Dependency Discovery via Multiscale Generalized Correlation

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Acknowledgment: NSF DMS, DARPA SIMPLEX.

1/23/2018

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- How are they related?

X	Y
brain connectivity	creativity / personality
brain shape	health
gene / protein	cancer
social networks	attributes
anything	anything else

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Without loss of generality, we shall assume F_{XY} has finite second moments.

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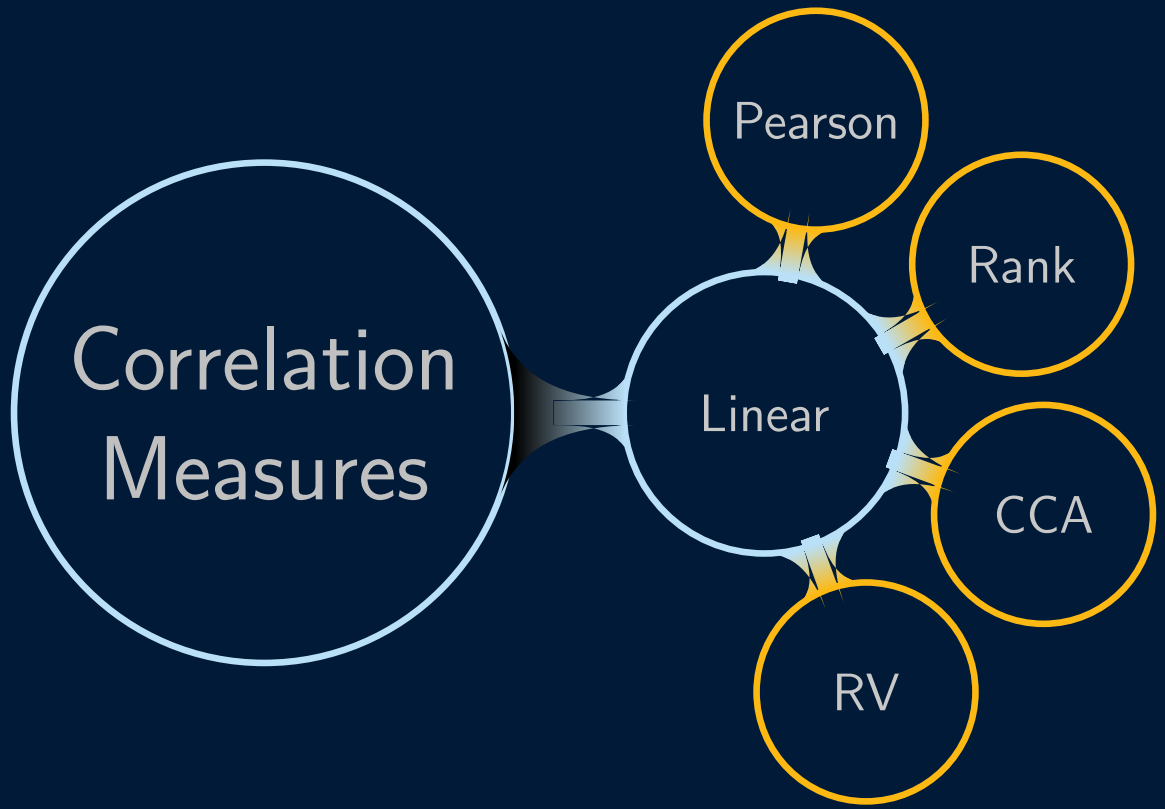

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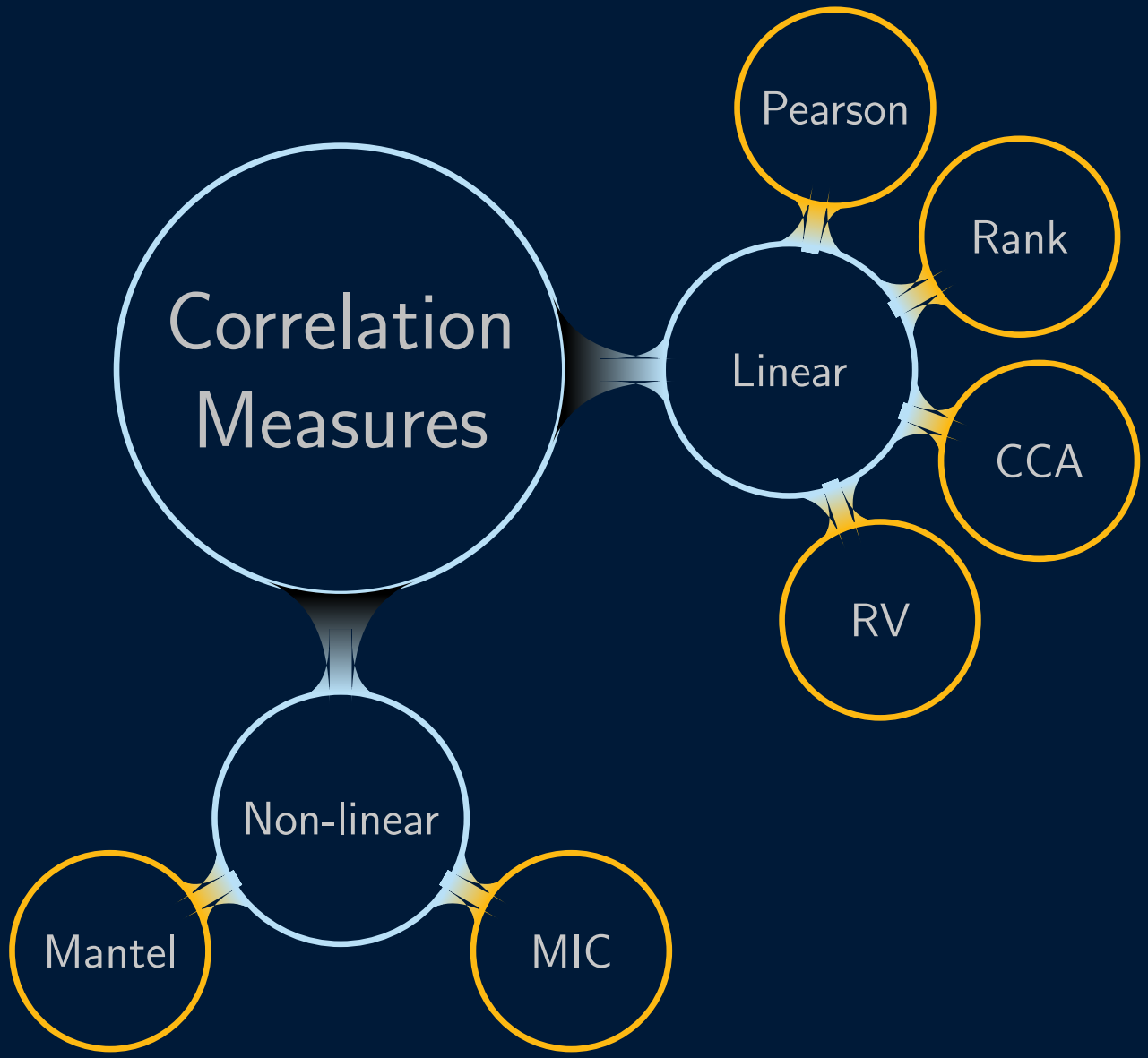
Correlation Measures
Linear
Pearson
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Mantel
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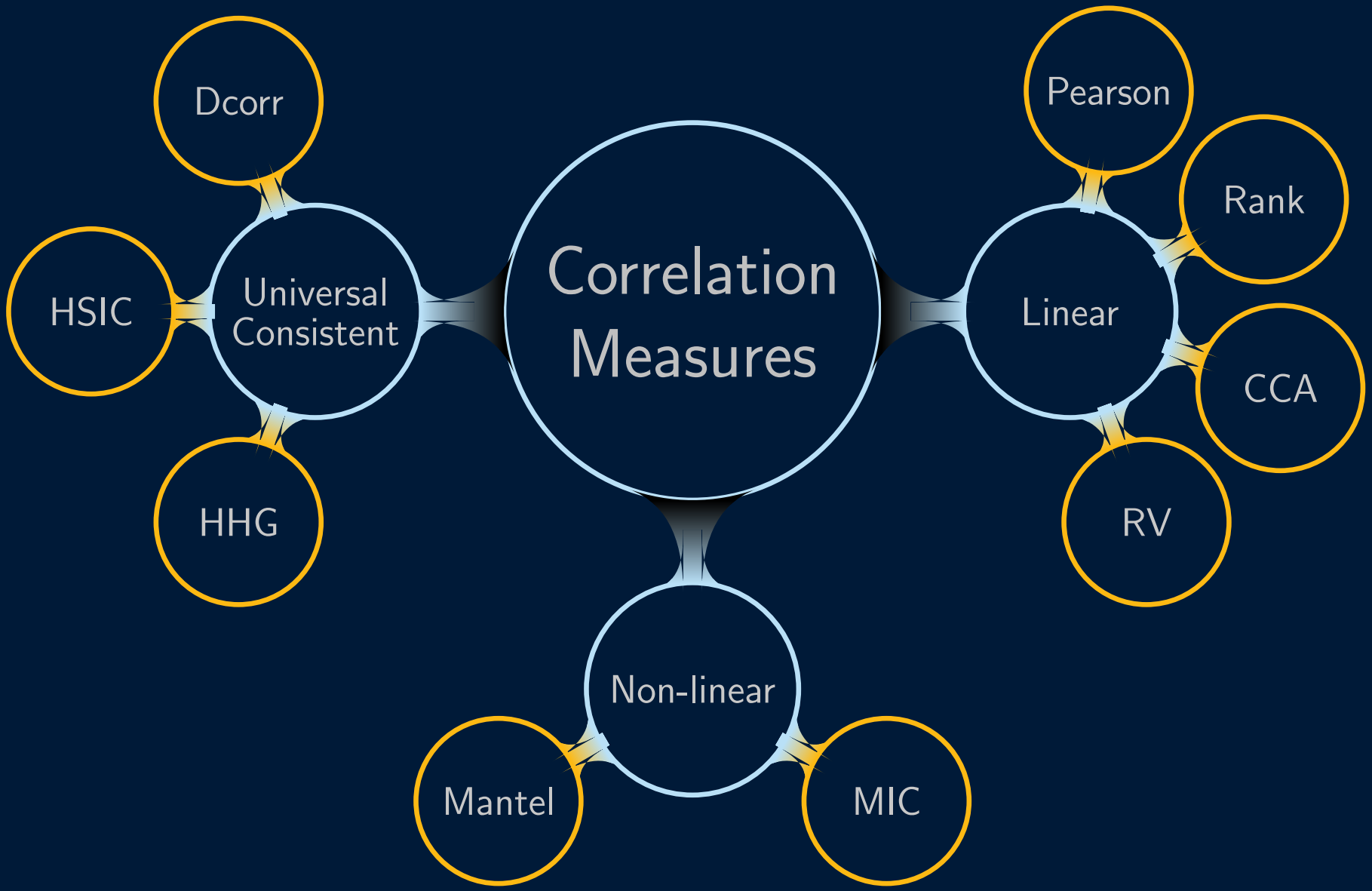
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To that end, we propose the **multiscale generalized correlation** in [*Shen et al.(2017a)*][1].

Overview

1. Illustration
2. Experiments
3. Theory
4. Summary

Illustration

Introducing MGC

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$(\mathcal{X}_n, \mathcal{Y}_n)$

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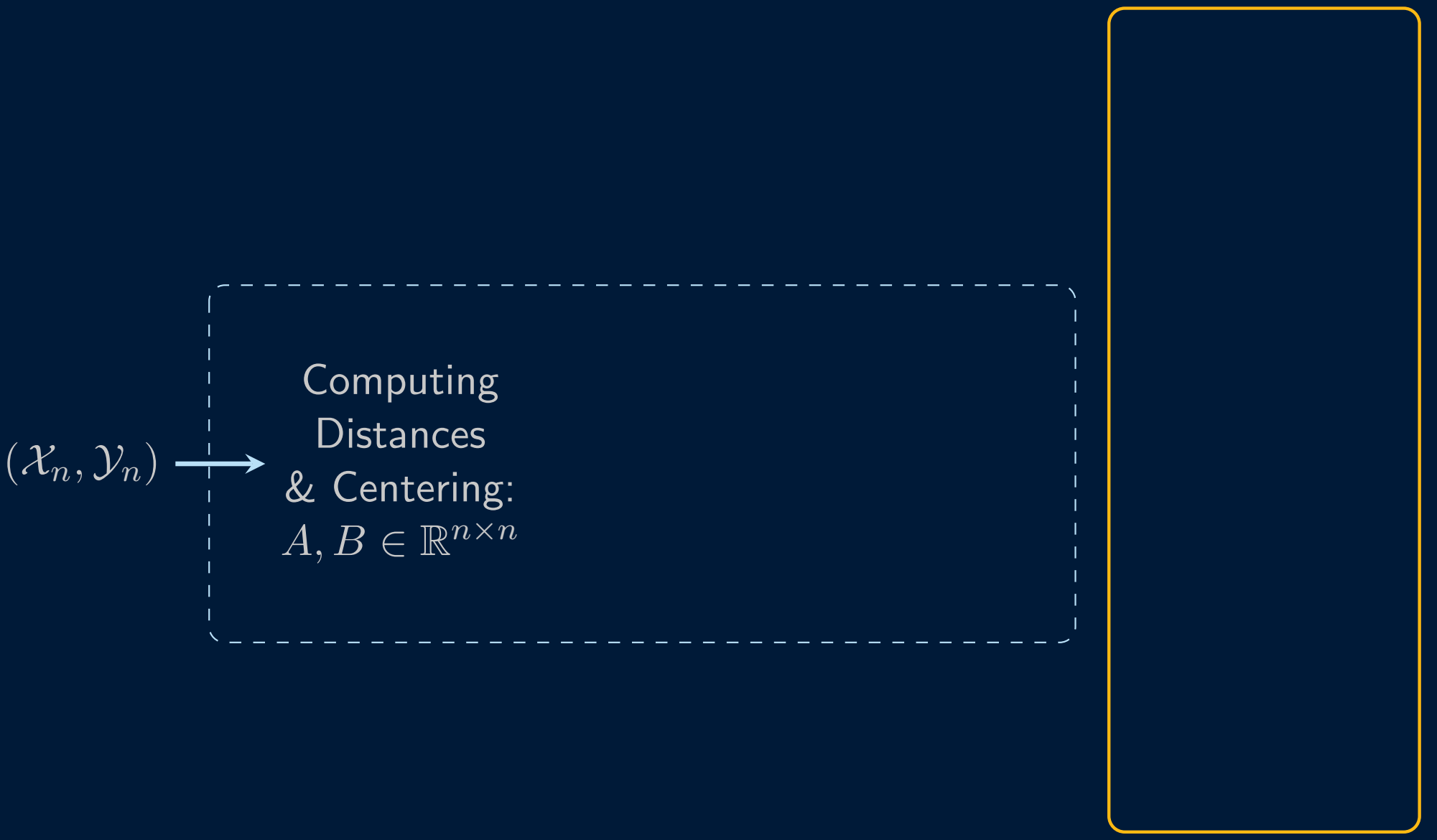

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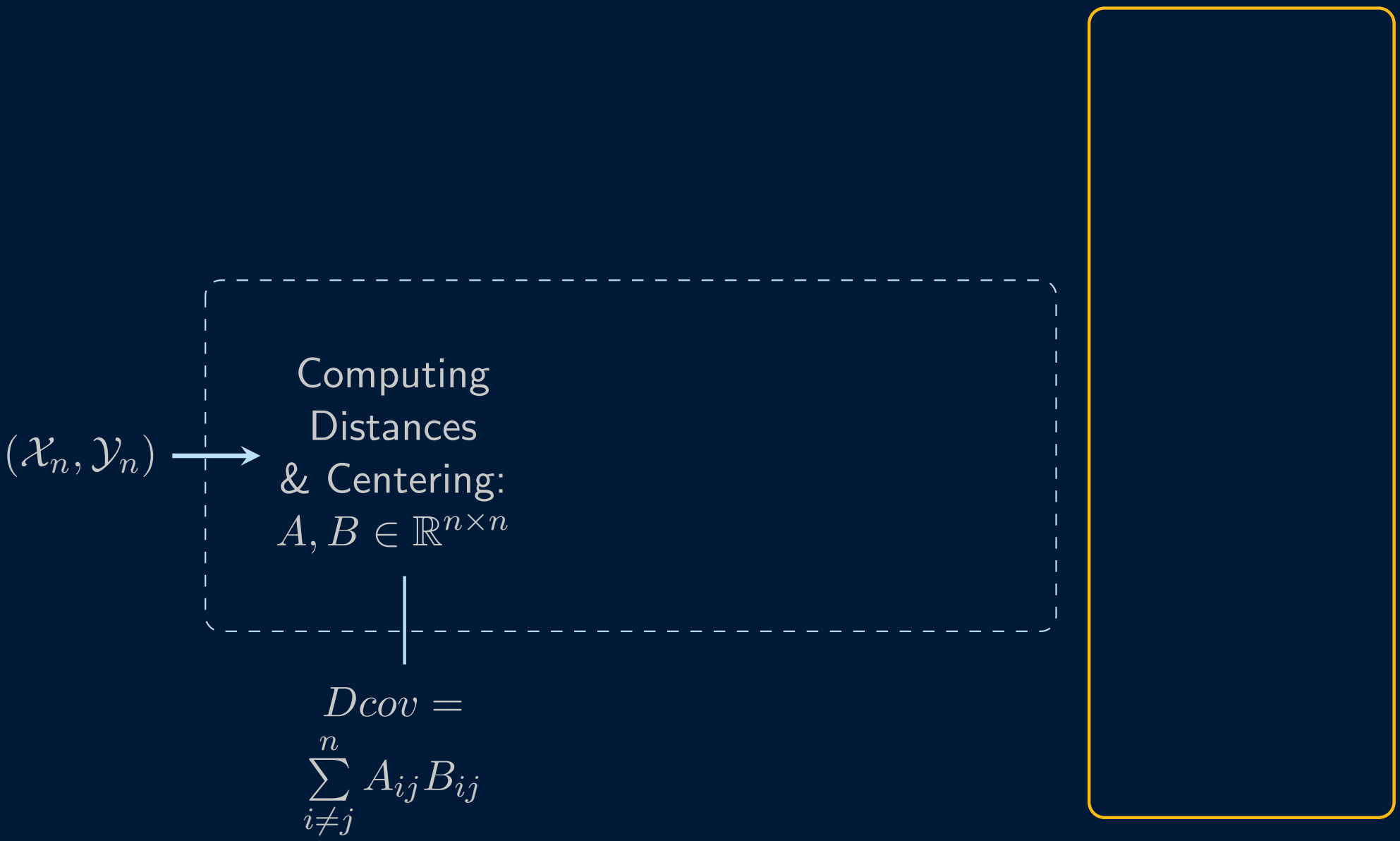

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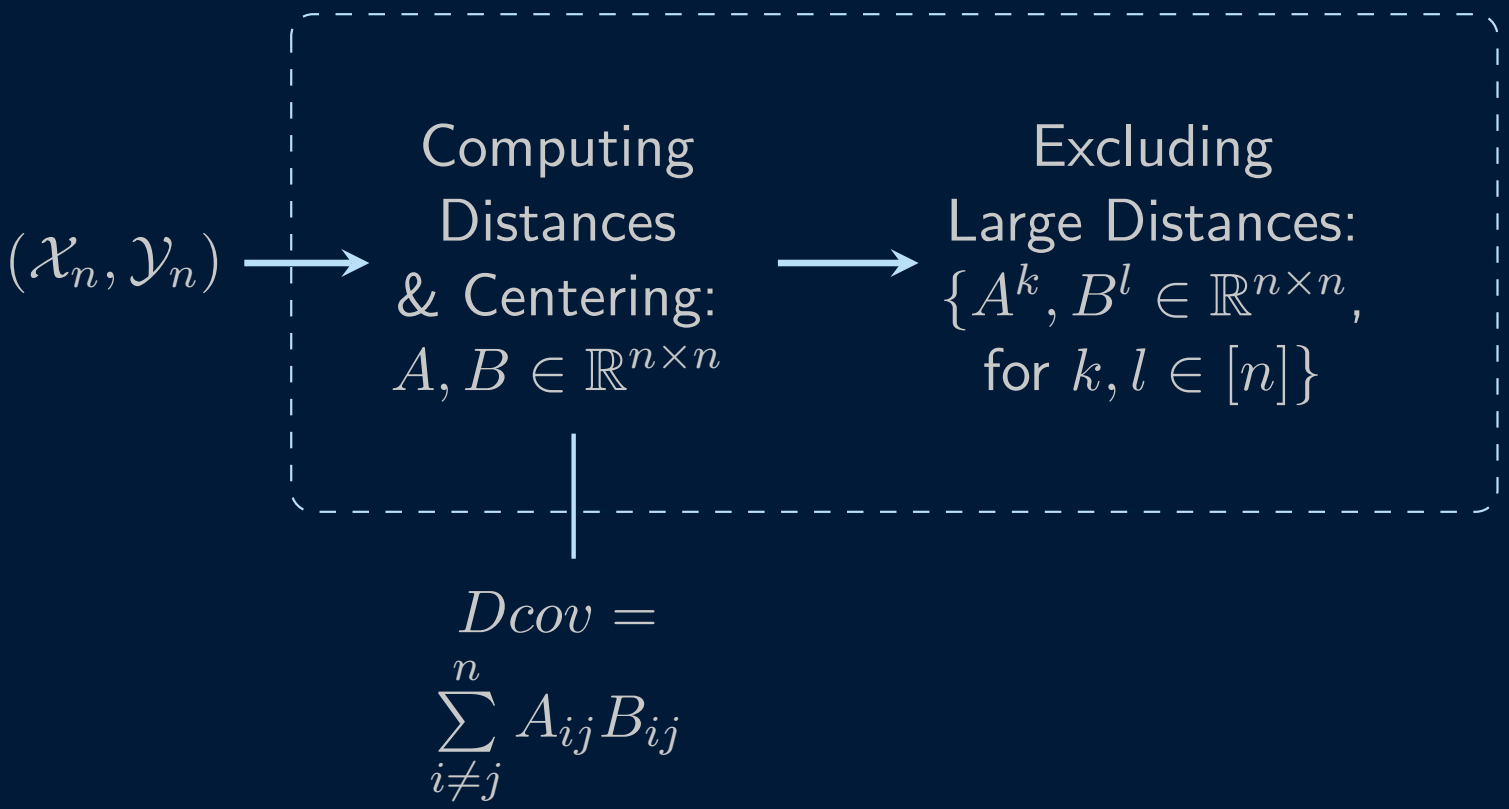

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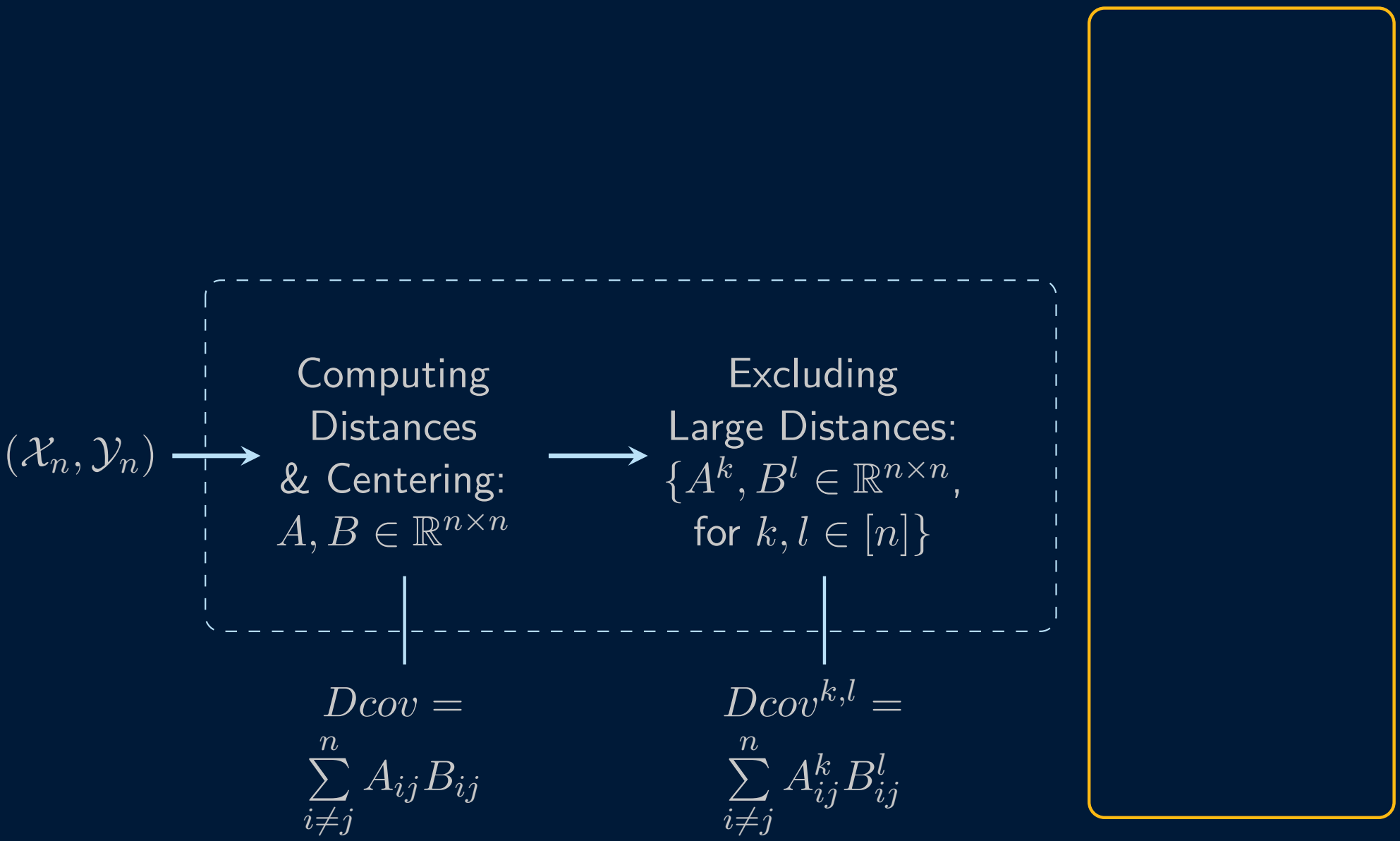

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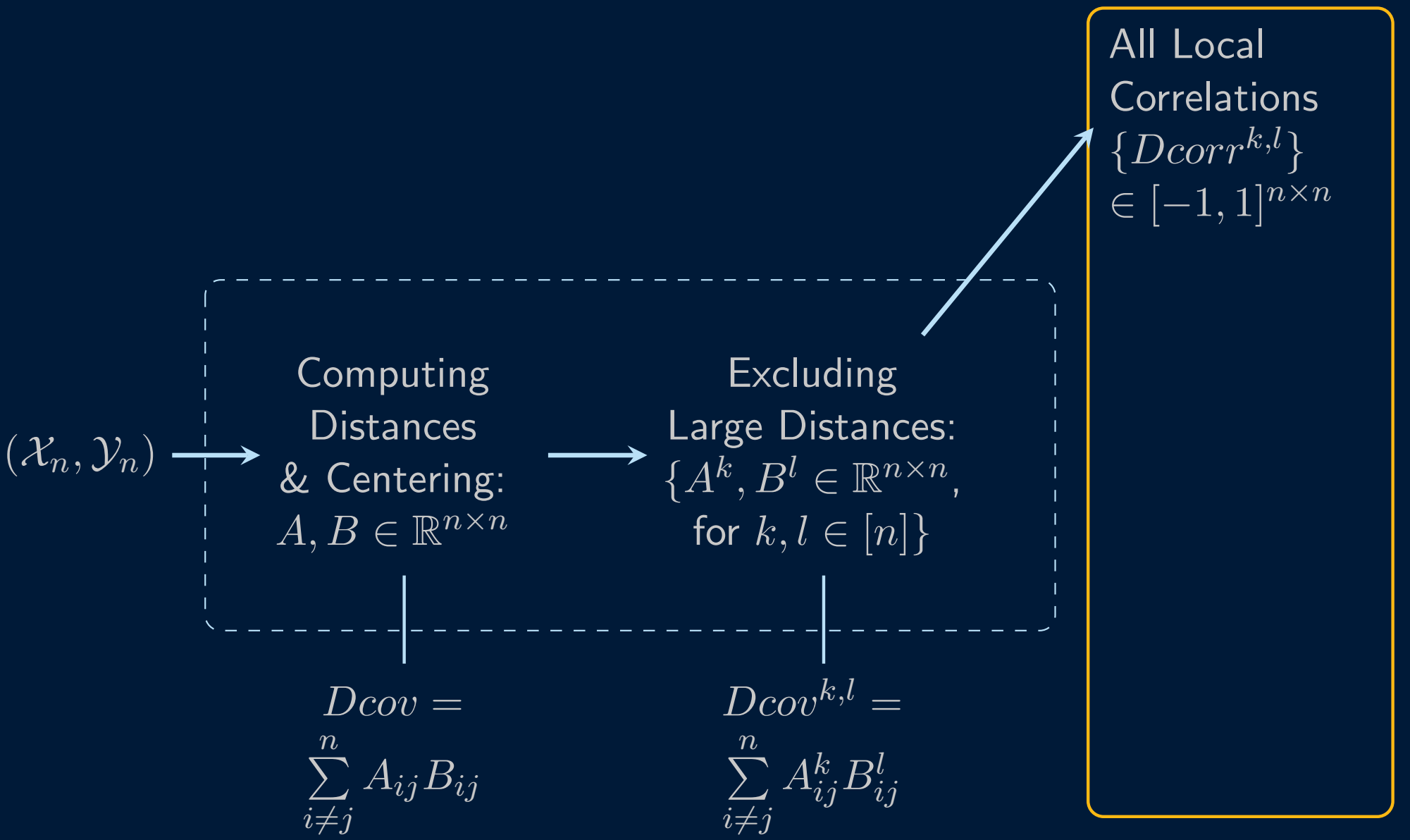

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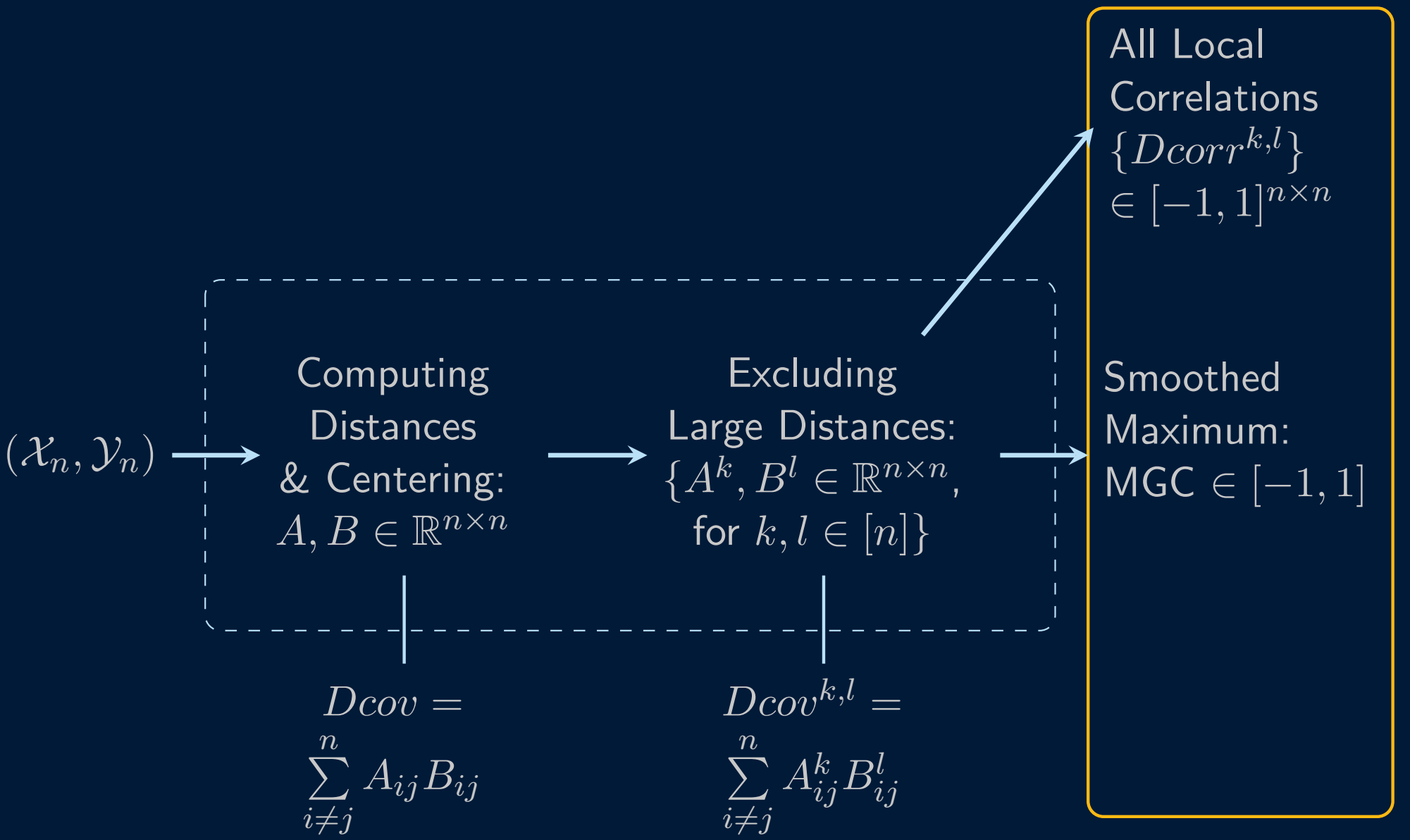

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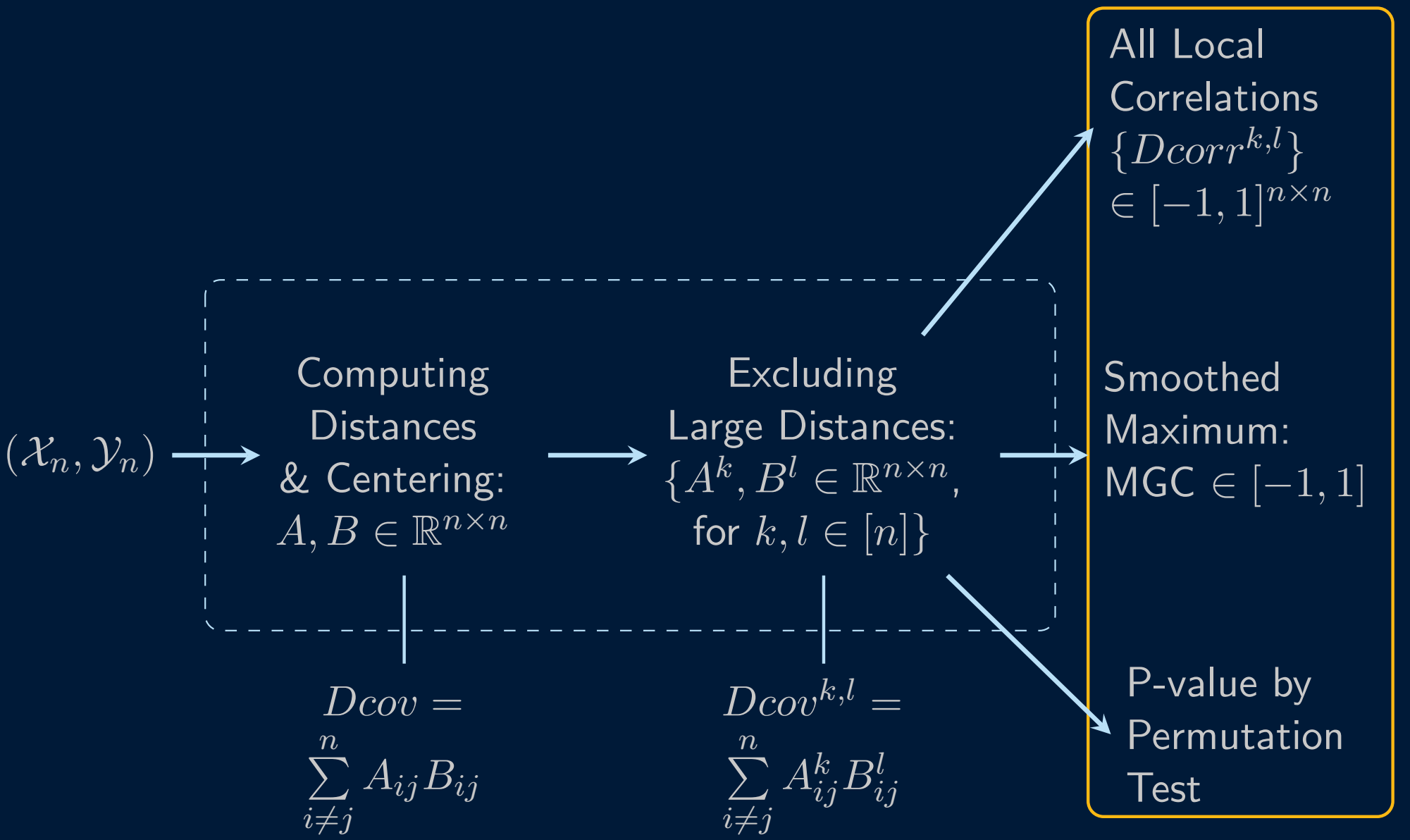

Direct Maximum

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Directly taking the maximum local correlation

$$\max_{(k,l)\in[n]^2} \{Dcorr^{k,l}(\mathcal{X}_n, \mathcal{Y}_n)\}$$

will yield a biased statistic under independence, i.e., the maximum is always larger than 0 in expectation even under independent relationship!

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It is a critical step for both the finite-sample performance and certain theoretical properties of MGC.

Examples

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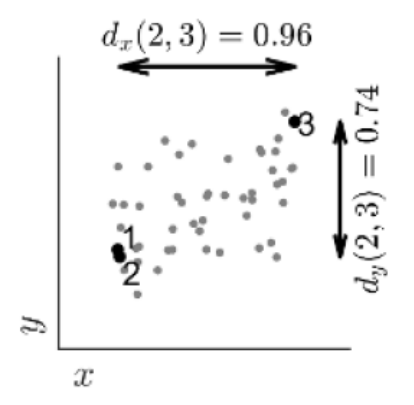

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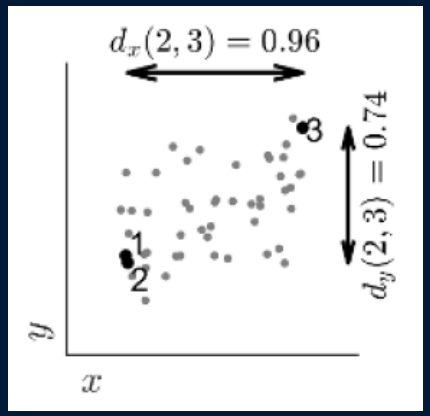

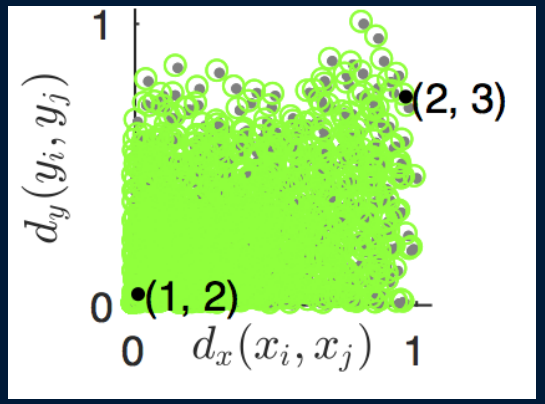

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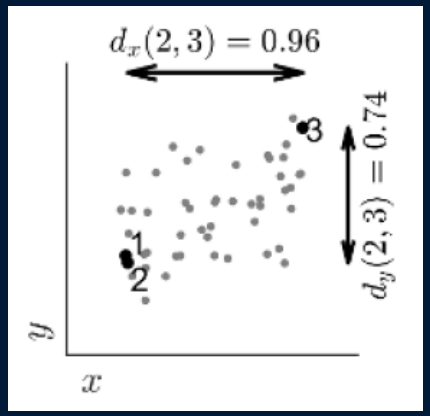

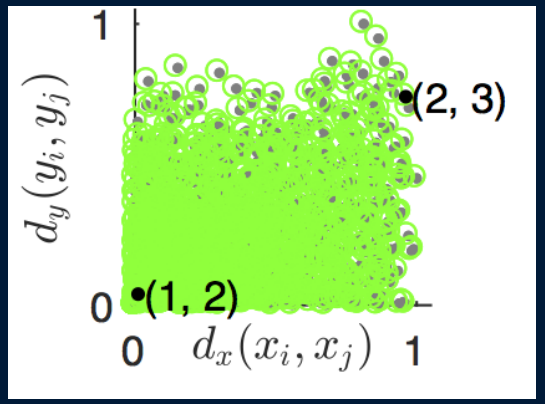

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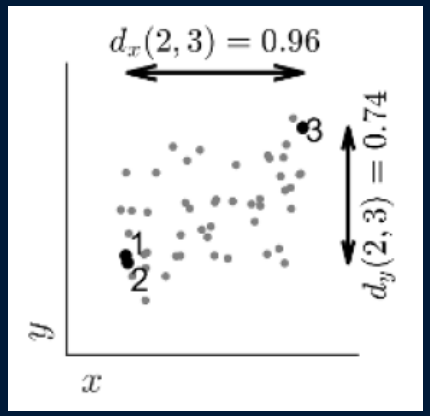

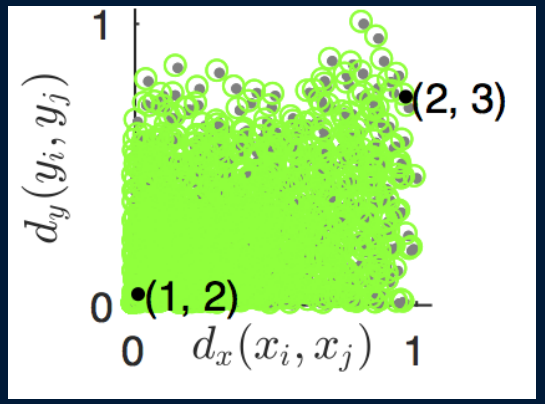

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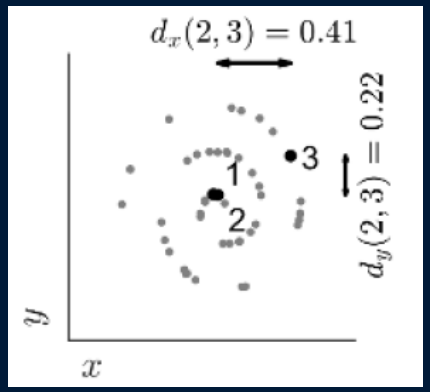

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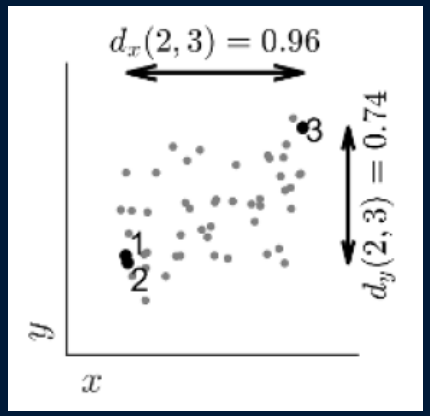

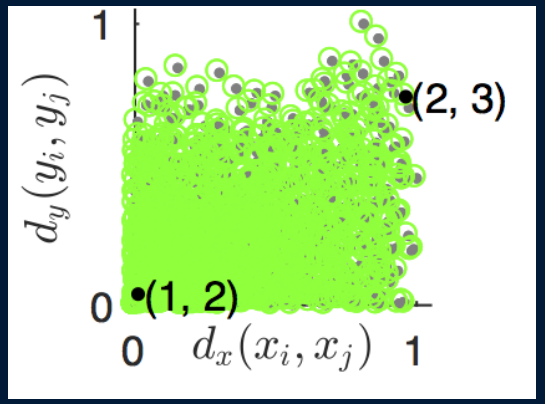

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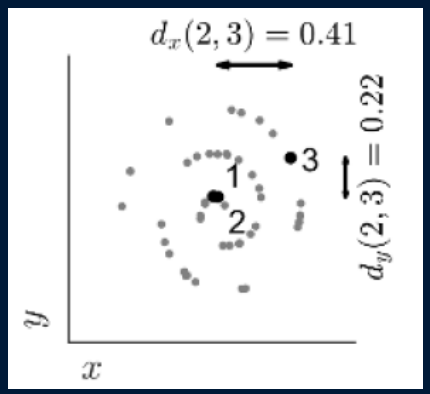

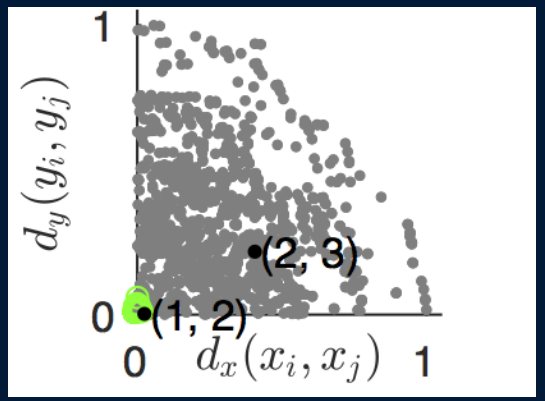

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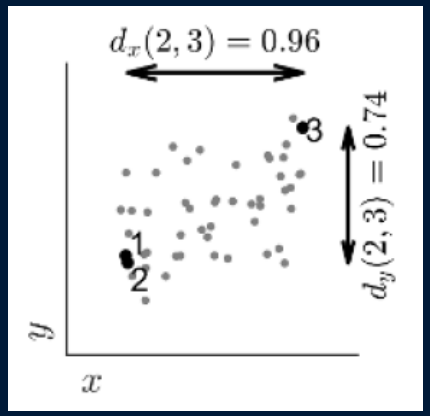

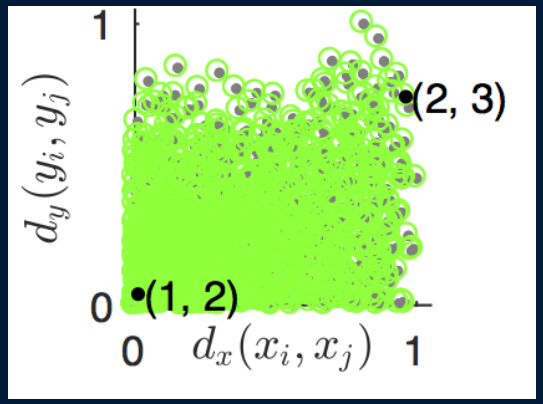

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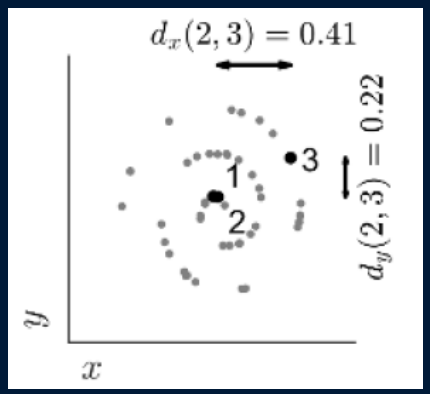

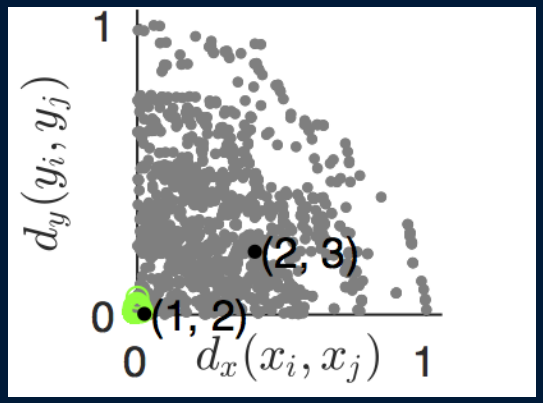

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Experiments

Visualizations of 20 Simulation Settings

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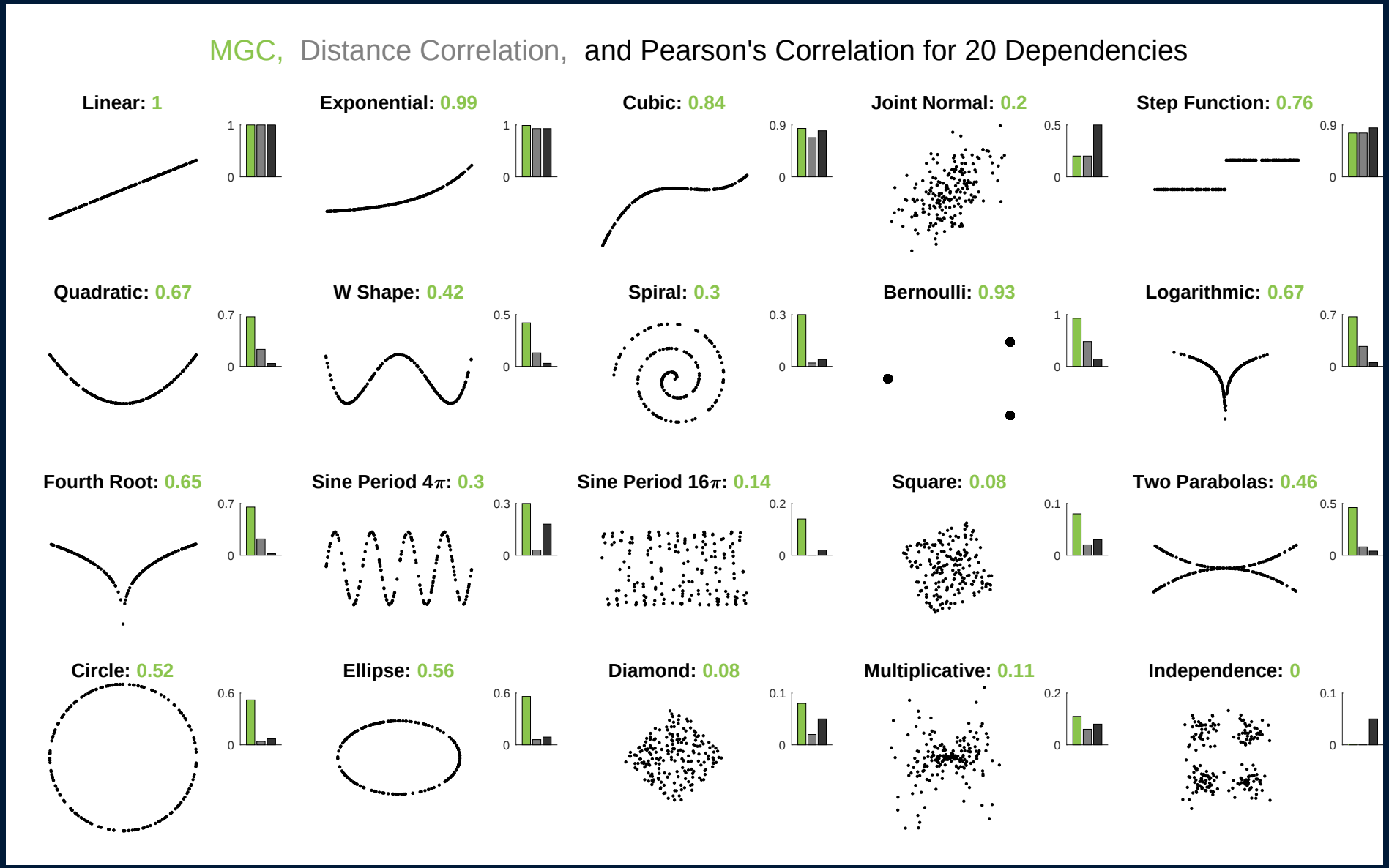

Evaluation Criterion

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- Required sample size $N_{\alpha,\beta}(c)$ to achieve a power of β at type 1 error level α using a statistic c.

Testing Power: Linear vs Nonlinear

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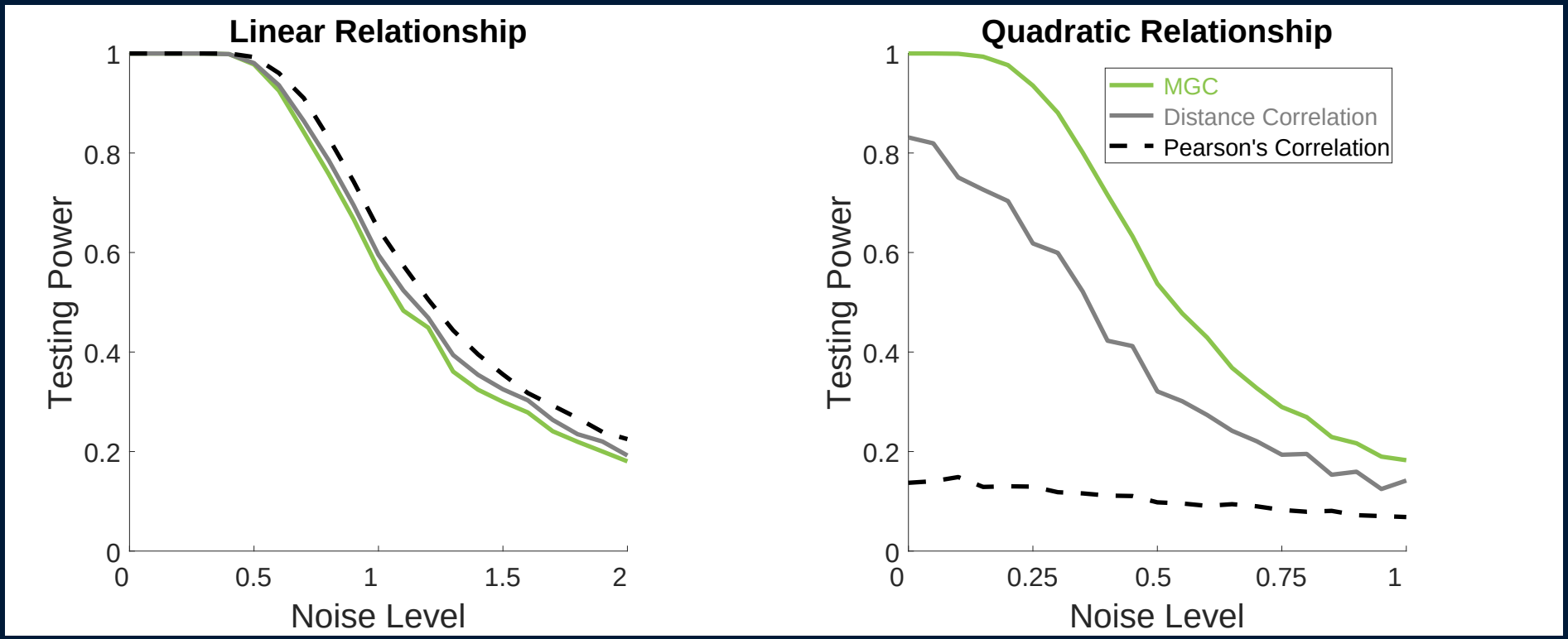

$$n = 30, p = q = 1,$$
$$X \sim Uniform(-1, 1),$$
$$\epsilon \sim Normal(0, noise),$$
$$Y = X + \epsilon \text{ and } Y = X^2 + \epsilon.$$

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We consider univariate (1D) and multivariate (10D) cases.

Median Size Table

Testing Methods	1D Lin	1D Non-Lin	10D Lin	10D Non-Lin
MGC	**50**	**90**	60	**165**
Dcorr	**50**	250	60	515
Pearson / RV / CCA	**50**	>1000	**50**	>1000
HHG	70	**90**	100	315
HSIC	70	95	100	400
MIC	120	180	n/a	n/a

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Adjusted for multiple testing, MGC uniquely revealed one particular protein, neurogranin, which is exclusively expressed in brain tissue among normal tissues and has not been linked with any other cancer type.

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If we compare kNN (K=3) leave-one-subject-error of these peptides:

Peptides	False Positives	True Positives
Neurogranin (MGC)	**2**	**5**
HSIC Features	4	**5**
HHG Features	**2**	1

Comparison and Verification

HSIC identifies two peptides, HHG identifies three peptides, and other methods do not identify any peptide as significant. However, there exists strong evidence that the other two peptides are upregulated in other cancers.

If we compare kNN (K=3) leave-one-subject-error of these peptides:

Peptides	False Positives	True Positives
Neurogranin (MGC)	**2**	**5**
HSIC Features	4	**5**
HHG Features	**2**	1

Theory

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Normalizing and taking a smoothed maximum yield population MGC.

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The last three properties also hold for any local correlation by $(\rho_k, \rho_l) = (\frac{k-1}{n-1}, \frac{l-1}{n-1})$.

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Conversely, the optimal scale being local (i.e., $MGC(X, Y) > Dcorr(X, Y)$) implies a non-linear relationship.

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They made MGC advantageous in theory and practice.

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MGC shares the same intrinsic idea as in nonlinear embedding, random forest, multiple kernel learning, deep learning.

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- MGC is infused with diffusion maps for testing between graph vertices and attributes [*Lee et al.(2017)*][3].
- MGC is utilized for iterative signal subgraph extraction in [*Wang et al.(2018)*][4].

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References

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