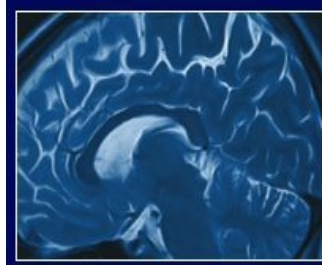




University of Wisconsin
**SCHOOL OF MEDICINE
AND PUBLIC HEALTH**



*The Waisman Laboratory
for Brain Imaging and Behavior*

Hyper Network Analysis on Paired Images

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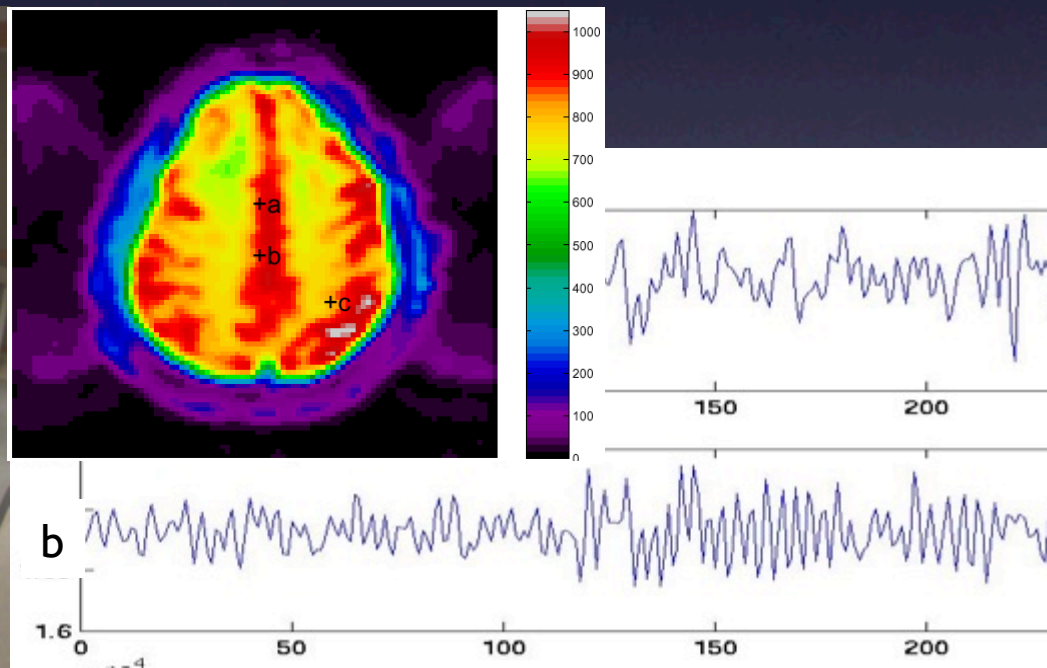
Twin functional-MRI study

11 monozygotic (MZ) twins

14 dizygotic (DZ) twins

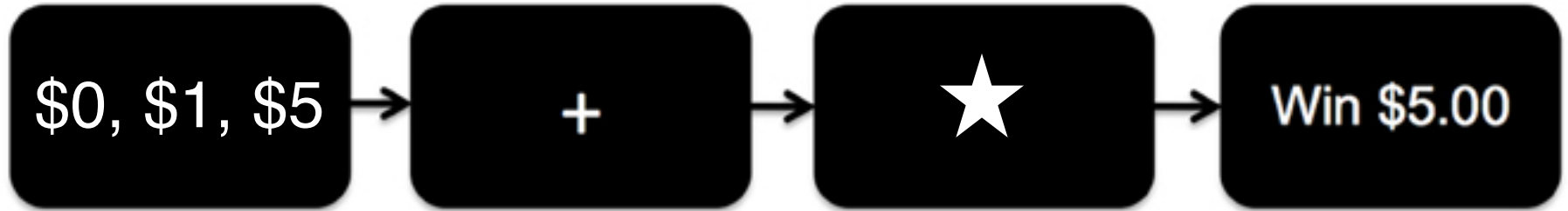
9 same-sex DZ pairs (5 male, 4 female)

5 different-sex DZ pairs



Paired statistical contrast images

Monetary incentive delay task



3 runs of 40 trials

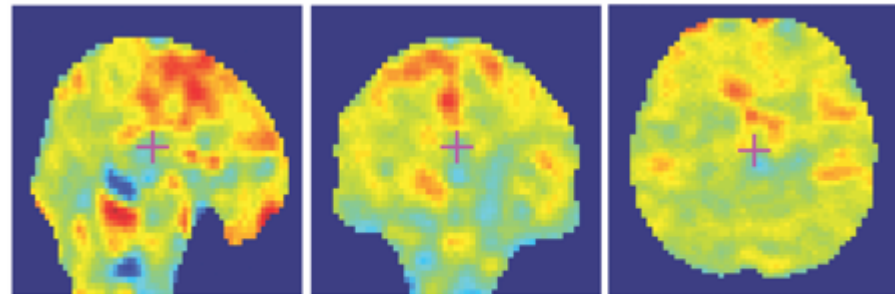
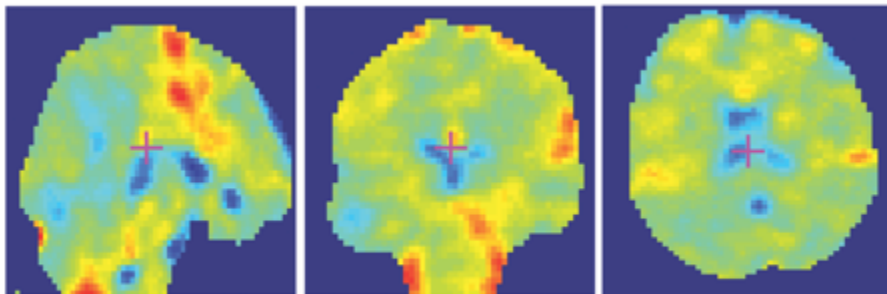
delay for \$0 trials
delay for \$1 trials
delay for \$5 trials

c

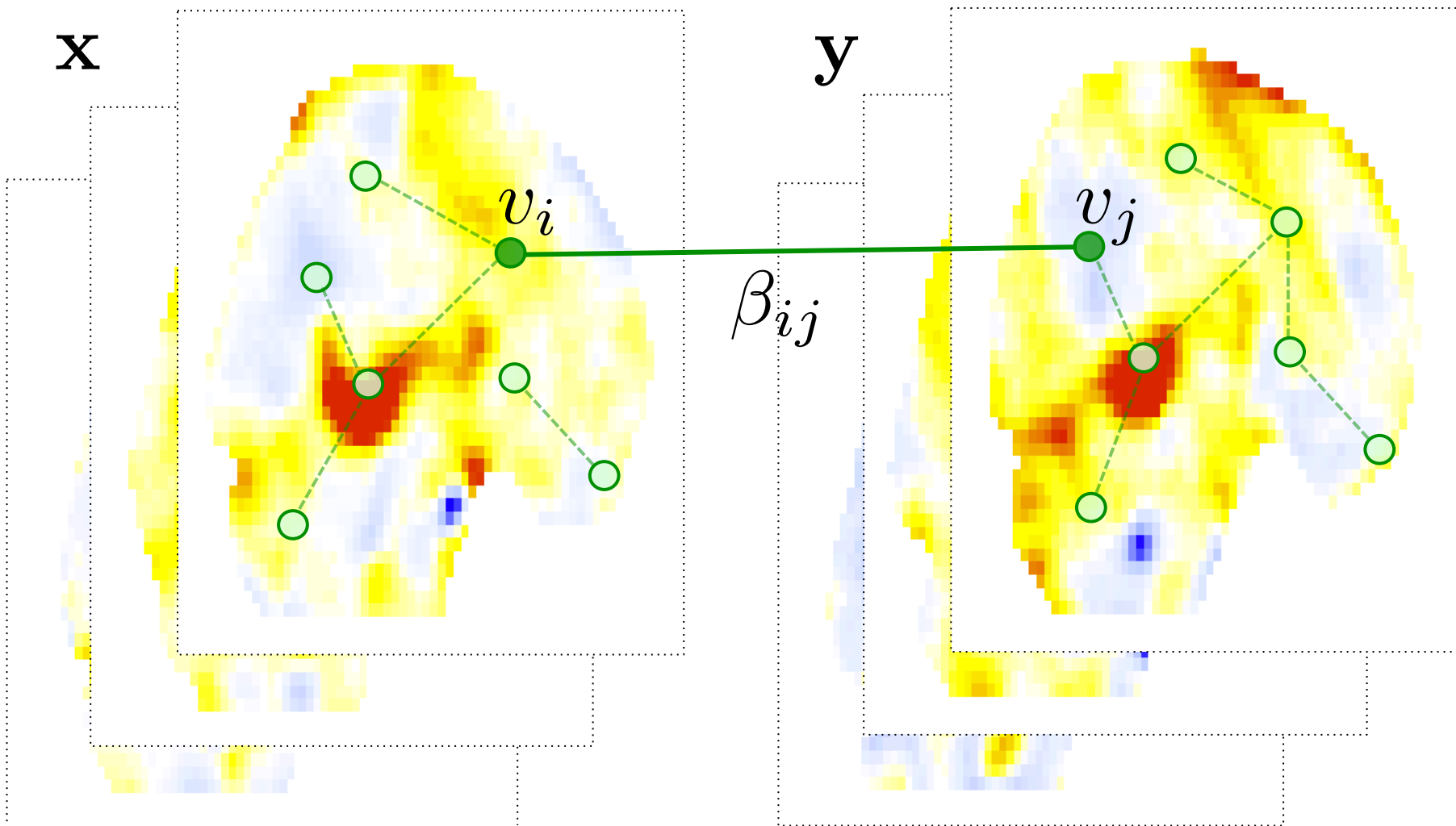
General Linear Model

$$W(v_i) = Zb(v_i) + \varepsilon(v_i)$$

$c^T b(v_i)$ Contrast map



Hyper-network across paired images



$$y(v_j) = \sum_{i=1}^p \beta_{ij} x(v_i) + e(v_j) \quad \dashrightarrow \quad y(v_j) = \beta_{ij} x(v_i) + e(v_j)$$

Dense connections

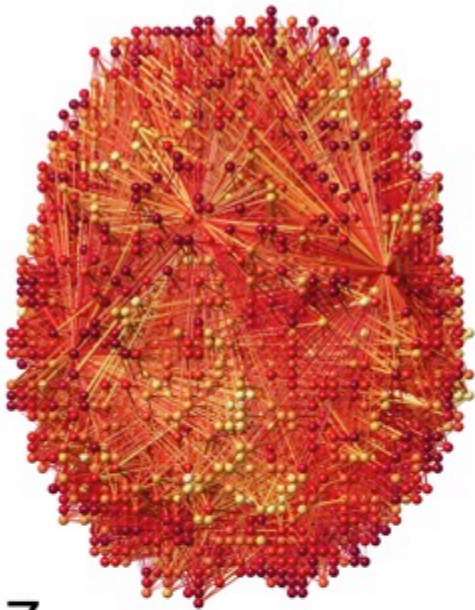
$$y(v_j) = \beta_{ij}x(v_i) + e(v_j)$$

Least squares

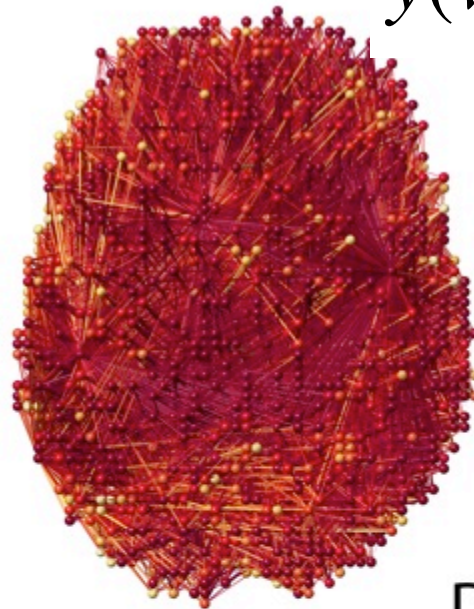
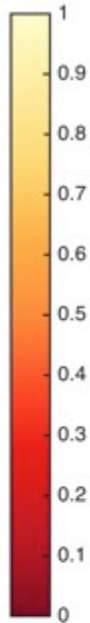
Estimation

$$\beta_{ij} = x'(v_i)y(v_j)$$

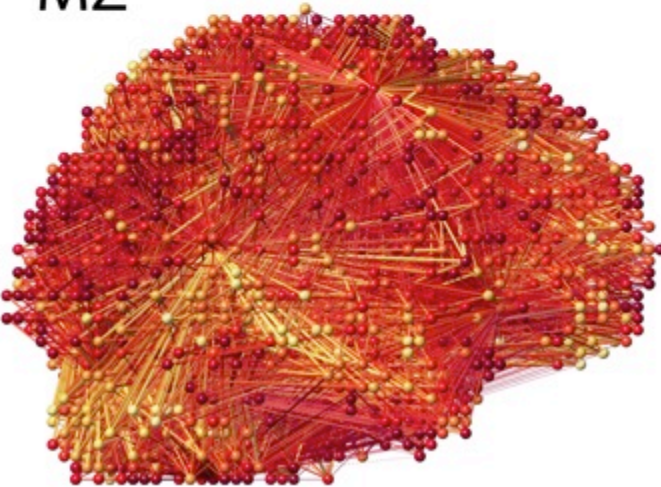
cross-correlation



MZ

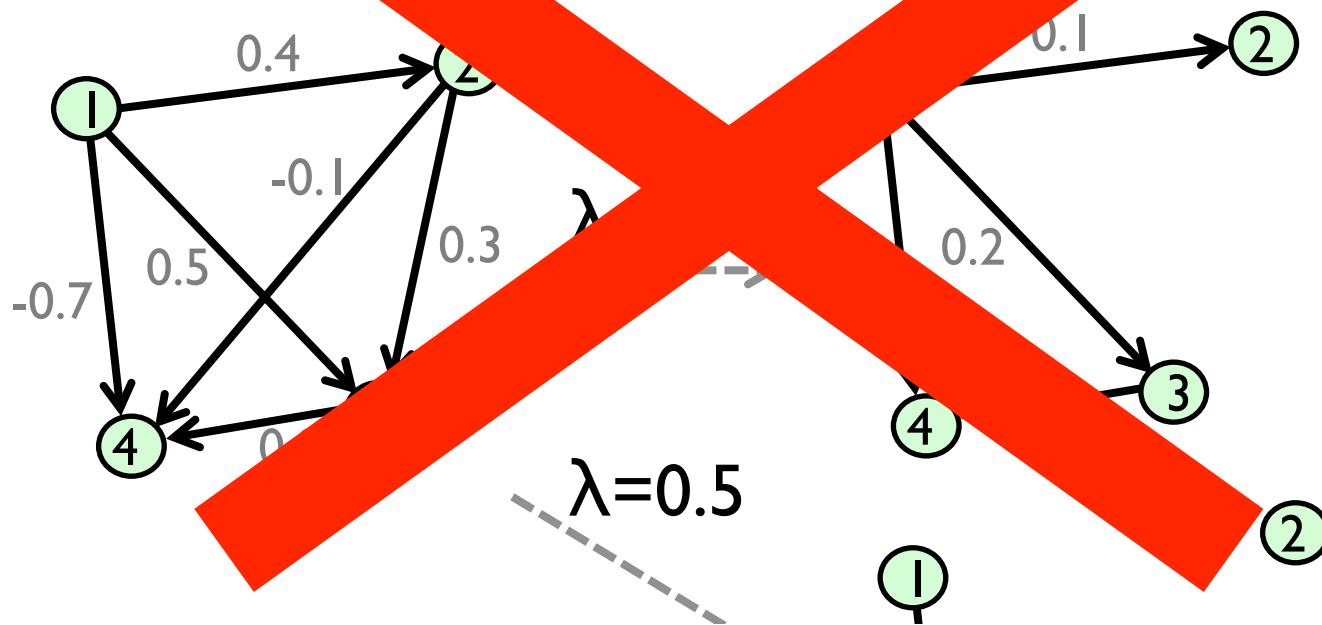


DZ



Sparse network model

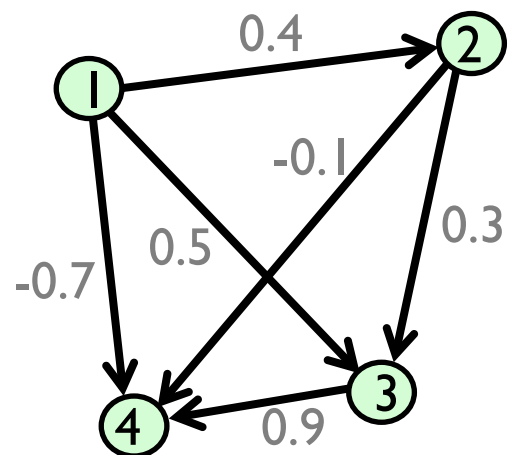
$$\hat{\beta}(\lambda) = \arg \min_{\beta} \frac{1}{2} \sum_{i=1}^p \sum_{j=1}^p \|y(v_j) - \beta_{ij} x(v_i)\|^2 + \lambda \sum_{i,j} |\beta_{ij}|$$



NOT A GOOD APPROACH!

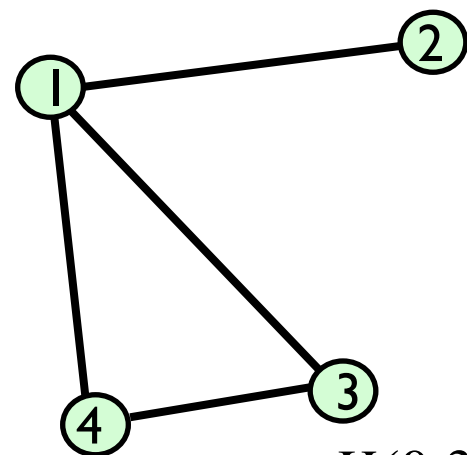
Sparse network + persistent homology

$$\hat{\beta} = \operatorname{argmin}_{\beta} \frac{1}{2} \sum_{i=1}^p \sum_{j=1}^p \|x(v_i) - \beta_{ij} y(v_j)\|^2 + \lambda \sum_{i,j} |\beta_{ij}|$$



Soft thresholding

$$\text{edge} = \begin{cases} 1 & \text{if } |x'(v_i)y(v_j)| > \lambda \\ 0 & \text{otherwise} \end{cases}$$

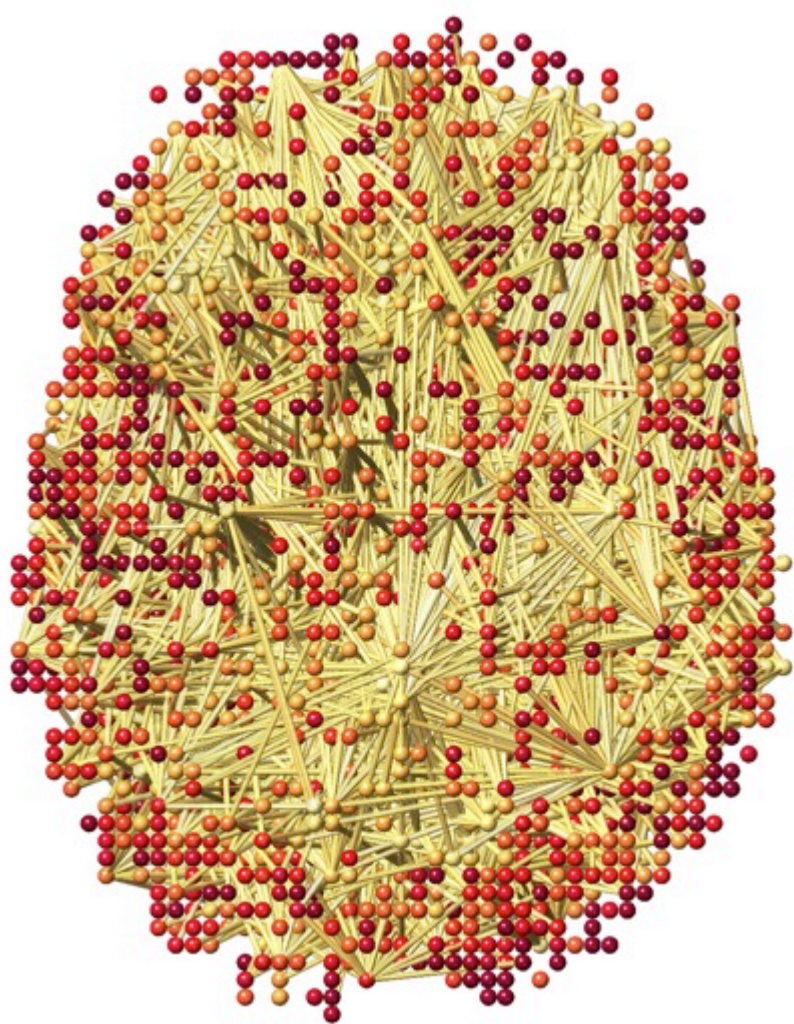


$H(0.3)$

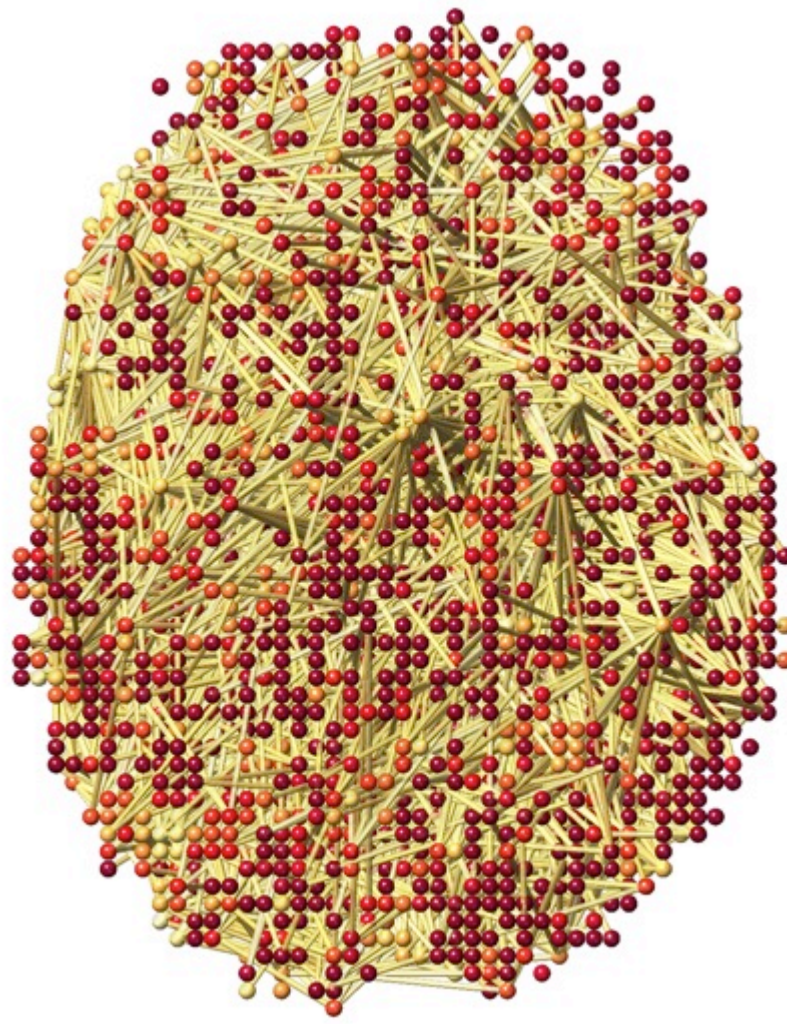
$$H(\lambda_1) \supset H(\lambda_2) \supset H(\lambda_3) \supset \dots$$

$$\text{for } \lambda_1 \leq \lambda_2 \leq \lambda_3 \leq \dots$$

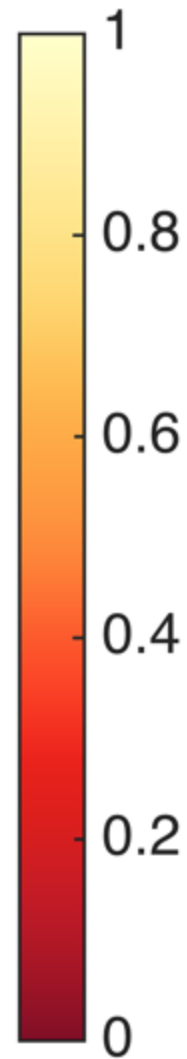
Networks at sparse parameter 0.7



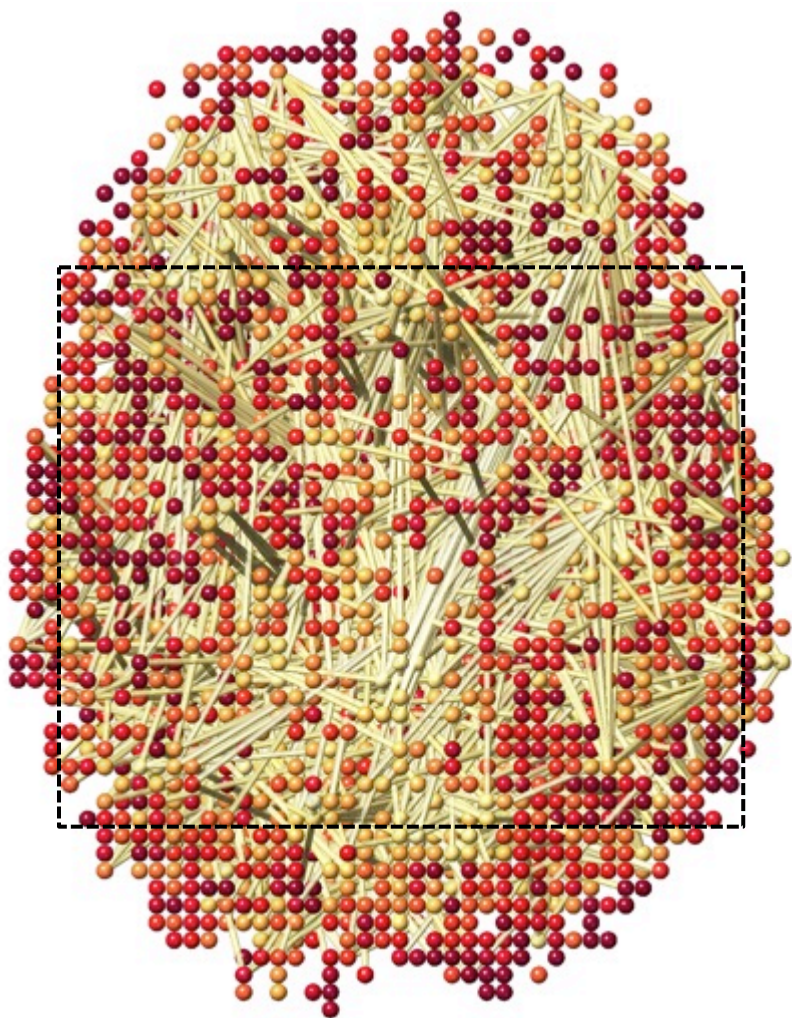
MZ-twins



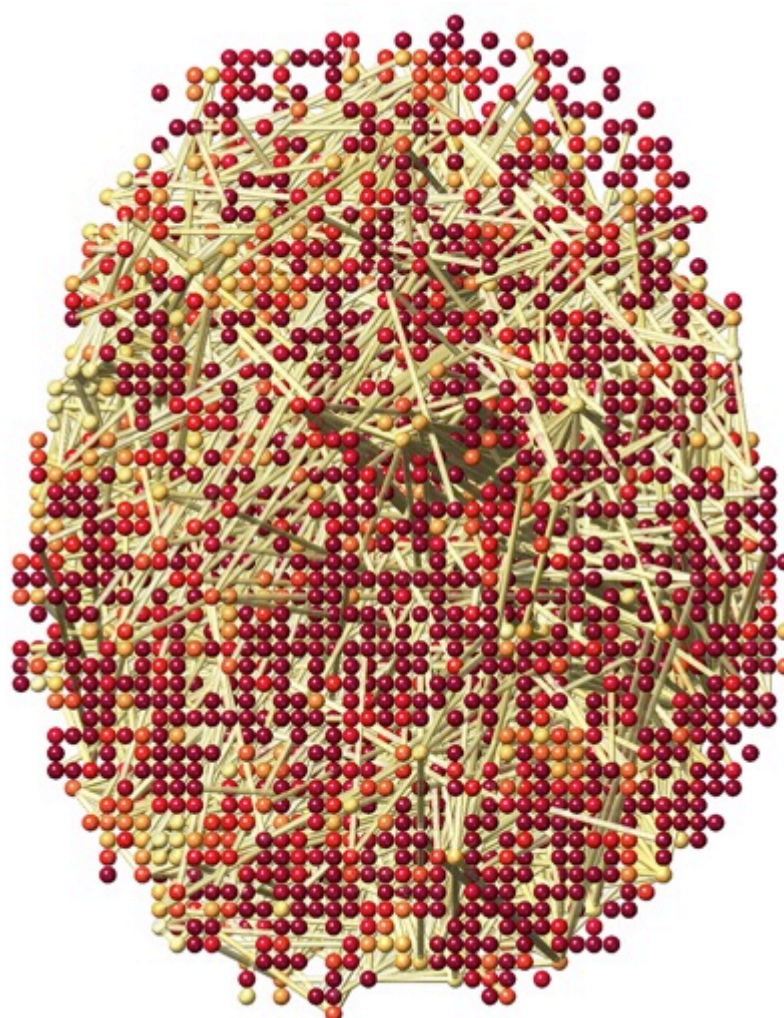
DZ-twins



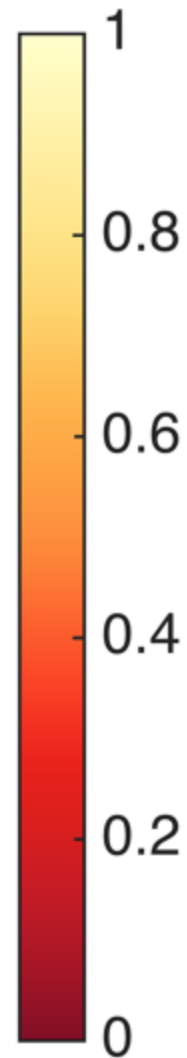
Networks at sparse parameter 0.8



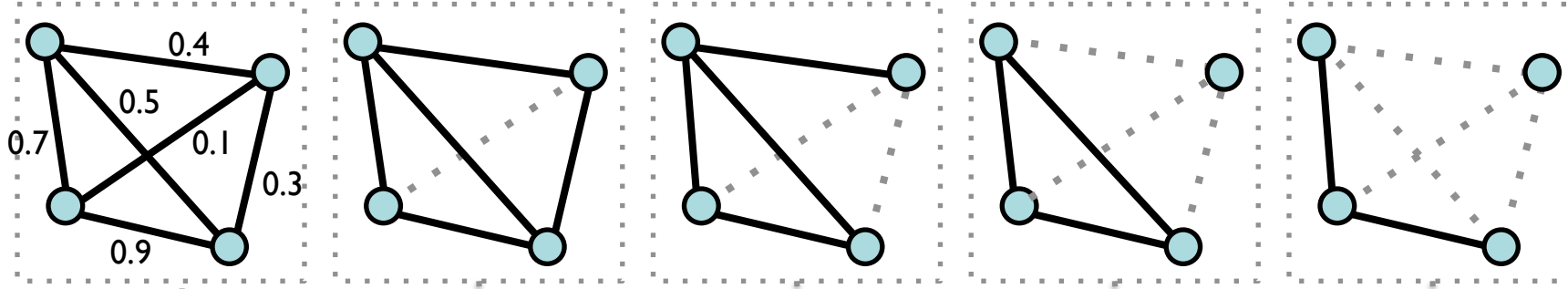
MZ-twins



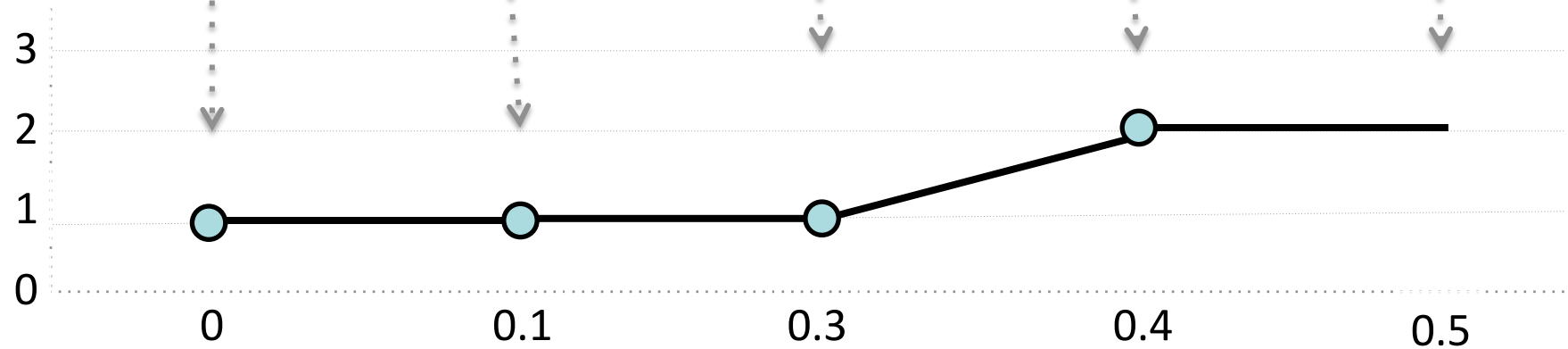
DZ-twins



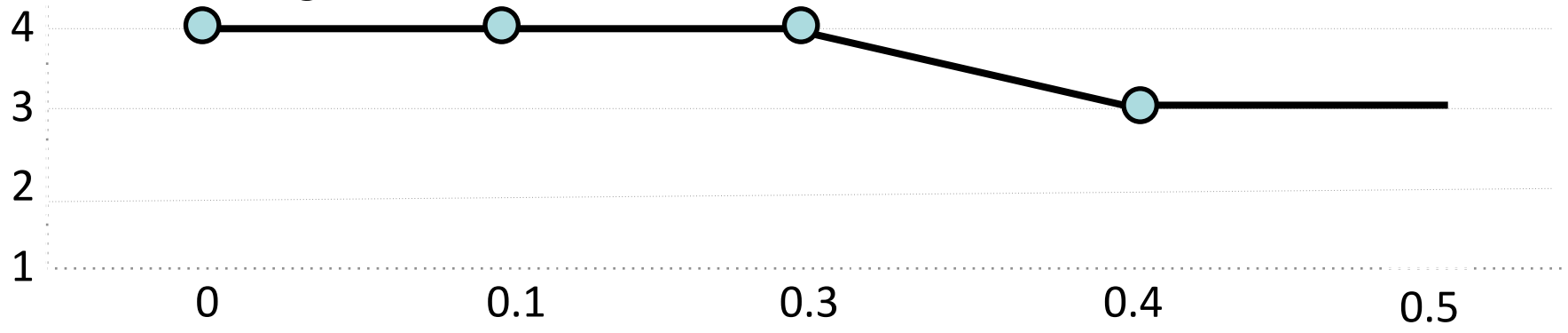
Persistent Homology



Number of connected components β_0

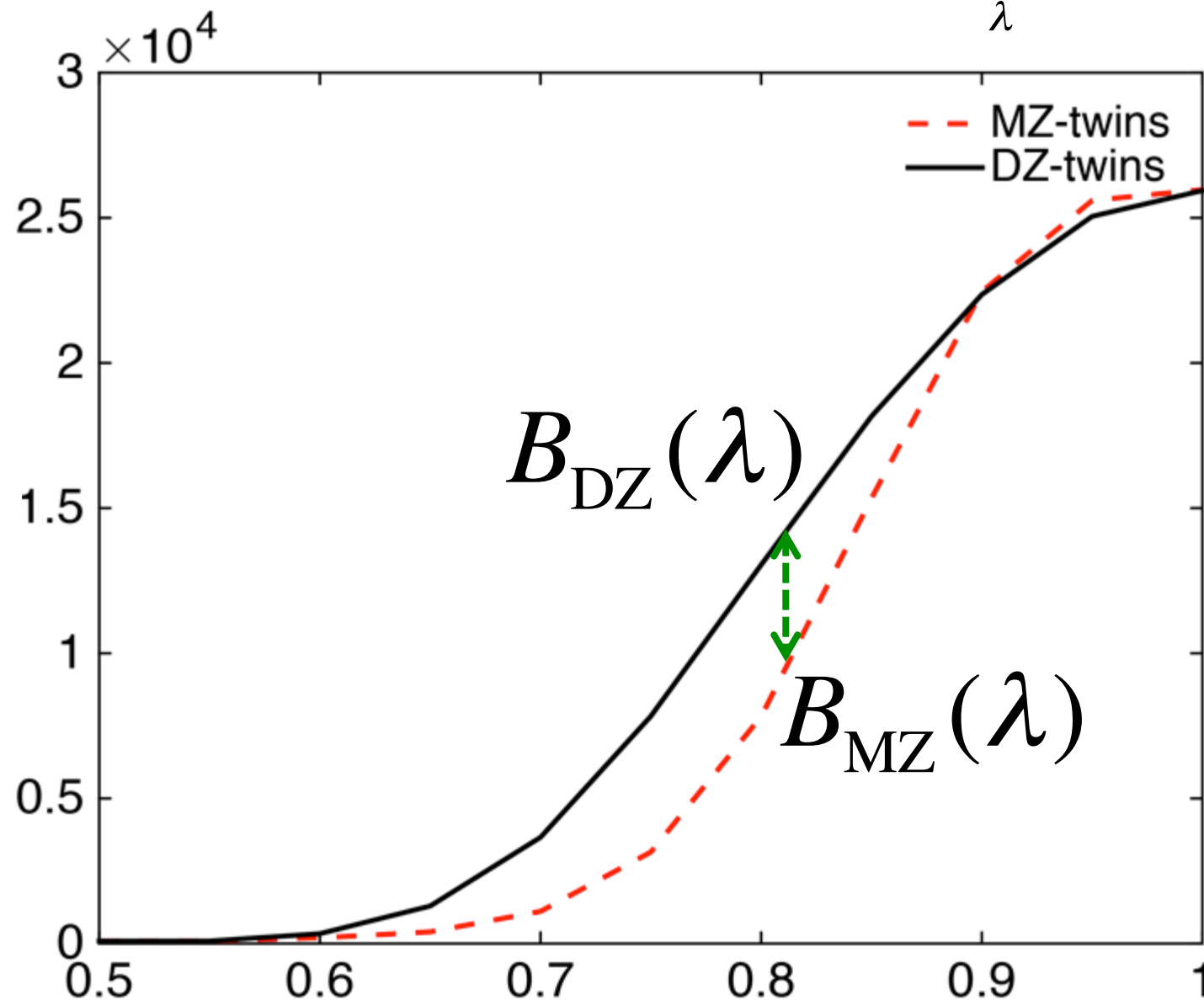


Size of the largest connected components



Distance between networks

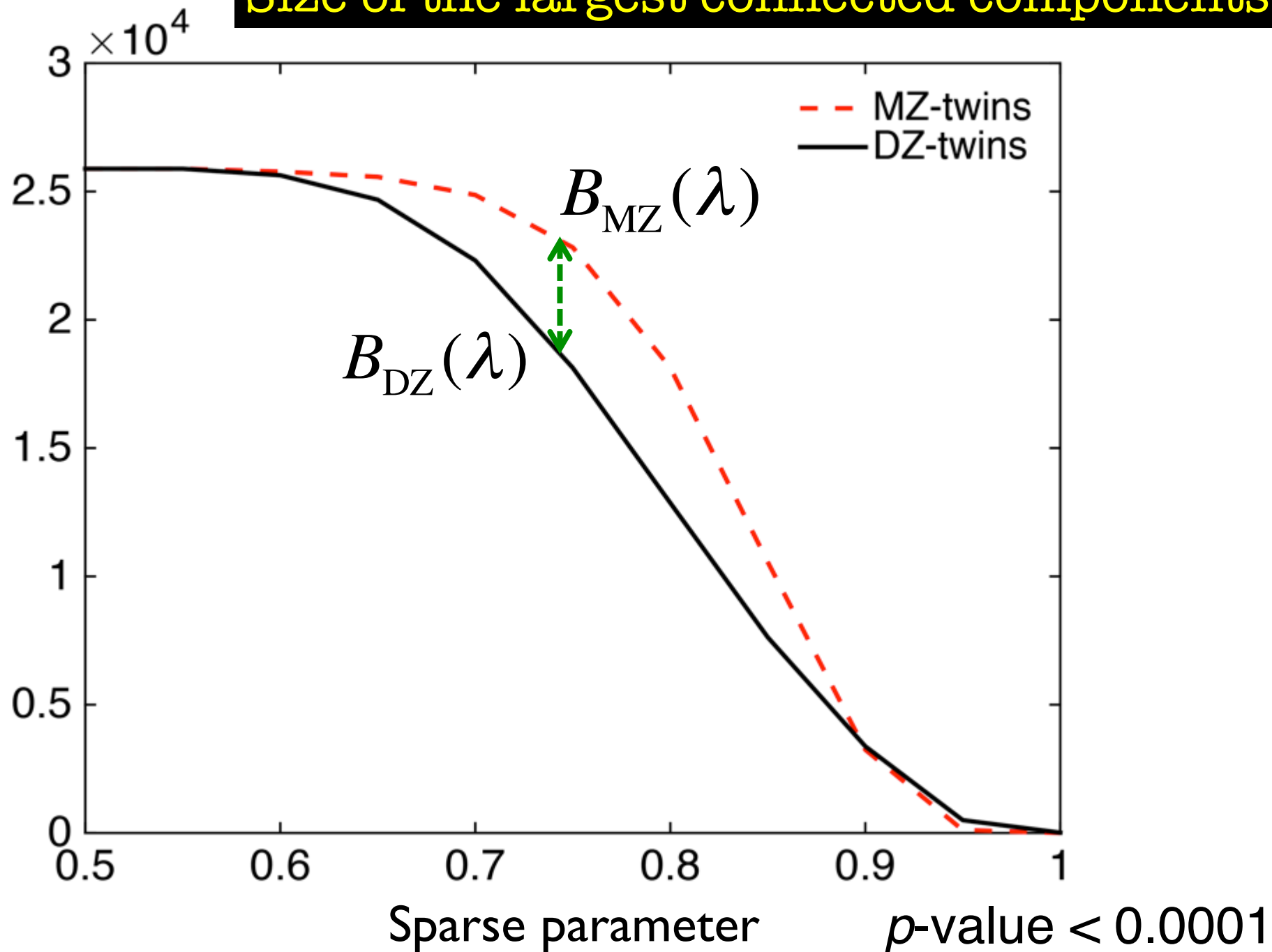
$$\sup_{\lambda} |B_{\text{MZ}}(\lambda) - B_{\text{DZ}}(\lambda)|$$



Sparse parameter

p -value < 0.0002

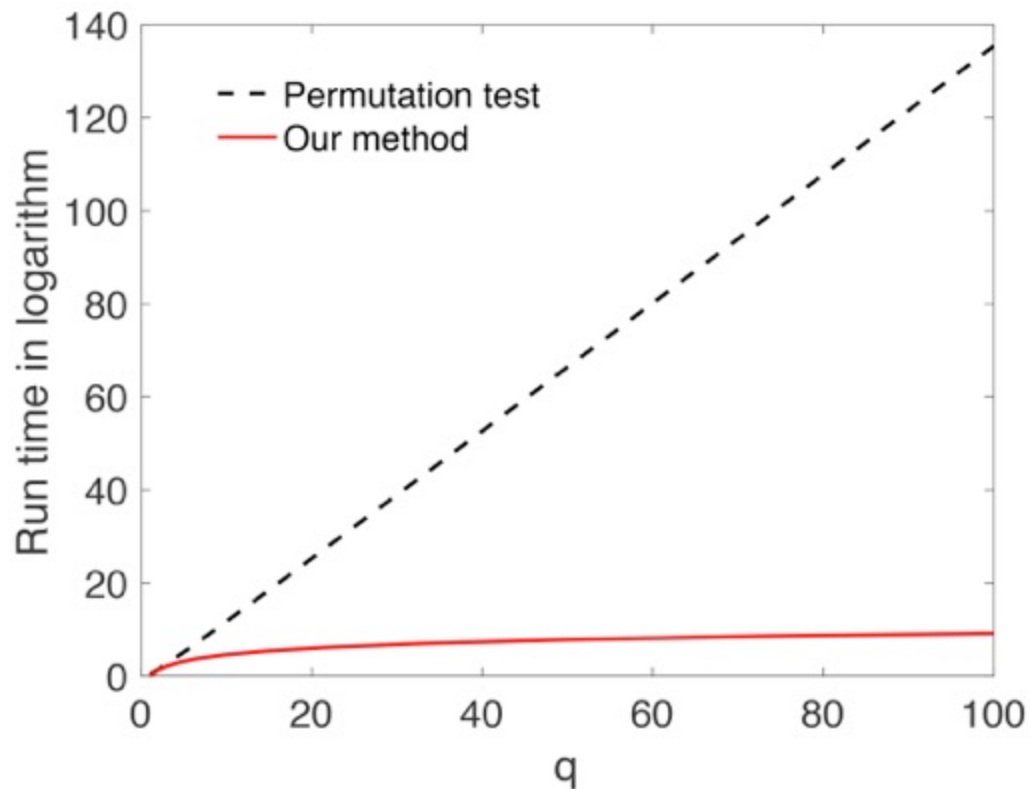
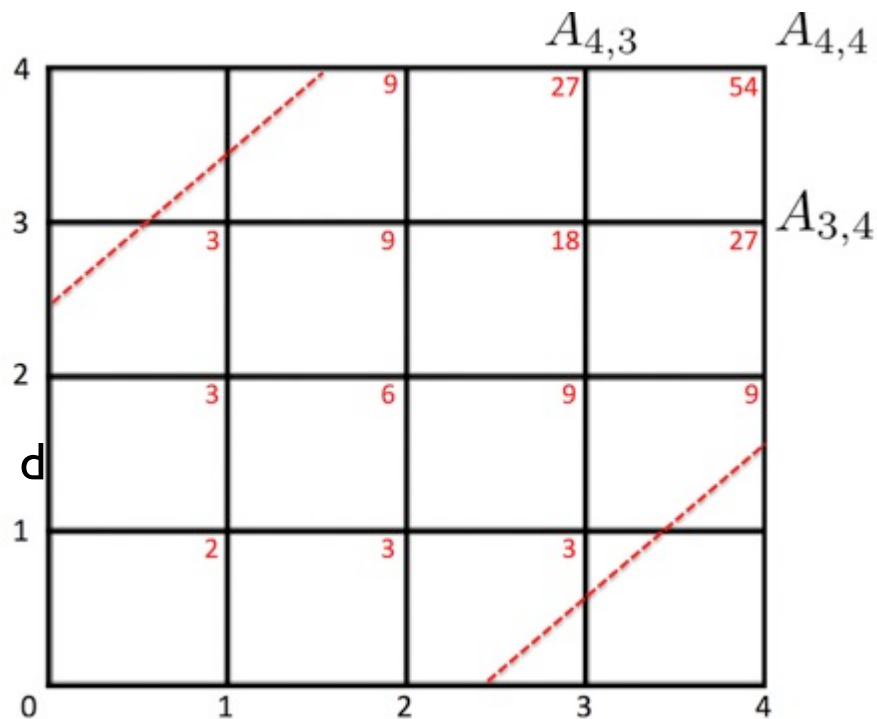
Size of the largest connected components



Exact permutation test

$$P\left(\sup_{1 \leq j \leq q} |\beta_0^1(\lambda_j) - \beta_0^2(\lambda_j)| > d\right) = 1 - \frac{A_{q,q}}{\binom{2q}{q}}$$

$$A_{u,v} = A_{u-1,v} + A_{u,v-1} \quad |u-v| < d$$



ACE model for twins

MZ-twins share 100% of genes

DZ-twins share 50% of genes

$$\rho_{\text{MZ}} = A + C$$

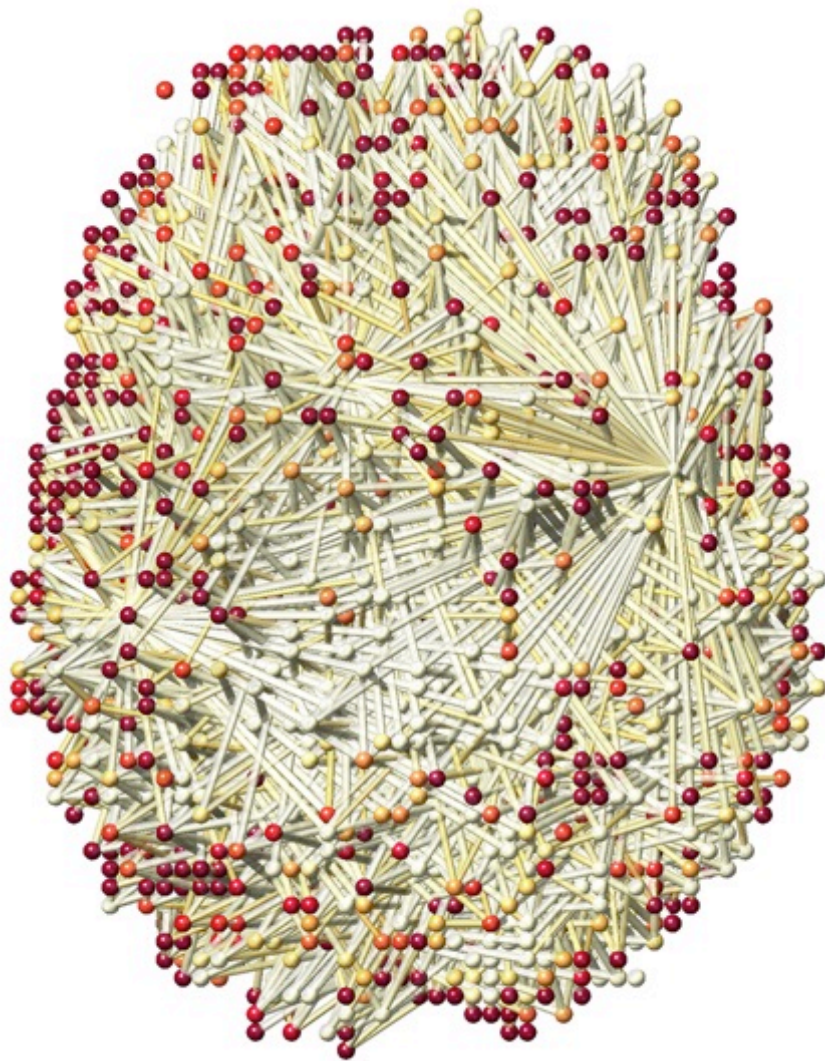
Additive genetics Common environment

$$\rho_{\text{DZ}} = A/2 + C$$

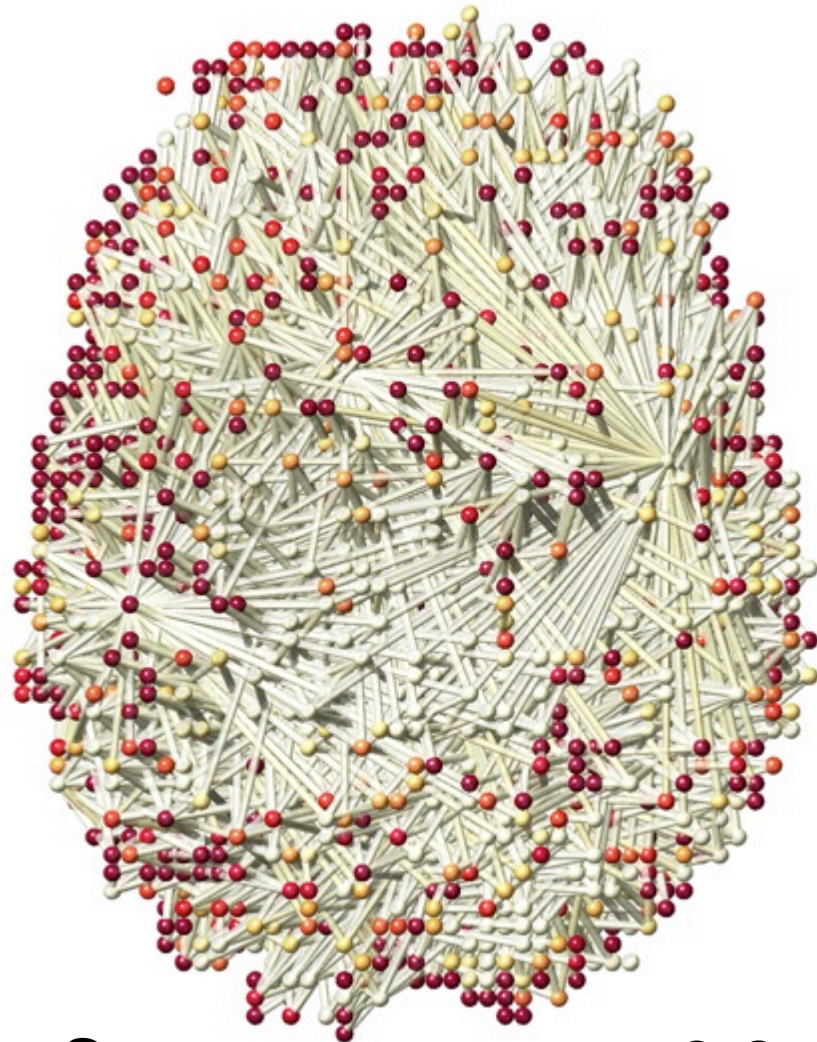
Falconer's formula for heritability index (HI)

$$\text{HI} = A = 2(\rho_{\text{MZ}} - \rho_{\text{DZ}})$$

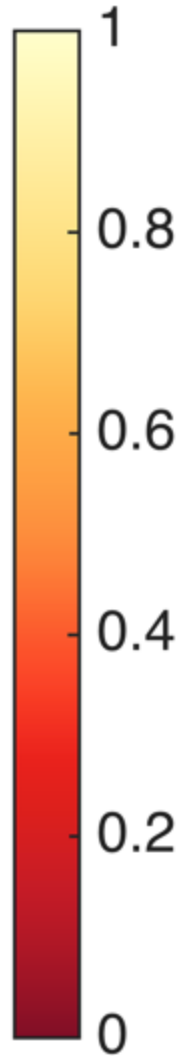
Heritability Index (both nodes and edges)



Sparse parameter 0.7



Sparse parameter 0.9



p -value < 0.0002



Thank you

MATLAB codes
google

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