

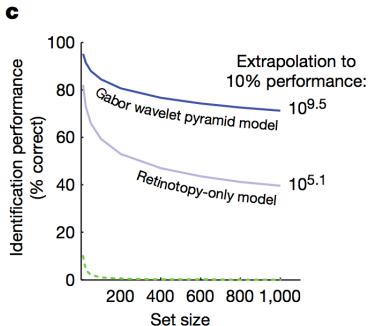
# Estimating mutual information for high-dimensional sparse relationships

Charles Zheng

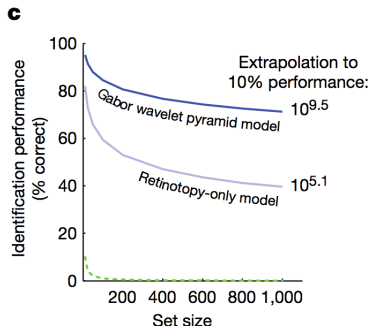
Stanford University

January 24, 2017

(Joint work with Yuval Benjamini, Hebrew University.)

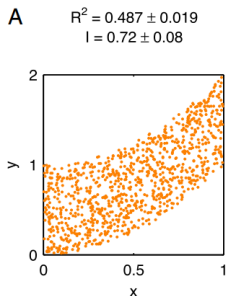


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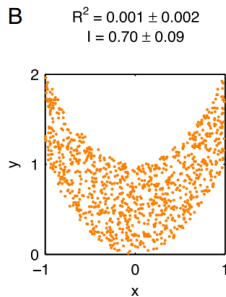
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- E.g.: Extrapolating classification accuracy curves (Z., Achanta, and Benjamini 2016)

# This talk

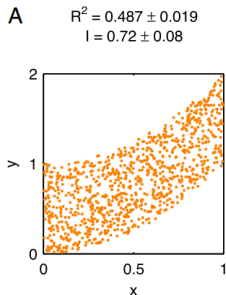


Mutual information  $I(\vec{X}; \vec{Y})$

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

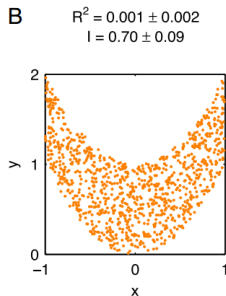


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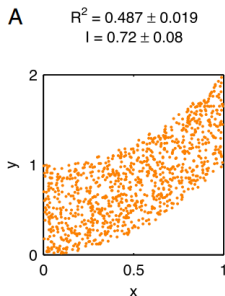


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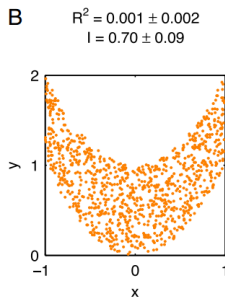


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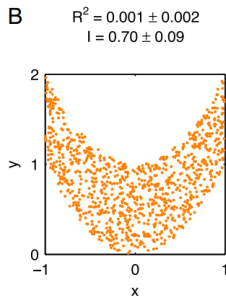
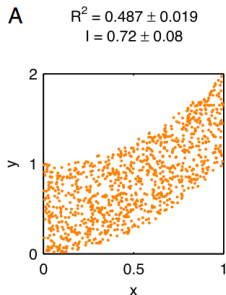


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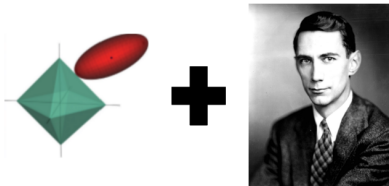
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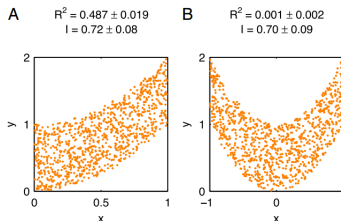
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We combine *machine learning* (sparse estimation) with *information theory* to obtain better estimates of  $I(\vec{X}; \vec{Y})$



# 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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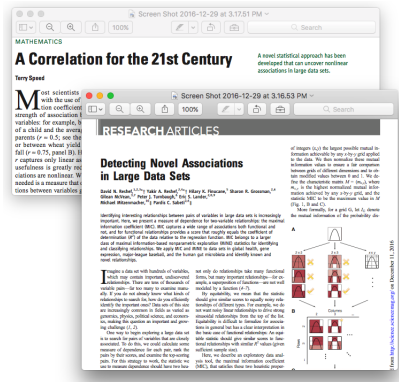
## Applications [\[ edit \]](#)

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](#) 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,

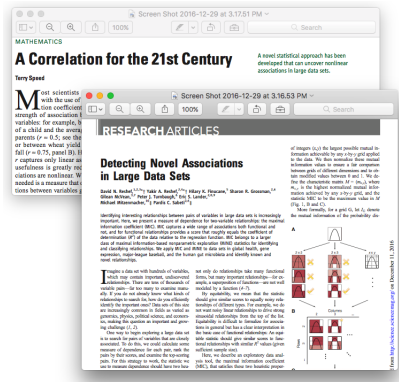
Engineering, biology, computer science, physics, medicine

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



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



- In many applications scientists are interested in *dependence*, not *correlation* (Reshef et al. 2011, Speed 2011).
- Only mutual information (and derived quantities) measures dependence directly.

# Problems with mutual information

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

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



# How to estimate $I(X; Y)$

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

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- Kernel density estimate approaches estimate  $p(x, y)$  (Beirlant et al. 2001, Ivanov and Rozhkova 1981)
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- **Plug-in estimate:**

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

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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

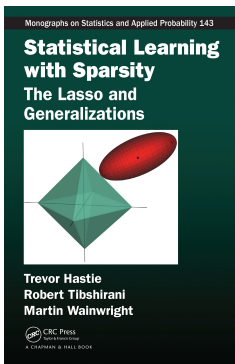
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- One approach is to assume joint multivariate normality of  $X, Y$ , but this reduces mutual information to a linear statistic.
- Other approaches: binning (Bialek et al. 1991, Paninski 2003), confusion matrix of a classifier (Treves 1997, Quiroga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

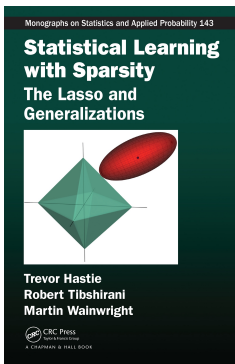
# New idea: Use sparsity!



- *Sparsity* refers to existence of low-dimensional structure hidden in high-dimensional data.

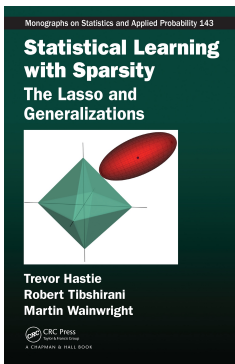


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- *Sparsity* refers to existence of low-dimensional structure hidden in high-dimensional data.
- E.g. suppose  $X$  is 100-dimensional but  $Y$  is only a function of  $(X_5, X_9)$ .
- Can we exploit sparsity to obtain a good estimate of  $I(X; Y)$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

# 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  $\mathbf{E}[\vec{Y}|\vec{X}]$ .
- 2 Assess the *prediction accuracy* of the model using *identification loss* (Kay et al. 2008)
- 3 Use the identification loss to obtain a lower bound for the mutual information  $I(X; Y)$

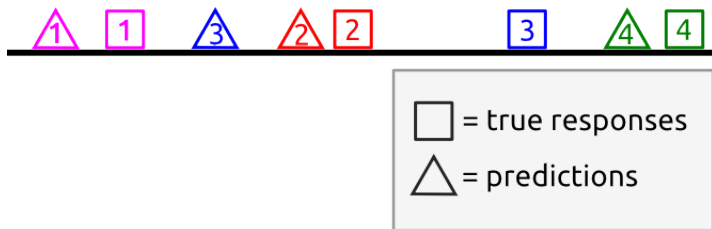
# Multiple-response regression

- 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),

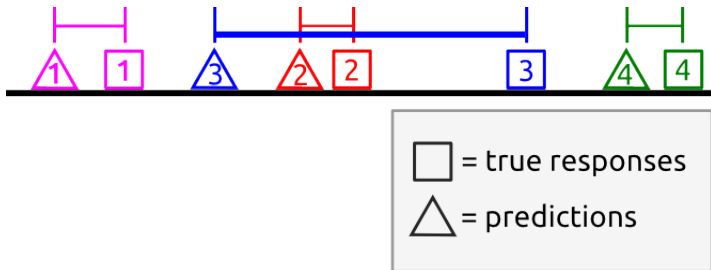
$$\hat{\beta}^{(i)} = \operatorname{argmin}_{\beta} \|\mathbf{X}^T \beta^{(i)} - Y^{(i)}\|^2 + \lambda_2 \|\beta^{(i)}\|_2^2 + \lambda_1 \|\beta^{(i)}\|_1$$

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

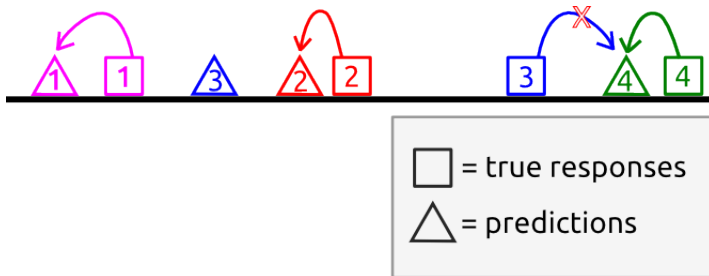
# Regression vs Identification loss



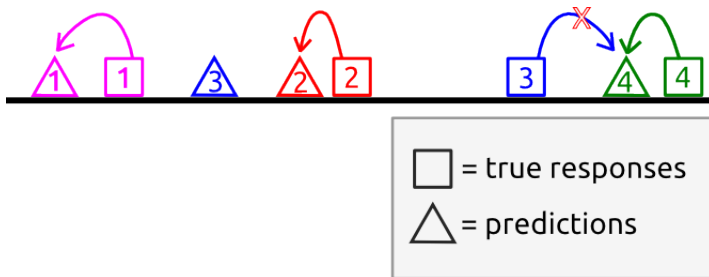
# Mean-squared error



# Identification loss



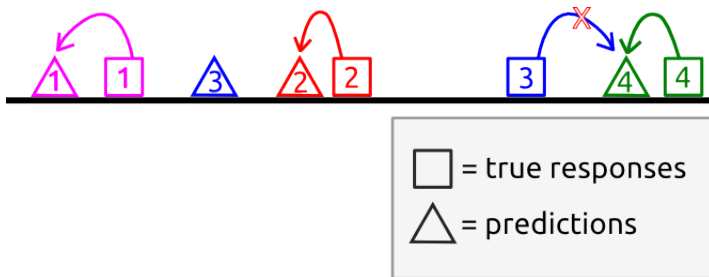
# Identification loss



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- We are the first to explore theoretical properties of the loss (e.g. connection to mutual information)

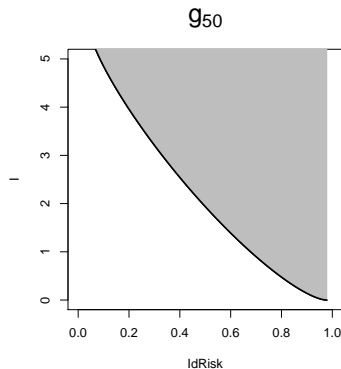
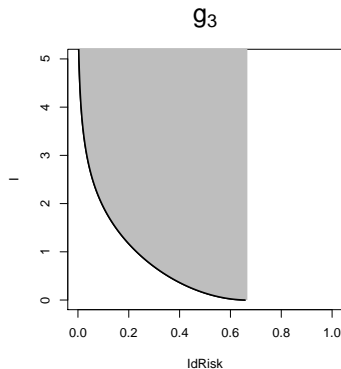
# Identification loss and mutual information

- Define the identification risk as the expected identification loss

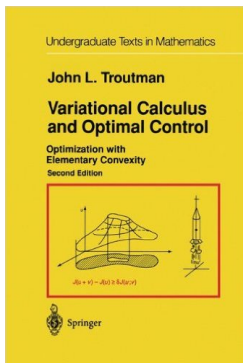
$$\text{IdRisk}_k = \mathbf{E}[\text{IdLoss}_k]$$

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

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

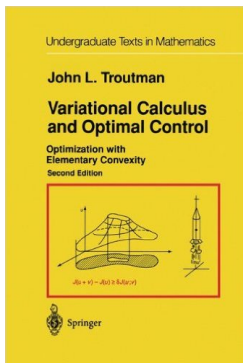


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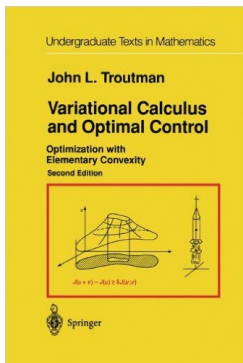


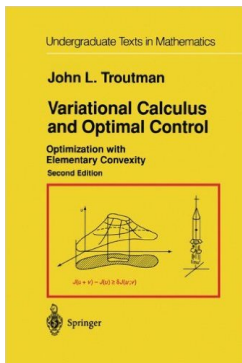
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$$I[p(x, y)] = \mathbf{E} \left[ \log \frac{p(X, Y)}{p(X)p(Y)} \right].$$

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

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





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

- $g_k(u)$  obtained by minimizing  $I[p(x, y)]$  subject to  $\text{BayesRisk}_k[p(x, y)] \leq u$ .

# Result

**Theorem.** (Z., Benjamini 2017) For any  $\iota > 0$  and  $k = 2, 3, \dots$ , 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, there exists a function  $g_k$  such that

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

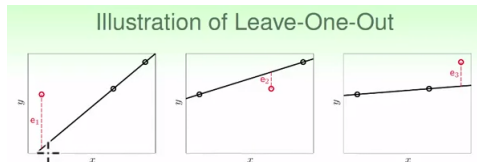
defined by

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

# 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  $\mathbf{E}[\vec{Y}|\vec{X}]$ .
- 2 Compute *identification loss*,  $\text{IdLoss}_k$ , using *leave-k-out*.



- 3 Estimate mutual information using

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

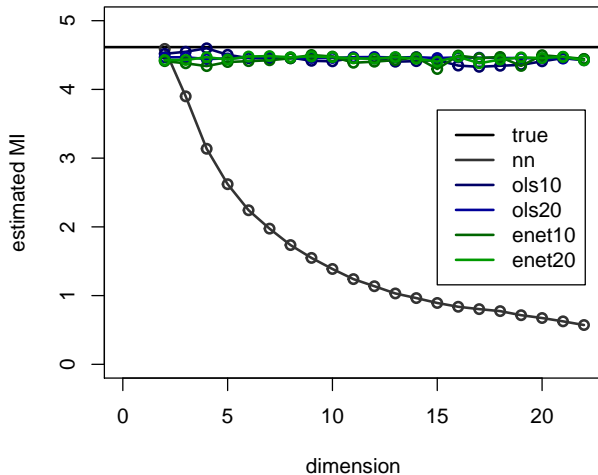


## Section 2

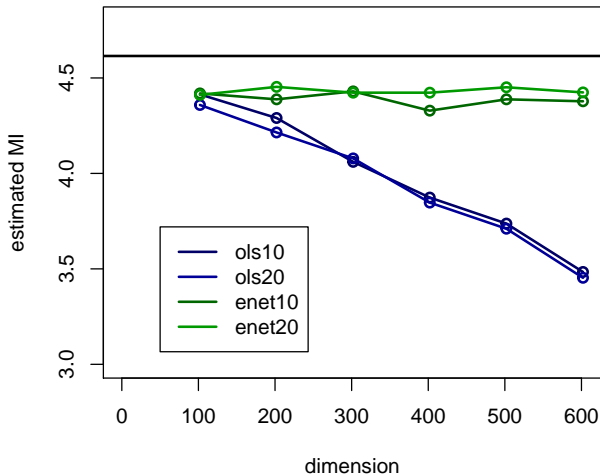
# Applications

- 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



# Simulation Results - III. high dimension



# Application to gene expression time series

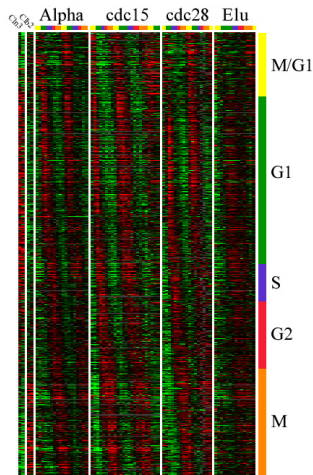
- Suppose we have *groups* of genes,  $\vec{X}^{(1)}, \dots, \vec{X}^{(m)}$ .
- Each group may consist of a different number of genes,  $p_i$ .
- Goal: estimate the mutual information

$$I(\vec{X}^{(i)}; \vec{X}^{(j)})$$

between each pair,  $i \neq j$ .

- Conclusion: find groups which are high predictive of each other—this may have biological significance.

# Application to gene expression time series



- Data from Spellman et al. 1998
- Expression levels of 6178 yeast genes during cell cycle
- Total 73 measurements 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					

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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					

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# Invariance properties

- Transform data from each group with random rotation...

$$\tilde{\mathbf{X}} = \mathbf{X}E$$

$$\tilde{\mathbf{Y}} = \mathbf{X}F$$

with  $E^T E = I$ ,  $F^T F = I$ .

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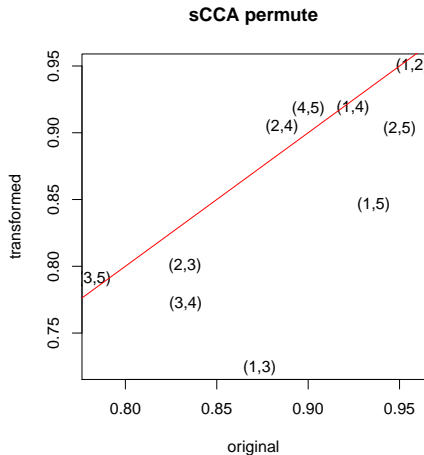
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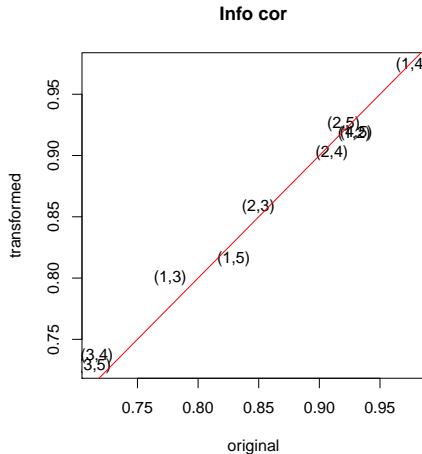
# Invariance properties

However, sparse CCA is not invariant.



# Invariance properties

Our method, on the other hand, is *robust* to rotation.



# 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,  $\text{IdLoss}_k$  into an estimate of  $I(\vec{X}; \vec{Y})$ .

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- 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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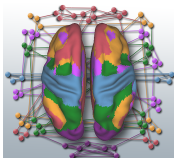


Image credit Simons Foundation

## Section 3

The End

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# Intuition behind identity

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

