



Turing-Roche knowledge event

Anthony Baptista

27/02/2024

Introduction

Statistical physics of liquids

Theoretical model for complex disorder

$$g_{ab}(r) = e^{-\beta v_{ab}(r) + h_{ab}(r) - c_{ab}(r) + b_{ab}(r)}$$

$$b_{ab}(r) = b_{ab}^{(CD)}(r) + b_{ab}^{(SD)}(r)$$

$$b_{ab}^{(CD)}(r) = \epsilon_1 \exp[-(r - \alpha_1)^2 / \kappa_1^2] - \epsilon_2 \exp[-(r - \alpha_2)^2 / \kappa_2^2]$$

$$b_{ab}(r) = \sum_{m \geq 3} \frac{1}{m!} \sum_{k \geq 3} \frac{1}{k!} \sum_{\alpha_1 \dots \alpha_k} \left(\prod_{l=1}^k \rho_{\alpha_l} \right) \int d\vec{r}_{13} \int d\vec{r}_{14} \dots \int d\vec{r}_{1k} \left(\prod_{l=1}^k h_{a\alpha_k}(r_{1k}) \right) c_{b\alpha_1 \dots \alpha_n}^{(k+1)}(\vec{r}_2, \vec{r}_3, \dots, \vec{r}_k)$$

AIP The Journal of Chemical Physics

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Home > The Journal of Chemical Physics > Volume 150, Issue 6 > 10.1063/1.5066598

No Access • Submitted: 16 October 2018 • Accepted: 26 January 2019 • Published Online: 13 February 2019

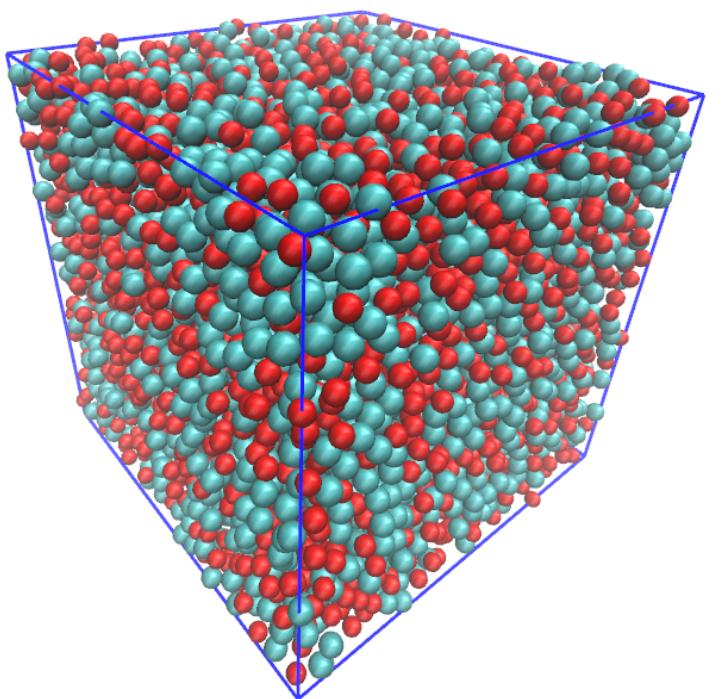
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Modeling micro-heterogeneity in mixtures: The role of many body correlations

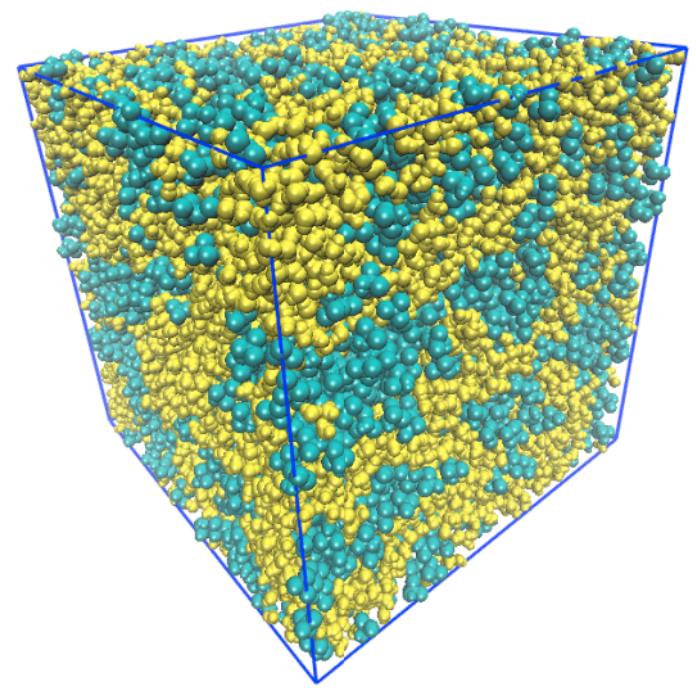
J. Chem. Phys. 150, 064504 (2019); <https://doi.org/10.1063/1.5066598>

Anthony Baptista and Aurélien Perera

Simulation based on molecular dynamics



Simple disorder



Complex disorder

Issue 18, 2019 Previous Article Next Article

PCCP From the journal: Physical Chemistry Chemical Physics

Microscopic origin of the scattering pre-peak in aqueous propylamine mixtures: X-ray and neutron experiments versus simulations

Check for updates

László Almásy, ^{ab} Alexander I. Kuklin, ^c Martina Požar, ^d Anthony Baptista, ^e and Aurélien Perera, ^{*e}

Network theory for biology



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Genetics



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Article | Open Access | Published: 01 July 2022

Universal multilayer network exploration by random walk with restart

Anthony Baptista , Aitor Gonzalez & Anaïs Baudot

RESEARCH

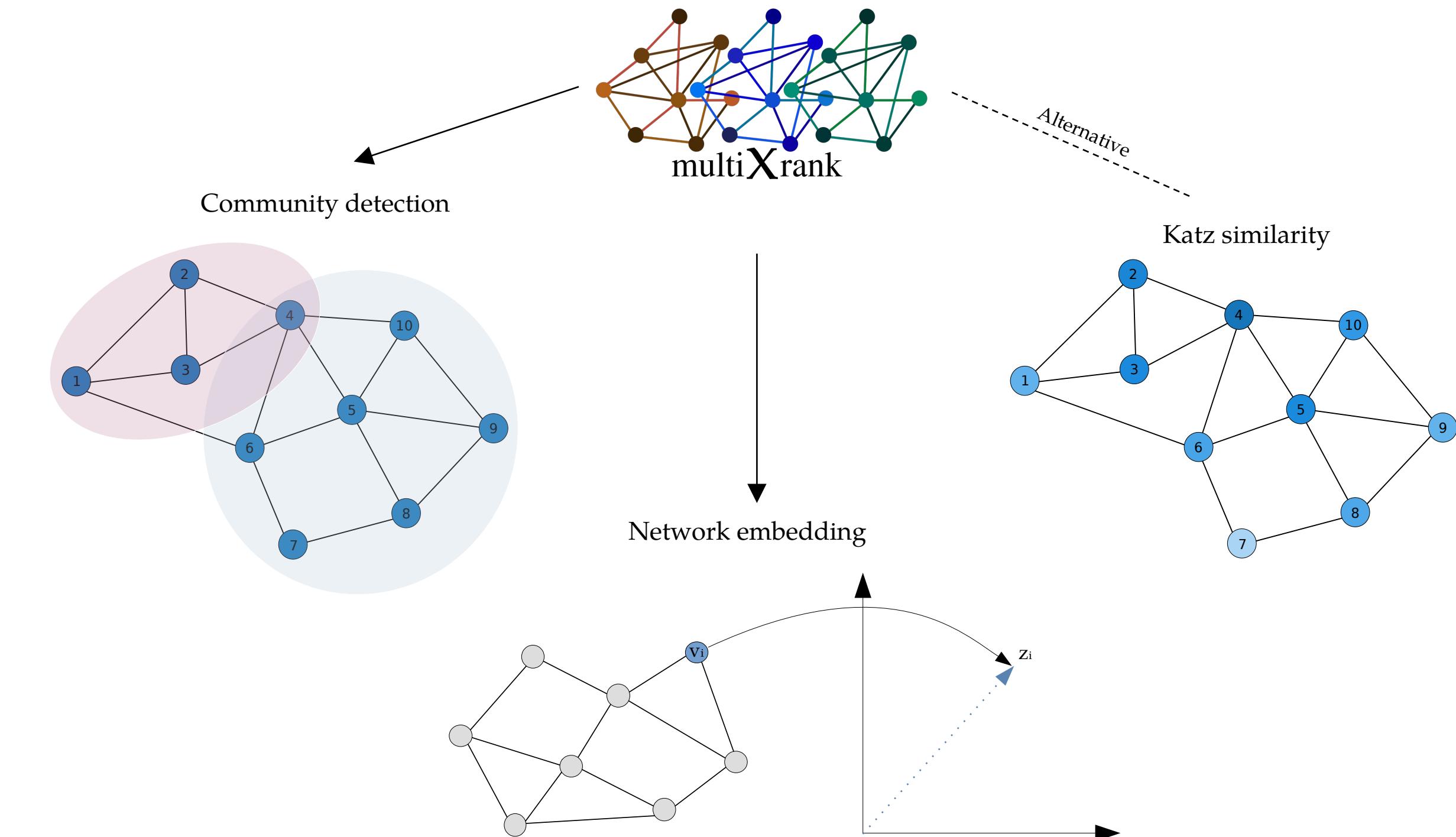
Random Walk with Restart on multilayer networks: from node prioritisation to supervised link prediction and beyond

Anthony Baptista^{1,2*}, Galadriel Brière³ and Anaïs Baudot^{4,5*}

TOPICAL REVIEW • OPEN ACCESS

Zoo guide to network embedding

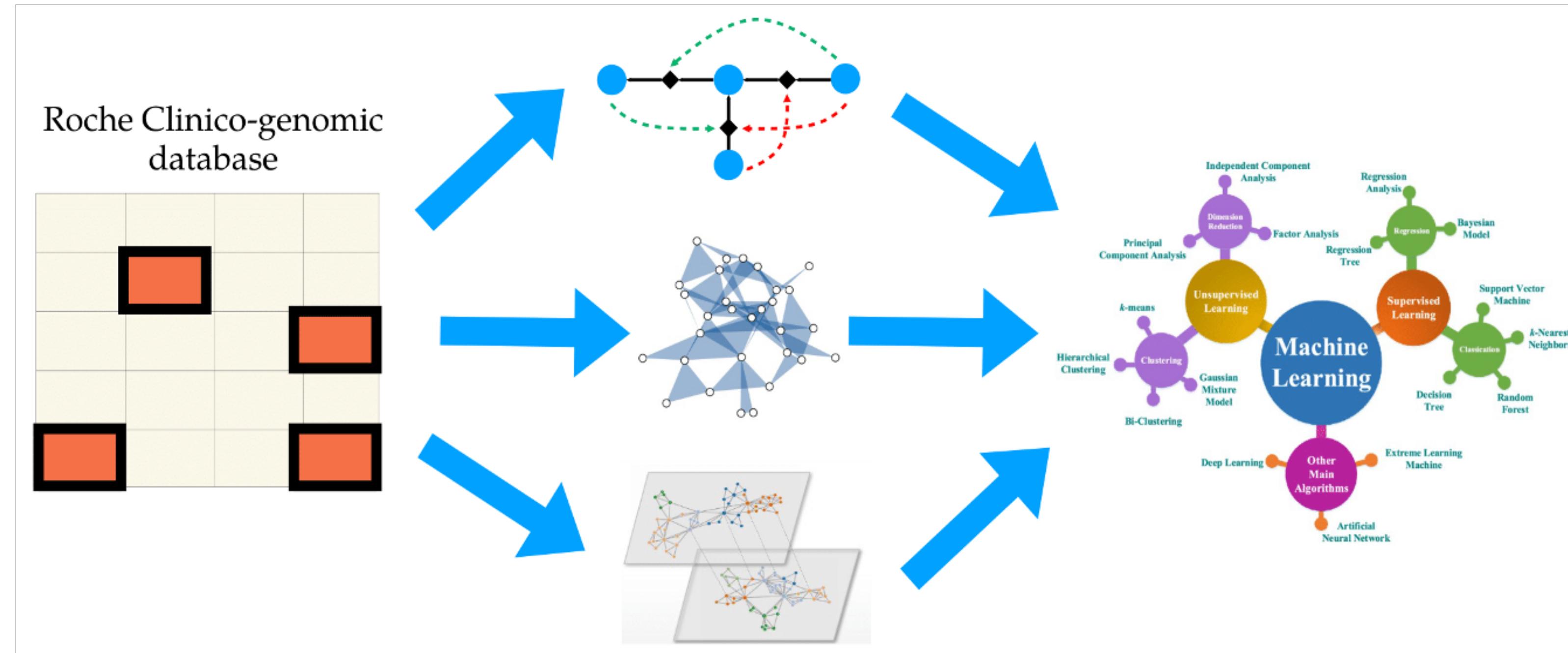
A Baptista^{8,1,2} , R J Sánchez-García^{2,3,4}, A Baudot^{5,6,7} and G Bianconi^{8,1,2}



The molecular landscape of premature aging diseases defined by
multilayer network exploration

Cécile Beust^{1,2,†}, Alberto Valdeolivas^{1,3,†}, Anthony Baptista^{1,4,5}, Galadriel Brière^{1,6}, Nicolas Lévy^{1,7}, Ozan Ozisik^{1,8}, and
Anaïs Baudot^{1,9,10}

Using network science to quantify the geometry of “missingness”



1

Characterize pairwise and higher-order interactions

2

Extract Structural Missingness Networks (SMNs)

3

Characterize the Geometry of SMNs



Professor Ginestra Bianconi



Dr Ruben Sanchez Garcia



Dr Anthony Baptista

Triadic interactions

Triadic interactions

Triadic interactions in both **continuous** and **discrete** real data

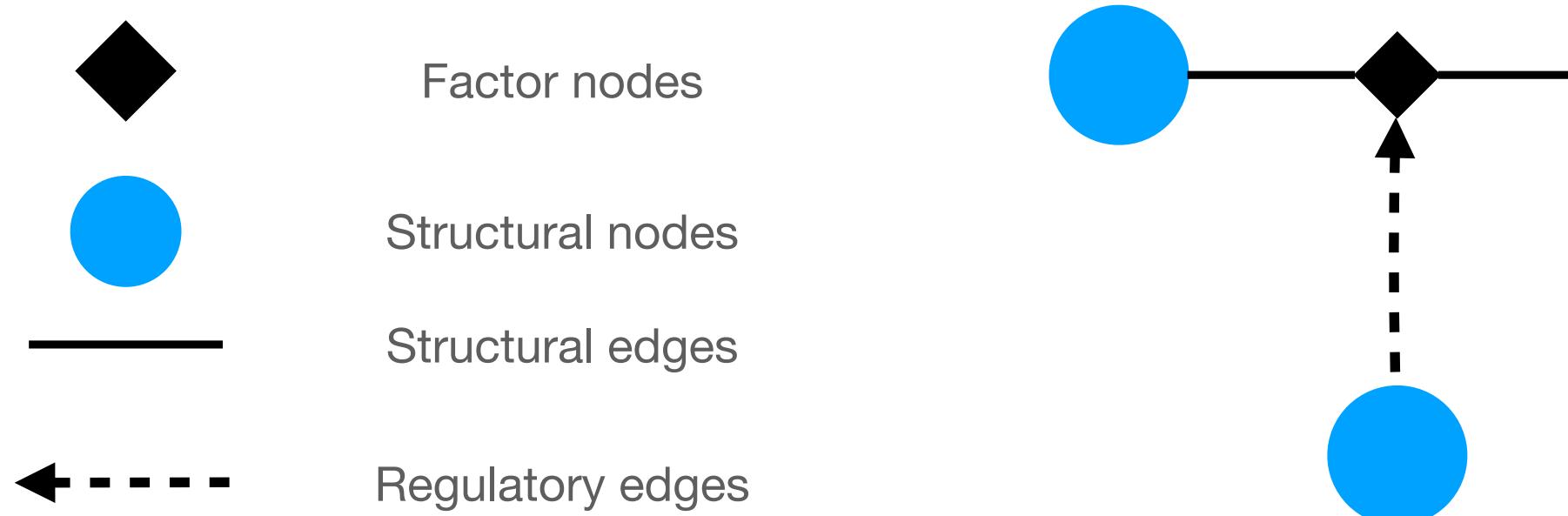
The structural network $G_S = (V, E_S)$

- * N nodes
 - * L edges

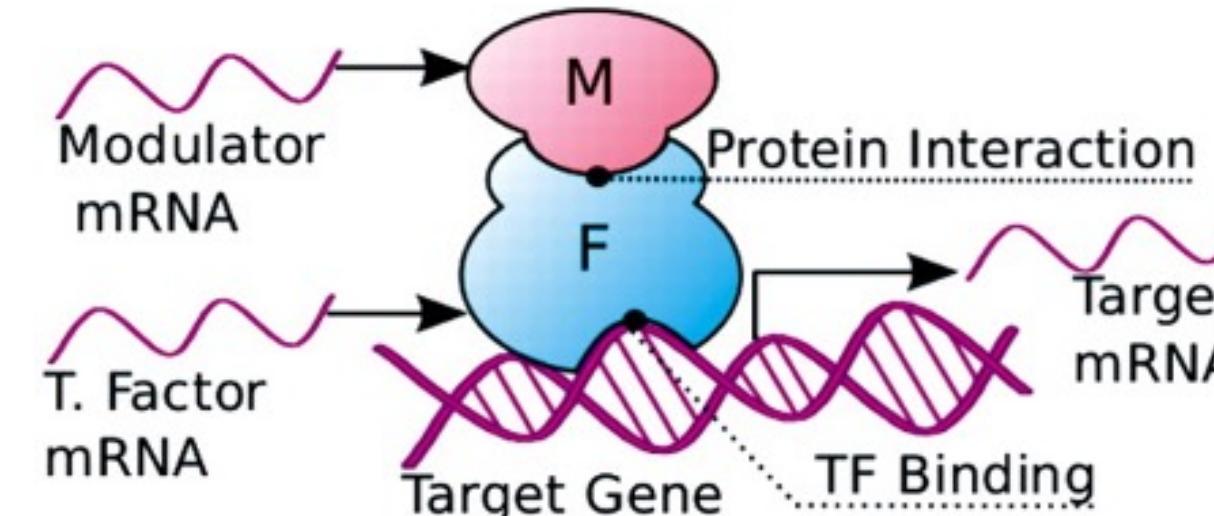
The regulatory network (bipartite)

$$G_R = (V, E_S, E_R)$$

- * Nodes given by V
 - * Nodes given by E_S
 - * Both types of nodes connected by the regulatory interactions E_R ($|E_R| = \hat{L}$).

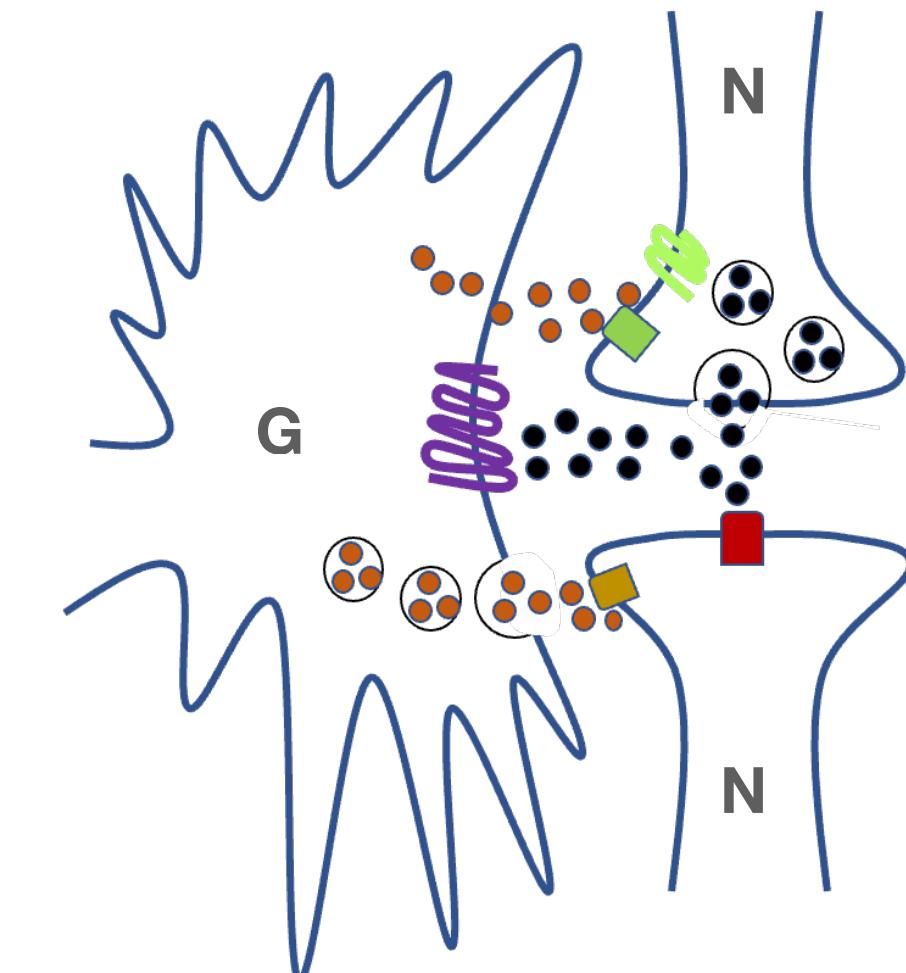


Gene regulatory network



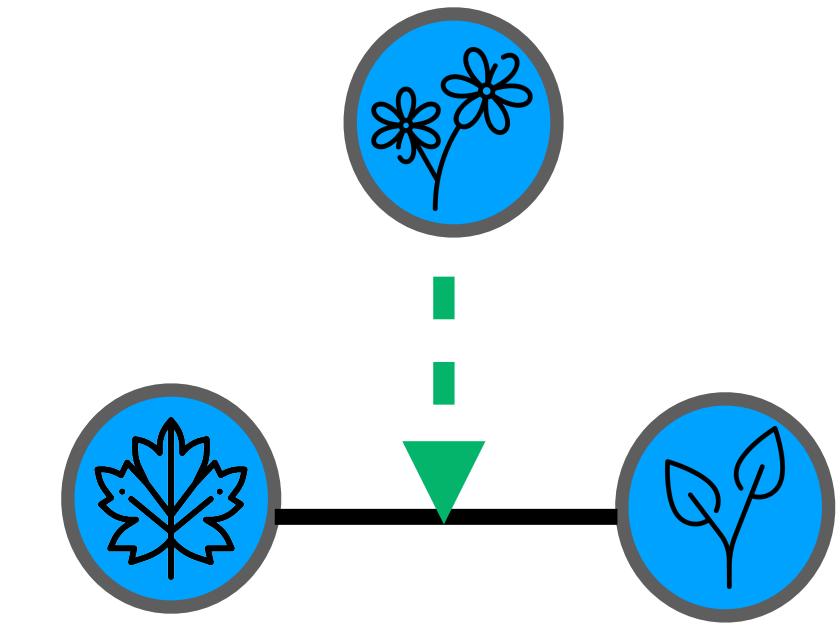
Wang, K. et al., Nat Biotechnol (2009)

Neurological network



Woo-Hyun C. et al., *Exp Neurobiol* (2016)

Ecological network

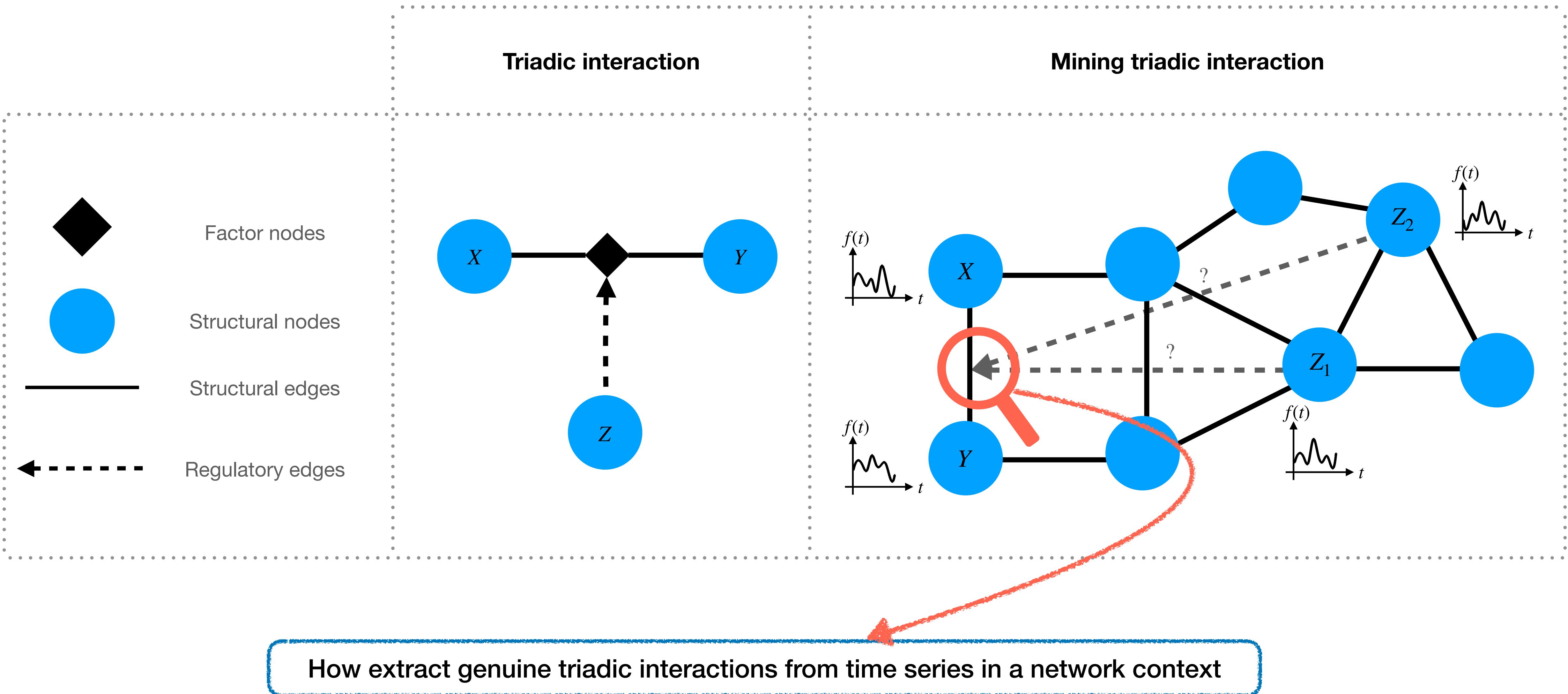


Grilli, J. et al., *Nature* (2017)
Bailey, E. Et al., *Nat Commun* (2016)

Structured missingness

Mitra, R., McGough, S.F., Chakraborti, T. *et al.*
Nat Mach Intell (2023)

Mining triadic interactions



Strength and sign of triadic interaction

Mutual information (given $Z = z$)

$$MI(X, Y | Z = z) = \sum_{x,y} p(x, y | z) \ln \frac{p(x, y | z)}{p(x | z)p(y | z)}$$

Conditional Mutual Information

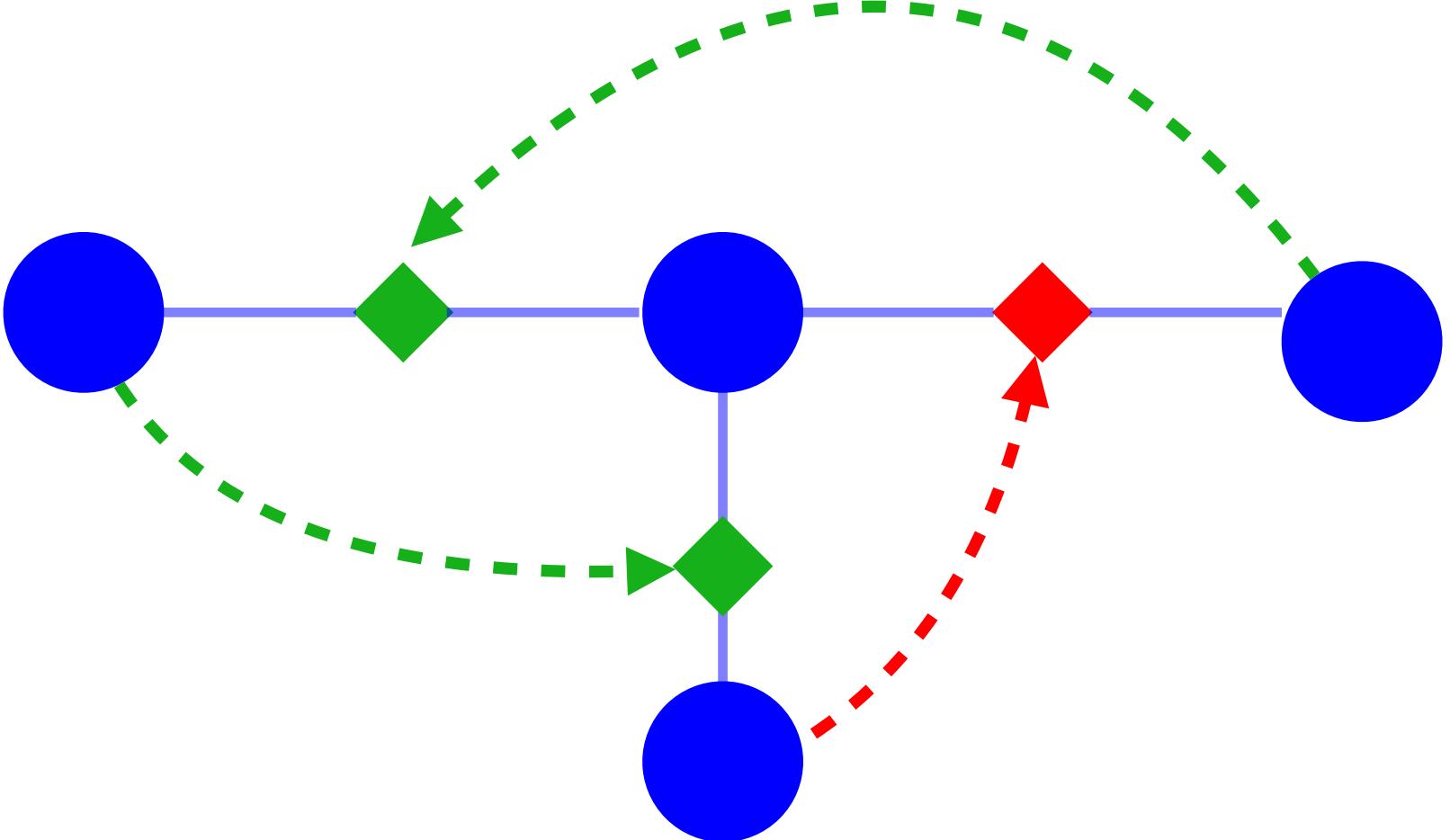
$$MI_{X,Y;Z} = \langle MI(X, Y | Z = z) \rangle = \sum_z p(z) MI(X, Y | Z = z)$$

Strength of triadic interaction

$$\Sigma_{X,Y;Z} = \sqrt{\sum_z p(z) [MI(X, Y | Z = z) - MI_{X,Y;Z}]^2} > 0$$

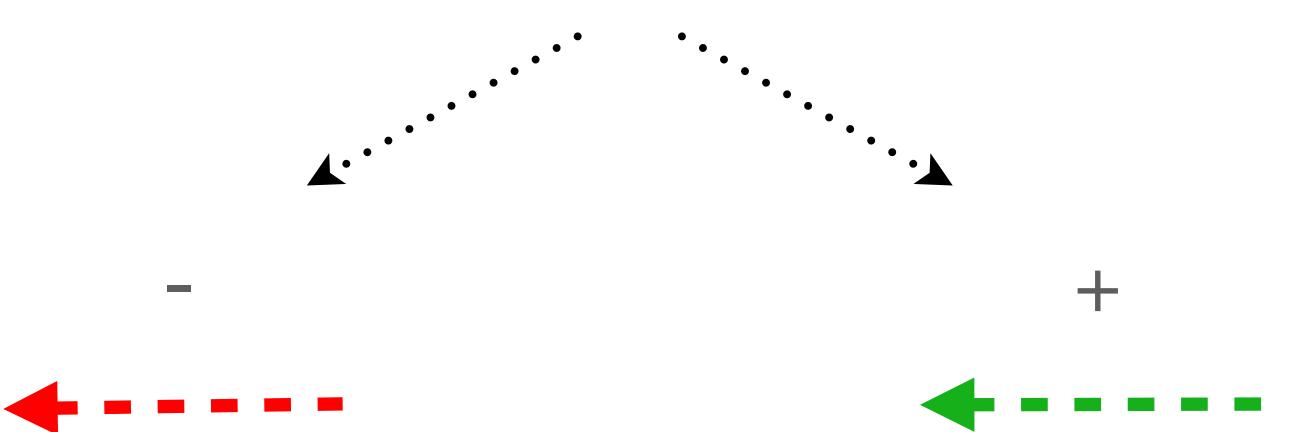
$$T_{X,Y;Z} = \max_z |MI(X, Y | Z = z) - MI_{X,Y;Z}| > 0$$

$$T_{nX,Y;Z} = \max_z |MI(X, Y | Z = z) - MI(X, Y | Z = z + \Delta z)| > 0$$

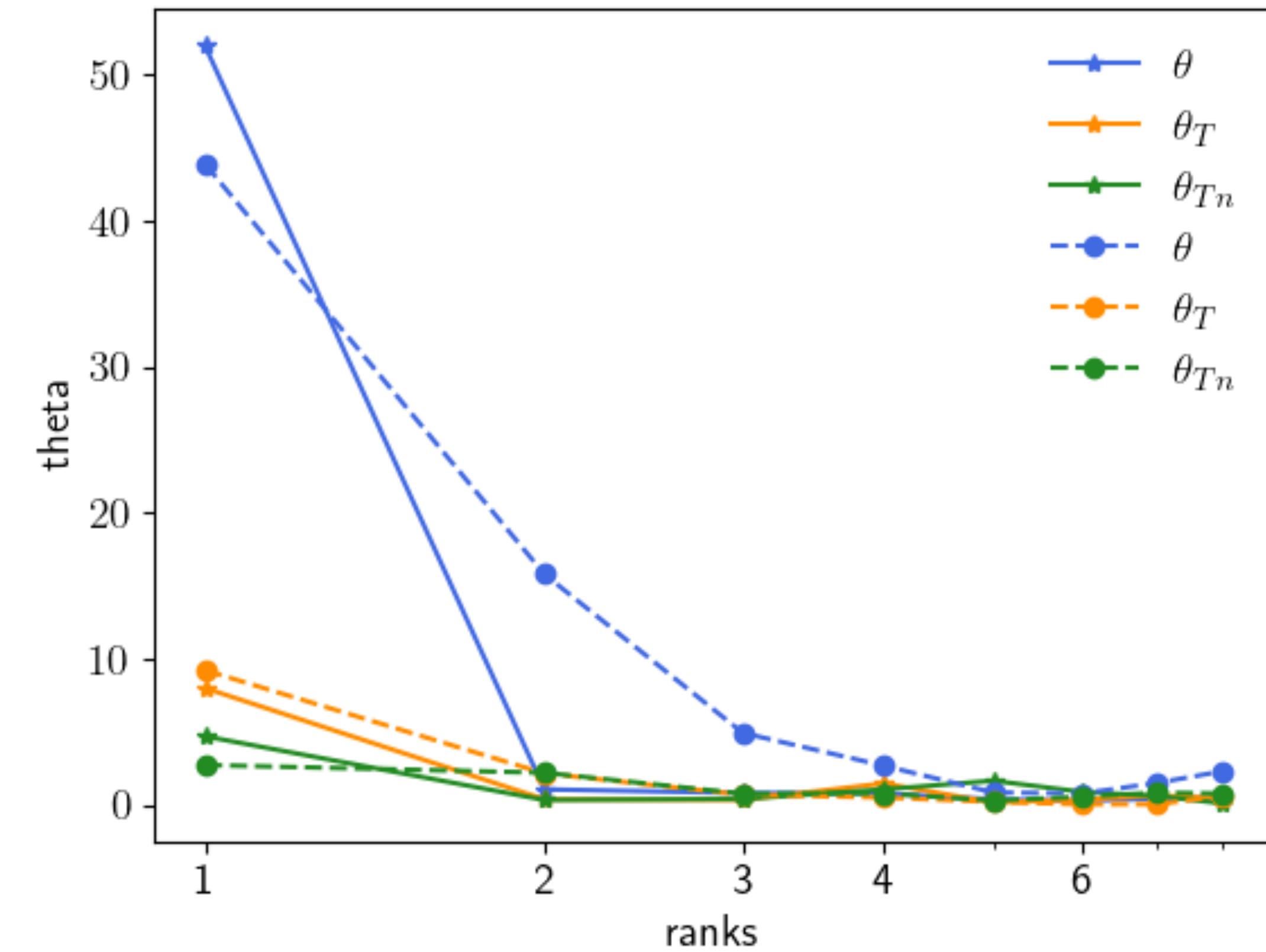
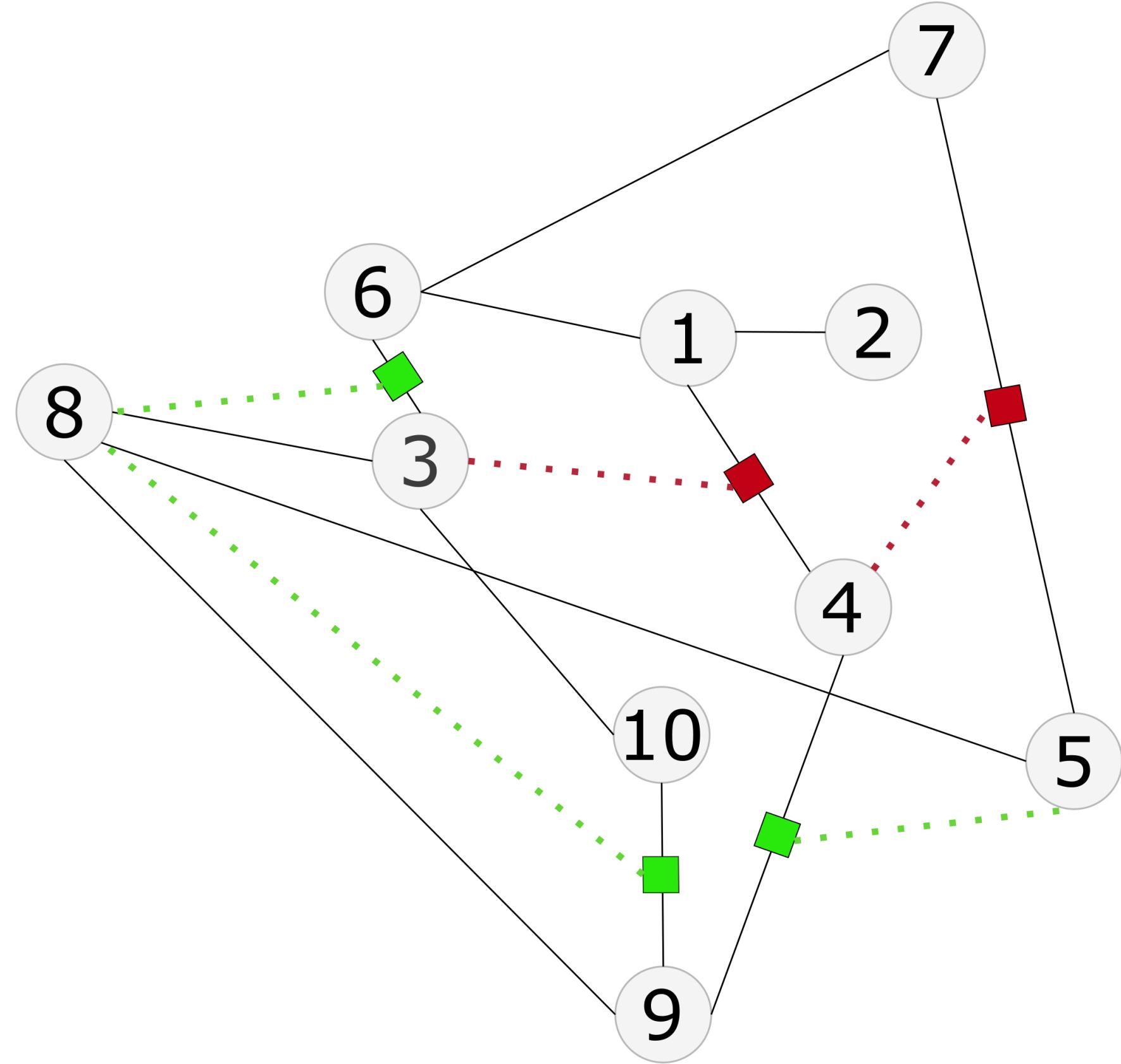


Sign of triadic interaction

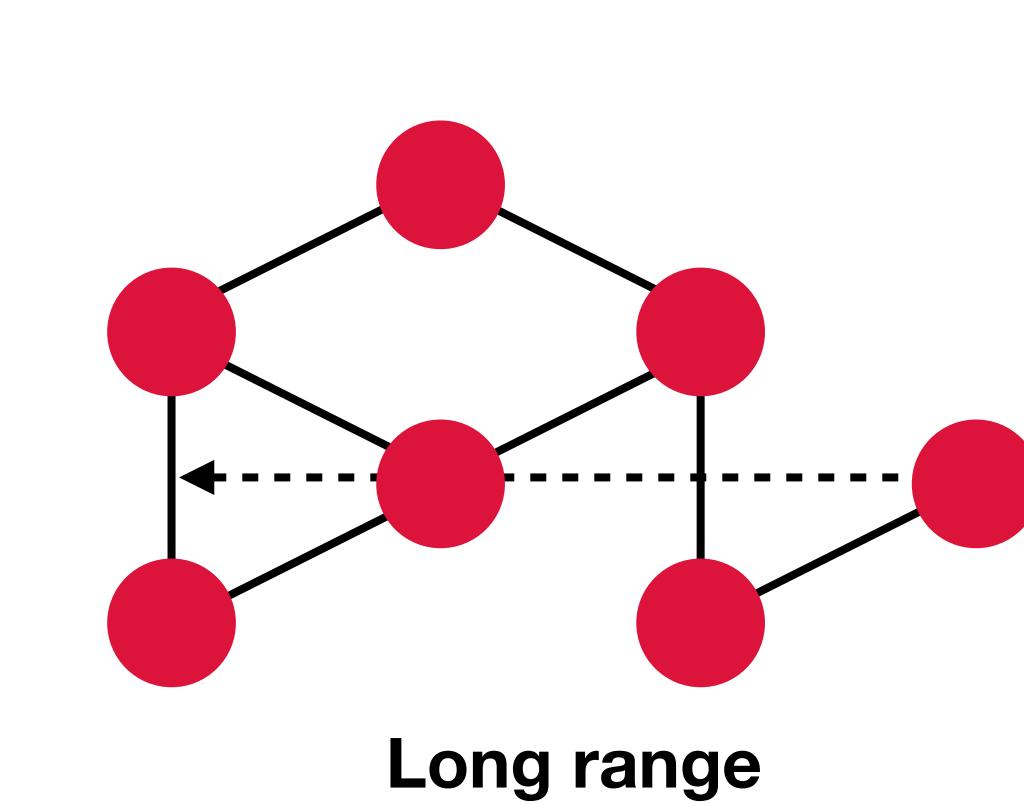
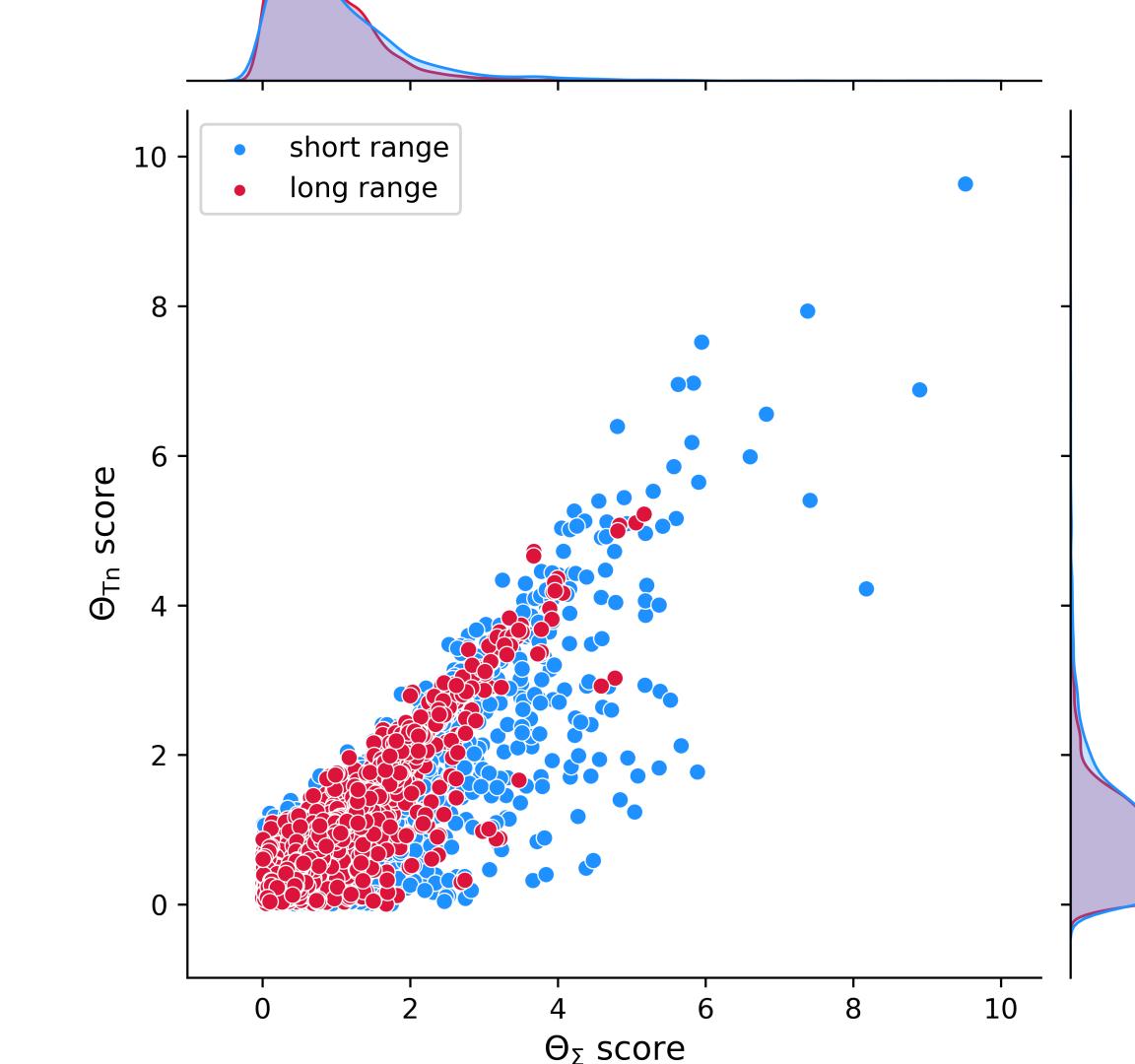
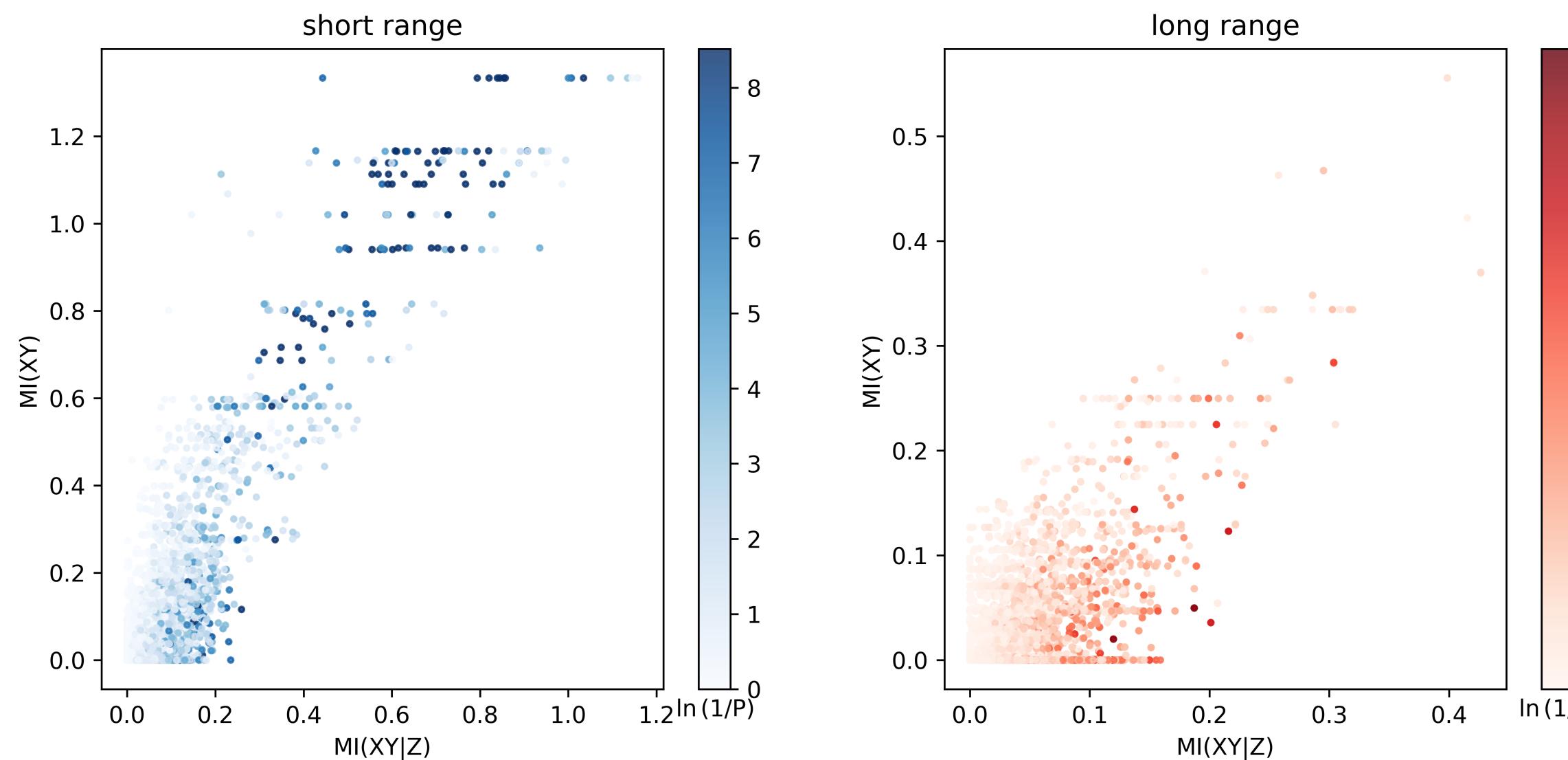
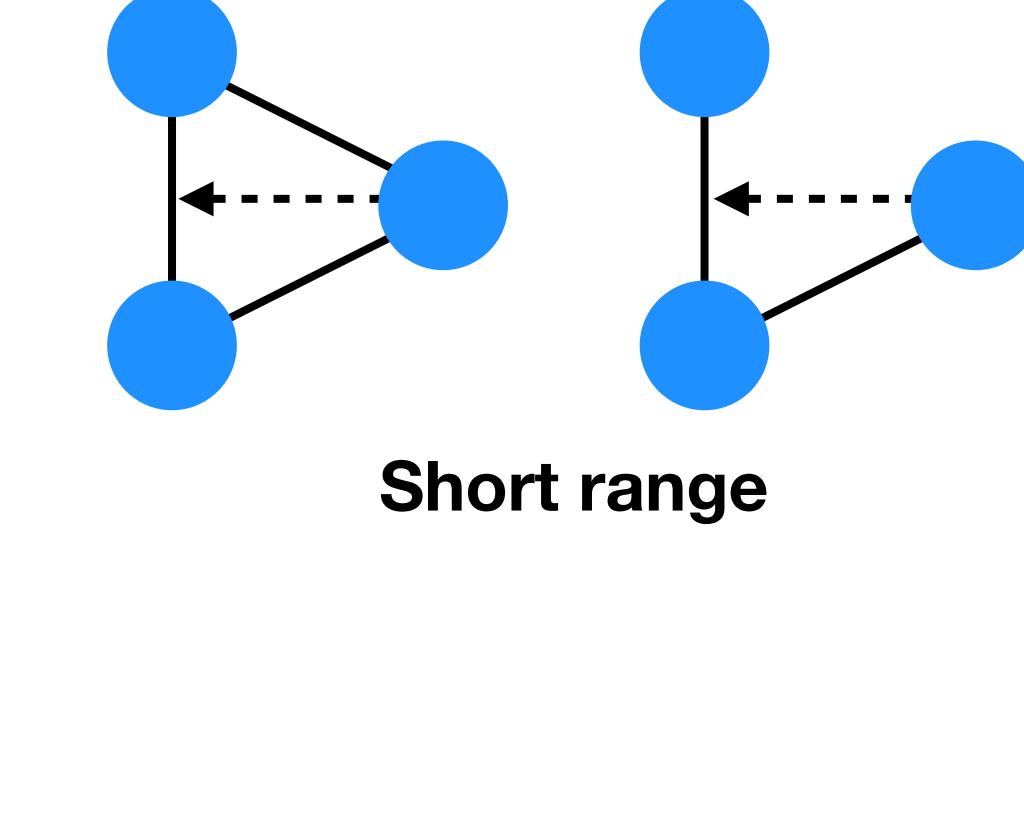
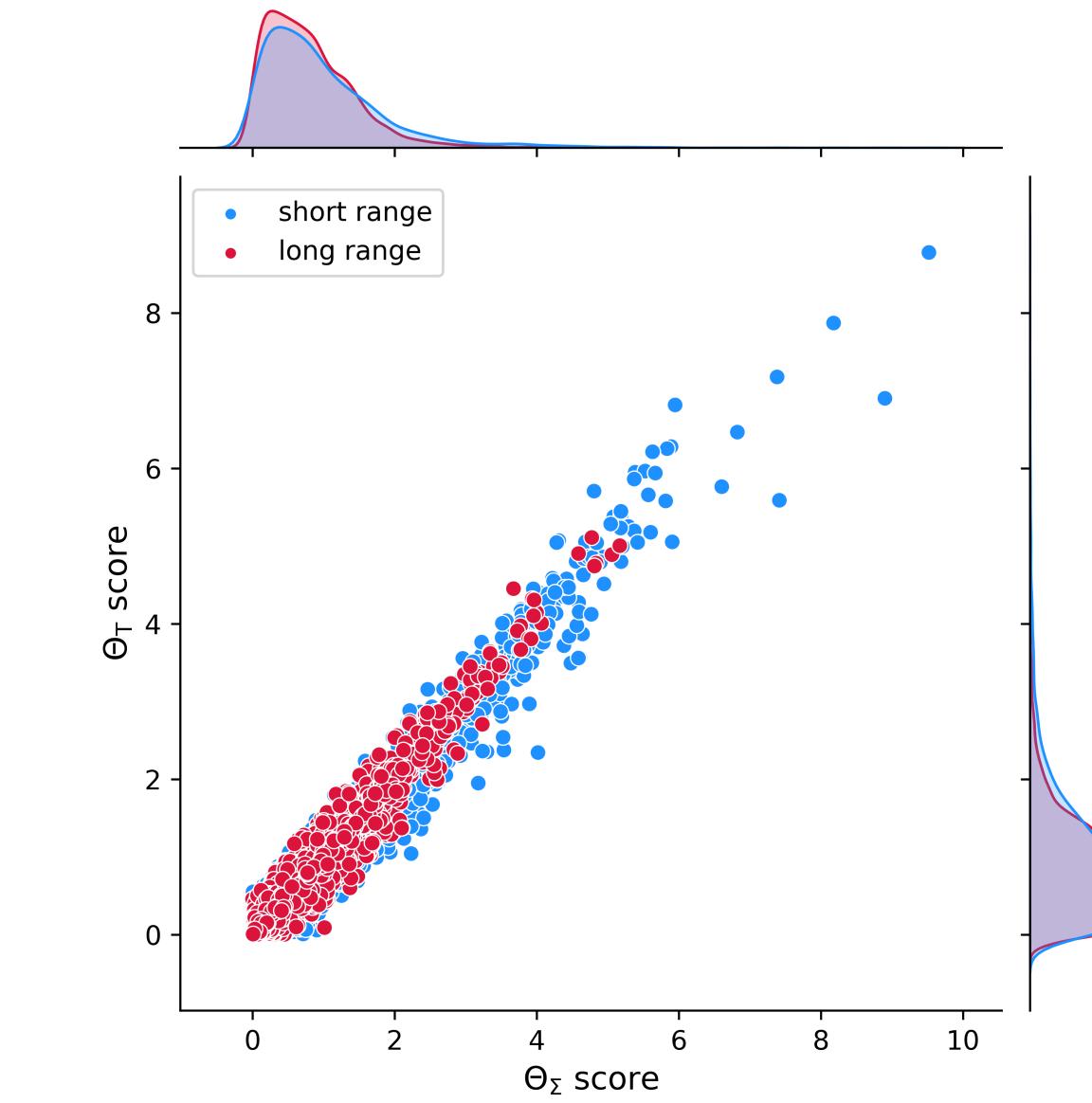
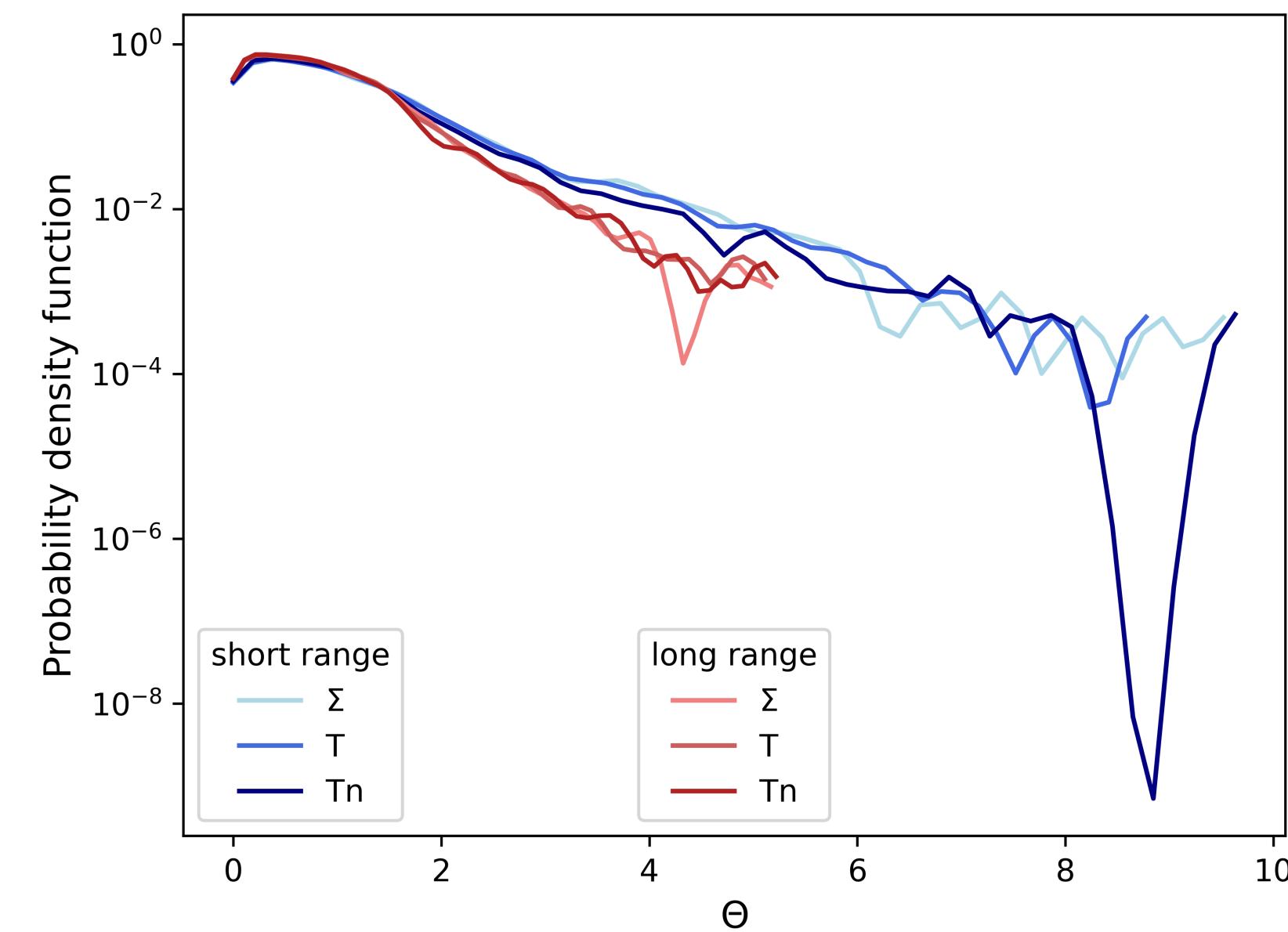
$$C = \frac{\langle z MI(X, Y | Z = z) \rangle - \langle z \rangle \langle MI(X, Y | Z = z) \rangle}{\sigma_z \sigma_{MI}}$$



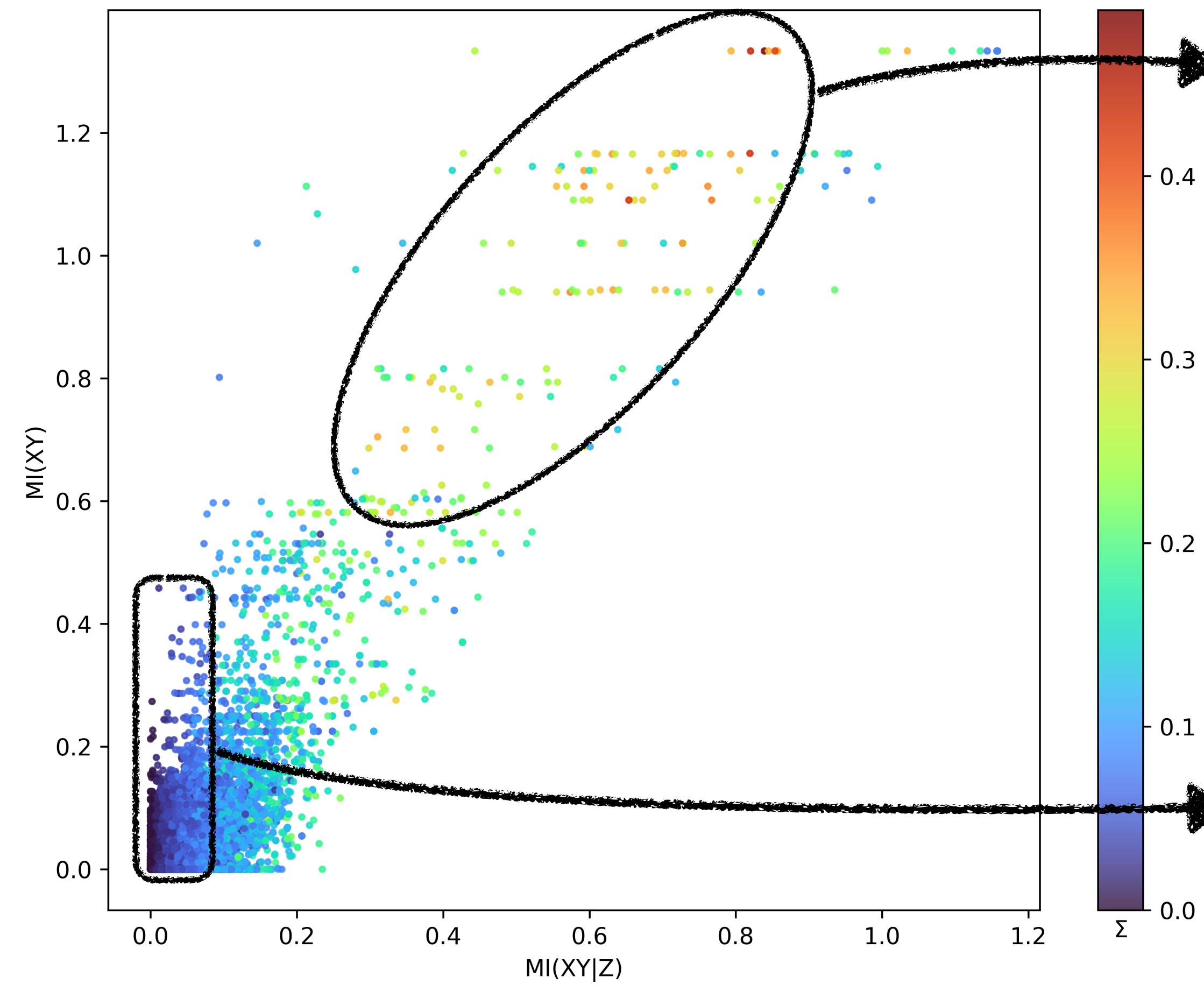
Toy model



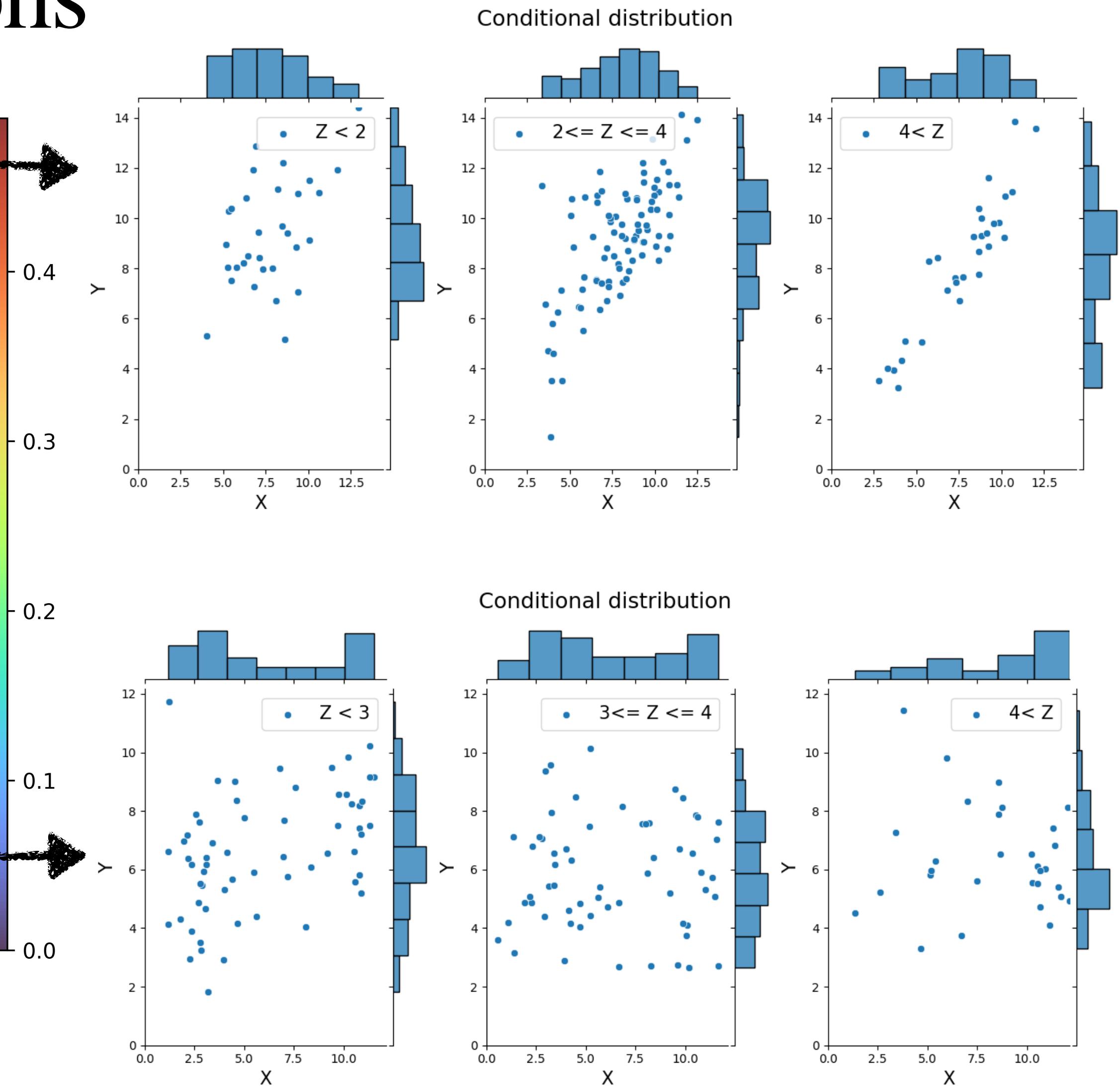
Comparison of measures to detect triadic interactions



Detection of triadic interactions



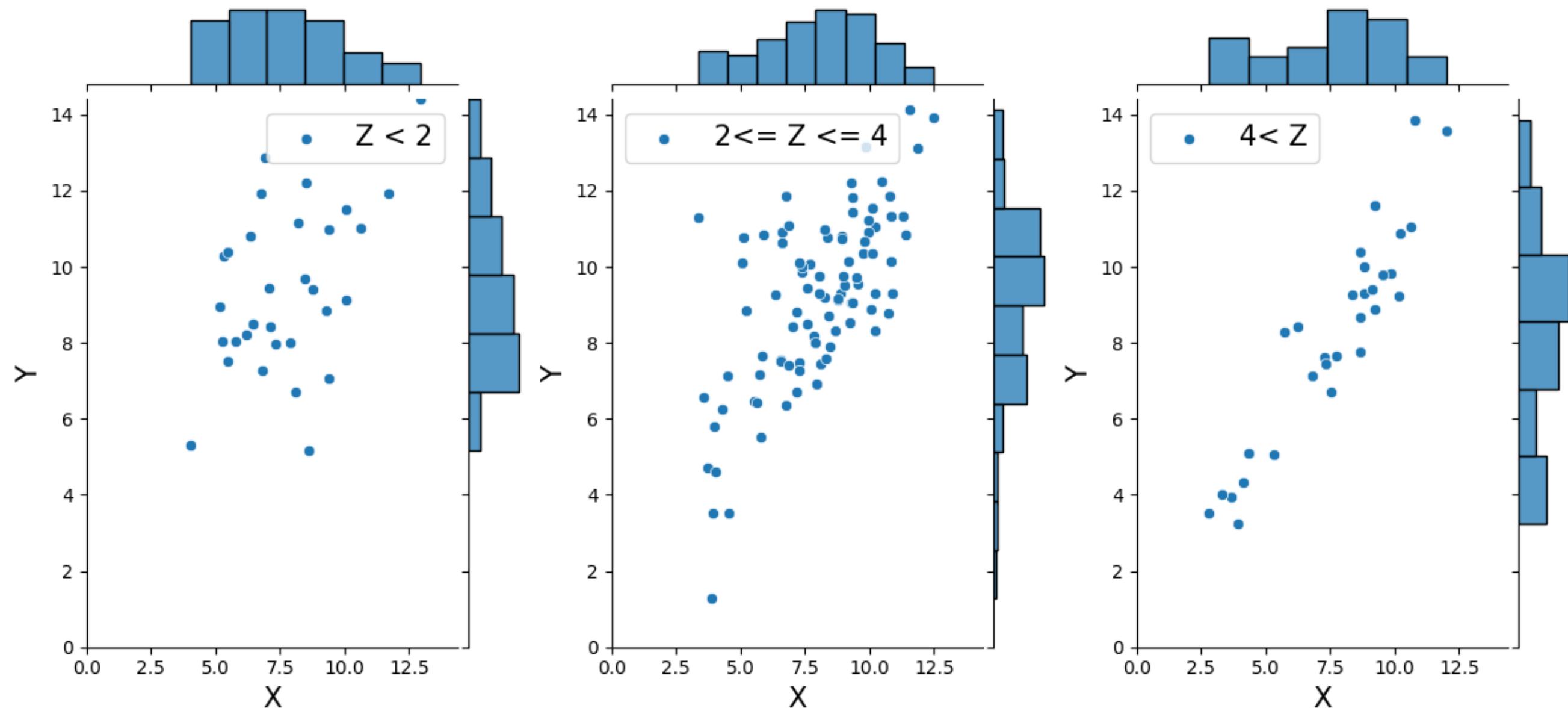
$$\Sigma_{X,Y;Z} = \sqrt{\langle (MI(X, Y | Z = z) - I(X, Y | Z))^2 \rangle} > 0$$



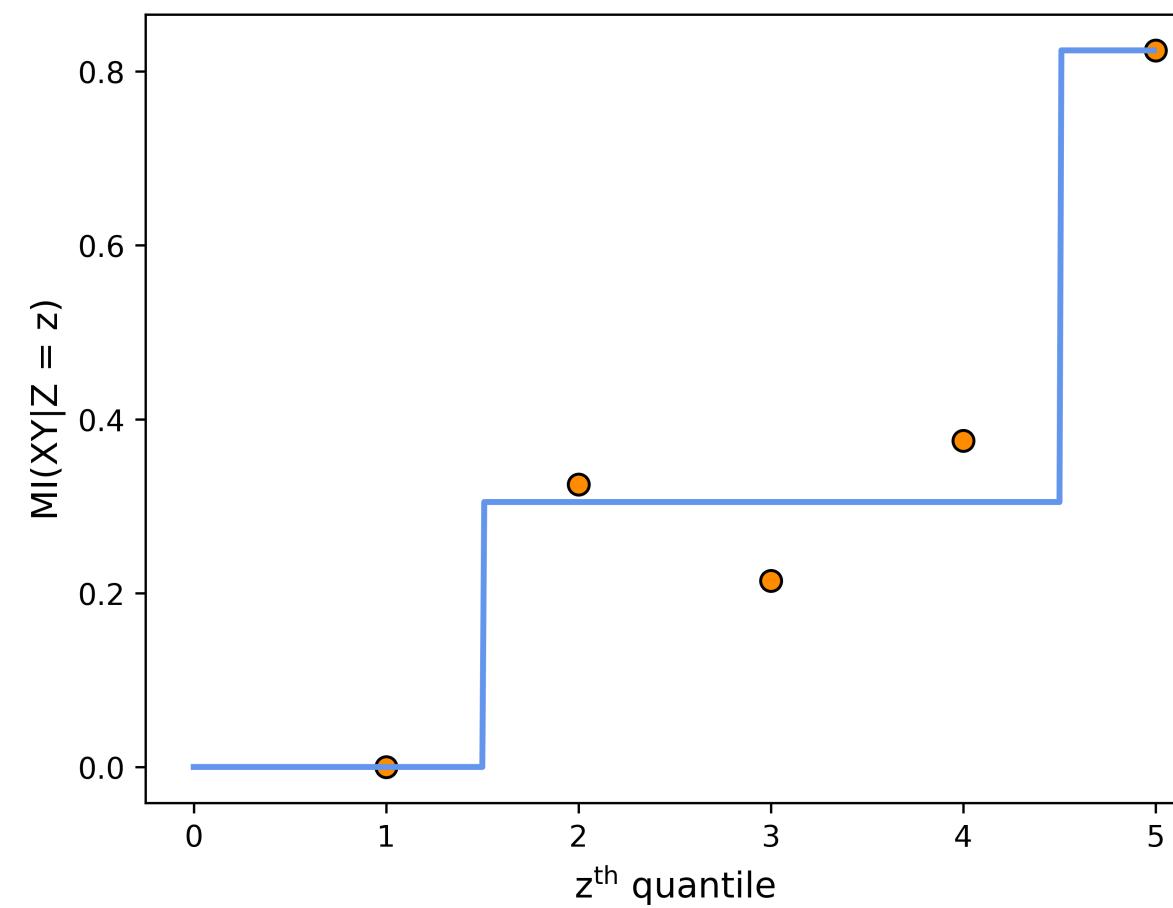
Σ scores separate strong triadic interactions from non triadic interactions

Detection of triadic interactions

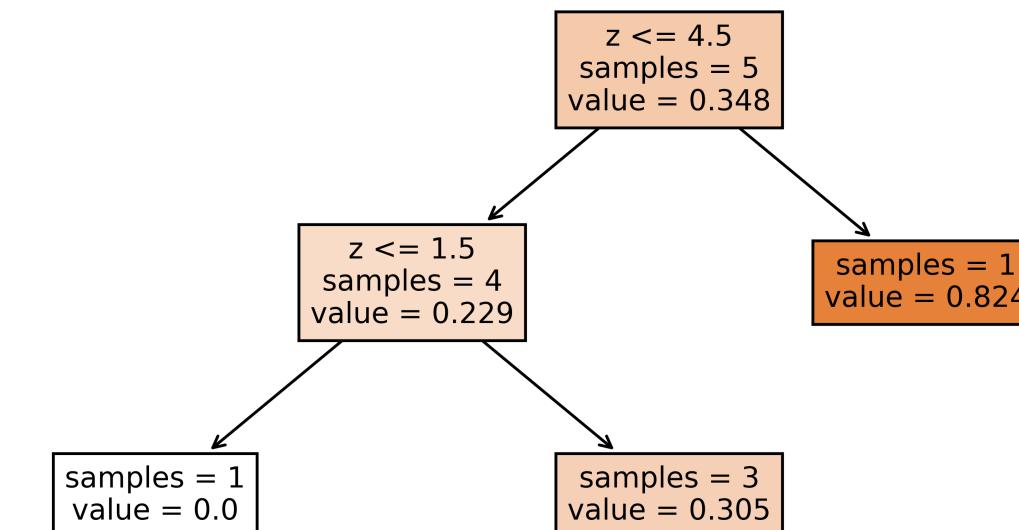
Conditional distribution



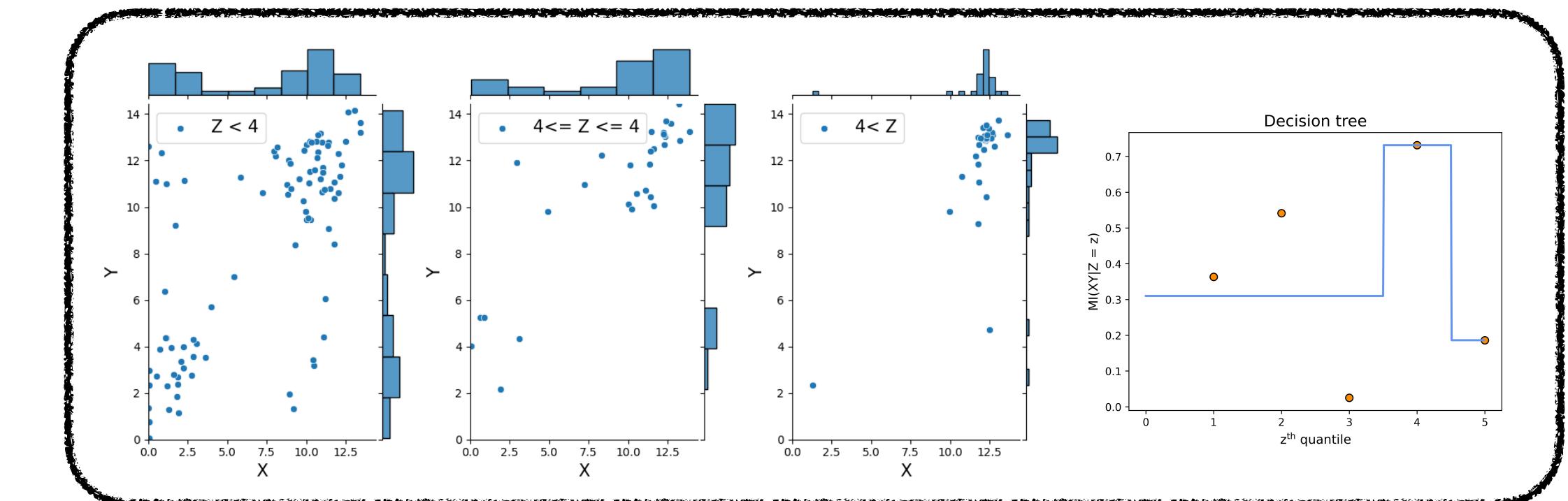
Regression plot



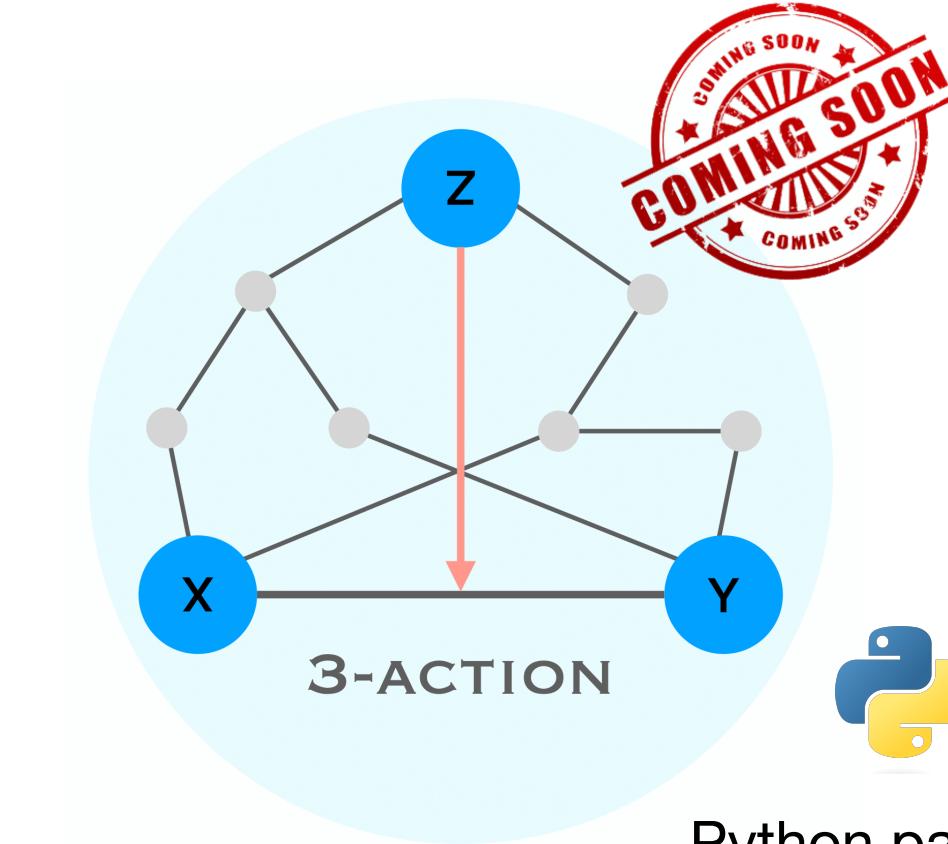
Decision tree



Non-monotonic



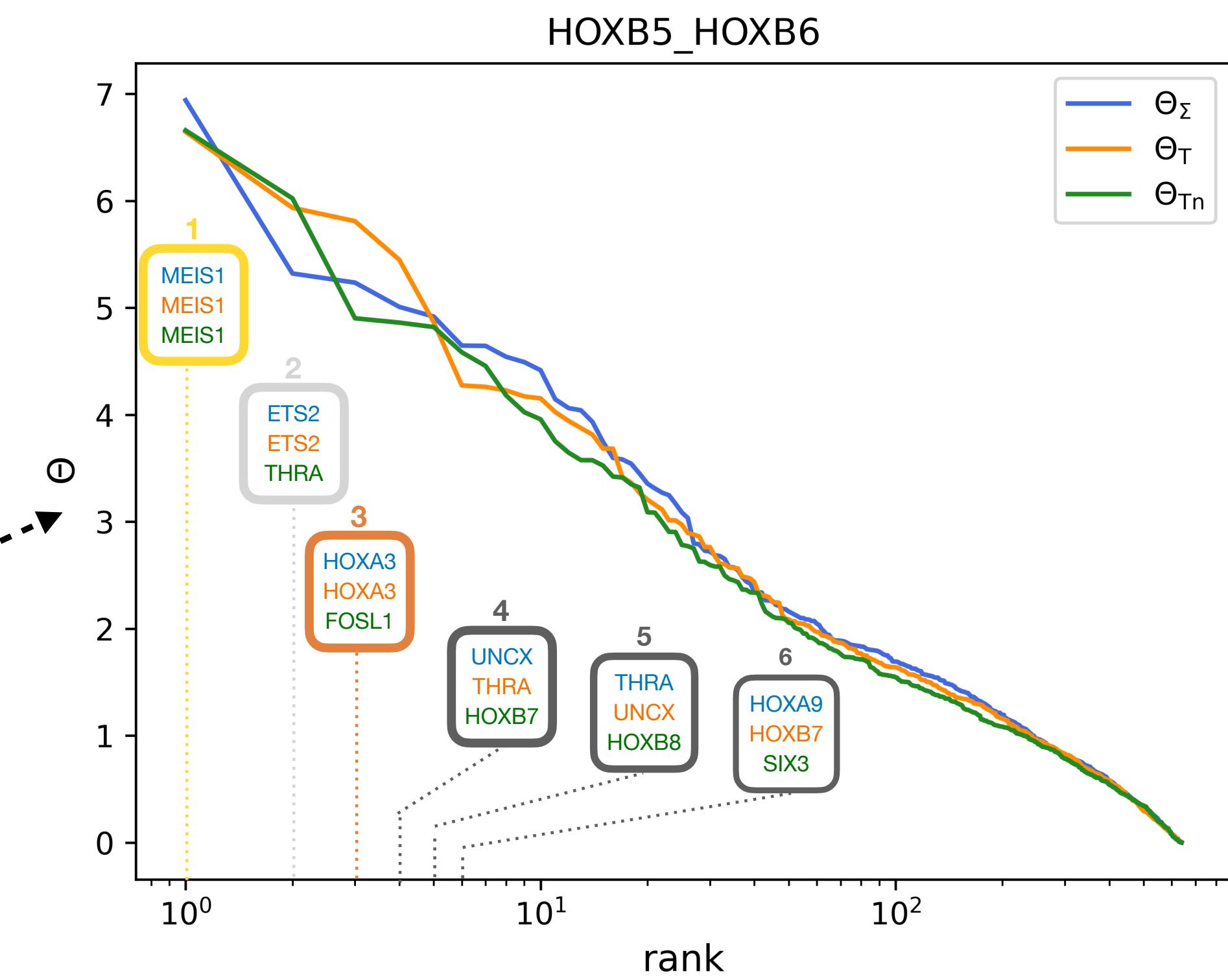
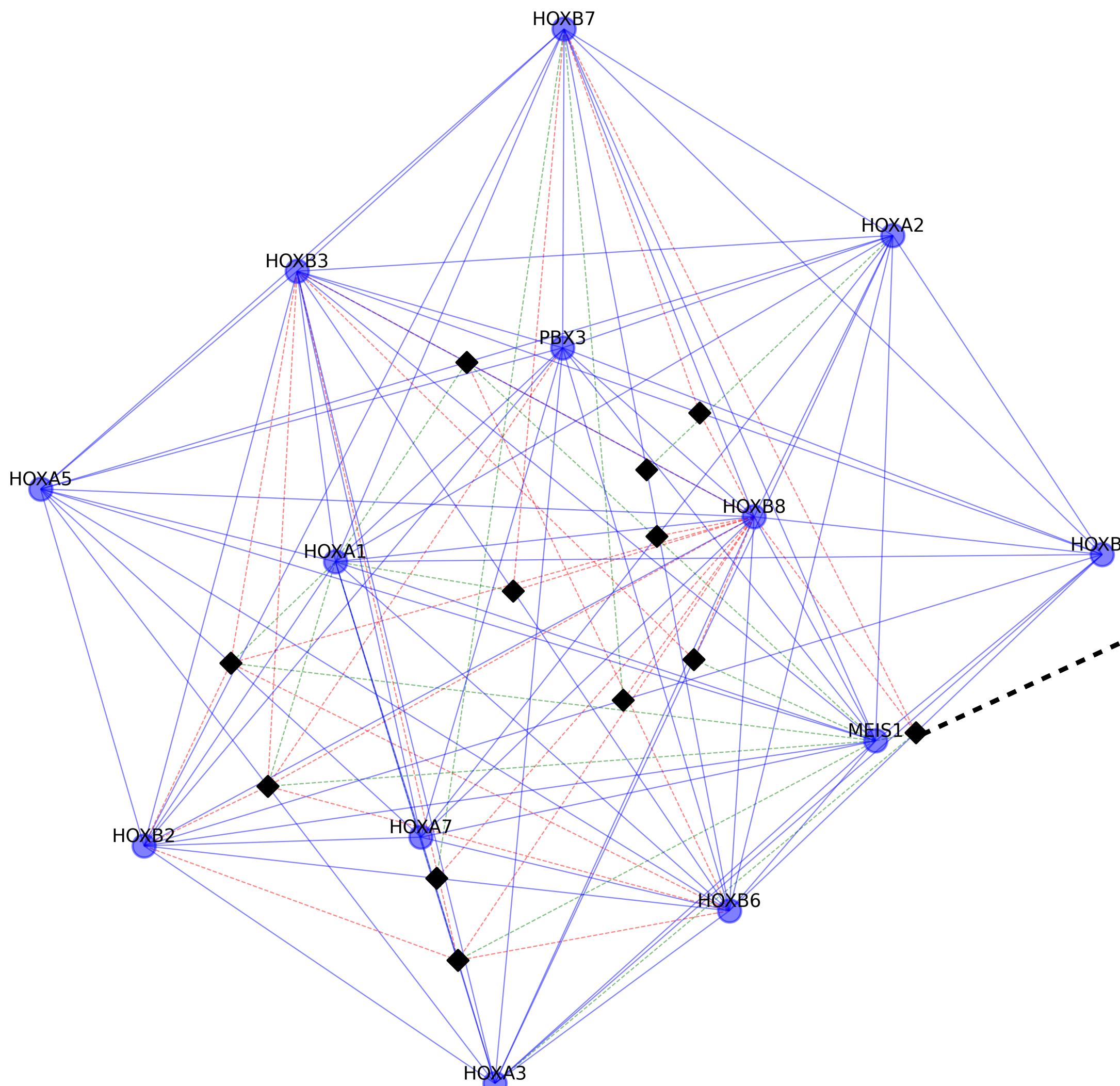
COMING SOON



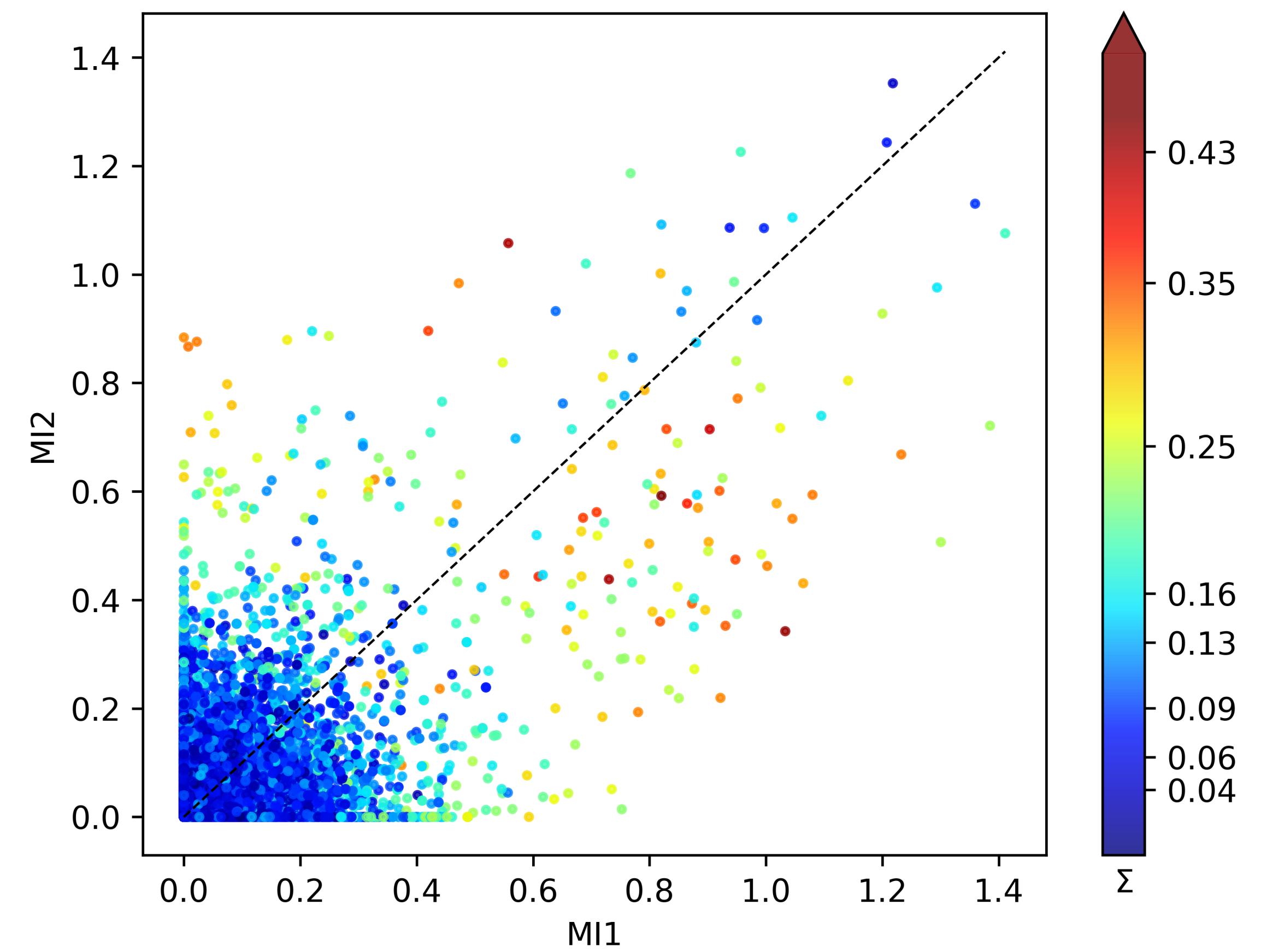
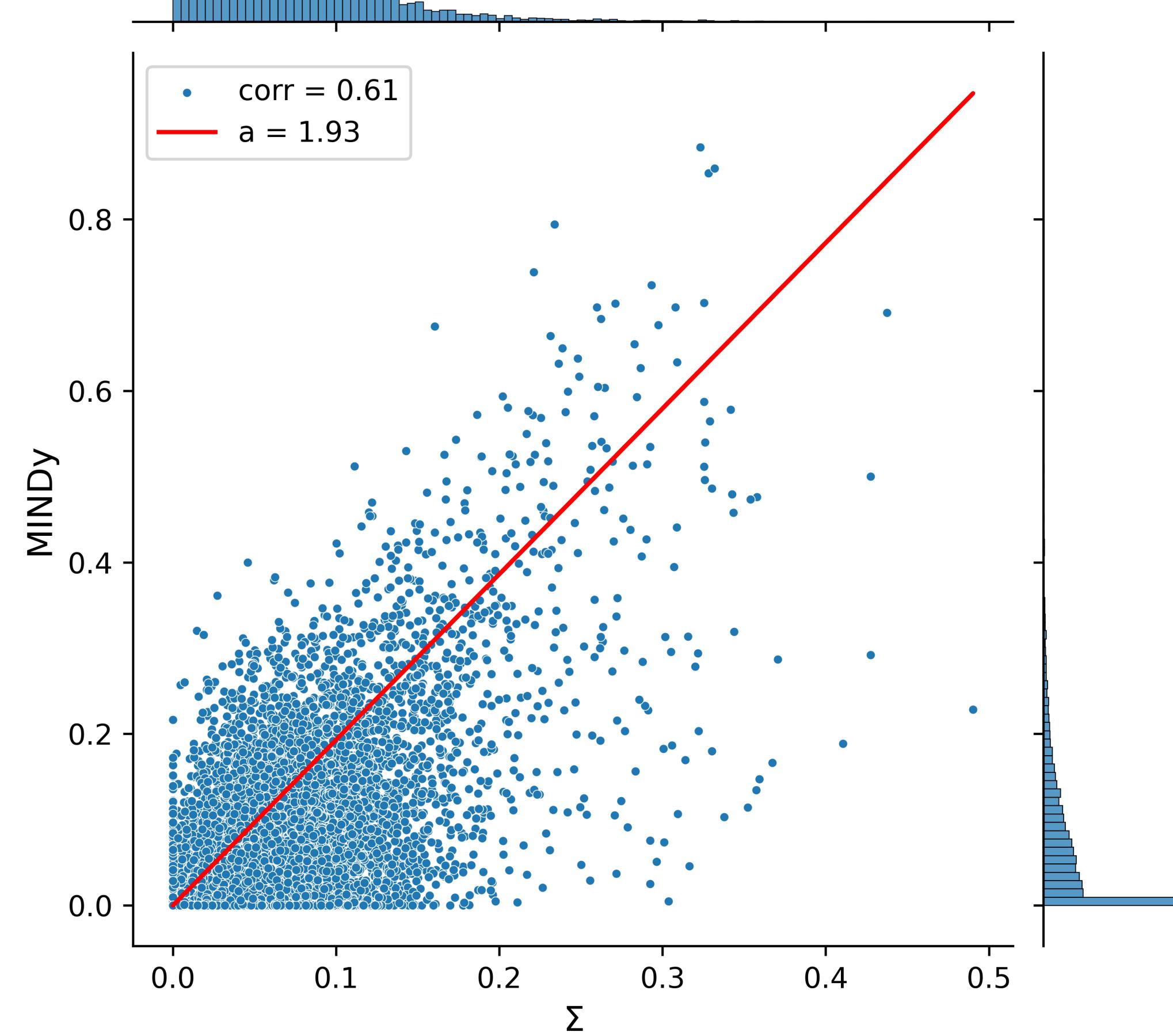
Python package

Triadic interaction network

Acute Myeloid Leukemia gene expression



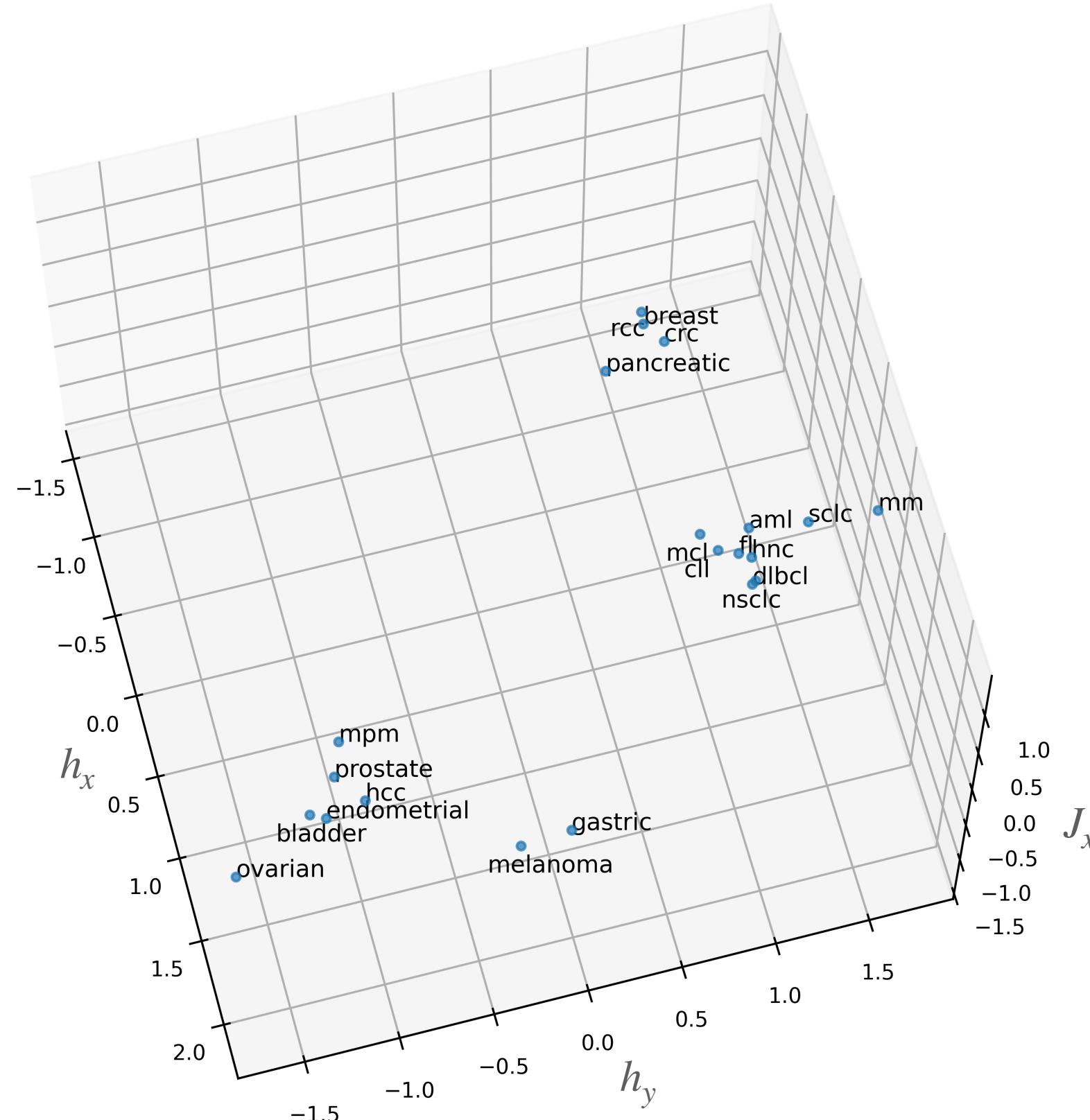
Comparison with former method (MINDy)



Detection of triadic interactions

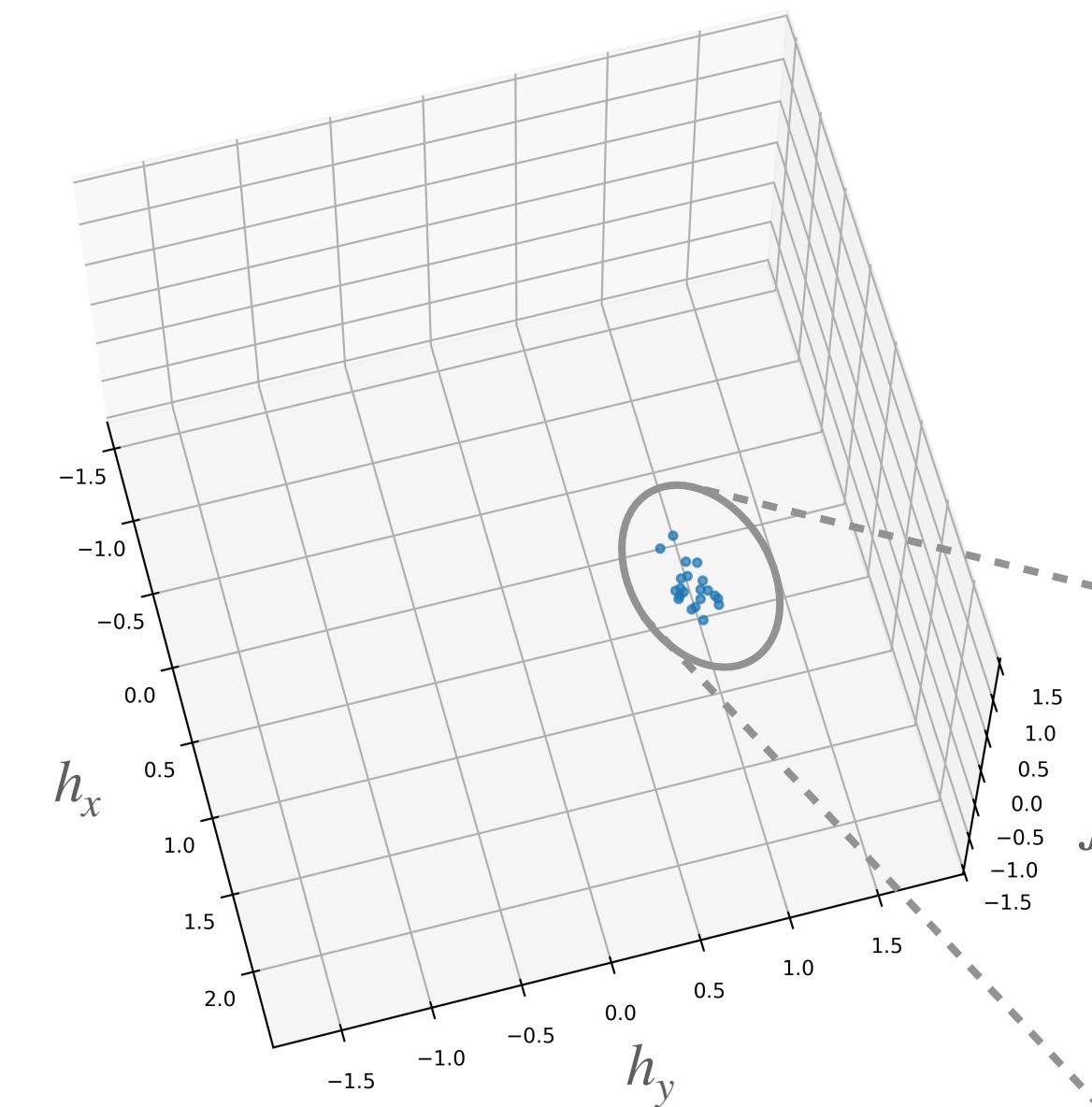
Structure missingness (bimodal variables)

Real data



	h_x	h_y	J_{xy}
Barycenter	-0.780	0.379	-0.023
Std	1.006	1.046	1.047
Max-dist	1.283	1.330	1.341

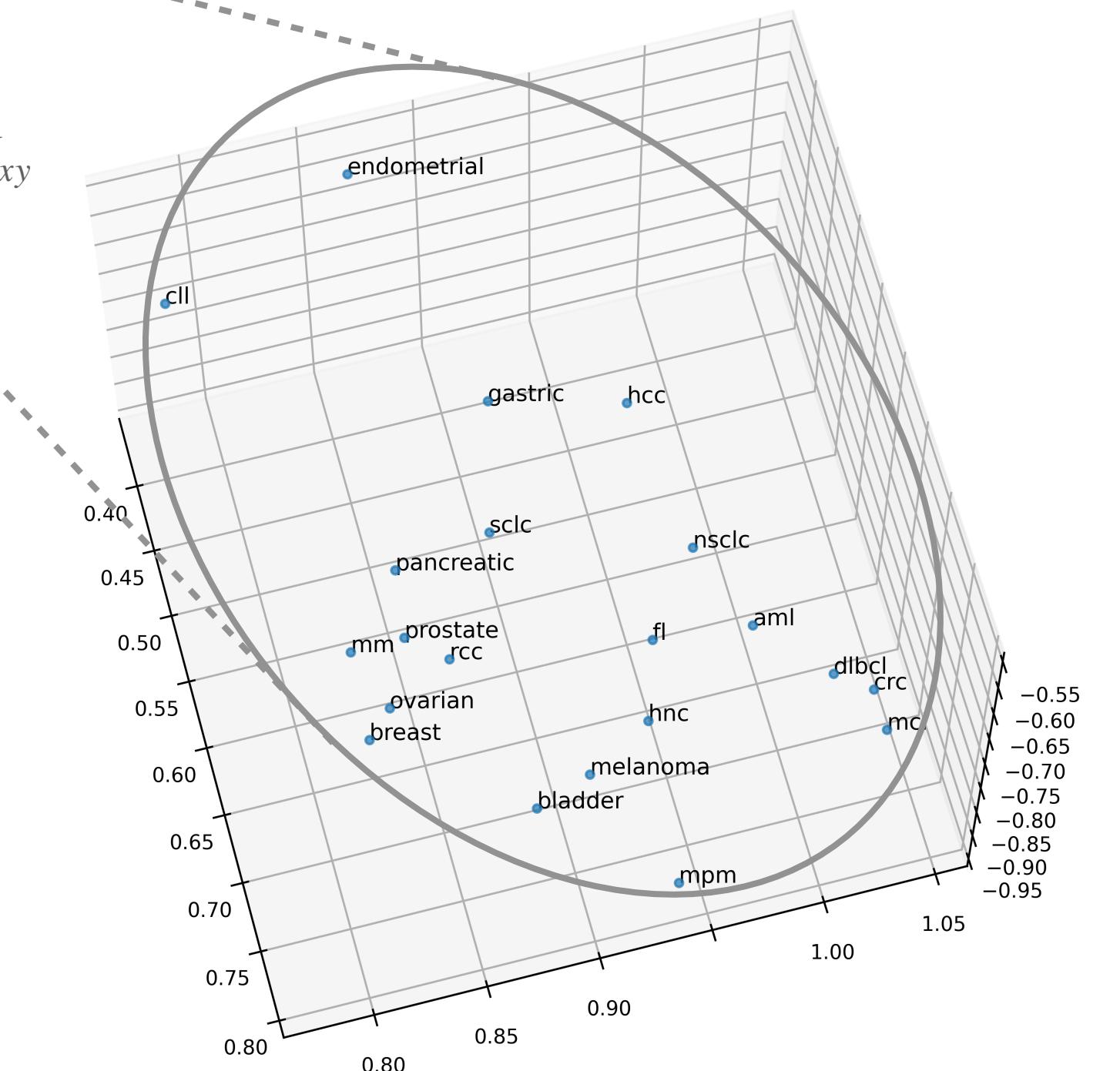
Null model



	h_x	h_y	J_{xy}	
	0.643	0.909	-0.745	Barycenter
	0.097	0.073	0.112	Std
	0.139	0.136	0.183	Max-dist

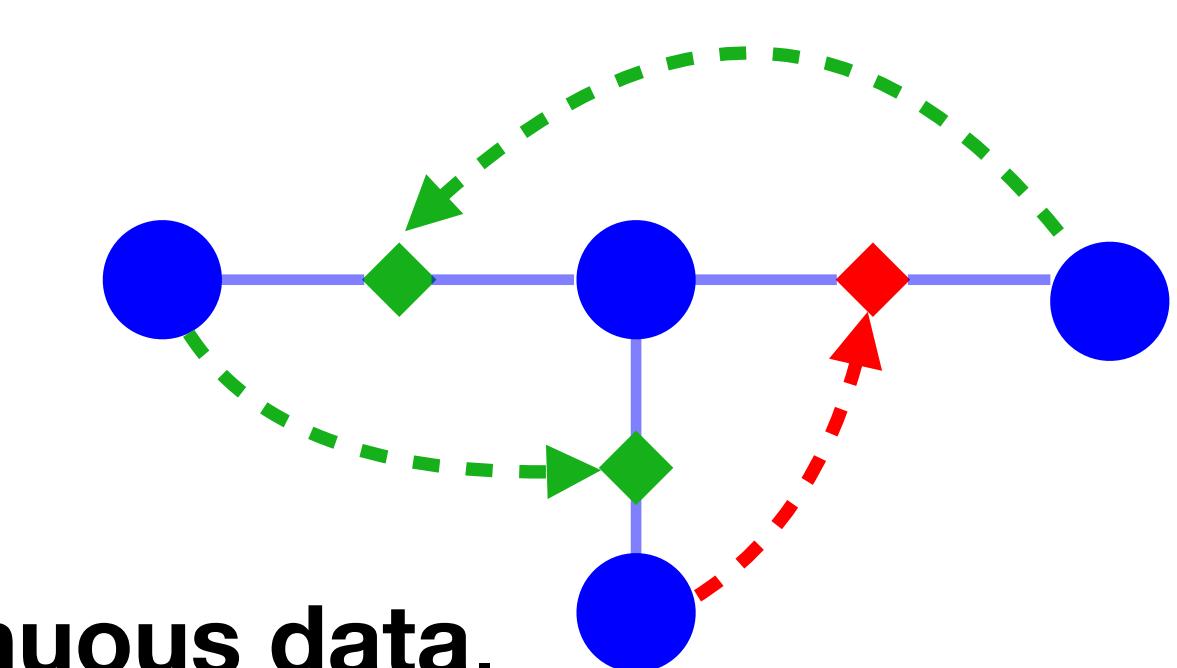
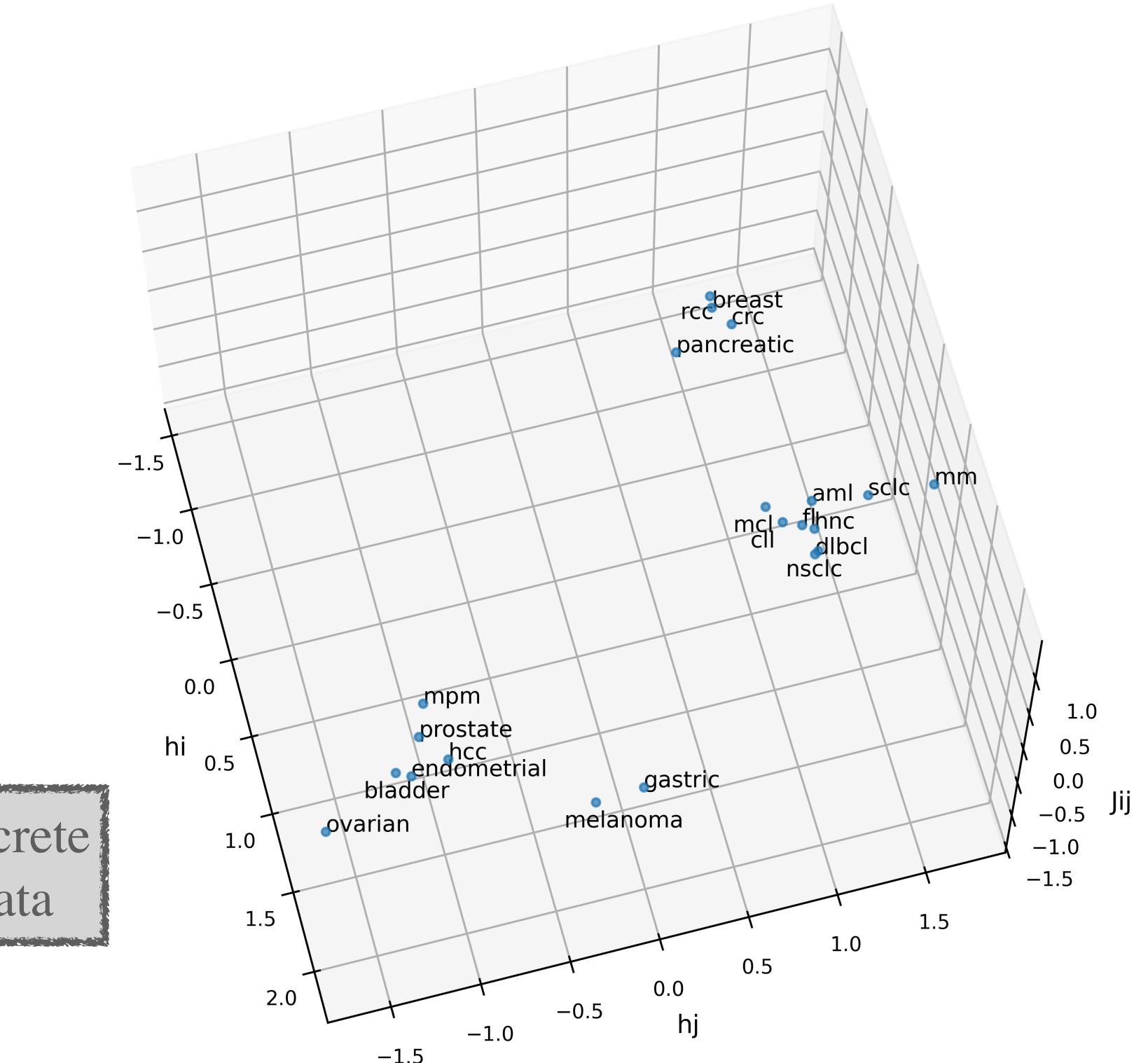
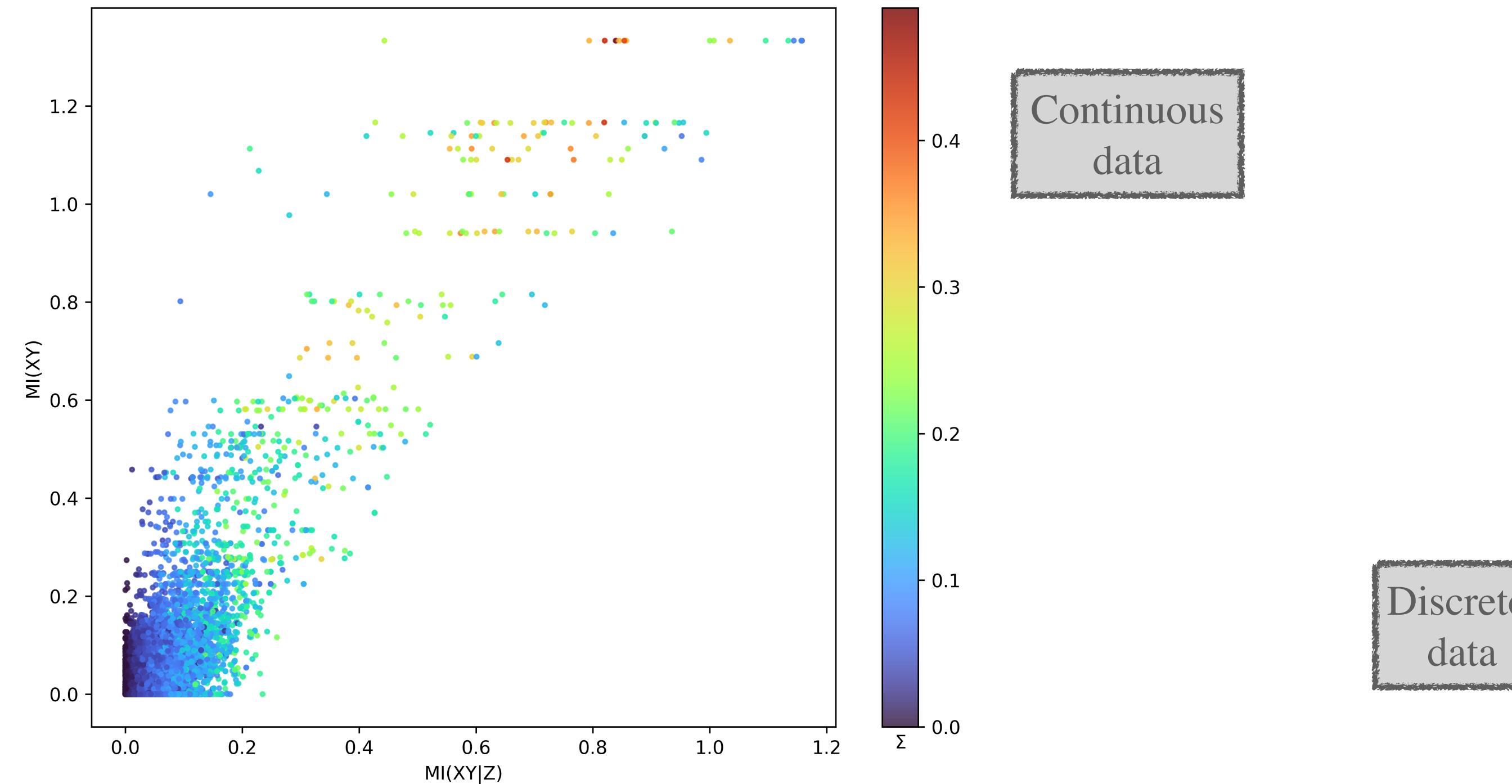
Indicator matrix

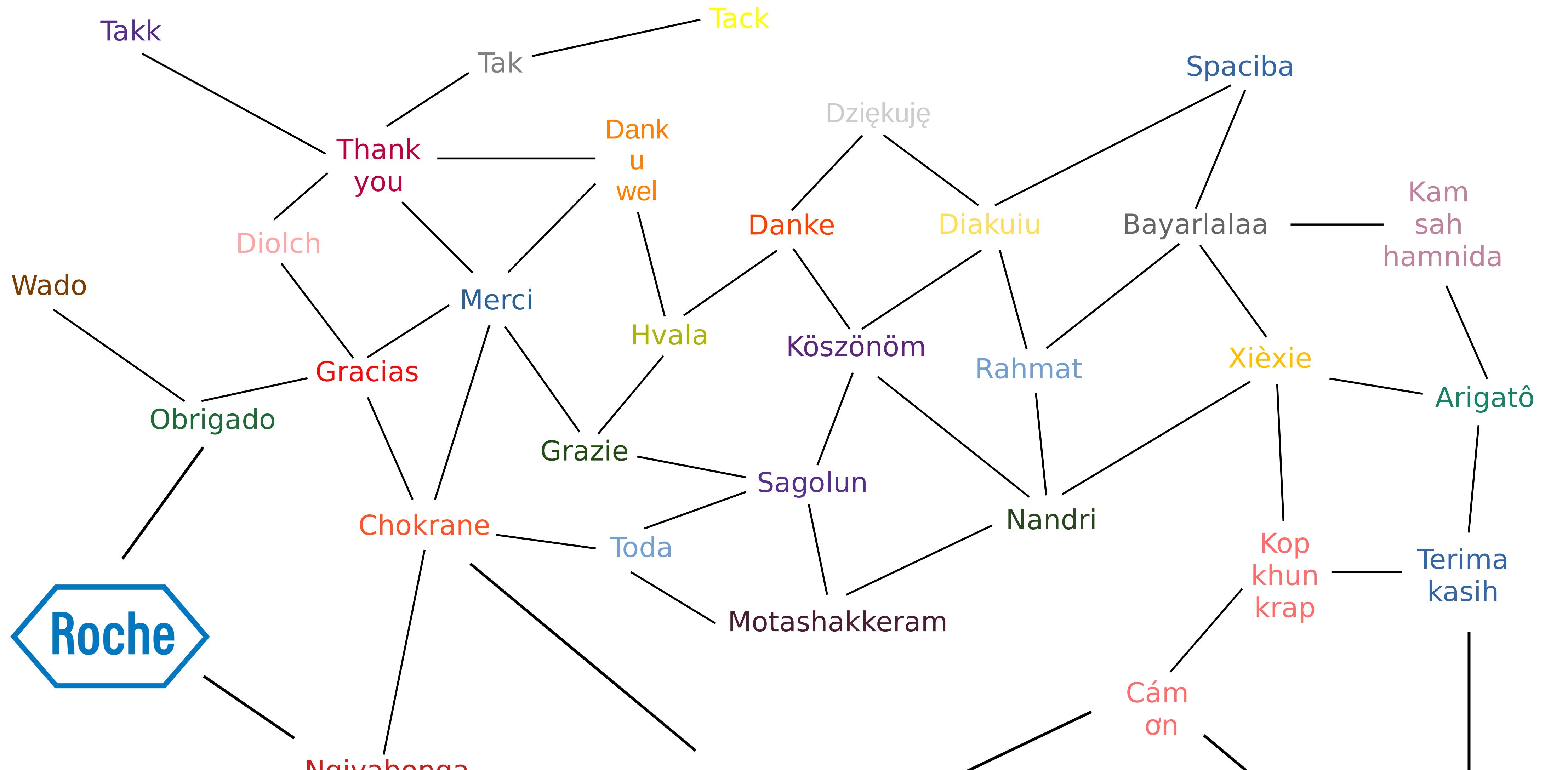
Role	X	Y	Z
Feature	Ismetastatic	tstage	Cancer type
Patient1			a
Patient2			a
Patient3			b
Patient4			b
Patient5			c



Conclusion

1. **Triadic interaction** manifests in **various systems**.
2. We have developed novel **measures** to identify triadic interactions in **continuous data**.
3. When dealing with **discrete data** (bimodal variables), we can quantitatively assess the intensity of triadic interactions.





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