

Heritability of Human Structural Connectomes

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What is heritability?

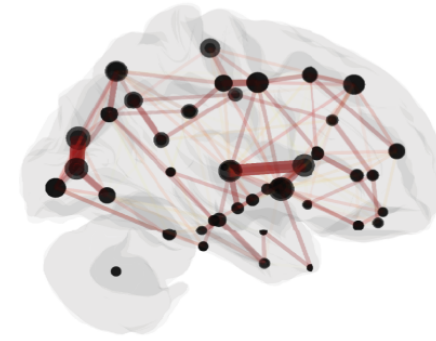
- Variations in phenotype caused by variations in genotype.
- Potentially discover relationships between diseases and genetics.

Are the patterns of brain connectivity heritable?

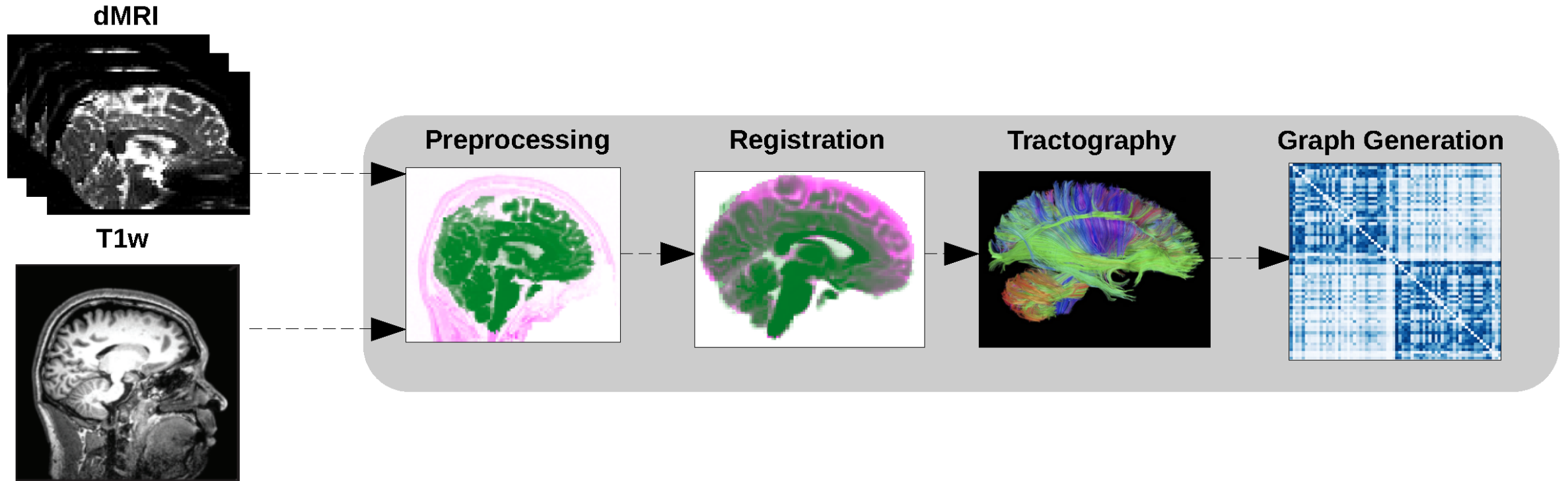
Brain connectivity as connectomes

(aka networks or graphs)

- Vertex: region of the brain
- Edges: connectivity measure between a pair of vertices
- Structural connectomes: estimated # of neuronal fibers
- Undirected: neurons have no direction


$$\begin{bmatrix} 0 & 3 & 0 & 0 & 1 & 0 \\ 3 & 0 & 2 & 0 & 1 & 0 \\ 0 & 2 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 6 \\ 1 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 6 & 0 & 0 \end{bmatrix}$$

How do we get structural connectomes?



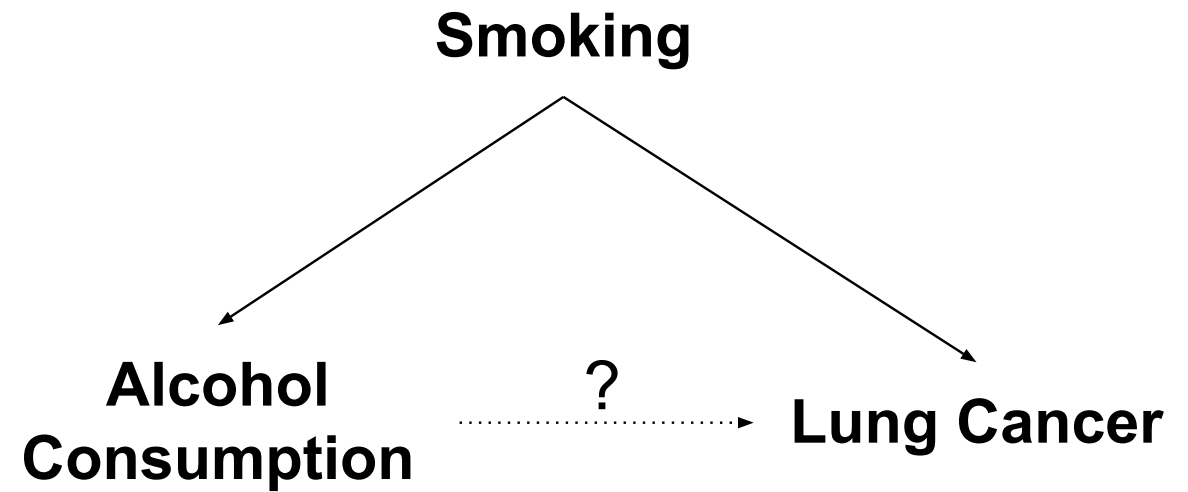
Quick detour to causal land

Directed acyclic graphs

- Representation of causal relationships of variables
 - From domain knowledge

Confounding

- Common cause for both exposure and outcome
 - Exposure: alcohol consumption
 - Outcome: lung cancer
- Causes spurious association!
- Solution: "condition" confounding



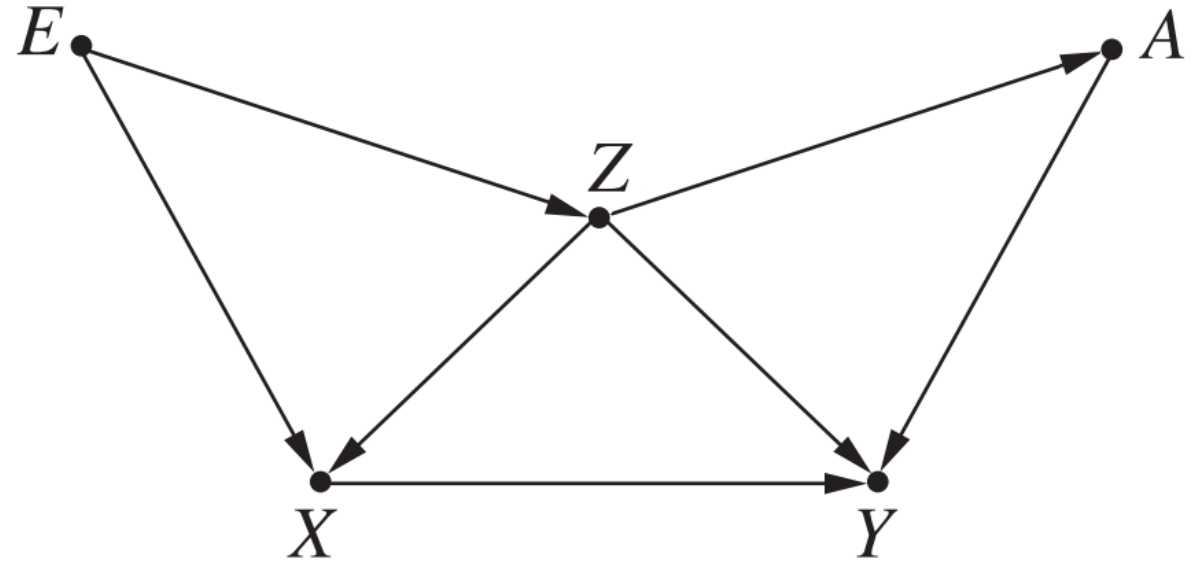
Toy example

- Smoking = $\mathcal{N}(5, 1)$
- Alcohol = Smoking + $\mathcal{N}(0, 1)$
- Lung Cancer = Smoking + $\mathcal{N}(0, 1)$
- n = 100

	Indep. Test	Conditional Indep. Test
Null Hypothesis	Alcohol \perp Lung cancer	Alcohol \perp Lung cancer Smoking
Alternate Hypothesis	Alcohol $\not\perp$ Lung cancer	Alcohol $\not\perp$ Lung cancer Smoking
Correlation (r)	≈ 0.66	≈ 0.006
p-value	≈ 0	≈ 1

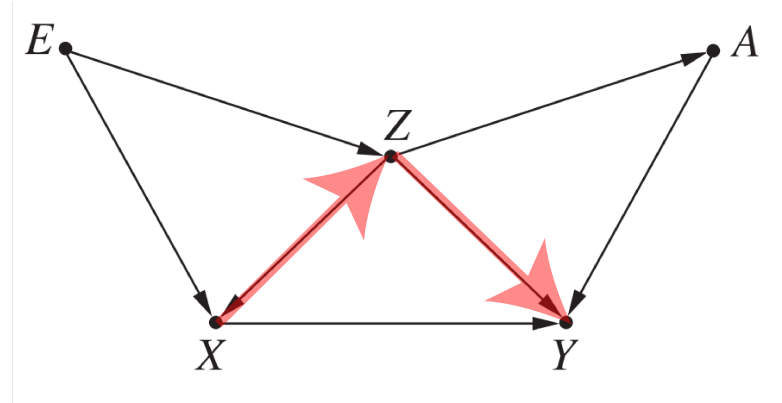
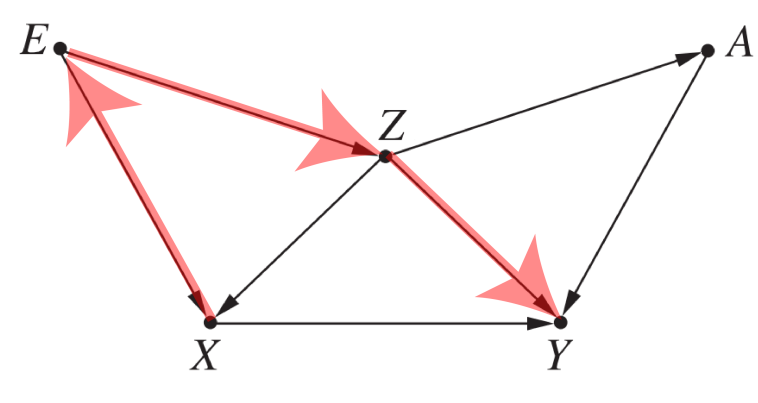
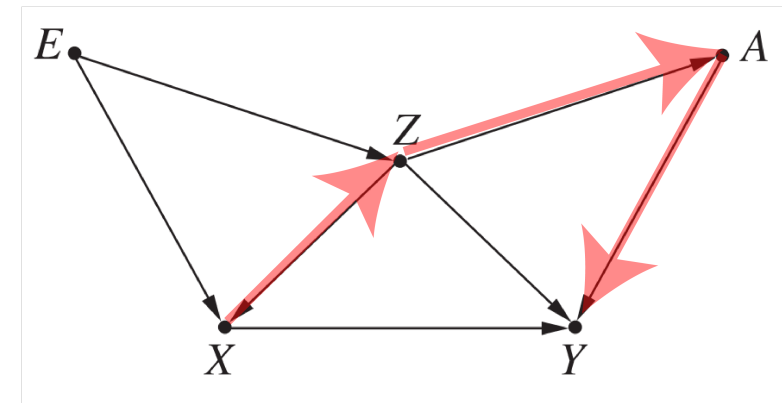
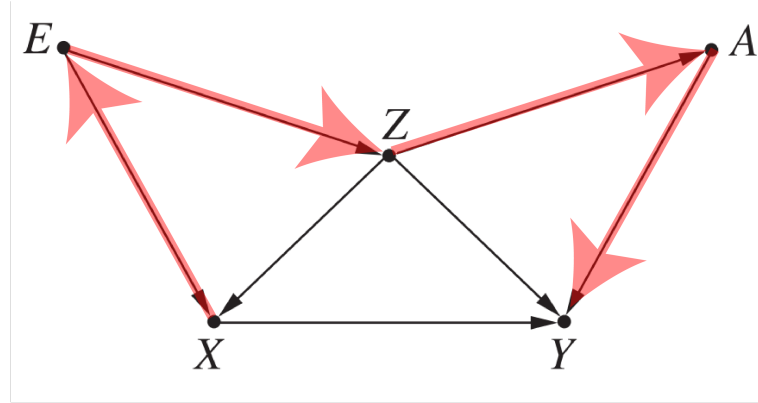
Backdoor paths

- Non-causal path from exposure to outcome
- Flow backwards out of exposure (arrow pointing towards exposure)
- Confounders create backdoor paths
- Path is blocked if a variable in the path is conditioned on.



Examples

- Four possible paths
- Condition sets:
 - $\{Z\}$
 - $\{Z, E\}$
 - $\{Z, A\}$
 - $\{Z, E, A\}$



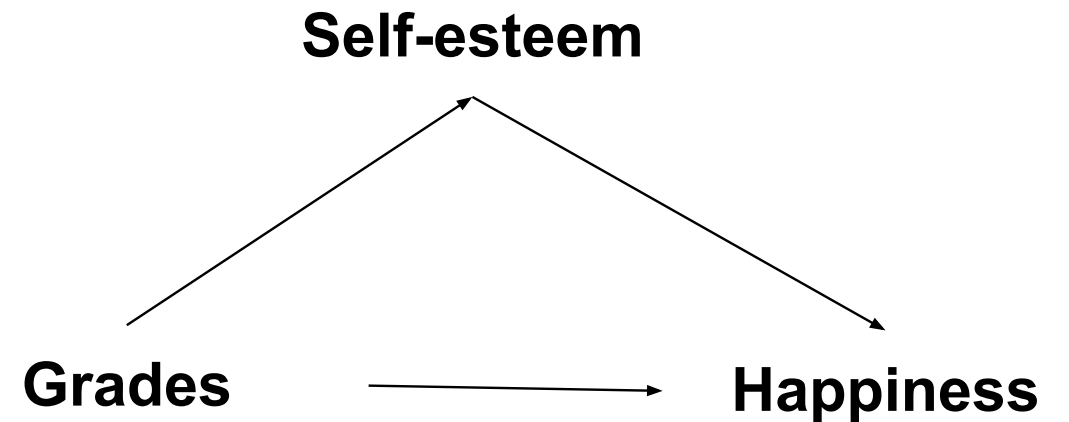
Backdoor criterion

Causal effect exists between exposure (X) and outcome (Y) if:

1. No backdoor paths from X to Y exist
2. Measured covariates Z block all backdoor paths from X and Y

Mediation

- Lies on the causal path between exposure and outcome
 - Exposure: grades
 - Outcome: happiness
 - Mediator: self-esteem
- Total effect: effect from both exposure and mediators
- Direct effect: effect only from exposure

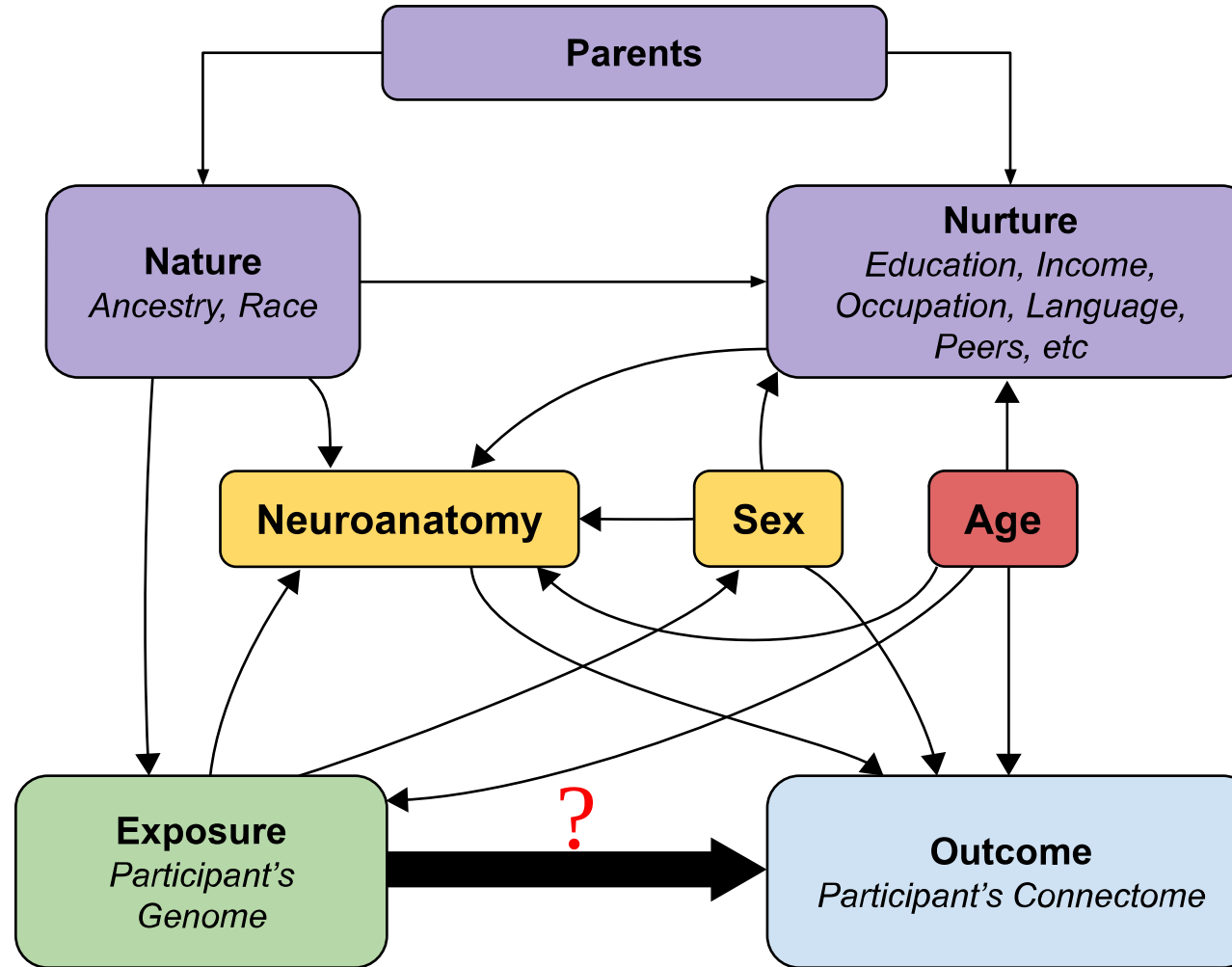


Toy example

- Grades = $\mathcal{N}(5, 1)$
- Self-esteem = Grades + $\mathcal{N}(0, 1)$
- Happiness = Grades + Self-esteem + $\mathcal{N}(0, 1)$
- n = 100

	Indep. Test	Conditional Indep. Test
Null Hypothesis	Grades \perp Happiness	Grades \perp Happiness Self-esteem
Alternate Hypothesis	Grades $\not\perp$ Happiness	Grades $\not\perp$ Happiness Self-esteem
Correlation (r)	≈ 0.89	≈ 0.63
p-value	≈ 0	≈ 0

Heritability as causal problem



Do genomes affect connectomes?

- Our hypothesis:

$$H_0 : F(\text{Connectome}|\text{Genome}) = F(\text{Connectome})$$

$$H_A : F(\text{Connectome}|\text{Genome}) \neq F(\text{Connectome})$$

- Alternatively:

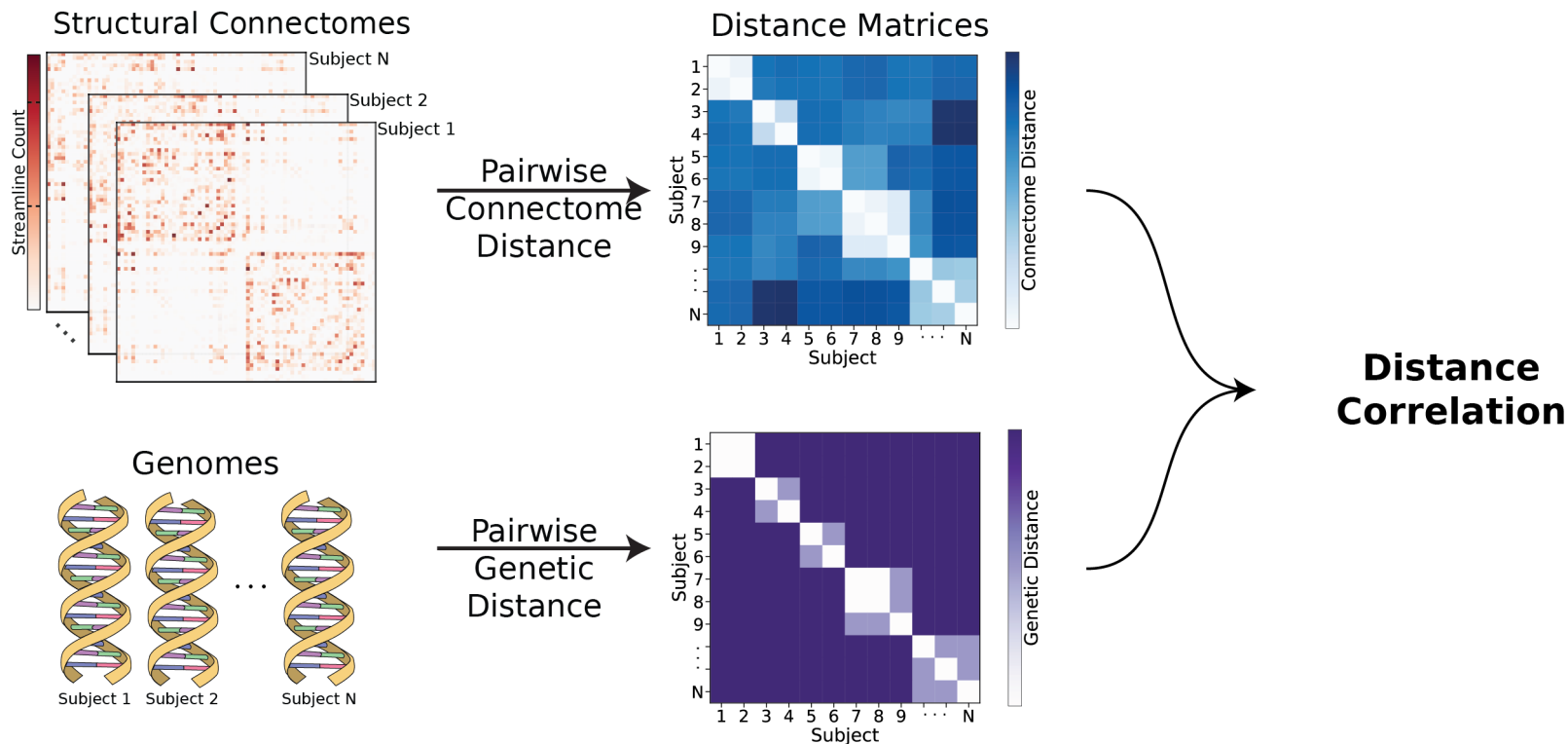
$$H_0 : F(\text{Connectome}, \text{Genome}) = F(\text{Connectome})F(\text{Genome})$$

$$H_A : F(\text{Connectome}, \text{Genome}) \neq F(\text{Connectome})F(\text{Genome})$$

- Known as independence testing
- Test statistic: *distance correlation* (*dcorr*)
- Implication if false: there exists an associational heritability.

Distance correlation

- Measures dependence between two *multivariate* quantities.
 - For example: connectomes, genomes.
- Can detect nonlinear associations.
- Measures correlation between pairwise distances.



Do genomes affect connectomes given covariates?

- Want to test:

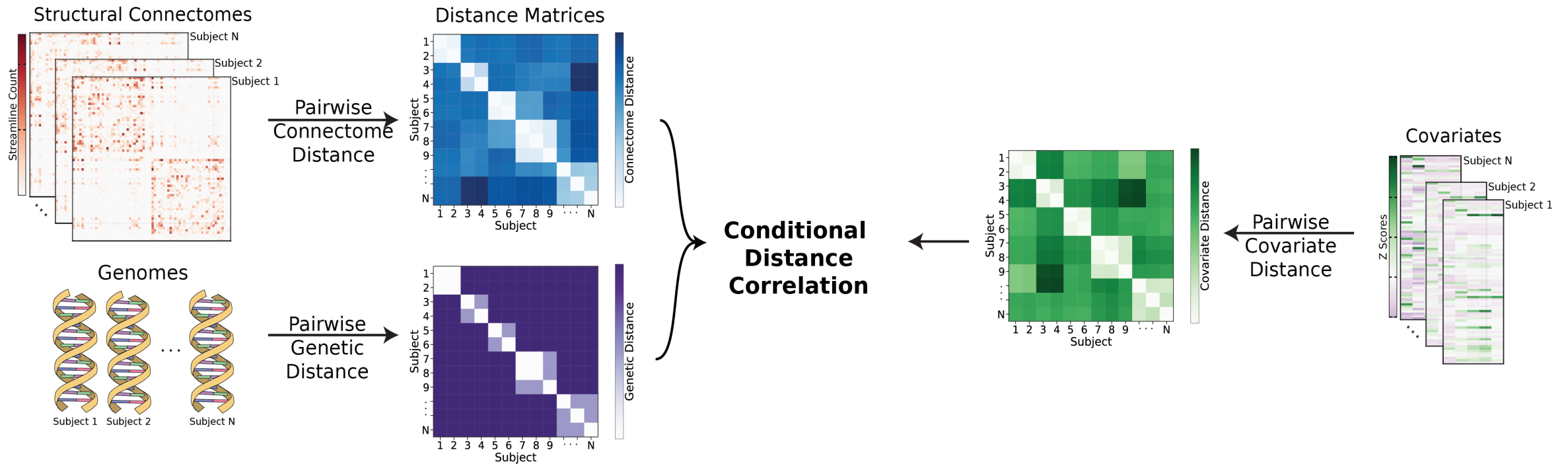
$$H_0 : F(\text{Conn.}, \text{Genome} | \text{Covariates}) = F(\text{Conn.} | \text{Covariates}) F(\text{Genome} | \text{Covariates})$$

$$H_A : F(\text{Conn.}, \text{Genome} | \text{Covariates}) \neq F(\text{Conn.} | \text{Covariates}) F(\text{Genome} | \text{Covariates})$$

- Known as conditional independence test
- Test statistic: Conditional distance correlation (cdcorr)
- Implication if false: there exists causal dependence of connectomes on genomes.

Conditional distance correlation

- Augment distance correlation procedure with third distance matrix.



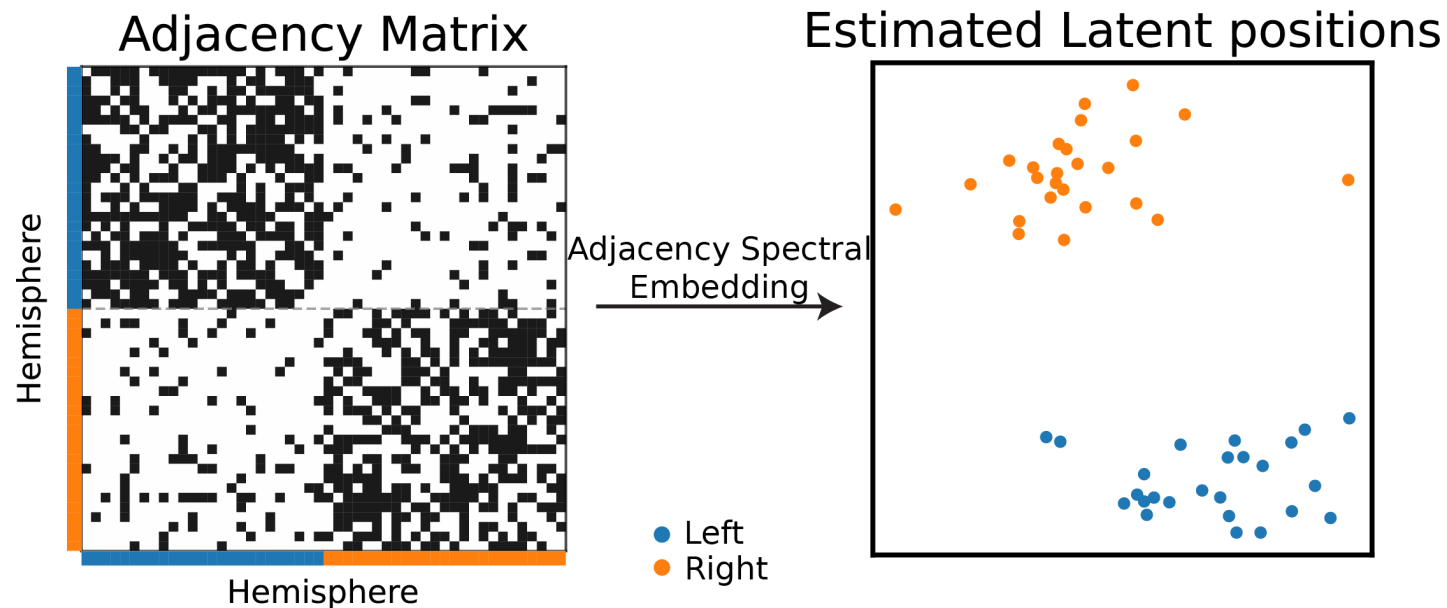
How do we compare genomes?

- Neuroimaging twin studies do not sequence genomes.
- Coefficient of kinship (ϕ_{ij})
 - Probabilities of finding a particular gene at a particular location.
- $d(\text{Genome}_i, \text{Genome}_j) = 1 - 2\phi_{ij}$.

Relationship	ϕ_{ij}	$1 - 2\phi_{ij}$
Monozygotic	$\frac{1}{2}$	0
Dizygotic	$\frac{1}{4}$	$\frac{1}{2}$
Non-twin siblings	$\frac{1}{4}$	$\frac{1}{2}$
Unrelated	0	1

How do we compare connectomes?

- Random dot product graph (RDPG)
 - Each vertex (region of interest) has a low d dimensional latent vector (position).
 - Estimate latent position matrix X via adjacency spectral embedding.



- $d(\text{Connectome}_k, \text{Connectome}_l) = ||X^{(k)} - X^{(l)} R||_F$

Neuroanatomy, Age (mediators)

- Literature show:
 - neuroanatomy (e.g. brain volume) is highly heritable.
 - age affects genomes and potentially connectomes
- $d(\text{Covariates}_i, \text{Covariates}_j) = \|\text{Covariates}_i - \text{Covariates}_j\|_F$

Human Connectome Project

- Brain scans from identical (monozygotic), fraternal (dizygotic), non-twin siblings.
- Regions defined using Glasser parcellation (180 regions).

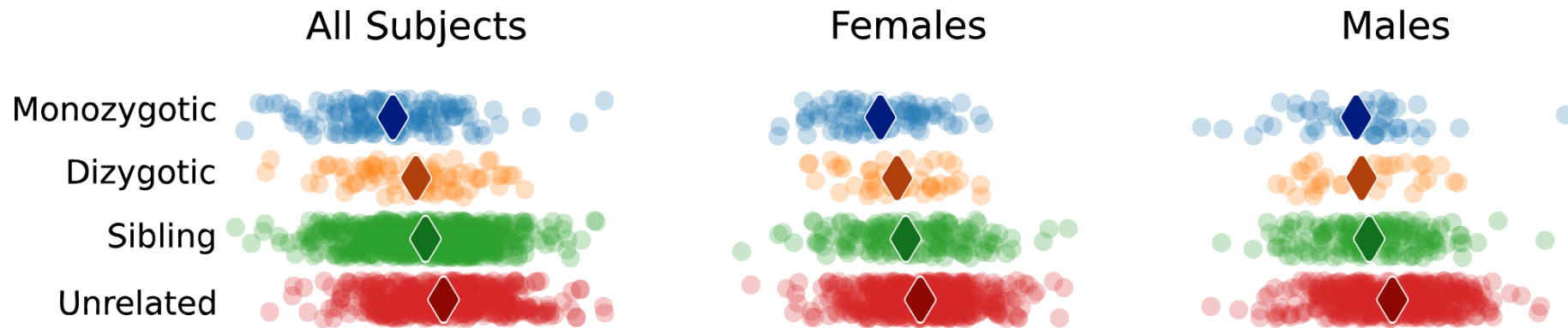
Zygosit y	Monozygoti c	Dizygotic	Non-twin siblings
N	322	212	490
Sex	196 F, 126 M	125 F, 87 M	237 F, 253 M
Age (mean)	29.6 (3.3)	28.9 (3.4)	28.3 (3.9)
Age (range)	22-36	22-36	22-37

Van Essen, David C., et al., The WU-Minn human connectome project: an overview (2013)

Glasser, Matthew F., et al. "A multi-modal parcellation of human cerebral cortex." Nature (2016).

Associational Test for Connectomic Heritability

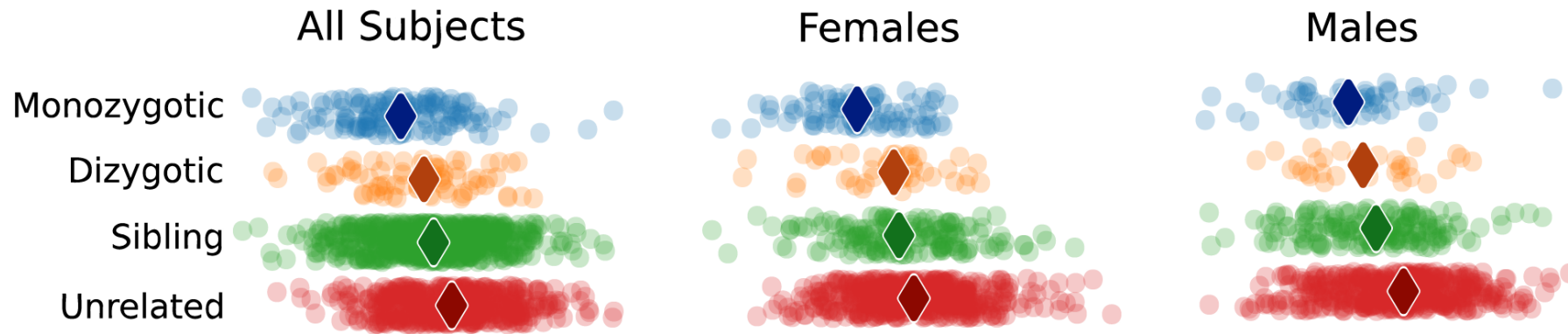
- $H_0 : F(\text{Connectome}, \text{Genome}) = F(\text{Connectome})F(\text{Genome})$
 $H_A : F(\text{Connectome}, \text{Genome}) \neq F(\text{Connectome})F(\text{Genome})$



Sex	All	Females	Males
p-value	$< 1 \times 10^{-5}$	$< 1 \times 10^{-3}$	$< 1 \times 10^{-2}$

Associational Test for Neuroanatomy

- $H_0 : F(\text{Neuroanatomy}, \text{Genome}) = F(\text{Neuroanatomy})F(\text{Genome})$
 $H_A : F(\text{Neuroanatomy}, \text{Genome}) \neq F(\text{Neuroanatomy})F(\text{Genome})$



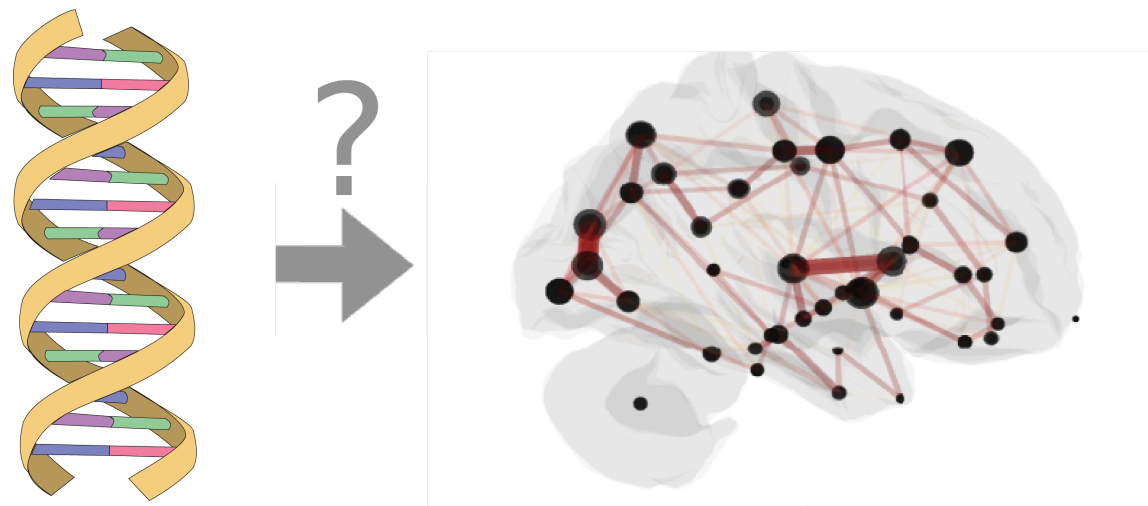
Sex	All	Females	Males
p-value	$< 1 \times 10^{-3}$	$< 1 \times 10^{-2}$	$< 1 \times 10^{-2}$

Causal Test for Connectomic Heritability

- $H_0 : F(\text{Conn.}, \text{Genome} | \text{Covariates}) = F(\text{Conn.} | \text{Covariates}) F(\text{Genome} | \text{Covariates})$
 $H_A : F(\text{Conn.}, \text{Genome} | \text{Covariates}) \neq F(\text{Conn.} | \text{Covariates}) F(\text{Genome} | \text{Covariates})$

Sex	All	Females	Males
p-value	$< 1 \times 10^{-2}$	$< 1 \times 10^{-2}$	$< 1 \times 10^{-2}$

Summary



- Present a causal model for heritability of connectomes.
- Leveraged recent advances:
 - i. Statistical models for networks, allowing meaningful comparison of connectomes.
 - ii. Distance and conditional distance correlation as test statistic for causal analysis¹.
- Connectomes are dependent on genome, suggesting heritability.

¹ Bridgeford, Eric W., et al. "Batch Effects are Causal Effects: Applications in Human Connectomics." (2021).

