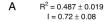
# Estimating mutual information for high-dimensional sparse relationships

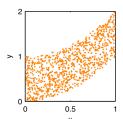
Charles Zheng

Stanford University

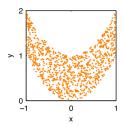
January 11, 2017

(Joint work with Yuval Benjamini.)





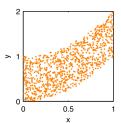
B 
$$R^2 = 0.001 \pm 0.002$$
  
I = 0.70 ± 0.09



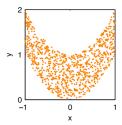
Mutual information  $I(\vec{X}; \vec{Y})$ 

• measures dependence between two random vectors,  $\vec{X}$  and  $\vec{Y}$ 

A  $R^2 = 0.487 \pm 0.019$ I = 0.72 ± 0.08

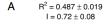


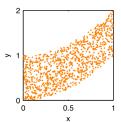
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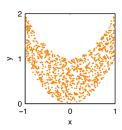
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- measures dependence between two random vectors,  $\vec{X}$  and  $\vec{Y}$
- applies to nonlinear and multidimensional relationships (unlike correlation)





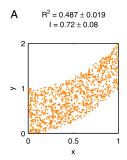
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# Mutual information $I(\vec{X}; \vec{Y})$

- measures dependence between two random vectors,  $\vec{X}$  and  $\vec{Y}$
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- is difficult to estimate in high dimensions

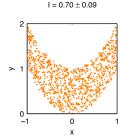
В



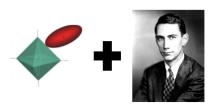
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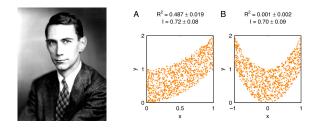
We combine machine learning (sparse estimation) with information theory to obtain better estimates of  $I(\vec{X}; \vec{Y})$ 



 $B^2 = 0.001 + 0.002$ 



# Mutual information I(X; Y)



Introduced in Shannon's 1948 paper, "A mathematical theory of communication"

Image credit Kinney et al. 2014.

# Applications of I(X; Y)

Mutual information has since been applied to many areas outside of information theory

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#### Applications [edit]

In many applications, one wants to maximize mutual information (thus

- In search engine technology, mutual information between phrases
- . In telecommunications, the channel capacity is equal to the mutua
- Discriminative training procedures for hidden Markov models have
- RNA secondary structure prediction from a multiple sequence alig
- Phylogenetic profiling prediction from pairwise present and disapp
- Mutual information has been used as a criterion for feature selectithe minimum redundancy feature selection.
- . Mutual information is used in determining the similarity of two diffe
- Mutual information of words is often used as a significance functio words; rather, one counts instances where 2 words occur adjacen another, goes up with N.
- Mutual information is used in medical imaging for image registratic reference image, this image is deformed until the mutual information
- · Detection of phase synchronization in time series analysis
- . In the infomax method for neural-net and other machine learning,

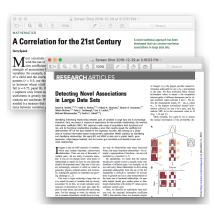
Engineering, biology, computer science, physics, medicine

# Comparing I(X; Y) with Pearson correlation



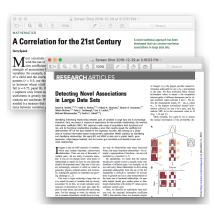
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- Only mutual information (and derived quantities) measures dependence directly

#### Problems with mutual information

- Hard to interpret (compared to  $R^2$ )
- Hard to estimate (compared to  $R^2$ )

# Can we make I(X; Y) easier to interpret?

• Define the "informational correlation" (Linfoot 1957)

$$Cor_{Info}(X, Y) = \sqrt{1 - e^{-2I(X;Y)}}$$

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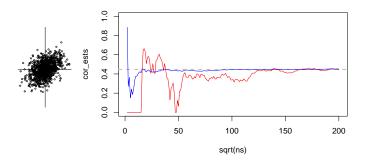
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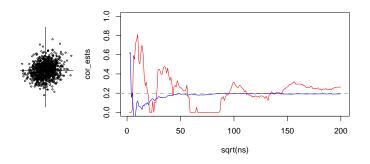
# Difficulty of estimating I(X; Y)

Example with  $Cor_{Pearson}(X, Y) = Cor_{Info}(X, Y) = 0.44$ .



# Difficulty of estimating I(X; Y)

Example with  $Cor_{Pearson}(X, Y) = Cor_{Info}(X, Y) = 0.2$ .



# How to estimate I(X; Y)

Suppose we observe pairs  $(X_i, Y_i)_{i=1}^n$  iid from density p(x, y)

• Definition of mutual information:

$$I(X;Y) = \int \log \left(\frac{p(x,y)}{p(x)p(y)}\right) p(x,y) dx dy$$

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- Kernel density estimate approaches estimate p(x, y) (Beirlant et al. 2001, Ivanov and Rozhkova 1981)
- Nearest neighbor estimators rely on distance-based computations (Mnatsakanov et al. 2008, Goria et al. 2005, Singh et. al. 2003)

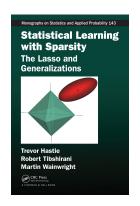
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- One approach is to assume joint multivariate normality of X, Y, but this reduces mutual information to a linear statistic.
- Other approaches: binning (Bialek et al. 1991, Paninski 2003), confusion matrix of a classifier (Treves 1997, Quiroga et al. 2009)

## First idea: Use sparsity!



- Suppose that  $Y \approx f(X) + \epsilon$ , where f depends sparsely on X.
- Can we exploit the sparsity to obtain an estimate of I(X; Y)?

# Second idea: link prediction accuracy to mutual information

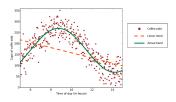
• If I(X; Y) > 0, then X carries information about Y and vice-versa.

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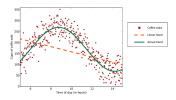
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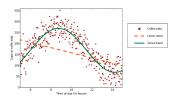
- If I(X; Y) > 0, then X carries information about Y and vice-versa.
- Therefore, we can predict Y from X (or X from Y)
- We know that often prediction accuracy implies a lower bound for mutual information (e.g. Fano 1952)



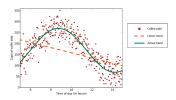
• Suppose you observe  $(\vec{X}^{(i)}, Y^{(i)})_{i=1}^n$  where  $Y^{(i)} = f(\vec{X}^{(i)}) + \epsilon$ , where f is an unknown function and  $\epsilon$  is noise. (Also, assume  $\mathbf{E}[\epsilon] = 0$ .)



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- The goal in regression is to recover the unknown function f.
- In *linear regression*, we assume *f* is linear.
- if we do not assume a particular form for f, we can use *nonparametric* regression.

# Background: Sparse regression

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# Background: Sparse regression

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- If the true function f only depends on a small number of components in  $\vec{X}$ , we can still do well if we use *sparse* regression methods.

	Classical	Sparse
Linear	Ordinary Least-Squares	Elastic net
	(Gauss 1975?)	(Zou 2008)
Nonpar.	LOWESS	Random forests
	(Cleveland 1979)	(Breiman 2001)

## Our proposal

Suppose we observe pairs  $(X_i, Y_i)_{i=1}^n$  iid from density p(x, y).

- **1** Estimate a (sparse) regression model for  $\mathbf{E}[y|x]$ .
- Assess the prediction accuracy of the model using identification risk
- ① Use the identification risk to obtain a lower bound for the mutual information I(X; Y)

# Multiple-response regression

- Pairs  $(x_i, y_i)_{i=1}^n$ , where X is p-dimensional and Y is q-dimensional.
- Data matrices  $\boldsymbol{X}_{n \times p}$ ,  $\boldsymbol{Y}_{n \times q}$ .
- For each column of Y, fit sparse model  $Y^{(i)} \approx X^T \beta^{(i)} + \epsilon$ , e.g. by using elastic net (Zou 2008),

$$\hat{\beta}^{(i)} = \mathsf{argmin}_{\beta} || \boldsymbol{X}^T \beta^{(i)} - Y^{(i)} ||^2 + \lambda_2 || \beta^{(i)} ||_2^2 + \lambda_1 || \beta^{(i)} ||_1$$

• Or, fit a random forest model for each column of Y (Breiman 2001)

# Regression vs Identification loss

- Independent test set  $(x_i^*, y_i^*)_{i=1}^k$ .
- Use model to predict  $\hat{y}_i^* = (x_i^*)^T \hat{B}$  for i = 1, ..., k.

Two ways to evaluate the predictive accuracy of the regression model:

• Regression (mean squared-error) loss:

MSE = 
$$\frac{1}{k} \sum_{i=1}^{k} ||y_i^* - \hat{y}_i^*||^2$$
.

Identification loss (Kay 2008):

$$IdLoss_k = \frac{1}{k} \sum_{i=1}^k (1 - I\{\hat{y}_i^* \text{ is nearest neighbor of } y_i^*\}).$$

[note: point out that while idloss was introduced by Kay, that we are the first to consider theory, and add slide about 1d example/robustness]

#### Identification loss and mutual information

Define the identification risk as the expected identification loss

$$IdRisk_k = \mathbf{E}[IdLoss_k]$$

• Define the Bayes risk as the identification risk given the *true* model parameters. Hence,

$$\mathsf{BayesRisk}_k \leq \mathsf{IdRisk}_k$$
.

• **Theorem.** (Z., Benjamini 2016) There exists a function  $g_k$  such that

$$I(X; Y) \ge g_k(\mathsf{BayesRisk}_k).$$

Resulting estimator:

$$\hat{I}_{IdLoss}(X;Y) = g_k(IdLoss_k).$$

### Cross-validated loss

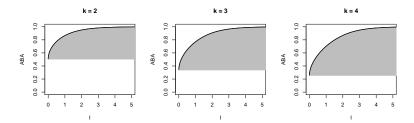
Leave-k-out cross-validation (LkoCV) can be used for both squared-error loss and identification loss.

- Start with a dataset  $(x_i, y_i)_{i=1}^N$ .
- Let n = N k. Consider all  $\binom{N}{k}$  partitions of the dataset into a test set (X, Y) and training set  $(X^*, Y^*)$ .
- For each partition, compute the loss.
- Define the LkoCV loss as the average loss over  $\binom{N}{k}$  partitions.

Computational note. One can subsample to avoid computing all  $\binom{N}{k}$  partitions. In particular, if m = N/k, then one can use m-fold cross-validation which uses m partitions that have disjoint test sets.

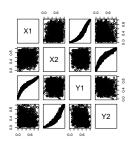
### **Functions**

Illustration of  $C_k = g_k^{-1}$ 



As information increases, the maximal identification risk goes to 0. [note: pictures need to be rotated]

### Simulation



- Generate data:  $(Y_1, Y_2) = f(X_1, X_2, \epsilon)$  where f is nonlinear.
- Add extra noise dimensions  $X_3, X_4, \ldots$
- n = 1000.
- Compare Nearest-Neighbor estimator (Mnatsakov et al, 2008, implemented in FNN) with our method using Random Forest.

### Simulation Results

True 
$$I(X; Y) = 4.615$$
.

Extra dim	NN	RF $k = 10$	RF $k = 20$
0	4.445	3.989	3.924
1	3.040	3.645	3.610
2	1.773	3.249	3.182

### Section 2

# Theory

### Functional formulation

Bayes identification risk BayesRisk<sub>k</sub>[p(x, y)] and mutual information I[p(x, y)] are both functionals of p(x, y).

$$\mathsf{BayesAcc}_k[p(x,y)] = \frac{1}{k} \int p_X(x_1) \dots p_X(x_k) \max_{i=1}^k p(y|x_i) dx_1 \dots dx_k dy.$$

$$I[p(x,y)] = \int p(x,y) \log \frac{p(x,y)}{p(x)p(y)} dxdy.$$

where  $BayesAcc_k = 1 - BayesRisk_k$ .

### Problem formulation

Take  $\iota > 0$ , and fix  $k \in \{2, 3, ...\}$ . Let p(x, y) be a joint density (where (X, Y) could be random vectors of any dimensionality.) Supposing

$$I[p(x,y)] \le \iota,$$

then can we find an upper bound,  $g_k^{-1}(\iota)$ , on BayesAcc<sub>k</sub>[p(x,y)]?

#### Proof outline

- Reduce problem to optimization over univariate densities.
- Oefine the Lagrangian functional

$$\mathcal{L}[q(x)] = -\mathsf{BayesAcc}_k[q(x)] + \lambda \int_0^1 q(x) dx + \nu \mathsf{I}[q(x)]$$

which maps the univariate density q(x) to a real number.

Compute the functional derivative of the Lagrangian

$$\nabla \mathcal{L}[q](x) = -t^{k-1} + \lambda + \nu(1 + \log q(x))$$

• Set  $\nabla \mathcal{L}[q](x) = 0$ , yielding

$$q^*(t) = \alpha e^{\beta t^{k-1}}.$$

Oheck that local minimizer is global minimizer.



#### Result

**Theorem**. For any  $\iota > 0$ , there exists  $\beta_{\iota} \geq 0$  such that defining

$$q_{eta}(t) = rac{\exp[eta t^{k-1}]}{\int_0^1 \exp[eta t^{k-1}]},$$

we have

$$\int_0^1 q_{eta_\iota}(t) \log q_{eta_\iota}(t) dt = \iota.$$

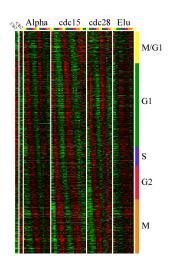
Then,

$$\sup_{I(X;Y)=\iota} \mathsf{BayesAcc}_k = \int_0^1 q_{eta_\iota}(t) t^{k-1} dt = g_k^{-1}(\iota).$$

### Section 3

# Conclusion

## Application to gene expression time series



- Data for expression levels of 6178 yeast genes during cell cycle
- Total 73 time points per gene

# Groups of genes

Group	No. genes
unknown	396
cell cycle	27
DNA replication	27
transport	19
cytoskeleton	17
chromatin structure	16

Total 145 different categories (only top 6 shown).

#### Canonical correlations between time series

Top canonical correlation (Hotelling 1936)

	CC	DR	Tr	Су	CS
CC		1	1	1	1
DR			1	0.99	0.99
Tr				0.99	0.98
Су					0.98
CS					

 $CC = cell\ cycle,\ DR = DNA\ replication,\ Tr = transport,$  $Cy = cytoskeleton,\ CS = chromatin\ structure$ 

# Sparse canonical correlations between time series

Using sparse CCA\* (Witten and Tibshirani 2009).

	CC	DR	Tr	Су	CS
CC		0.93	0.79	0.88	0.87
DR			0.76	0.76	0.91
Tr				0.65	0.68
Су					0.83
CS					

$$CC = cell\ cycle,\ DR = DNA\ replication,\ Tr = transport,$$
  
 $Cy = cytoskeleton,\ CS = chromatin\ structure$ 

<sup>\*:</sup> Default settings in R package PMA

#### Information correlations between time series

Taking the max of  $\hat{I}(X; Y)$  and  $\hat{I}(Y; X)$ .

	CC	DR	Tr	Су	CS
CC		0.92	0.79	0.97	0.81
DR			0.85	0.90	0.92
Tr				0.73	0.71
Су					0.93
CS					

 $CC = cell\ cycle,\ DR = DNA\ replication,\ Tr = transport,$  $Cy = cytoskeleton,\ CS = chromatin\ structure$ 

### Related work and future directions

to be contd

### Section 4

### The End

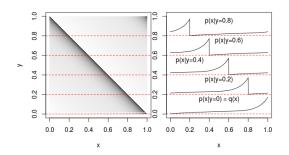
#### Reduced Problem

Rather than show the whole proof, we consider a simplified problem to illustrate the methods.



Actually, the simplified problem is equivalent to the full problem and we get the same answer (but this is non-trivial).

#### Reduced Problem



- p(x, y) on unit square with uniform marginals.
- The conditional distributions p(x|y) are just "shifted" copies of a common density, q(x), on [0,1]

$$p(x|y) = q(x - y + I\{x < y\})$$

• Furthermore, q(x) is increasing in x.

# Simplified formulae

The information and average Bayes error can be written in terms of q(x).

$$I[p(x,y)] = \int_0^1 q(x) \log q(x) dx$$

$$\mathsf{BayesAcc}_k[p(x,y)] = \int_{[0,1]^k} \max_{i=1}^k q(x_i) dx_1 \cdots dx_k$$

# Simplified formulae

Overload the notation and "redefine" information and average Bayes error as functionals of q(x).

$$I[q(x)] \stackrel{\text{def}}{=} \int_0^1 q(x) \log q(x) dx$$

$$\mathsf{BayesAcc}_k[q(x)] \stackrel{\text{def}}{=} \frac{1}{k} \int_{[0,1]^k} \max_{i=1}^k q(x_i) dx_1 \cdots dx_k$$

# Optimization problem

We now pose the question: how do we find q(x) which maximizes BayesAcc $_k[q(x)]$  subject to  $I[q(x)] \leq \iota$ ?

- Domain of the optimization: Recall that q(x) satisfies  $q(x) \ge 0$ ,  $\int_0^1 q(x) dx = 1$ , and is increasing in x. Let  $\mathcal Q$  denote the space of functions on  $[0,1] \to [0,\infty)$  which are increasing in x.
- Constraints: We have two remaining constraints,  $I[q(x)] \le \iota$  and  $\int_0^1 q(x) dx = 1$ .

Hence the problem is

 $\mathsf{maximize}_{q(x) \in \mathcal{Q}} \; \mathsf{BayesAcc}_k[q(x)] \; \mathsf{subject} \; \mathsf{to} \; \int_0^1 q(x) dx = 1 \; \mathsf{and} \; \mathsf{I}[q(x)] \leq \iota.$ 

# Optimization problem

$$\mathsf{maximize}_{q(x) \in \mathcal{Q}} \; \mathsf{BayesAcc}_k[q(x)] \; \mathsf{subject} \; \mathsf{to} \; \int_0^1 q(x) dx = 1 \; \mathsf{and} \; \mathsf{I}[q(x)] \leq \iota.$$

- Does a solution exist? Yes, because the space of measures with density q(x) satisfying  $I[q(x)] \le \iota$  is tight, and both the constraints and objective are continuous wrt to the topology of weak convergence.
- Given a solution  $q^*(x)$  exists, there exist Lagrange multipliers  $\lambda \in \mathbb{R}$  and  $\nu > 0$  such that  $q^*$  minimizes

$$egin{aligned} \mathcal{L}[q(x)] &= -\mathsf{BayesAcc}_k[q(x)] + \lambda \int_0^1 q(x) dx + 
u \mathsf{I}[q(x)] \ &= \int_0^1 (-t^{k-1} + \lambda + 
u \log q(x)) q(x) dx. \end{aligned}$$

#### Functional derivatives

- Taylor explansions are a useful trick for computing functional derivatives
- ullet We can compute the functional derivative of  $\mathcal{L}[q(x)]$  by writing

$$\begin{split} \mathcal{L}[q(x) + \epsilon \xi(x)] \\ &= \int_0^1 (-t^{k-1} + \lambda + \nu \log(q(x) + \epsilon \xi(x)))(q(x) + \epsilon \xi(x)) dx. \\ &\approx \int (q(x) + \epsilon \xi(x))(-t^{k-1} + \lambda + \nu \{\log q(x) + \frac{\epsilon \xi(x)}{q(x)}\}) dx \\ &\approx \mathcal{L}[q(x)] + \int_0^1 (-t^{k-1} + \lambda + \nu (1 + \log q(x)) \epsilon \xi(x) dx. \end{split}$$

Hence

$$\nabla \mathcal{L}[q](x) = -t^{k-1} + \lambda + \nu(1 + \log q(x))$$

# Variational magic!

Suppose we set the functional derivative to 0,

$$0 = \nabla \mathcal{L}[q](t) = -t^{k-1} + \lambda + \nu + \nu \log q(t).$$

Then we conclude that the optimal  $q^*(t)$  takes the form

$$q^*(t) = \alpha e^{\beta t^{k-1}}$$

for some  $\alpha > 0$ ,  $\beta > 0$ .

From the constraint  $\int q(t)dt = 1$ , we get

$$q_{eta}(t) = rac{e^{eta t^{k-1}}}{\int e^{eta t^{k-1}} dt}.$$

#### Result

**Theorem**. For any  $\iota > 0$ , there exists  $\beta_{\iota} \geq 0$  such that defining

$$q_{eta}(t) = rac{\exp[eta t^{k-1}]}{\int_0^1 \exp[eta t^{k-1}]},$$

we have

$$\int_0^1 q_{eta_\iota}(t) \log q_{eta_\iota}(t) dt = \iota.$$

Then,

$$\sup_{I(X;Y)=\iota} \mathsf{BayesAcc}_k = \int_0^1 q_{eta_\iota}(t) t^{k-1} dt = g_k^{-1}(\iota).$$