

Estimating mutual information for high-dimensional sparse relationships

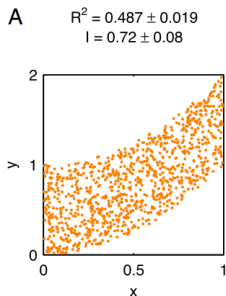
Charles Zheng

Stanford University

January 16, 2017

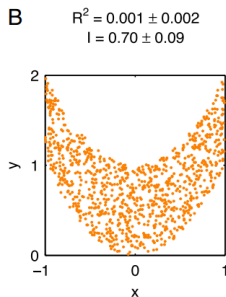
(Joint work with Yuval Benjamini, Hebrew University.)

Overview

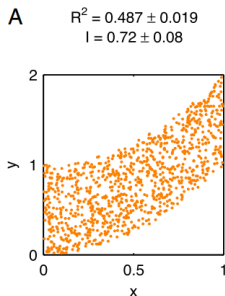


Mutual information $I(\vec{X}; \vec{Y})$

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

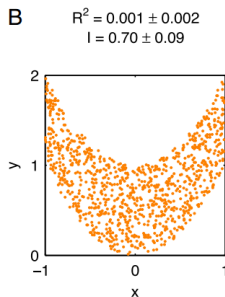


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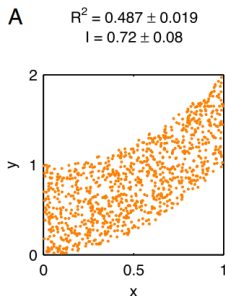


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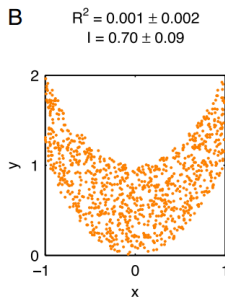


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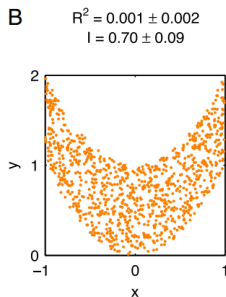
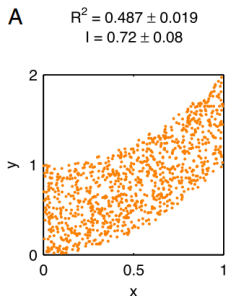


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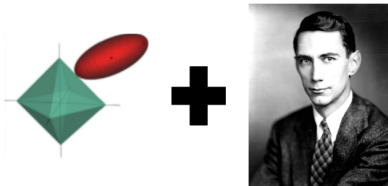
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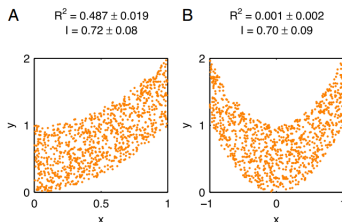
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We combine *machine learning* (sparse estimation) with *information theory* to obtain better estimates of $I(\vec{X}; \vec{Y})$



Mutual information $I(X; Y)$



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

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

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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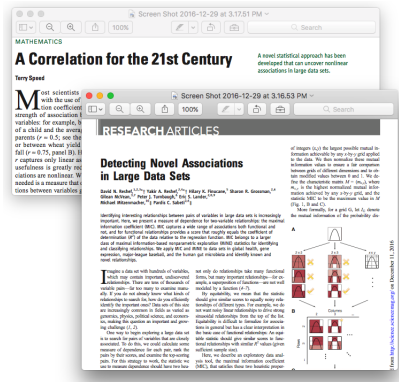
Applications [\[edit \]](#)

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 mutual information
- [Discriminative training](#) procedures for [hidden Markov models](#) have
- [RNA secondary structure](#) prediction from a [multiple sequence alignment](#)
- [Phylogenetic profiling](#) prediction from pairwise presence and absence
- Mutual information has been used as a criterion for [feature selection](#) the [minimum redundancy feature selection](#).
- Mutual information is used in determining the similarity of two documents
- Mutual information of words is often used as a significance function for word pairs; rather, one counts instances where 2 words occur adjacent to each other, goes up with N.
- Mutual information is used in [medical imaging](#) for [image registration](#); given a reference image, this image is deformed until the mutual information is maximized
- Detection of [phase synchronization](#) in [time series](#) analysis
- In the [infomax](#) method for neural-net and other machine learning,

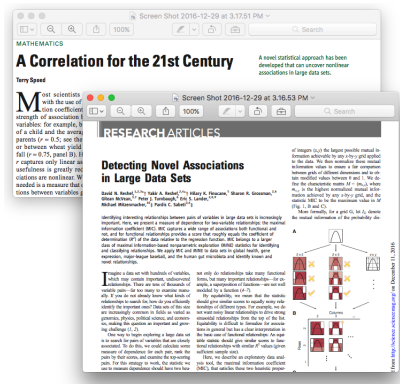
Engineering, biology, computer science, physics, medicine

Comparing $I(X; Y)$ with Pearson correlation



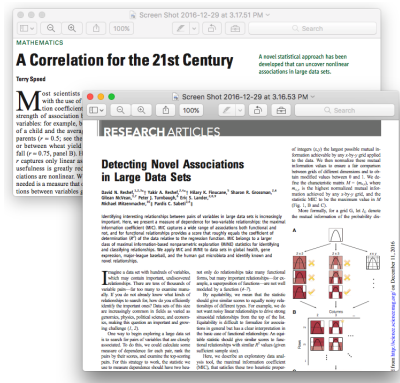
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Problems with mutual information

- 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)

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- For (X, Y) bivariate normal,

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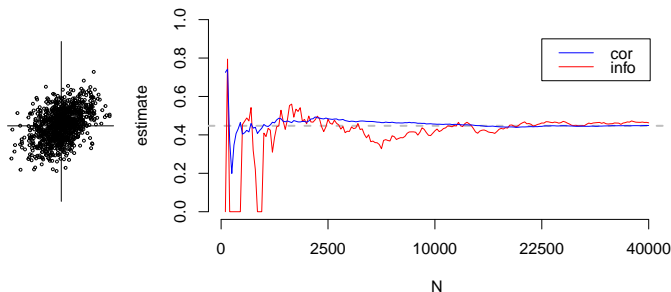
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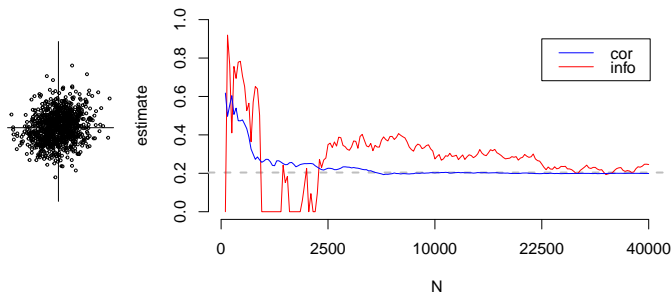
Difficulty of estimating $I(X; Y)$

Example with $\text{Cor}_{\text{Pearson}}(X, Y) = \text{Cor}_{\text{Info}}(X, Y) = 0.44$.



Difficulty of estimating $I(X; Y)$

Example with $\text{Cor}_{\text{Pearson}}(X, Y) = \text{Cor}_{\text{Info}}(X, Y) = 0.2$.



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:

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- **Plug-in estimate:**

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Problems in high dimensions

- Density estimation is known to have *exponential complexity* with respect to dimensionality.
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- Many applications with high-dimensional X, Y .
 - Gene expression time series
 - Functional magnetic resonance imaging

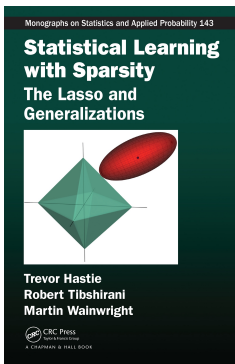
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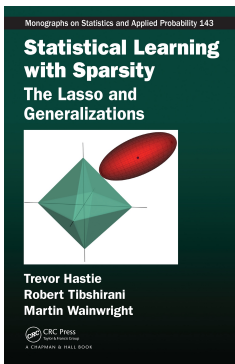
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- One approach is to assume joint multivariate normality of X, Y , but this reduces mutual information to a linear statistic.
- Other approaches: binning (Bialek et al. 1991, Paninski 2003), confusion matrix of a classifier (Treves 1997, Quiroga et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

First idea: Use sparsity!



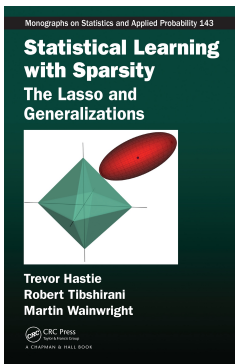
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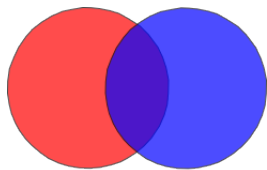
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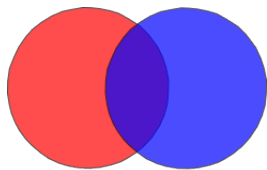
- *Sparsity* refers to existence of low-dimensional structure hidden in high-dimensional data.
- E.g. suppose X is 100-dimensional but Y is only a function of (X_5, X_9) .
- Can we exploit sparsity to obtain a good estimate of $I(X; Y)$ even under low sample sizes?

Dimension reduction vs. sparsity?

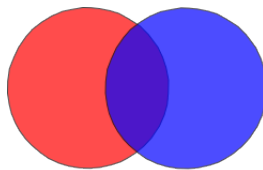


Unsupervised dimension reduction

Dimension reduction vs. sparsity?



Unsupervised dimension reduction



Sparsity = supervised dim. reduction

Second idea: link prediction accuracy to mutual information

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

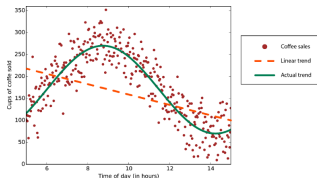
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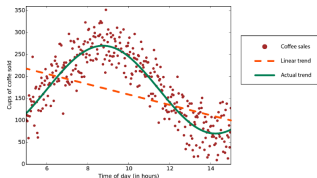
- If $I(X; Y) > 0$, then X carries information about Y and vice-versa.
- Therefore, we can *predict* Y from X (or X from Y)
- We know that often *prediction accuracy* implies a lower bound for *mutual information* (e.g. Fano 1952)

Background: Regression



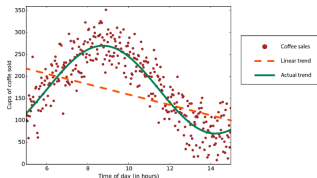
- Suppose you observe $(\vec{X}^{(i)}, Y^{(i)})_{i=1}^n$ where $Y^{(i)} = f(\vec{X}^{(i)}) + \epsilon$, where f is an unknown function and ϵ is noise. (Also, assume $\mathbf{E}[\epsilon] = 0$.)

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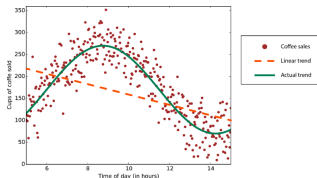
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- if we do not assume a particular form for f , we can use *nonparametric regression*.

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| | <i>Classical</i> | <i>Sparse</i> |
|----------------|---|----------------------------------|
| <i>Linear</i> | Ordinary Least-Squares (Legendre 1805) | Elastic net (Zou 2008) |
| <i>Nonpar.</i> | LOWESS (Cleveland 1979) | Random forests (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 $\mathbf{E}[y|x]$.
- 2 Assess the *prediction accuracy* of the model using *identification risk*
- 3 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 $\mathbf{X}_{n \times p}$, $\mathbf{Y}_{n \times q}$.
- For each column of Y , fit sparse model $Y^{(i)} \approx X^T \beta^{(i)} + \epsilon$, e.g. by using elastic net (Zou 2008),

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

- 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 $i = 1, \dots, k$.

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

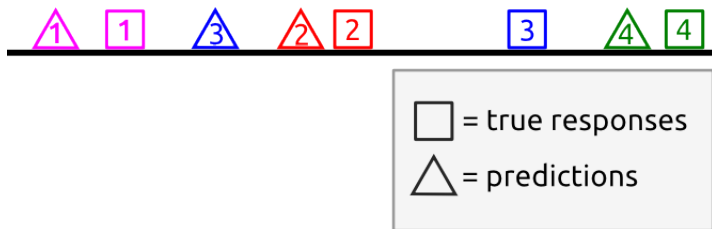
- Regression (mean squared-error) loss:

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

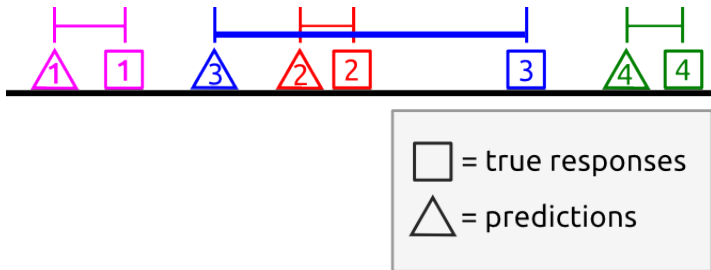
- Identification loss (Kay 2008):

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

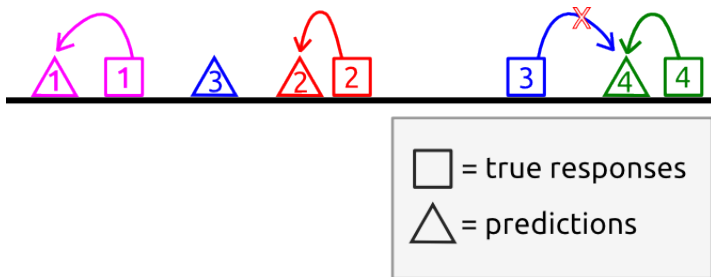
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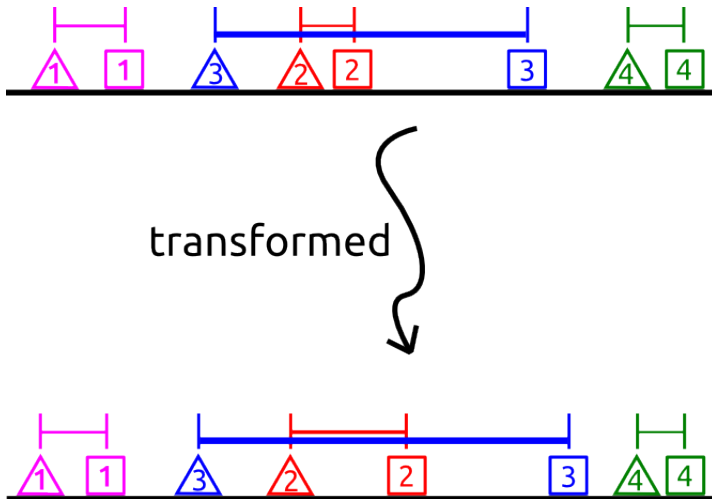
Mean-squared error



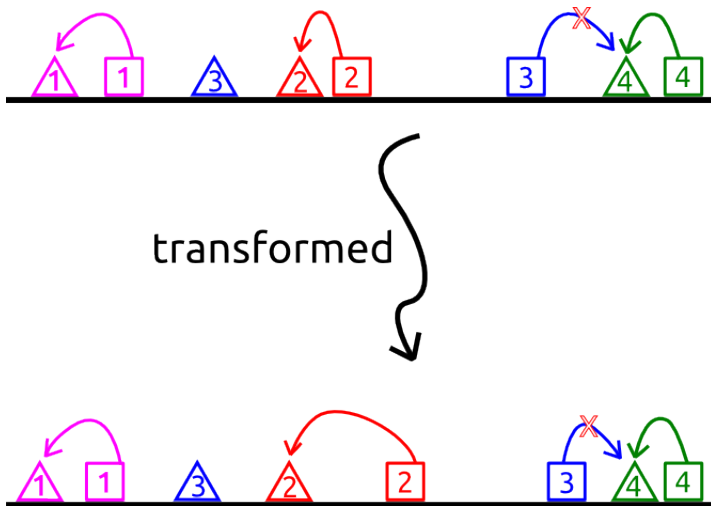
Identification loss



Mean-squared error changes under nonlinear scaling



Identification loss robust under nonlinear scaling



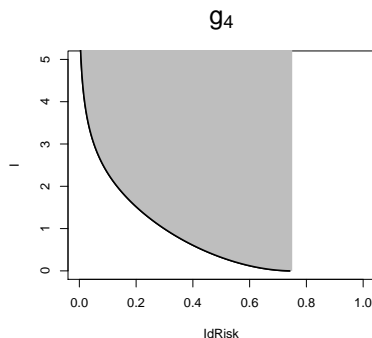
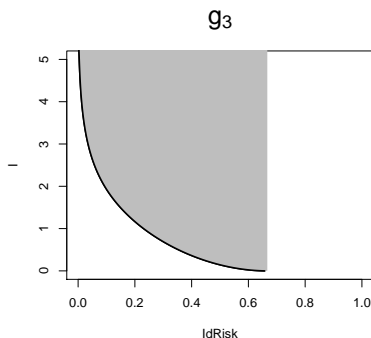
Identification loss and mutual information

- Define the identification risk as the expected identification loss

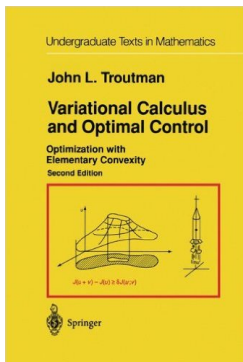
$$\text{IdRisk}_k = \mathbf{E}[\text{IdLoss}_k]$$

- Theorem.** (Z., Benjamini 2017) There exists a function g_k such that

$$I(X; Y) \geq g_k(\text{IdRisk}_k).$$



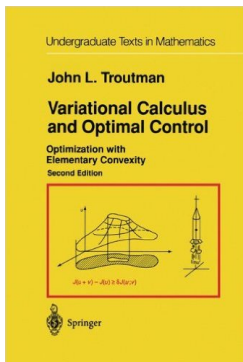
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- Mutual information is a functional of $p(x, y)$.

$$I[p(x, y)] = \mathbf{E} \left[\log \frac{p(X, Y)}{p(X)p(Y)} \right].$$



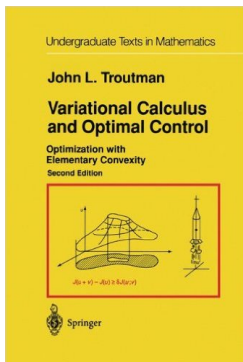
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- Identification risk is *lower-bounded* by another functional—the *Bayes risk*.

$$\text{BayesRisk}_k[p(x, y)] = 1 - \mathbf{E} \left[\max_{i=1}^k p(Y|X_i) \right].$$



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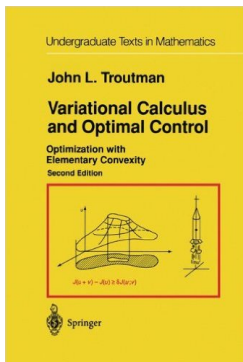
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- $g_k(u) = \inf_{p(x, y)} I[p(x, y)]$

subject to $\text{BayesRisk}_k[p(x, y)] \geq u$.



Our proposal

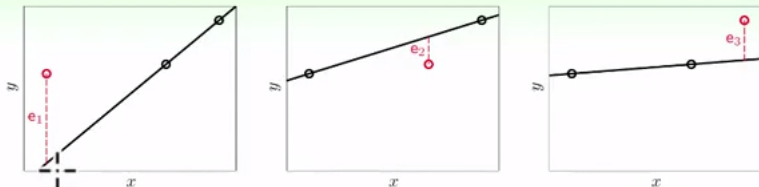
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- 1 Estimate a (sparse) regression model for $\mathbf{E}[y|x]$.
- 2 Compute *identification loss*, IdLoss_k , using *leave-k-out*.
- 3 Estimate mutual information using

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

What is leave-k-out cross-validation?

Illustration of Leave-One-Out



- Randomly hold out a subset of size k .
- Use remaining data to predict the held-out data.
- Obtain the average prediction error.

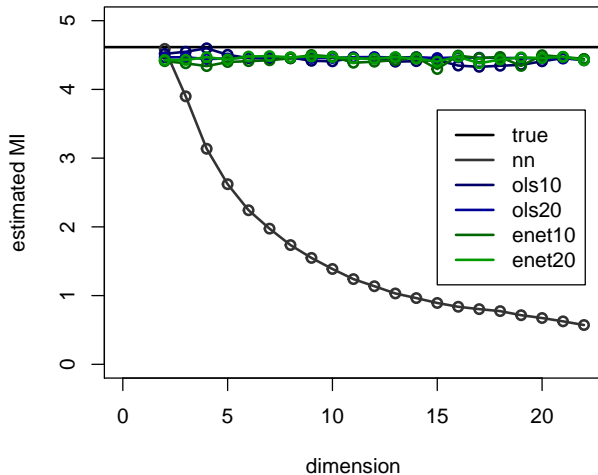
Image credit Hsuan-Tien Lin

Section 2

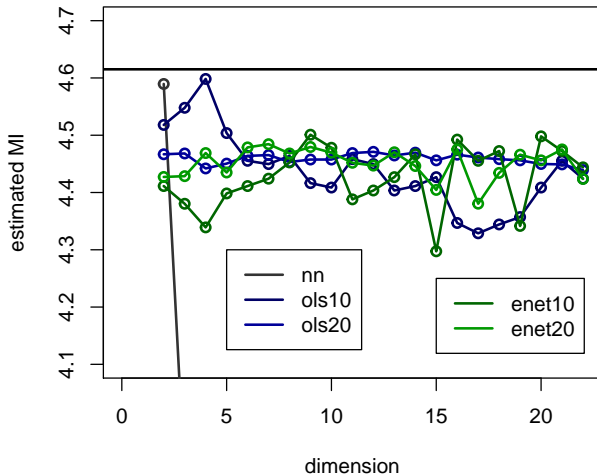
Applications

- Generate data: $(Y_1, Y_2) = (X_1, X_2)^T B + \epsilon$ where B is a randomly generated coefficient matrix.
- Add extra noise dimensions X_3, X_4, \dots
- $n = 1000$.
- Compare Nearest-Neighbor estimator (Mnatsakov et al, 2008, implemented in FNN) with our method using OLS and elastic net (sparse).

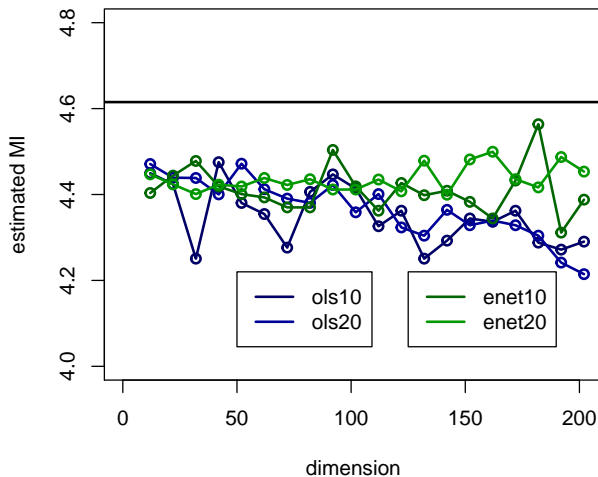
Simulation Results - I. low dimension



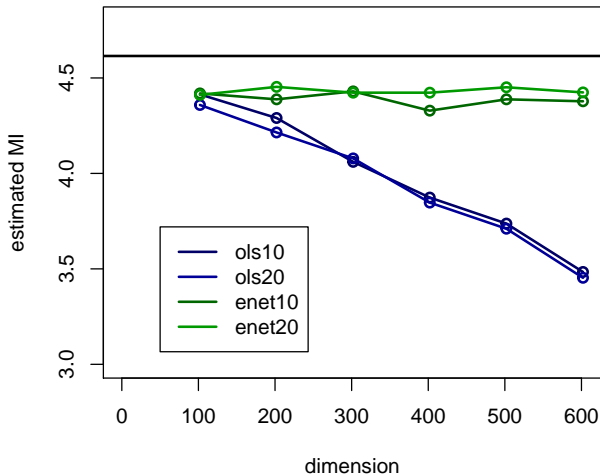
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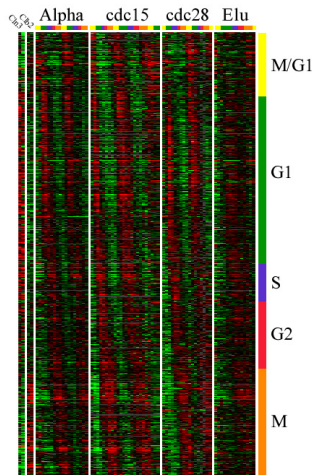
Simulation Results - II. medium dimension



Simulation Results - III. high dimension



Application to gene expression time series



- Data from Spellman et al. 1998
- 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 | Cy | CS |
|----|----|----|----|------|------|
| CC | | 1 | 1 | 1 | 1 |
| DR | | | 1 | 0.99 | 0.99 |
| Tr | | | | 0.99 | 0.98 |
| Cy | | | | | 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 | Cy | CS |
|----|----|------|------|------|------|
| CC | | 0.96 | 0.87 | 0.92 | 0.94 |
| DR | | | 0.83 | 0.88 | 0.95 |
| Tr | | | | 0.83 | 0.78 |
| Cy | | | | | 0.90 |
| CS | | | | | |

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

*: using CCApermute in R package PMA

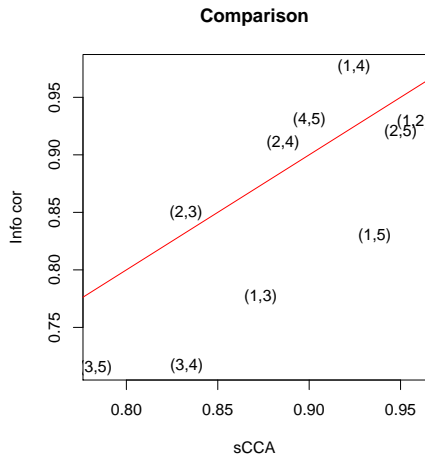
Information correlations between time series

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

| | CC | DR | Tr | Cy | CS |
|----|----|------|------|------|------|
| CC | | 0.93 | 0.78 | 0.98 | 0.83 |
| DR | | | 0.85 | 0.91 | 0.92 |
| Tr | | | | 0.72 | 0.71 |
| Cy | | | | | 0.93 |
| CS | | | | | |

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

Comparing sparse CCA and Cor_{Info}



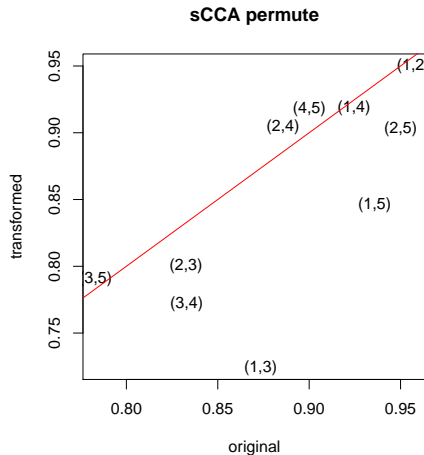
(1) cell cycle, (2) DNA replication, (3) transport,
(4) cytoskeleton, (5) chromatin structure

Invariance properties

Transform data from each group with random rotation...

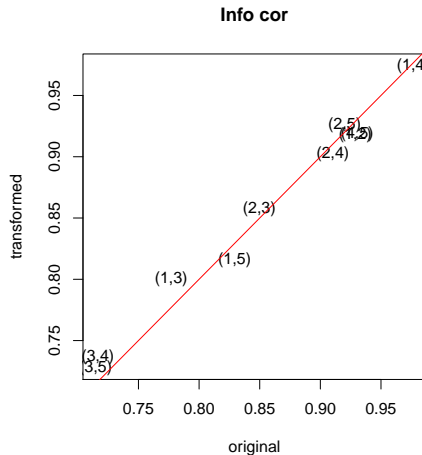
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Invariance properties

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Conclusions

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- How to use: choose a regression model suited to the model assumptions. Our method allows you to convert the prediction accuracy of the model, IdLoss_k into an estimate of $I(\vec{X}; \vec{Y})$.
- Example application: measure of joint information between two tables which is robust to transformations.

Related work and future directions

- What if data is high-dimensional, but not sparse? We have another method based on high-dimensional asymptotics (ZB 2016).

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Related work and future directions

- What if data is high-dimensional, but not sparse? We have another method based on high-dimensional asymptotics (ZB 2016).
- Estimating quantities related to mutual information, such as *transfer information*, *stimulus-specific information* and *redundancy* (Borst and Theunissen 1999)
- Inferring resting-state brain networks.

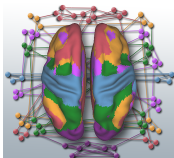


Image credit Simons Foundation

Section 3

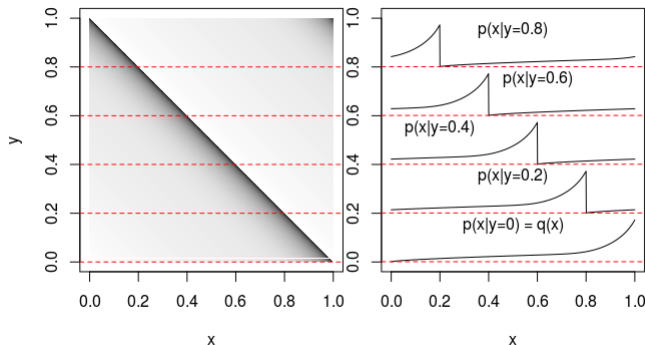
The End

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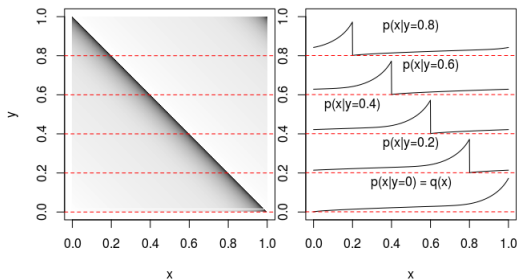
Reduced Problem

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 .

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

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

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

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

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

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

Optimization problem

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

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

Hence the problem is

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

Optimization problem

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

- Does a solution exist? Yes, because the space of measures with density $q(x)$ satisfying $I[q(x)] \leq \iota$ 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

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

Functional derivatives

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

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

- 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

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

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

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

we have

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

Then,

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