Dependency Discovery via Multiscale Generalized Correlation

Cencheng Shen

Johns Hopkins University

Collaborators: Joshua T. Vogelstein, Carey E. Priebe, Shangsi Wang, Youjin Lee, Mauro Maggioni, Qing Wang, Alex Badea.

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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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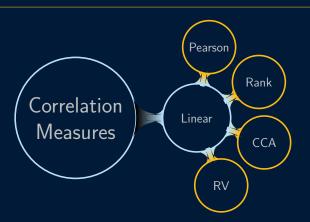
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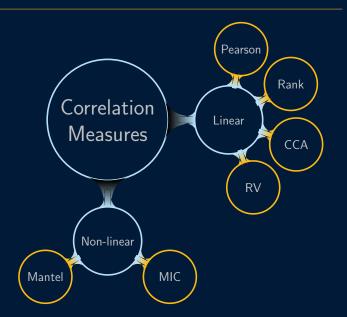
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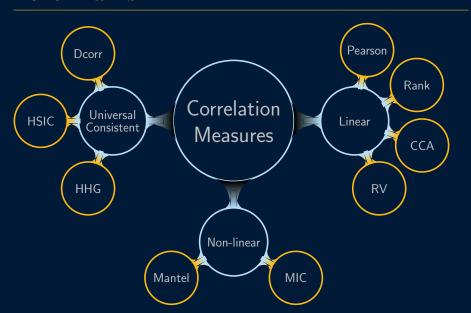
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Without loss of generality, we shall assume ${\cal F}_{XY}$ has finite second moments.









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

Overview

1. Illustration

2. Experiments

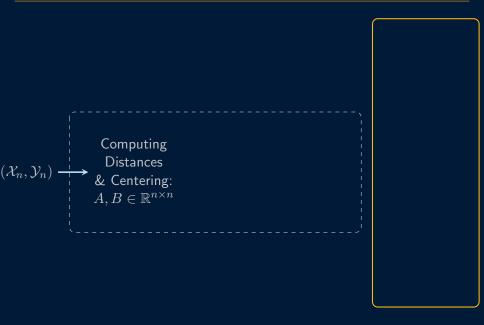
3. Theory

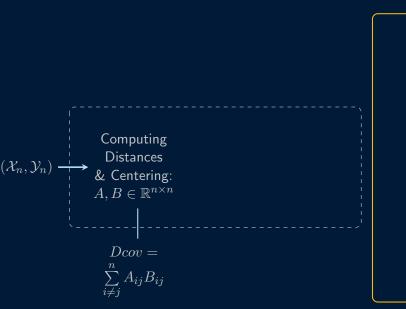
4. Summary

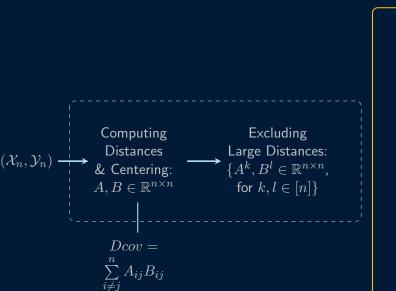
Illustration

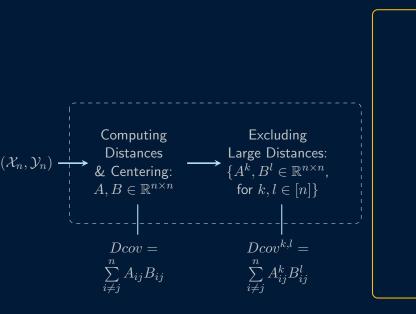
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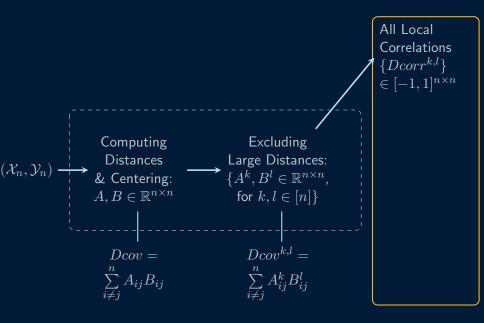


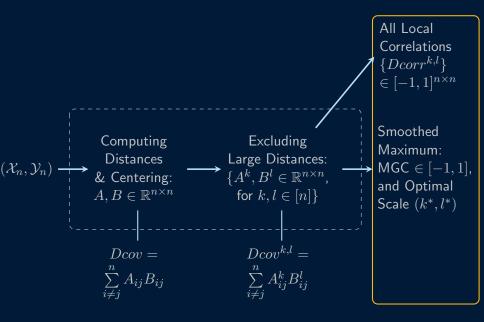


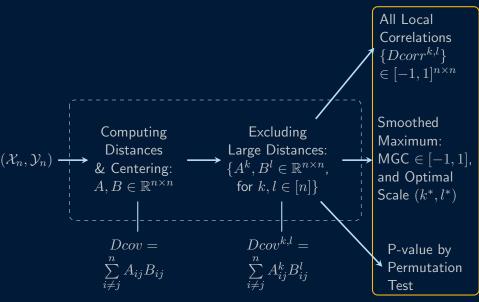












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Direct Maximum

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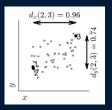
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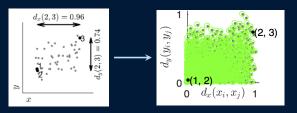
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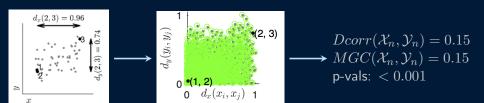
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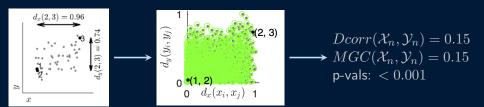
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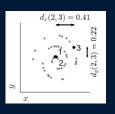
It is a critical step for both the finite-sample performance and certain theoretical properties of MGC.

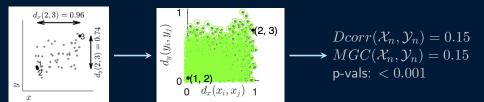


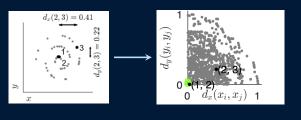


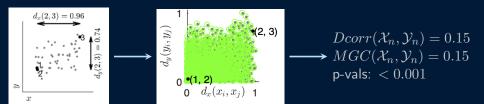














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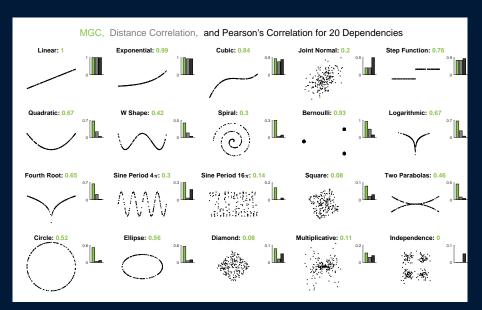
Experiments

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Visualizations of 20 Simulation Settings

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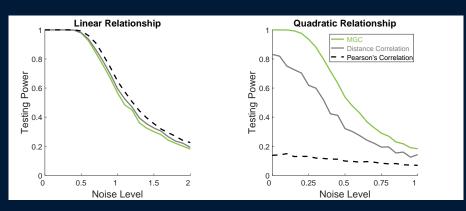
- Power is the probability of rejecting the null when the alternative is true.
- Required sample size $N_{\alpha,\beta}(c)$ to achieve a power of β at type 1 error level α using a statistic c.

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Testing Power: Linear vs Nonlinear

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

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When noise=1, p=q=1, the required sample size $N_{\alpha=0.05,\beta=0.85}(c)$:

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Next we compute the size for each simulation, and summarize by the median over close-to-linear (type 1-5) and strongly non-linear relationships (type 6-19).

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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.

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.

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Theory

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Theorem 1 (Well-behaved Correlation Measure)

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for $\rho_k, \rho_l \in [0, 1]$.

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$$Dcov^{\rho_k=1,\rho_l=1}(X,Y) = \int_{t,s} |g_{XY}(t,s) - g_X(t)g_Y(s)|^2 dw(t,s),$$

see [Shen et al.(2017b)][2].

Theorem 3 (Convergence, Mean and Variance)

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

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Theorem 5 (Optimal Scale of MGC Implies Geometry Structure)

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.

Summary

MGC builds on distance correlation, the locality principle, and taking a smoothed maximum.

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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 utilized for iterative signal subgraph extraction in [Wang et al.(2018)][4].

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