Hyeji Kim*, Weihao Gao*, Sreeram Kannan+, Sewoong Oh*, Pramod Viswanath*

University of Illinois at Urbana-Champaign*, University of Washington+

INTRODUCTION

Discovering associations in large datasets

Example: Data for 300 indicators for 200 countries

Which pairs of indicators are associated?

~ 900,000 pairs of indicators!

Associations are used to make policy decisions

Important both in industry and scientific research



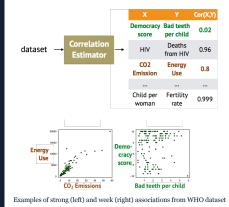
World Health Organization (WHO)

BACKGROUND

Correlation analysis to discover associations

Estimate correlation coefficients for all pairs of indicators

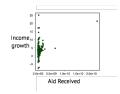
Pairs w. large corr coeff: candidates for strong association



PROBLEM STATEMENT

Motivation:

Existing correlation estimators discover average correlations but fail to discover potential correlations



Discovering potential correlations can affect policy decisions and lead to scientific findings

Goal: discover potential correlations

METHOD

1. Propose 7 axioms for a measure of potential correlation

 $0 \le \rho(X, Y) \le 1$

 $\rho(X,Y) = 0 \text{ iff } X \text{ and } Y \text{ are independent}$ $\rho(X,Y) = 1 \text{ if } Y = f(X) \text{ for } (X,Y) \in \mathcal{X}_r \times \mathcal{Y} \text{ for some } \mathcal{X}_r \subseteq \mathcal{X}$





2. Show hypercontractivity coefficient satisfies all axioms

$$s(X;Y) \equiv \sup_{U-X-Y} \frac{I(U;Y)}{I(U;X)}$$

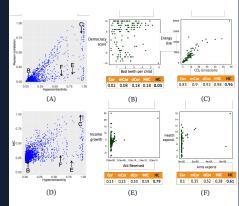
- 3. Propose a novel estimator
 - based on an alternative definition

$$\begin{split} s(X;Y) = \sup_{r(x) \neq p(x)} \frac{D_{\mathrm{KL}}(r(y) \| p(y))}{D_{\mathrm{KL}}(r(x) \| p(x))} \\ \text{where} \quad r(y) = \sum r(x) p(y|x) \end{split}$$

via joint optimization and estimation

EXPERIMENTS

1. WHO dataset



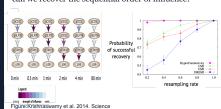
- (A): Scatter plot of Pearson correlation vs. HC
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- (B): All correlations are small
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- (E) and (F): Only HC discovers potential correlations

2. Genetic Pathway Recovery

Gene expression time series data for four genes

Biological fact:

can we recover the sequential order of influence?



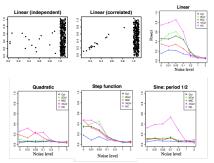
Hypercontractivity: robust measure strength of influence

EXPERIMENTS

3. Power test

Binary hypothesis testing of potential correlations

Power: true positive rate for a fixed false positive rate



HC is more powerful than others in hypothesis testing of canonical examples of potential correlations

CONCLUSION

- We postulate a set of natural axioms that we expect a measure of potential correlation to satisfy
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- 3. We provide a novel estimator for HC
- Experimental results:
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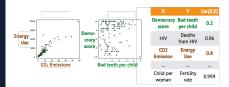
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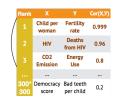
Correlation analysis to discover associations

Estimate correlation coefficients for all pairs of indicators



Rank pairs according to correlation coefficients





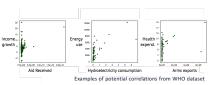
Different correlation estimators discover diff, associations



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Discover potential correlations

Our Approach:

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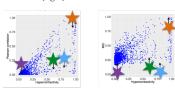
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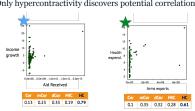
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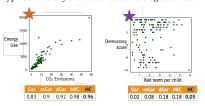
Scatter plots of Pearson correlation vs. HC (left) and MIC vs. HC (right)



Only hypercontractivity discovers potential correlations



Hypercontracitivy & others discover average correlations



2. Genetic Pathway Recovery

Gene expression time series data for four genes

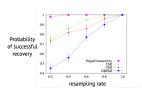


can we recover the sequential order of influence?



EXPERIMENTS

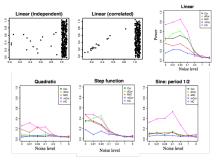
Hypercontractivity: robust measure strength of influence



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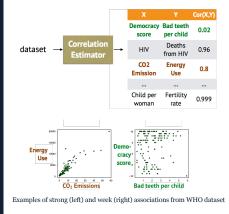
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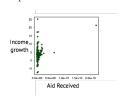


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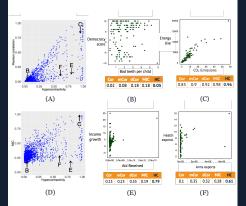
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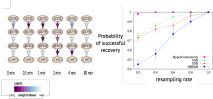
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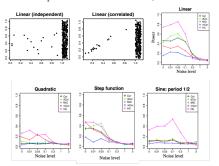
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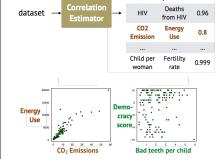
Democracy Bad teeth

ner child

CORRELATION ANALYSIS

Estimate correlation coefficients for all pairs of indicators

Correlation coefficients: measure strength of association



Different correlation estimators discover diff. associations

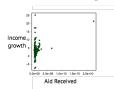
Example: Pearson correlations - linear associations

Maximal correlations - Functional associations

POTENTIAL CORRELATION

Goal

Discover potential correlation from large datasets



Problem

All correlation estimators discover average correlations

Fail to discover potential correlation

Our Approach

Provide a measure of potential correlation and estimator

(1) Propose axioms for a measure of potential correlation

$$\begin{split} 0 &\leq \rho(X,Y) \leq 1 \\ \rho(X,Y) &= 0 \text{ iff } X \text{ and } Y \text{ are independent} \\ \rho(X,Y) &= 1 \text{ if } Y = f(X) \text{ for } (X,Y) \in \mathcal{X}_r \times \mathcal{Y} \text{ for some } \mathcal{X}_r \subseteq \mathcal{X} \end{split}$$





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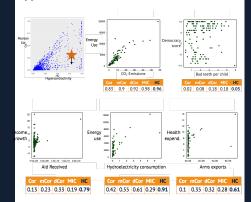
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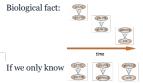
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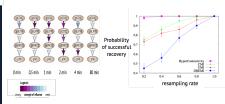
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Gene expression time series data for four genes



can we recover the sequential order of influence?

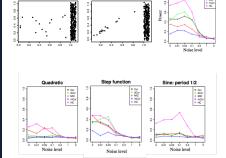


Hypercontractivity: robust measure strength of influence

EXPERIMENTS

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CONCLUSION

- 1. We postulate a set of natural axioms that we expect a measure of potential correlation to satisfy $% \left\{ 1,2,...,n\right\}$
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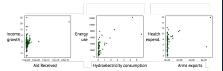
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PROBLEM STATEMENT

Motivation

Exist. correlation estimators discover average correlation Fail to discover *potential* correlation



Examples of potential correlations from WHO dataset

Discovering potential correlations between aid received vs. income growth: affect policy decisions

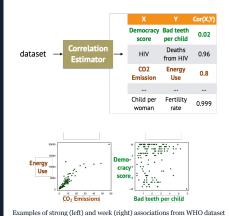
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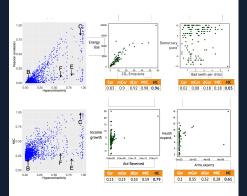
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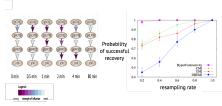
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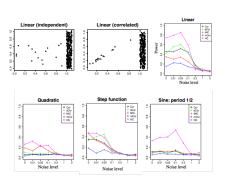
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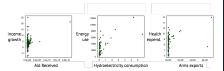
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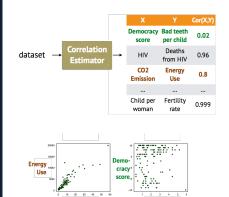
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Examples of strong (left) and week (right) associations from WHO dataset

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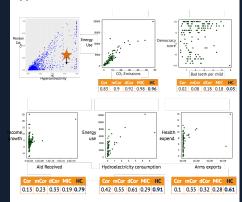
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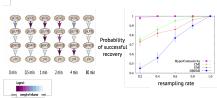
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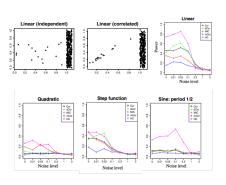
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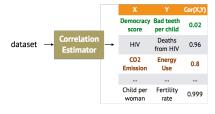
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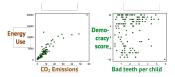
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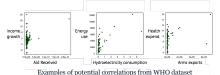


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$$\begin{split} 0 &\leq \rho(X,Y) \leq 1 \\ \rho(X,Y) &= 0 \text{ iff } X \text{ and } Y \text{ are independent} \\ \rho(X,Y) &= 1 \text{ if } Y = f(X) \text{ for } (X,Y) \in \mathcal{X}_r \times \mathcal{Y} \text{ for some } \mathcal{X}_r \subseteq \mathcal{X} \end{split}$$





2. Show hypercontractivity coefficient satisfies all axioms

$$s(X;Y) \equiv \sup_{U-X-Y} \frac{I(U;Y)}{I(U;X)}$$

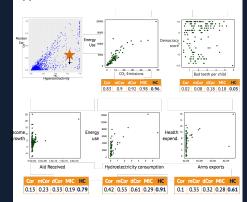
- 3. Propose a novel estimator for HC
 - based on equivalent definition of s(X;Y):

$$\begin{split} s(X;Y) = \sup_{r(x) \neq p(x)} \frac{D_{\mathrm{KL}}(r(y) || p(y))}{D_{\mathrm{KL}}(r(x) || p(x))} \\ \text{where } \ r(y) = \sum_{x} r(x) p(y|x) \end{split}$$

- joint optimization and estimation

EXPERIMENTS

(1) WHO dataset



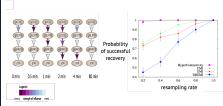
- (A) and (D): Scatter plot of correlation measures
- (B): All correlations are small
- (C): All correlations are large
- (E) and (F): Only HC discovers potential correlations

(2) Genetic Pathway Recovery

Gene expression time series data for four genes



can we recover the sequential order of influence?



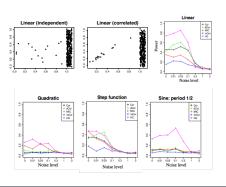
Hypercontractivity: robust measure strength of influence

EXPERIMENTS

(3) Power test

Binary hypothesis testing of potential correlation

Power: true positive rate for a fixed false positive rate



CONCLUSION

- We postulate a set of natural axioms that we expect a measure of potential correlation to satisfy
- We show that rate of information bottleneck, i.e., the hypercontractivity coefficient (HC), satisfies all the proposed axioms
- 3. We provide a novel estimator for HC
- 4. Experimental results:
 WHO datasets, genetic pathway recovery, power tests

ACKNOWLEDGEMENTS





Hyeji Kim*, Weihao Gao*, Sreeram Kannan+, Sewoong Oh*, Pramod Viswanath*

University of Illinois at Urbana-Champaign*, University of Washington+

INTRODUCTION

Discovering associations in large datasets

Example: Data for 300 indicators for 200 countries

Which pairs of indicators are associated?

~ 900,000 pairs of indicators!

Associations are used to make policy decisions

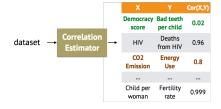
Important both in industry and scientific research

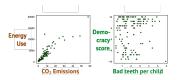
		?	~?	
	Population	Energy Use		CO ₂ Emissions
Afghanistan	26088	470		0.02
Albania	3172	761		0.98
Zambia	11696	620		0.21
Zimbabwe	13228	741		0.94

World Health Organization (WHO)

Correlation analysis to discover associations

Correlation coefficient: a measure to quantify association Estimate correlation coefficients for all pairs of indicators Pairs w. large corr coeff: candidates for strong association



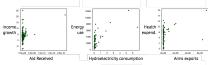


Examples of strong (left) and week (right) associations from WHO dataset

POTENTIAL CORRELATION

Goal

Discover potential correlation from large datasets



Examples of potential correlations from WHO dataset

Problem

Exist. correlation estimators discover average correlation Fail to discover *potential* correlation

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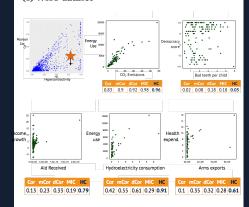
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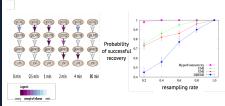
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Gene expression time series data for four genes

If we only know

can we recover the sequential order of influence?



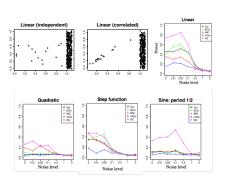
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