# Dependency Discovery via Multiscale Generalized Correlation

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*Acknowledgment: NSF DMS, DARPA SIMPLEX.*

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| $X$ | $Y$ |
|---|---|
| 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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Correlation
Measures

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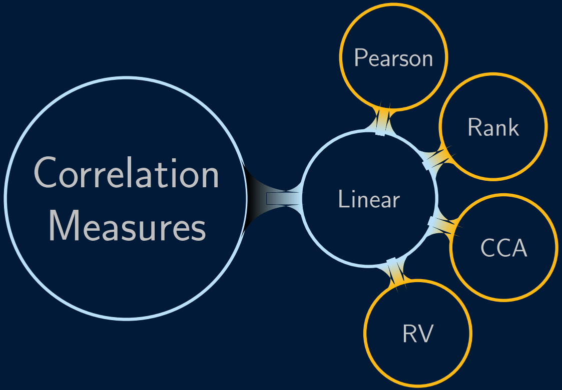

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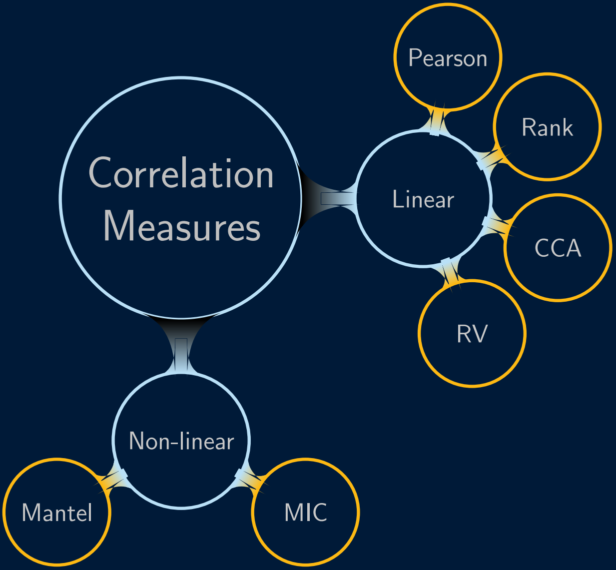
Correlation Measures
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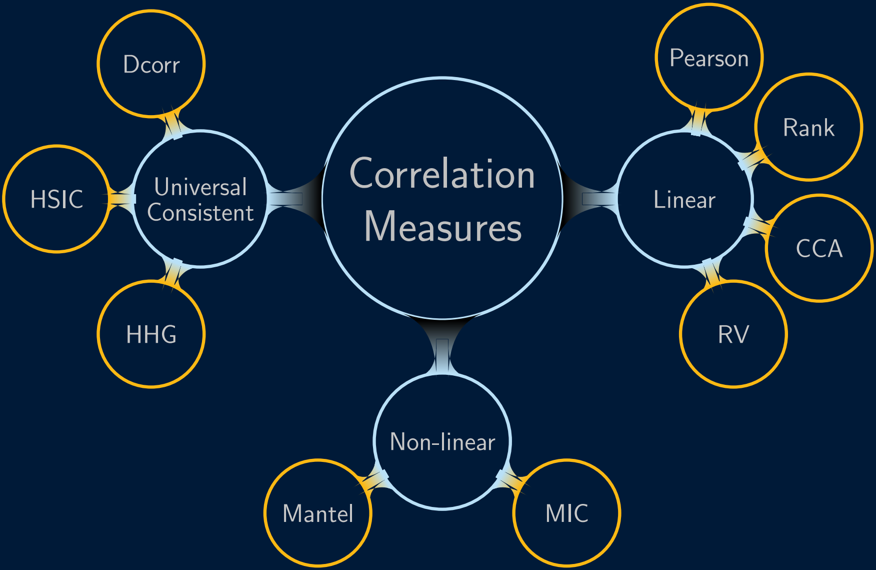
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To that end, we propose the **multiscale generalized correlation** in [*Shen et al.(2017a)*][1].

# Overview

1. Illustration

2. Experiments

3. Theory

4. Summary

# Illustration

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P-value by Permutation Test

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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.

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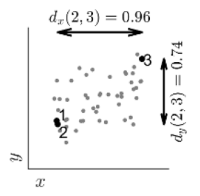

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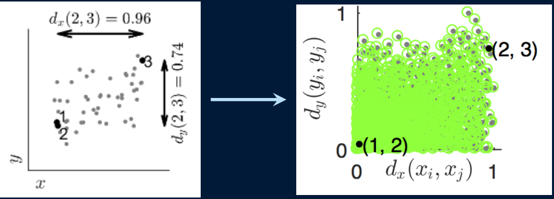

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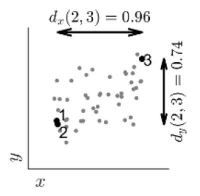


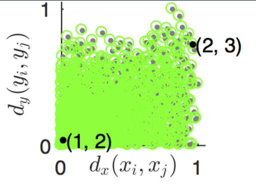


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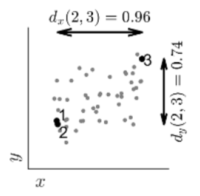


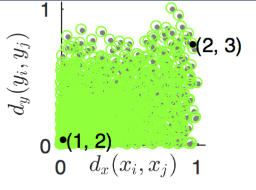


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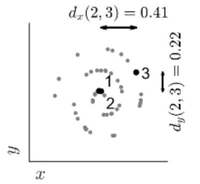

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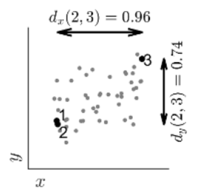


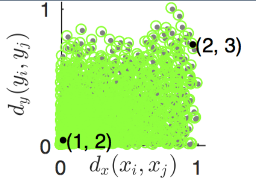


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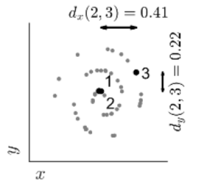


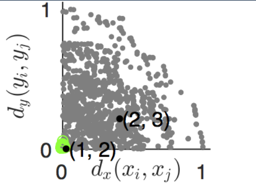

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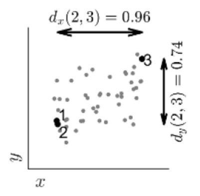


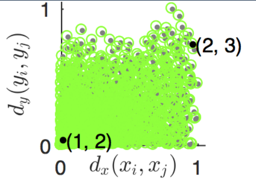


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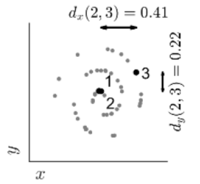


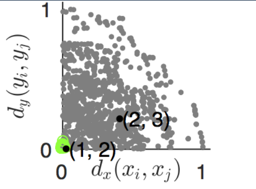


$$Dcorr(\mathcal{X}_n, \mathcal{Y}_n) = 0.01$$
$$MGC(\mathcal{X}_n, \mathcal{Y}_n) = 0.13$$
p-vals: $0.3$ vs $< 0.001$

# Experiments

# Visualizations of $20$ Simulation Settings

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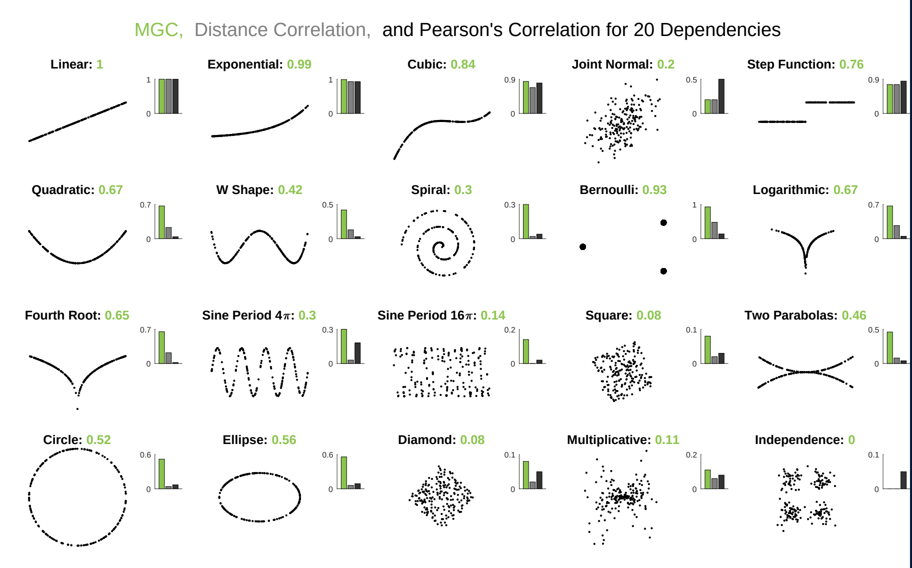

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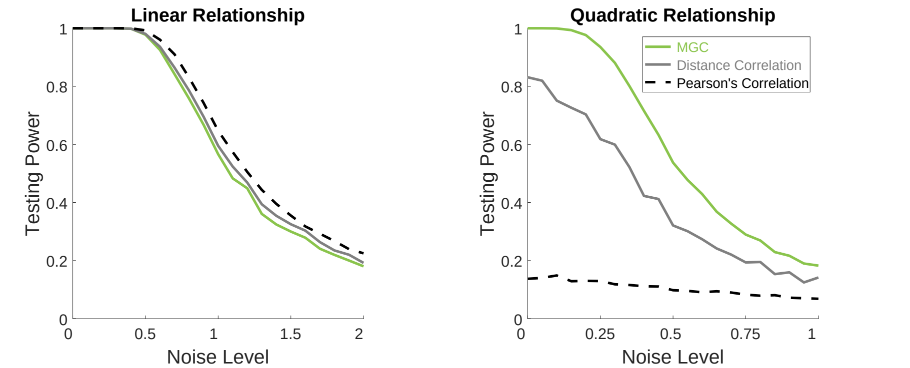


$n = 30, p = q = 1,$

$X \sim Uniform(-1, 1),$

$\epsilon \sim Normal(0, noise),$

$Y = X + \epsilon$ 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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*3. Invariant:* $c(\mathcal{X}_n, \mathcal{Y}_n) = c(\{\phi(x_i)\}, \{\delta(y_i)\})$ *for any linear transformation* $\phi, \delta$ *(i.e., rotation, scaling, translation, reflection).*

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The population local covariance can be defined as

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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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*If the relationship is linear (or with independent noise), the global scale is always optimal and* $MGC(X, Y) = Dcorr(X, Y)$.

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

# MGC is applicable to similarity / kernel matrix

**Theorem 6 (Transforming kernel to distance)**

*For a positive definite kernel function $k(\cdot,\cdot)$, define an induced semi-metric as*

$$d(\cdot,\cdot) = 1 - k(\cdot,\cdot)/\max\{k(\cdot,\cdot)\}.$$

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For any sample kernel matrices $K_{n\times n}$, one can transform it to a dissimilarity matrix by

$$D = J - K/\max_{i,j\in[1,\ldots,n]^2}\{K(i,j)\},$$

and apply MGC / Dcorr to the transformed dissimilarity matrices.

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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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