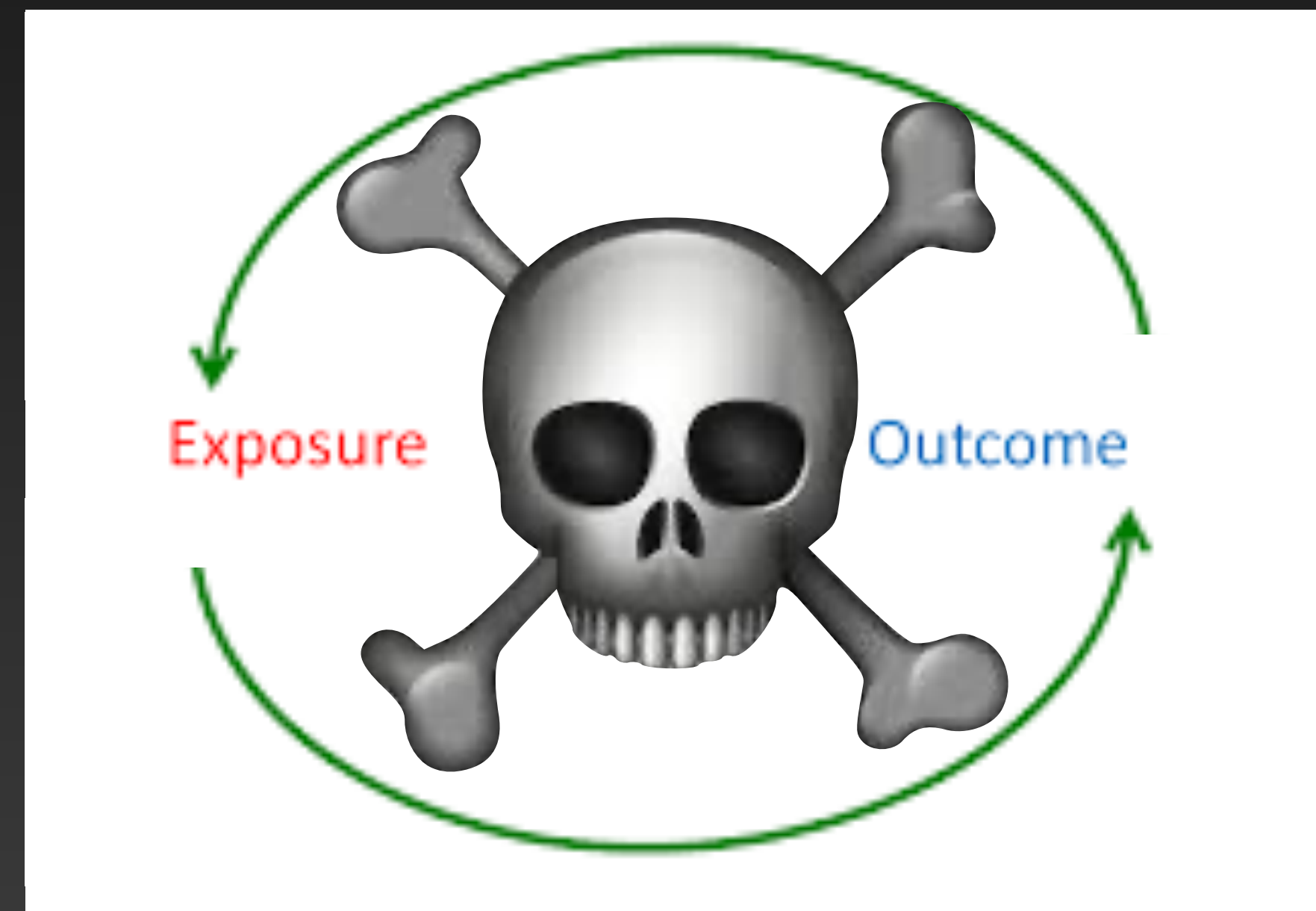




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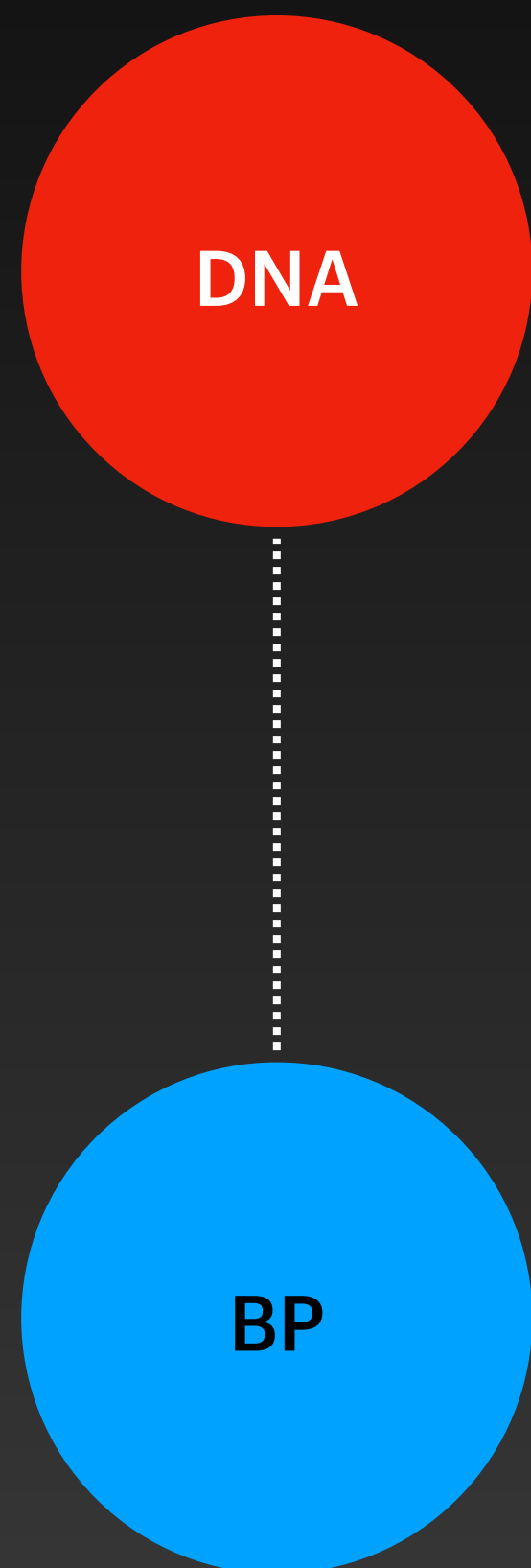
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**Methodology motivated by an  
epigenetic question**

# Does *DNA*m $\rightarrow$ *BP* or *BP* $\rightarrow$ *DNA*m?

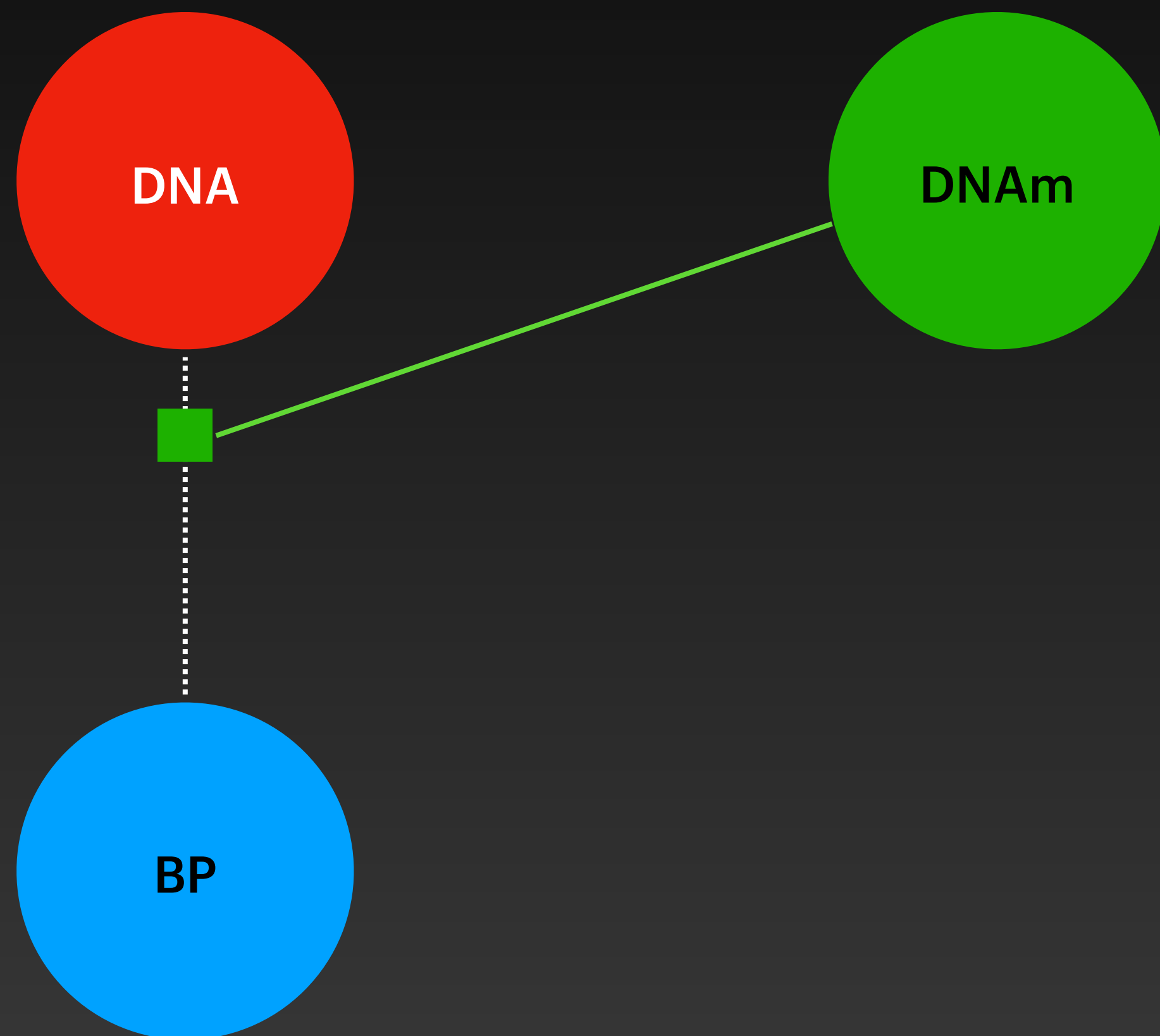
Early Life Exposures in Mexico to Environmental Toxicants (*ELEMENT*) cohort study



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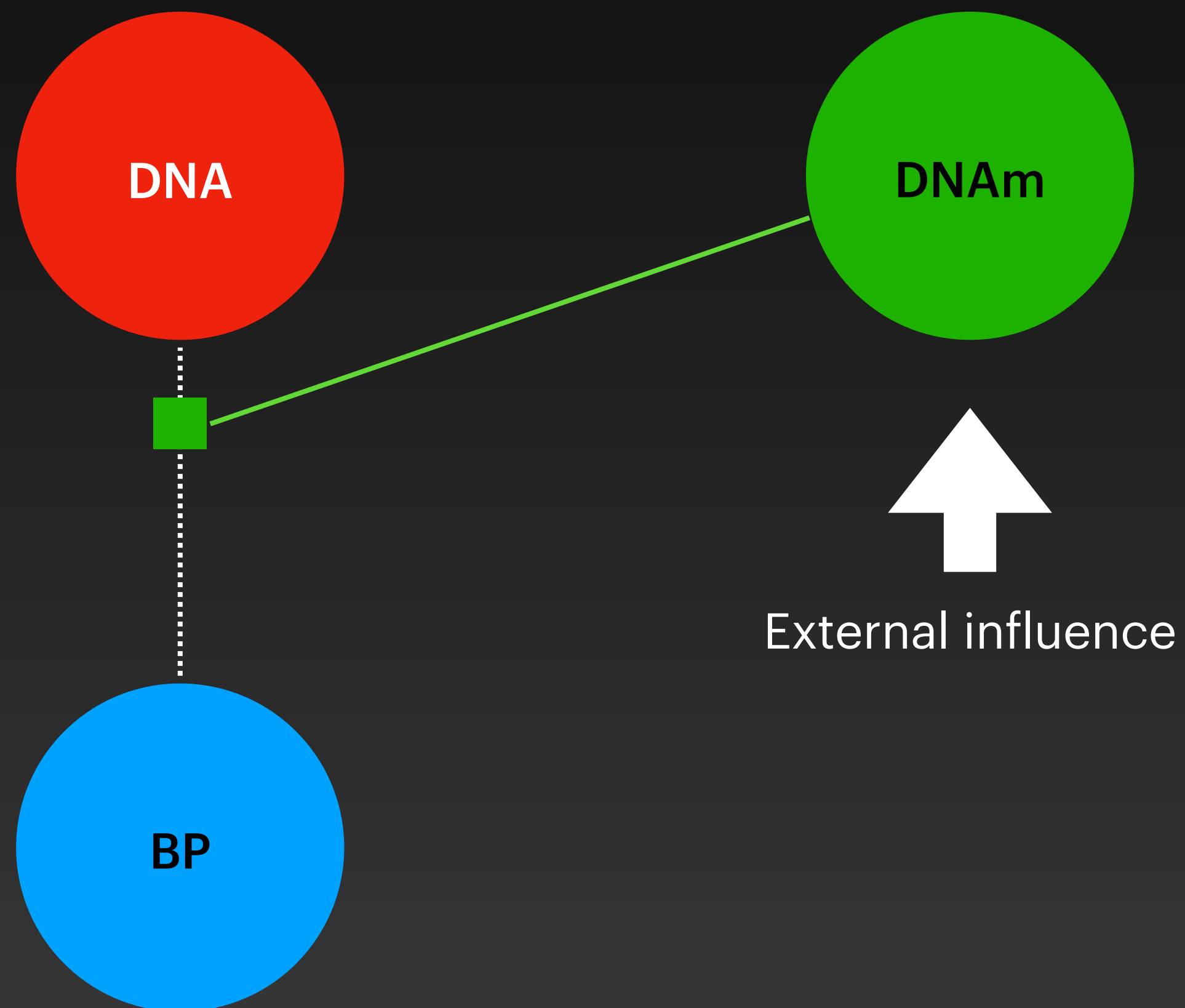
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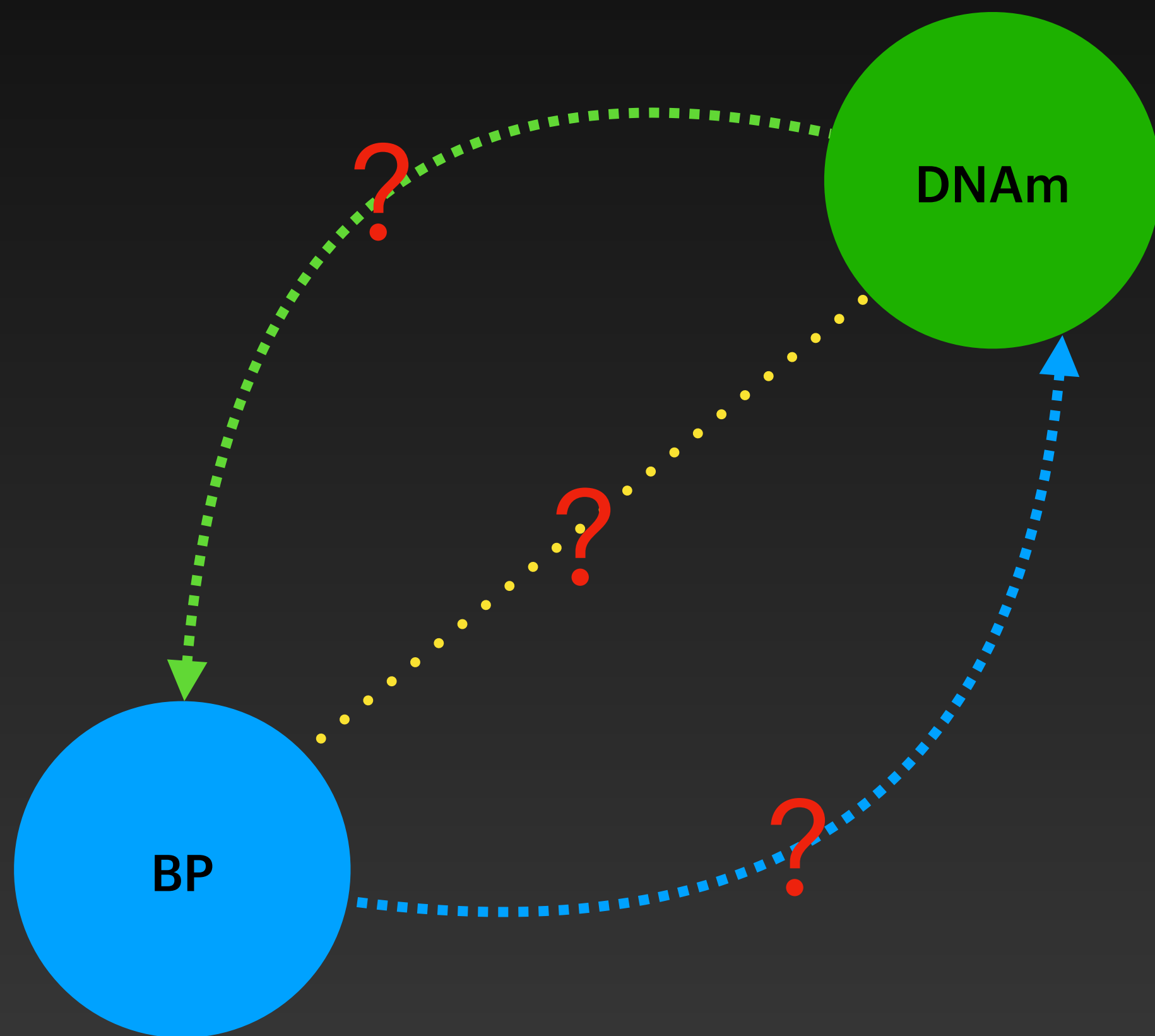
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Early Life Exposures in Mexico to Environmental Toxicants (*ELEMENT*) cohort study



- 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. ***DNA*m  $\rightarrow$  *BP* or *BP*  $\rightarrow$  *DNA*m?**

# Deliverables

Does  $X \rightarrow Y$  or  $Y \rightarrow X$ ?

**Directed Mutual Information (DMI)**

1. **Asymmetric predictability:** well-justified framework for studying statistical asymmetries between cause and effect.



Does  $X \rightarrow Y$  or  $Y \rightarrow X$ ?

**Directed Mutual Information (DMI)**

1. **Asymmetric predictability:** well-justified framework for studying statistical asymmetries between cause and effect.
2. New information theory-based measure: **Directed Mutual Information (DMI)**.
  - A. DMI can test for independence.
  - B. DMI can quantify and estimate “asymmetries” between cause and effect.

**Asymmetric predictability**

# Some information theoretic concepts

Entropy decomposition equation:

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$$MI = 0 \iff X \perp Y$$

Symmetric!

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Study independence with  
*MI*.

Depends only on copula  $c_{XY}$

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Marginal entropies  $H(X)$  and  $H(Y)$

Symmetric!

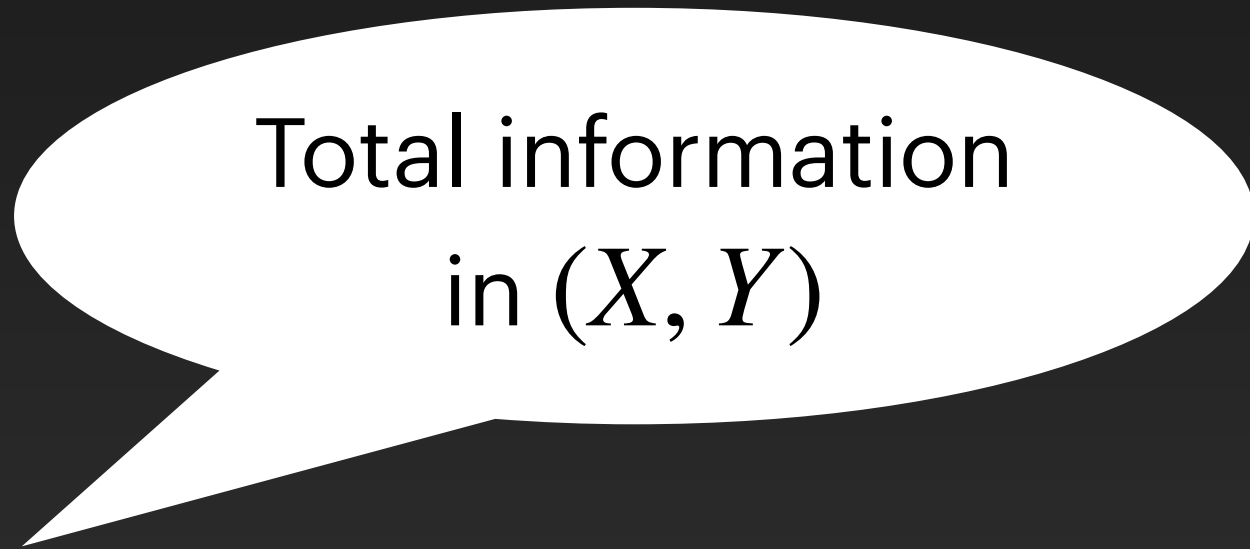
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Total information  
in  $(X, Y)$

Marginal entropies  $H(X)$  and  $H(Y)$

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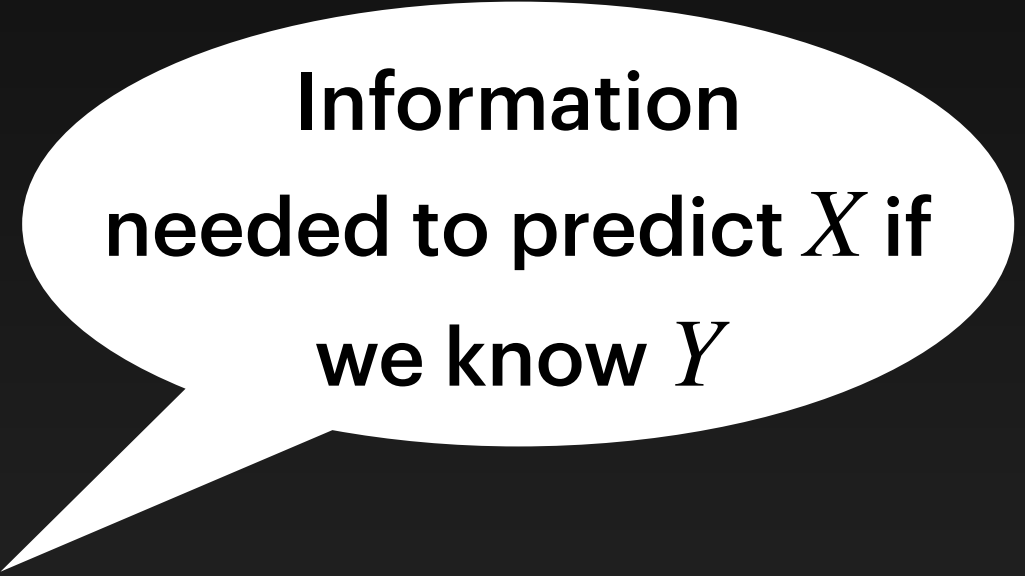
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Information  
needed to predict  $X$  if  
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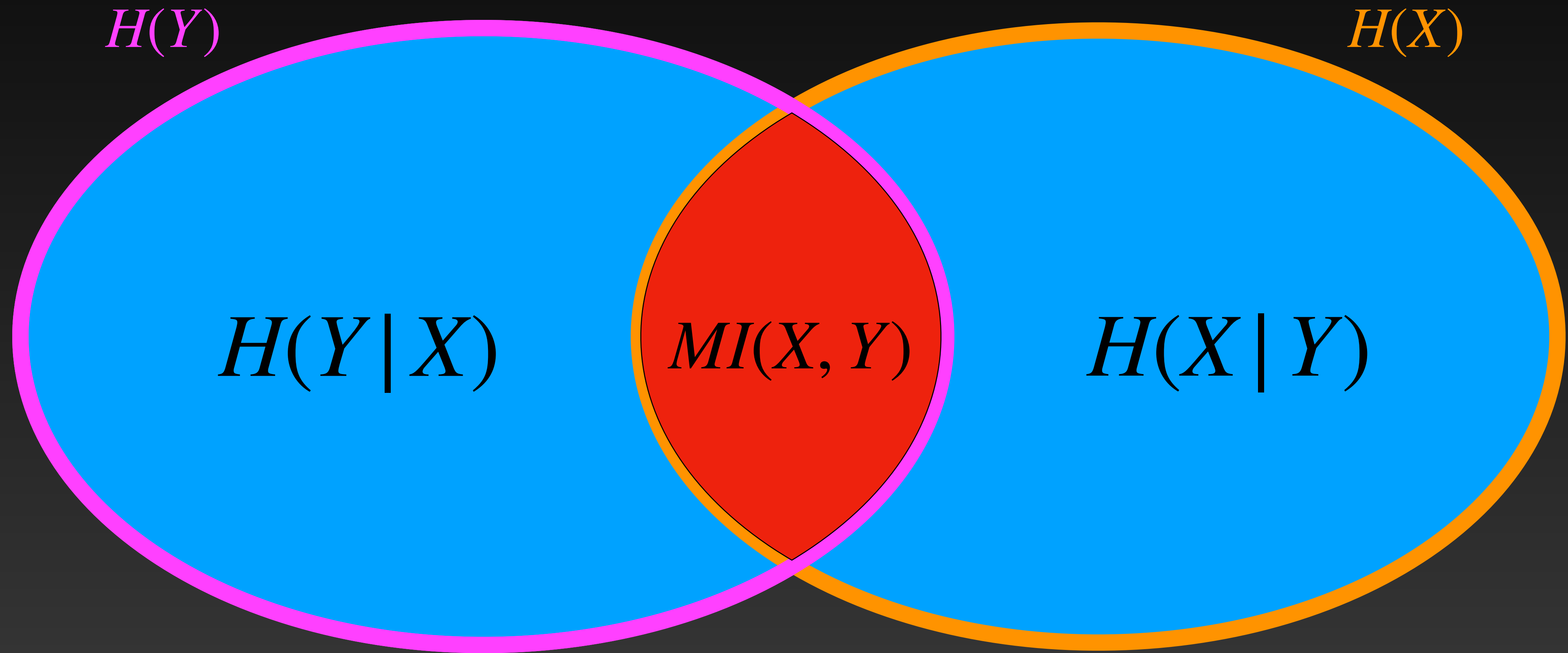
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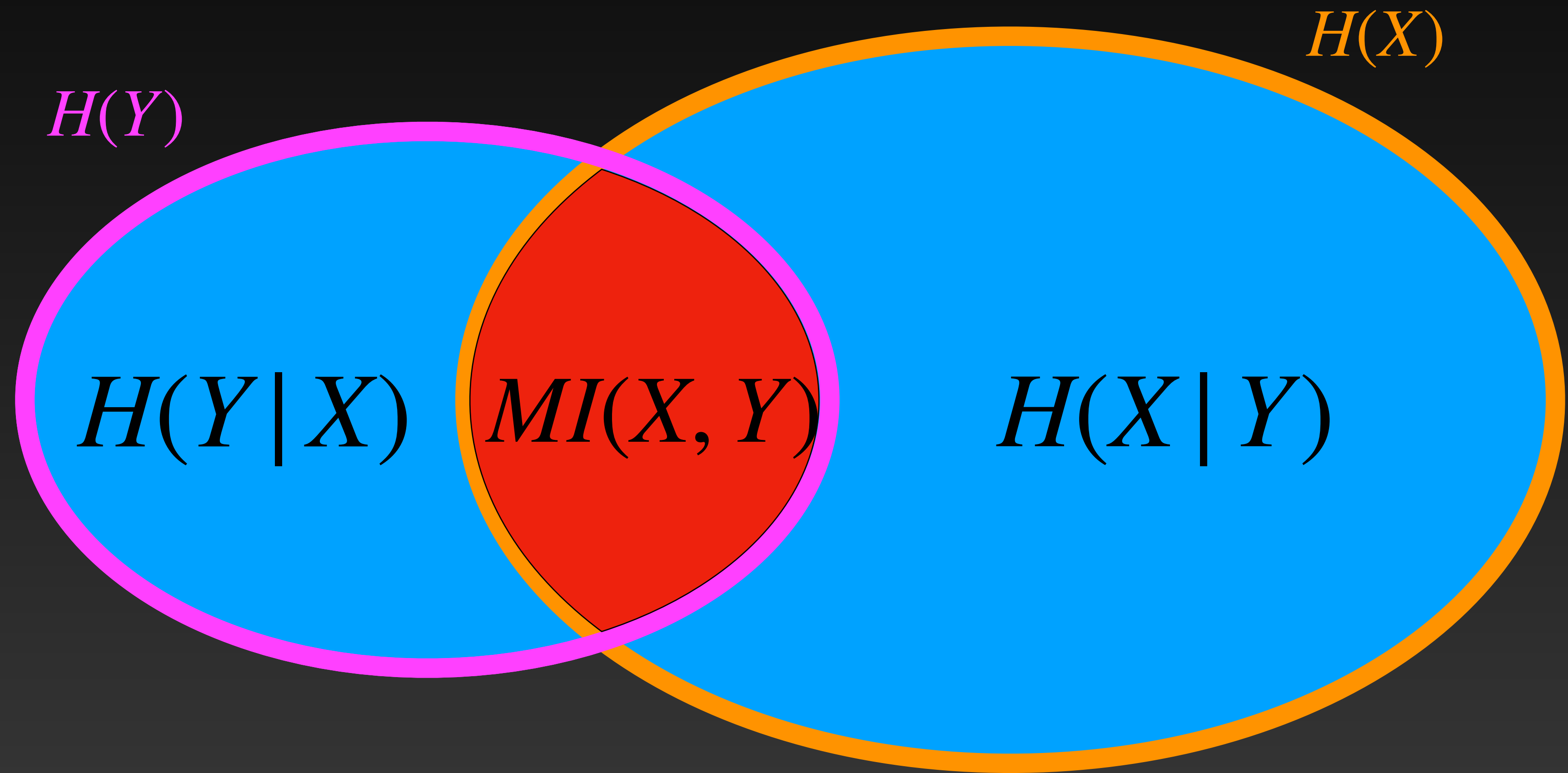
**Symmetric entropy decomposition**



Symmetric/balanced

# Comparing conditional entropies

## Asymmetric entropy decomposition



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

# Asymmetric predictability

## Causality in information space

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

**Postulate:** If  $X \rightarrow Y$ , the density  $f_X$  and the function  $g$  are “independent”.

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### References:

Janzing, D., et al. (2012). *Information-geometric approach to inferring causal directions.*

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**Towards defining DMI**



# Entropy ratio

## Definition and properties

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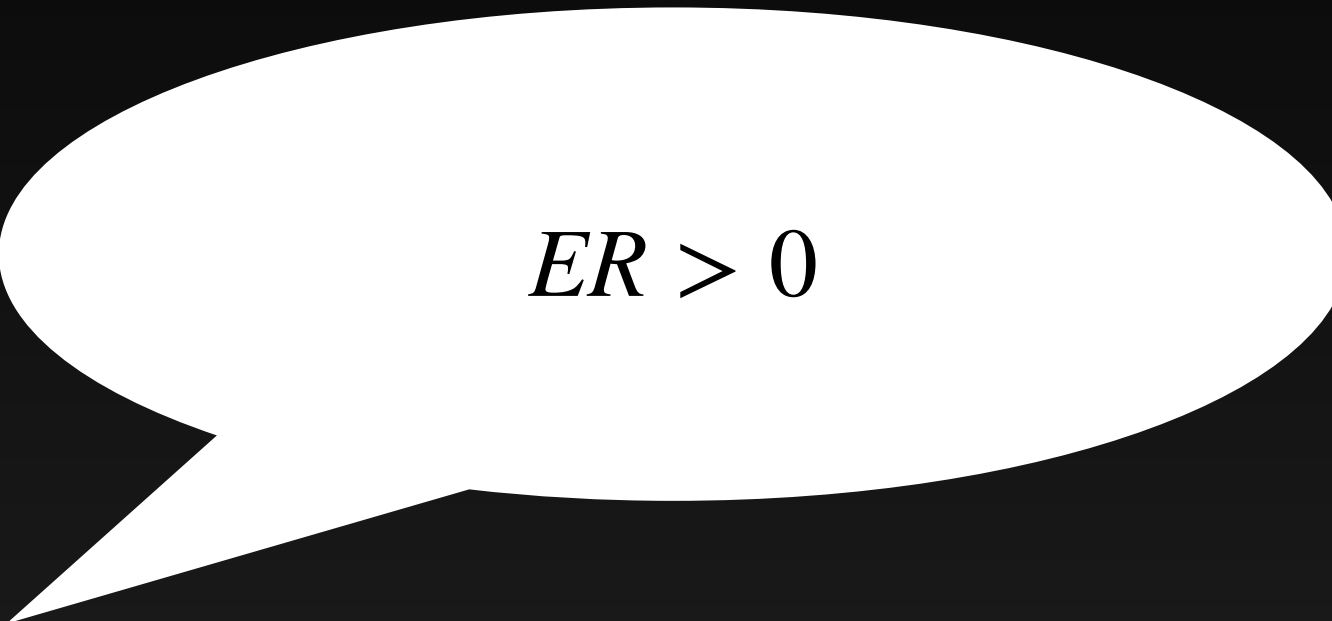
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$$ER > 0$$

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

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## Definition and properties

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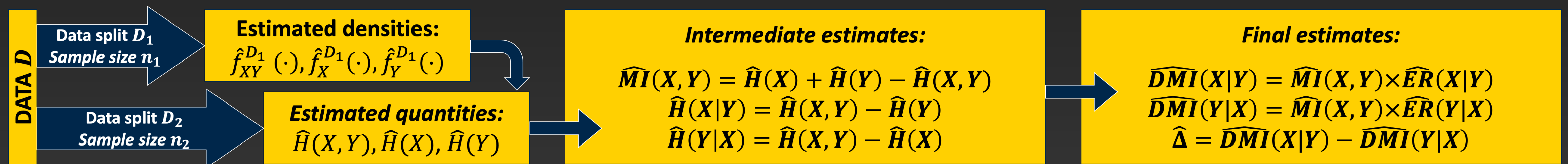
# Estimation and inference using DMI



# 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

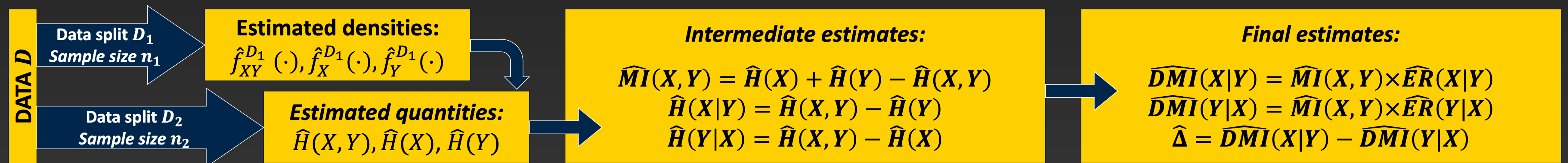


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**Sample splitting eliminates bias due to nuisance parameter estimation.**

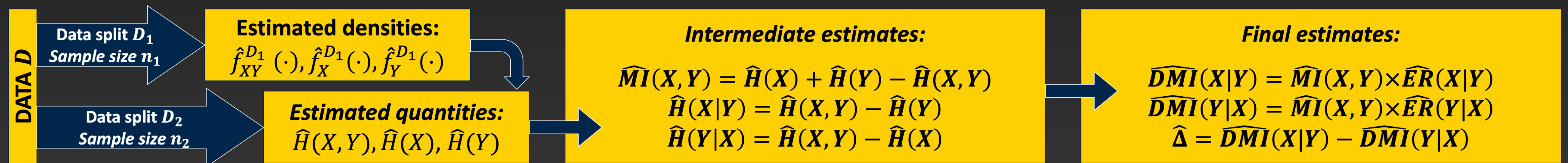


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**Cross-fitting yields improved empirical performance.**



# Directed Mutual Information (DMI)

## Theoretical guarantees

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

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.**

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

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# New epigenetic insights using DMI

Does *DNA*m  $\rightarrow$  BP or BP  $\rightarrow$  *DNA*m

**Application of DMI to methylation studies**

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

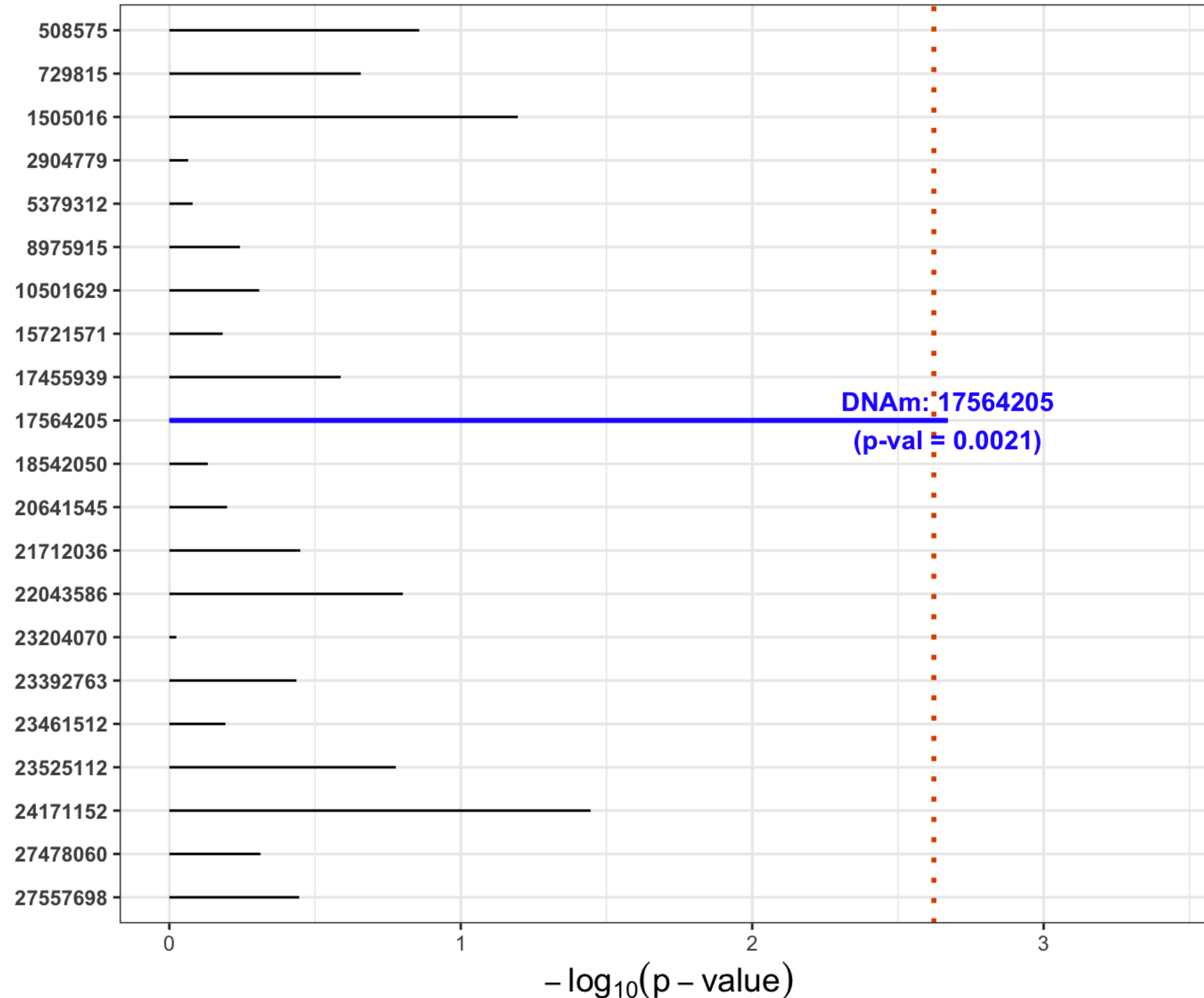
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    - Mildly correlated methylation sites: 21 for ***ATP2B1***, 21 for ***FGF5***, and 51 sites for ***PRDM8***.
1. Test for association between *DNAm* site and BP for a given gene.
  2. Aggregate all *DNAm*-findings using Cauchy combination test for each gene.
  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* → BP or BP → *DNAm*?

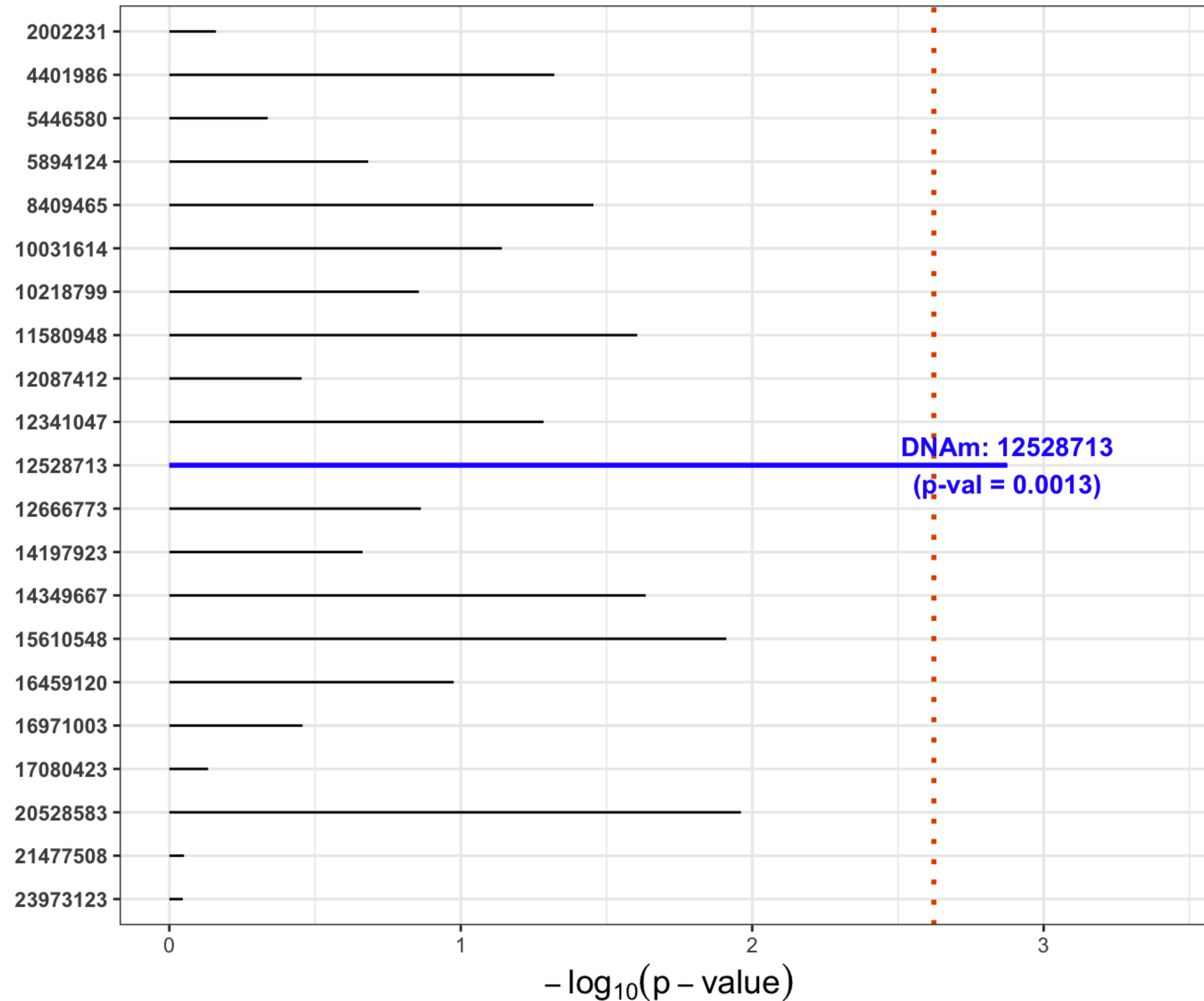
CCT-based combined p-value for association of ATP2B1 gene with DBP: 0.042



## Finding 2: DNAm site #125287 in *FGF5*

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

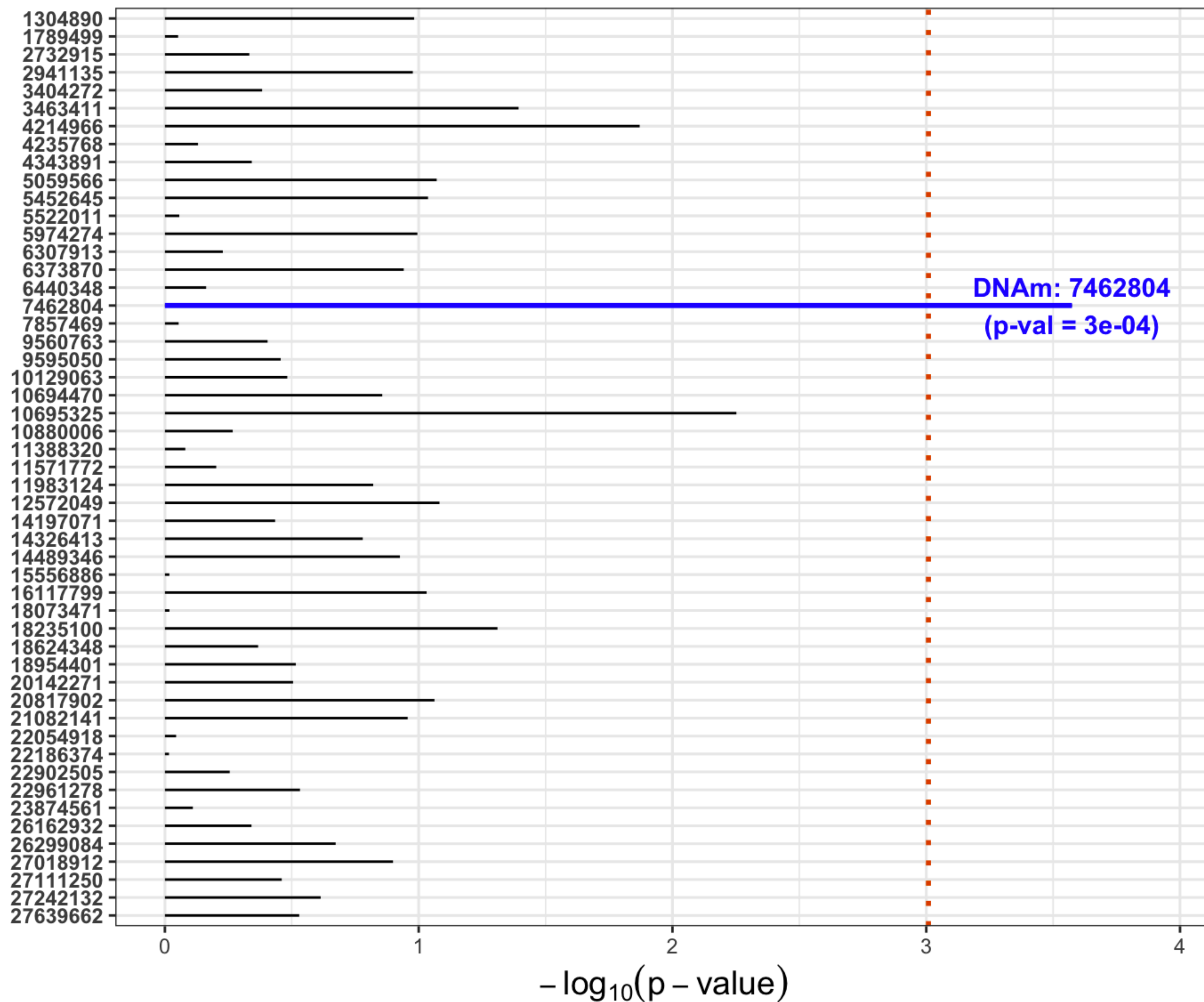
CCT-based combined p-value for association of *FGF5* gene with SBP: 0.019



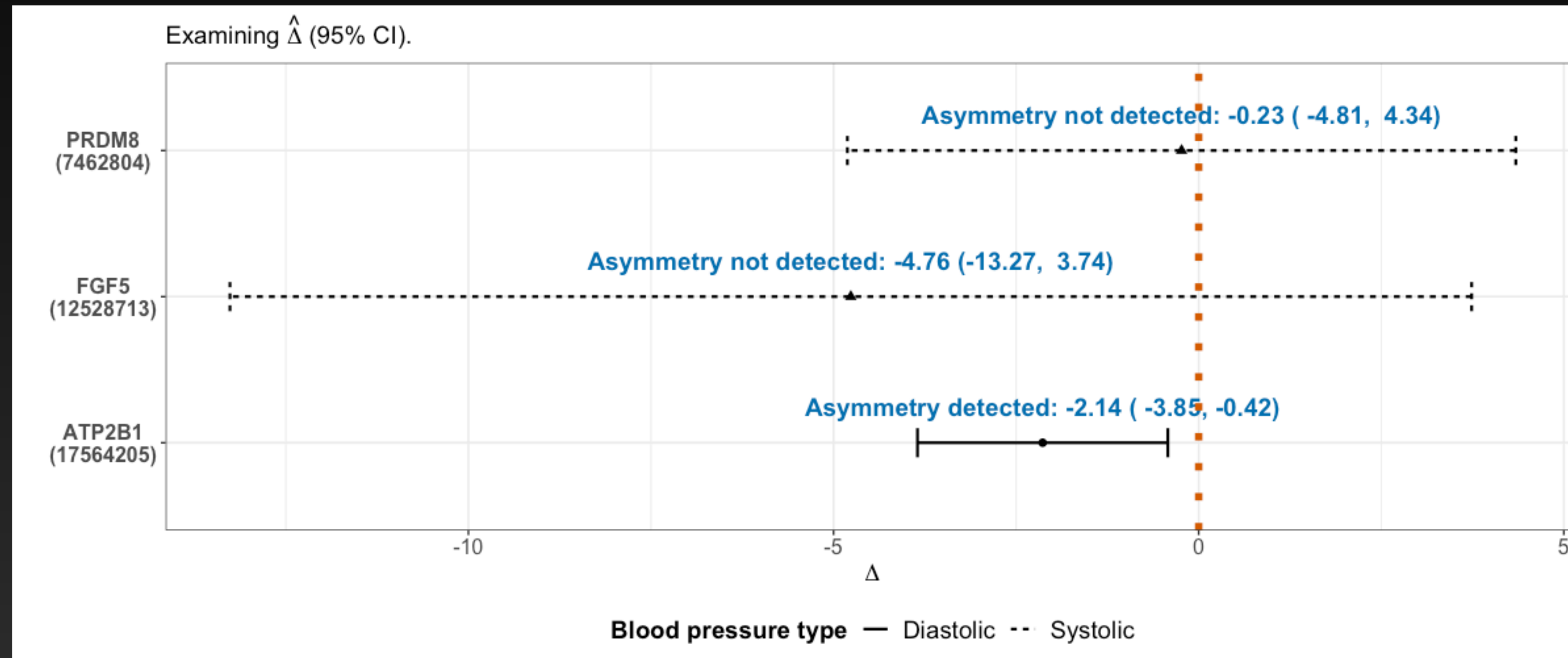
## Finding 3: DNAm site #7462804 in PRDM8

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

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



# Finding 4: DBP → #17564205 in *ATP2B1*



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

**Thank you for your  
time!**

[soumikp@umich.edu](mailto:soumikp@umich.edu)

# References

- **ELEMENT study reference**

- Perng, Wei, et al. "Early life exposure in Mexico to environmental toxicants (ELEMENT) project." *BMJ open* 9.8 (2019): e030427.

- **Motivation of entropy ratio**

- Varin, Cristiano, Manuela Cattelan, and David Firth. "Statistical modelling of citation exchange between statistics journals." *Journal of the Royal Statistical Society. Series A, (Statistics in Society)* 179.1 (2016): 1.

- **Information geometric causal inference**

- Janzing, D., et al. (2012). Information-geometric approach to inferring causal directions. *Artificial Intelligence*, 182–183, 1–31. <https://doi.org/10.1016/j.artint.2012.01.002>
- Daniusis, P., et al. (2012). Inferring deterministic causal relations. *arXiv*. <https://doi.org/10.48550/arXiv.1203.3475>

- **Sample splitting and cross-fitting**

- Zivich, P. N., & Breskin, A. (2021). Machine learning for causal inference: on the use of cross-fit estimators. *Epidemiology (Cambridge, Mass.)*, 32(3), 393.