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Tokyo Workshop on Statistically Sound Data Mining - February 16th 2015

Statistically Correcting for Chance using the Adjusted and Standardized Mutual Information Measures

James Bailey



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Statistically Correcting for Chance using the Adjusted and Standardized Mutual Information Measures

James Bailey

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Definition of Mutual Information

Mutual Information (MI) quantifies the *information shared* between two **categorical** random variables X and Y:

$$MI(X, Y) = \sum_{x \in \mathcal{X}} \sum_{y \in \mathcal{Y}} p_{X,Y}(x, y) \log \frac{p_{X,Y}(x, y)}{p_X(x)p_Y(y)}$$
$$= H(Y) - H(Y|X)$$

where *H* is the entropy function which quantifies *uncertainty*. MI intuitively quantifies the uncertainty of *Y* explained by X^1 .

Characteristics

- MI(X, Y) = 0 if X and Y are independent;
- MI is maximized when one variable is a deterministic function of the other. E.g. $Y = f(X) \Rightarrow MI(X, Y) = H(Y)$.

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¹In this talk we use natural logarithms.

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Extension to continuous random variables

MI can also quantify the dependency between two continuous random variables:

$$\mathsf{MI}(X,Y) = \int_{-\infty}^{+\infty} \int_{-\infty}^{+\infty} f_{X,Y}(x,y) \log \frac{f_{X,Y}(x,y)}{f_X(x)f_Y(y)}$$

Characteristics

• MI(X, Y) = 0 if X and Y are independent;

Importance of MI

MI is a compelling tool to assess the strength of the dependency between features because it is based on a *well-established theory* and quantifies *non-linear* interactions which might be missed if e.g. the Pearson's correlation coefficient r(X, Y) is used.

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Estimation of MI

Categorical variables

The estimation for the categorical case is straightforward: the empirical probability distribution for $p_{X,Y}(x, y), p_X(x)$, and $p_Y(y)$ is computed on data and plugged in the MI formula. In this case, MI is also a linear function of the *G*-statistics used in likelihood-ratio tests : $G = 2N \cdot MI$ with *N* number of records.

Continuous variables

A number of different estimators have been proposed for MI in the continuous case. The standard approach consists in *discretizing* the space of possible values for X and Y. There are also many possible approaches for discretization [Garcia et al., 2013], however the straightforward way is to discretize X and Y according to equal-width or equal-frequency binning.

Group	Туре	Citation
Discretization based	Discretization equal width Discretization equal frequency Adaptive Discretization	[Steuer et al., 2002] [Steuer et al., 2002] [Cellucci et al., 2005]
Others	Nearest Neighbour Kernel Density Estimation	[Kraskov et al., 2004] [Moon et al., 1995]

Table: List of possible estimators.

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Non-exhaustive list of other dependency measures

Information theory gave birth to some new dependency measures (also based on discretization) in the last few years:

Acronym	Name	Citation
MIC	Maximal Information Coefficient	[Reshef et al., 2011]
GMIC	Generalized Mean Information Coefficient	[Luedtke and Tran, 2013]
MID	Mutual Information Dimension	[Sugiyama and Borgwardt, 2013]

Of course the number of possible non-linear dependency measures in use is large:

Acronym	Name	Citation
dCorr RDC	Distance Correlation Randomized Dependency Coefficient	[Székely et al., 2009] [Lopez-Paz et al., 2013]
HSIC	Hilbert-Schmidt Independence Criterion	[Gretton et al., 2005]

However, information theory provides a well-established framework and it has been successfully employed for a variety of applications...

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Applications

Supervised data mining

- ▶ Feature selection [Nguyen et al., 2014b, Nguyen et al., 2014a];
- Decision tree induction [Criminisi et al., 2012].

Unsupervised data mining

- External clustering validation [Romano et al., 2014];
- Generation of alternative or multi-view clusterings [Dang and Bailey, 2015, Müller et al., 2013];
- The exploration of the clustering space using results from the Meta-Clustering algorithm [Caruana et al., 2006].

Exploratory data mining

- Analysis of neural time-series data [Cohen, 2014];
- Reverse engineering of biological networks [Villaverde et al., 2013];

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Application examples

Remark:

In the rest of the talk we focus on MI for **categorical** variables or the **discretized** version of continuous variables.

Examples:

To gain intuition about MI computation we describe in detail 2 application examples:

- 1. External clustering validation;
- 2. Decision tree induction.

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Application example (1): external clustering validation

Task: Compare a clustering solution B to a reference clustering A.

Example

N = 15 data points

reference clustering ${\bm A}$ with 2 clusters, stars $\overleftarrow{{\bm \mathcal M}}$ and circles ${\bm O}$



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Application example (1): external clustering validation

Task: Compare a clustering solution B to a reference clustering A.



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MI computed on a contingency table

MI is estimated on data via a contingency table that assess the amount of overlap between ${\bf A}$ and ${\bf B}$



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MI computation

MI between the two clusterings **A** and **B** is computed on a contingency table \mathcal{M} using the empirical probability distributions $\frac{n_{ij}}{M}, \frac{a_{ij}}{M}$, and $\frac{b_{j}}{M}$:

$$\mathsf{MI}(\mathbf{A}, \mathbf{B}) = \sum_{i=1}^{r} \sum_{j=1}^{c} \frac{n_{ij}}{N} \log \frac{n_{ij}N}{a_i b_j}$$

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	a_1	<i>n</i> ₁₁	• • •	•	• • •	n _{1c}
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Contingency table ${\mathcal M}$

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 $a_i = \sum_j n_{ij}$ are the row marginals and $b_j = \sum_i n_{ij}$ are the column marginals.

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Application example (2): decision tree induction

Task: Find the most informative feature F to the target class C.

 $\mathsf{MI}(F,C)$ is still computed on a contingency table. In this scenario MI is also known as the Information Gain: $\mathsf{IG}(F,C)=\mathsf{MI}(F,C)$

E.g. if the class C = cancer and a feature F = smoker.



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Limitations

MI is a well-established tool to compare two random variables but it is has some limitations that can be overcome by its **statistical adjustments**.

Limitation and solution

Non-intuitive range of variation

 \Rightarrow Solution: the Normalized Mutual Information (NMI) [Kvalseth, 1987]; Ensure the range of the measure is in the range [0, 1]

Non-zero baseline

 \Rightarrow Solution: the Adjusted Mutual Information (AMI) [Vinh et al., 2009]; Value of measure is expected to be zero when sampling at random features to be correlated.

Selection bias

 \Rightarrow Solution: the Standardized Mutual Information (SMI) [Romano et al., 2014]; Avoid preferring features with many bins/categories.

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Definition of the Normalized Mutual Information

Limitation of MI

MI has a non-intuitive range of variation. What does an MI of 5.6 mean ?

Solution

MI can be normalized by its maximum value in order to vary in the interval [0,1]:

$$\mathsf{NMI} = \frac{\mathsf{MI}}{\mathsf{max}\,\mathsf{MI}}$$

Many possible upper bounds for MI(A, B):

$$\min \left\{ H(\mathbf{A}), H(\mathbf{B}) \right\} \le \sqrt{H(\mathbf{A}) \cdot H(\mathbf{B})} \le \frac{1}{2} (H(\mathbf{A}) + H(\mathbf{B})) \le \max \left\{ H(\mathbf{A}), H(\mathbf{B}) \right\} \le H(\mathbf{A}, \mathbf{B})$$

Depending on the chosen upper bound, it is possible to obtain information theoretic distance measures with metric properties [Vinh et al., 2010]. A distance measure with metric properties is indeed useful for designing efficient algorithms that exploit the nice geometric properties of metric spaces [Meilă, 2012].

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Normalization of Mutual Information

In [Vinh et al., 2010] we propose a review of possible normalization choices for MI.

Name	Expression	Range	Related sources
NMI _{joint}	$\frac{MI(A,B)}{H(A,B)}$	[0,1]	[Yao, 2003]
NMI _{max}	$\frac{MI(\mathbf{A},\mathbf{B})}{\max\{H(\mathbf{A}),H(\mathbf{B})\}}$	[0,1]	[Kvalseth, 1987]
NMI _{sum}	$\frac{2MI(\mathbf{A},\mathbf{B})}{H(\mathbf{A})+H(\mathbf{B})}$	[0,1]	[Kvalseth, 1987]
NMI _{sqrt}	$\frac{\dot{M}(\mathbf{A}, \dot{\mathbf{B}})}{\sqrt{H(\mathbf{A})H(\mathbf{B})}}$	[0,1]	[Strehl and Ghosh, 2002]
NMI _{min}	$\frac{MI(\mathbf{A},\mathbf{B})}{\min\{H(\mathbf{A}),H(\mathbf{B})\}}$	[0,1]	

Table: Normalization of Mutual Information.

Table: Distance measures based on MI.

Name	Expression	Range	Metric	Related sources
D _{joint} (VI) (Variation of Information)	$H(\mathbf{A},\mathbf{B})-MI(\mathbf{A},\mathbf{B})$	[0,log N]	\checkmark	[Yao, 2003] [Meilă, 2005]
D _{max}	$\max{H(\mathbf{A}), H(\mathbf{B})} - MI(\mathbf{A}, \mathbf{B})$	[0,log N]	\checkmark	
$D_{sum} (\equiv \frac{1}{2} D_{joint})$	$\frac{1}{2}[H(\mathbf{A}) + H(\mathbf{B})] - MI(\mathbf{A}, \mathbf{B})$	[0,log N]	\checkmark	
D _{sqrt}	$\sqrt[n]{H(\mathbf{A})H(\mathbf{B})} - MI(\mathbf{A}, \mathbf{B})$	[0,log N]	×	
D _{min}	$\min\{H(\mathbf{A}), H(\mathbf{B})\} - MI(\mathbf{A}, \mathbf{B})$	[0,log N]	X	

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Successful applications and limitations

NMI has been shown to be successful in:

- Clustering comparisons scenarios [Strehl and Ghosh, 2003, Wu et al., 2009];
- Decision tree induction [Quinlan, 1993];
- ▶ Feature selection [Estévez et al., 2009].

However NMI has some limitations

NMI does not have constant 0 baseline value for independent variables A and B.

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Limitation on case study: external clustering validation

Task: Compare a clustering solution B to reference clustering A.

Experiment

N = 500 data points

A with 10 clusters



Figure: If the clustering solution **B** is generated independently from **A** at random with *c* clusters the average value of MI and NMI increases at the increase of the number of clusters.

Needs of statistical correction for MI

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Little affect of other approaches:

A correction for MI has already been proposed a while ago [Miller, 1955]:

MI (Miller correction) = MI -
$$\frac{(r-1)(c-1)}{2N}$$

with r,c number of bins and N number of records. However it seems not effective in the general case:



Figure: Clustering solutions B generated independently from A. Miller correction is not effective.

To address this issue we propose to statistically adjust MI for chance

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The Adjusted Mutual Information

Limitation of NMI

MI and NMI have non-zero baseline.

Solution

Statistically adjust MI by the subtraction of its expected value under the null hypothesis of independence. The **Adjusted Mutual Information** (AMI) is defined as [Vinh et al., 2009]:

$$AMI = \frac{MI - E[MI]}{\max MI - E[MI]}$$

The resulting measure is statistically normalized: it is equal to 0 when MI is equal to the *expected value obtained by chance*.

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Adjustment for chance

We compute the **expected value** of MI under the **null hypothesis** of independent clusterings A and B.

we make use of the **permutation model** to compute it analytically: the distribution of MI is computed using all possible contingency tables \mathcal{M} obtained by permutations.

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Expected Value

E[MI] is obtained by summation over all possible contingency tables $\mathcal M$ obtained by permutations.

$$E[\mathsf{MI}] = \sum_{\mathcal{M}} \mathsf{MI}(\mathcal{M}) P(\mathcal{M}) = \sum_{\mathcal{M}} \sum_{i,j} \frac{n_{ij}}{N} \log \frac{n_{ij}N}{a_i b_j} P(\mathcal{M})$$

- No method to exhaustively generate M
- extremely time expensive (permutations O(n!))

However, it is possible to swap the inner summation with the outer summation:

$$E[\mathsf{MI}] = \underbrace{\sum_{\mathcal{M}} \sum_{i,j} n_{ij}}_{\text{to swap}} \frac{n_{ij}}{N} \log \frac{n_{ij}N}{a_i b_j} P(\mathcal{M}) = \underbrace{\sum_{i,j} \sum_{n_{ij}} n_{ij}}_{\text{swapped}} \frac{n_{ij}N}{N} \log \frac{n_{ij}N}{a_i b_j} P(n_{ij})$$

- n_{ij} has a known hypergeometric distribution,
- Computation time dramatically reduced!

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According to the different upper bound to MI used we obtain different versions of the Adjusted Mutual Information (AMI):

Name	Expression	Range
AMI _{max}	$\frac{MI(\mathbf{A},\mathbf{B})\!-\!E[MI(\mathbf{A},\mathbf{B})]}{\max{\{\mathcal{H}(\mathbf{A}),\mathcal{H}(\mathbf{B})\}}\!-\!E[MI(\mathbf{A},\mathbf{B})]}$	$[0, 1]^*$
AMI _{sum}	$\frac{MI(\mathbf{A},\mathbf{B})\!-\!E[MI(\mathbf{A},\mathbf{B})]}{\frac{1}{2}(H(\mathbf{A})\!+\!H(\mathbf{B}))\!-\!E[MI(\mathbf{A},\mathbf{B})]}$	$[0, 1]^*$
AMI _{sqrt}	$\frac{MI(\mathbf{A},\mathbf{B})\!-\!E[MI(\mathbf{A},\mathbf{B})]}{\sqrt{\mathcal{H}(\mathbf{A})\!\cdot\!\mathcal{H}(\mathbf{B})\!-\!E[MI(\mathbf{A},\mathbf{B})]}}$	$[0, 1]^*$
AMI _{min}	$\frac{MI(\textbf{A},\textbf{B})\!-\!\textit{E}[MI(\textbf{A},\textbf{B})]}{\min\left\{\textit{H}(\textbf{A}),\!\textit{H}(\textbf{B})\right\}\!-\!\textit{E}[MI(\textbf{A},\textbf{B})]}$	$[0, 1]^*$

Table: Adjusted Mutual Information [Vinh et al., 2010].

* These measures are normalized in a statistical sense.

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Speed considerations

The computational complexity of NMI depends just on the number of clusters:

 $\mathcal{O}(\mathbf{rc})$

The computational complexity of AMI is linear in the number of records N:

 $\mathcal{O}(\max{rN, cN})$

However

Useful when the number of data points is small because

$$\lim_{N\to+\infty} E[\mathsf{MI}] = 0$$

Somebody has recently parallelized it [Schmidt et al., 2014].

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Successful application

Task: Compare a clustering solution B to reference clustering A.

Experiment

N = 500 data points **A** with 10 clusters



Figure: AMI obtains 0 baseline when clusterings B are generated at random.

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Successful applications and limitations

AMI is becoming a popular tool to compare clusterings.



Figure: AMI is a polar tool for clustering comparisons.

However even AMI has some limitations:

AMI is affected by selection bias.

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Task: Select the most similar clustering solution B to a reference clustering A.

Experiment

N = 500 data points **A** with 10 clusters

Each B is generated independently from A:

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Task: Select the most similar clustering solution B to a reference clustering A.

Experiment

- N = 500 data points
- A with 10 clusters

Each B is generated independently from A:

• One clustering solution **B** on c = 2 clusters

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Task: Select the most similar clustering solution B to a reference clustering A.

Experiment

- N = 500 data points
- A with 10 clusters

Each B is generated independently from A:

- One clustering solution **B** on c = 2 clusters
- One clustering solution **B** on c = 6 clusters

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Task: Select the most similar clustering solution B to a reference clustering A.

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A with 10 clusters

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- One clustering solution **B** on c = 6 clusters
- One clustering solution **B** on c = 10 clusters

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A with 10 clusters

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- One clustering solution B on c = 2 clusters
- One clustering solution **B** on c = 6 clusters
- One clustering solution **B** on c = 10 clusters
- One clustering solution **B** on c = 14 clusters

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A with 10 clusters

Each B is generated independently from A:

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- One clustering solution **B** on c = 6 clusters
- One clustering solution B on c = 10 clusters
- One clustering solution **B** on c = 14 clusters
- One clustering solution **B** on c = 18 clusters

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Experiment

N = 500 data points

A with 10 clusters

Each B is generated independently from A:

- One clustering solution B on c = 2 clusters
- One clustering solution **B** on c = 6 clusters
- One clustering solution **B** on c = 10 clusters
- One clustering solution **B** on c = 14 clusters
- One clustering solution **B** on c = 18 clusters
- One clustering solution **B** on c = 22 clusters

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Task: Select the most similar clustering solution B to a reference clustering A.

Experiment

- N = 500 data points
- A with 10 clusters

Each B is generated independently from A:

- One clustering solution B on c = 2 clusters
- One clustering solution **B** on c = 6 clusters
- One clustering solution B on c = 10 clusters
- One clustering solution **B** on c = 14 clusters
- One clustering solution **B** on c = 18 clusters
- One clustering solution **B** on c = 22 clusters

Select the **B** that yields the maximum MI(**A**, **B**)

Give a **win** to the solution that gets the highest value

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Task: Select the most similar clustering solution B to a reference clustering A.

Experiment

N = 500 data points

A with 10 clusters

Each B is generated independently from A:

- One clustering solution B on c = 2 clusters
- One clustering solution **B** on c = 6 clusters
- One clustering solution B on c = 10 clusters
- One clustering solution **B** on c = 14 clusters
- One clustering solution **B** on c = 18 clusters
- One clustering solution B on c = 22 clusters

Select the **B** that yields the maximum MI(**A**, **B**)

Give a **win** to the solution that gets the highest value

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Selection Bias

MI unfairly selects more often the solution with c = 22 clusters.



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Also AMI is affected by selection bias

$$\mathsf{AMI} = \frac{\mathsf{MI} - \mathsf{E}[\mathsf{MI}]}{\sqrt{H(\mathbf{A}) \cdot H(\mathbf{B})} - \mathsf{E}[\mathsf{MI}]}$$



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Also AMI is affected by selection bias

$$\mathsf{AMI} = \frac{\mathsf{MI} - \mathsf{E}[\mathsf{MI}]}{\sqrt{H(\mathbf{A}) \cdot H(\mathbf{B})} - \mathsf{E}[\mathsf{MI}]}$$



We have to take into account full distributional properties of MI: we proceed by subtracting its **expected value** and dividing by its **standard deviation**:

we propose to statistically standardize MI

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Non-standardized variance

Limitation of AMI

MI, NMI, and AMI are affected by selection bias.

Solution

This behaviour is due to the non-standardized variance of $\mathsf{AMI} \Rightarrow \mathsf{need}$ of standardization.



Figure: AMI values have bigger variation when the number of clusters c for **B** is high.

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Definition of Standardized Mutual Information

The Standardized Mutual Information (SMI) is defined as [Romano et al., 2014]:

$$SMI = rac{MI - E[MI]}{\sqrt{Var(MI)}}$$

where we compute the **expected value** and the **variance** of Mutual Information under the **null hypothesis** of independent clusterings **A** and **B**.

The SMI value is the number of standard deviations the mutual information is away from the expected value.

As in [Vinh et al., 2009] we make use of the **permutation model** to compute the expected value and the variance:

 \Rightarrow The distribution of MI is computed using all possible contingency tables ${\cal M}$ obtained by permutations.

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Variance Computation

We have to compute MI's second moment:

$$\begin{split} E[\mathsf{MI}^2] &= \sum_{\mathcal{M}} \mathsf{MI}(\mathcal{M})^2 P(\mathcal{M}) = \sum_{\mathcal{M}} \left(\sum_{i=1}^r \sum_{j=1}^c \frac{n_{ij}}{N} \log \frac{n_{ij}N}{a_i b_j} \right)^2 P(\mathcal{M}) \\ &= \sum_{\mathcal{M}} \sum_{\substack{i,j,i',j' \\ \text{to swap}}} \frac{n_{ij}}{N} \log \frac{n_{ij}N}{a_i b_j} \cdot \frac{n_{i'j'}}{N} \log \frac{n_{i'j'}N}{a_{i'} b_{j'}} P(\mathcal{M}) \\ &= \sum_{\substack{i,j,i',j' \\ \text{swapped}}} \sum_{\substack{n_{ij} \\ n_{i'j'} \\ \text{swapped}}} \frac{n_{ij}}{N} \log \frac{n_{ij}N}{a_i b_j} \cdot \frac{n_{i'j'}}{N} \log \frac{n_{i'j'}N}{a_{i'} b_{j'}} P(n_{ij}, n_{i'j'}) \end{split}$$

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Variance Computation

We have to compute MI's second moment:

$$E[\mathsf{MI}^{2}] = \sum_{\mathcal{M}} \mathsf{MI}(\mathcal{M})^{2} P(\mathcal{M}) = \sum_{\mathcal{M}} \left(\sum_{i=1}^{r} \sum_{j=1}^{c} \frac{n_{ij}}{N} \log \frac{n_{ij}N}{a_{i}b_{j}} \right)^{2} P(\mathcal{M})$$
$$= \underbrace{\sum_{\mathcal{M}} \sum_{i,j,i',j'} \frac{n_{ij}}{N} \log \frac{n_{ij}N}{a_{i}b_{j}} \cdot \frac{n_{i'j'}}{N} \log \frac{n_{i'j'}N}{a_{i'}b_{j'}} P(\mathcal{M})}_{\text{to swap}}$$
$$= \underbrace{\sum_{i,j,i',j'} \sum_{n_{ij}} \sum_{n_{i'j'}} \frac{n_{ij}}{N} \log \frac{n_{ij}N}{a_{i}b_{j}} \cdot \frac{n_{i'j'}}{N} \log \frac{n_{i'j'}N}{a_{i'}b_{j'}} P(n_{ij}, n_{i'j'})}_{\text{swapped}}$$

Contribution: $P(n_{ij}, n_{i'j'})$ computation is **technically challenging**. We use the hypergeometric model: drawings from a urn with *N* marbles with 3 colors, red, blue, and white.

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Characteristics of standardized measures					

Bias Towards More Clusters Correction

MI and AMI unfairly select more often the solution with c = 22 clusters:



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Bias Towards Fewer Data Points Correction

Reference clustering **A** on N = 100 data points with 4 clusters

B induced independently on N = 20, 40, 60, 80, 100 data points with 4 clusters.



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Characteristics of standardized measures						

Unification property

The ability to compute a variance term allows extension of the existing measures:

- Variation of Information
- G-statistic

Definitions:

$$SVI = \frac{E[VI] - VI}{\sqrt{Var(VI)}}, SG = \frac{G - E[G]}{\sqrt{Var(G)}}$$

Theorem: The standardization unifies information theoretic measures:

$$SMI = SVI = SG$$

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Speed considerations

The computational complexity of SMI is dominated by the computational complexity of $E[MI^2]$:

```
\mathcal{O}\left(\max\left\{rcN^{3},c^{2}N^{3}\right\}\right)
```

However

- Useful when the number of data points is small;
- Faster than using the full distribution (compared to the p-value for the Fisher's exact test);
- Easily parallelizable.

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	100	150	200	250	300	350
SMI	0.65	1.53	2.94	5.00	7.59	11.00
SMI (4 cores)	0.30	0.51	0.97	1.52	2.33	3.35
Fisher's	0.65	11.32	242.67	844.62	N/A	N/A

Time in seconds for 4×4 tables with N records

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Summary

We discussed some enhancements to mutual information obtained by *statistical* correction for chance.

Limitation and solution

Non-intuitive range of variation

 \Rightarrow Solution: the Normalized Mutual Information (NMI) [Kvalseth, 1987];

Non-zero baseline

 \Rightarrow Solution: the Adjusted Mutual Information (AMI) [Vinh et al., 2009];

Selection bias

 \Rightarrow Solution: the Standardized Mutual Information (SMI) [Romano et al., 2014];

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Take Away Message

Each variant is useful in some specific scenarios and there is a trade-off in computational complexity:



Table: Complexity when comparing two clusterings A and B with r and c clusters on N records.

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Open issues

There is a number of open issues for SMI:

▶ SMI achieves strength toward selection bias at the loss of normalization in the range [0,1]

 \Rightarrow need of statistical adjustment which allows normalization;

- SMI computational complexity might be problematic ⇒ at the large number of records N, G-statistic (G = 2N · MI) can be approximated with a χ² distribution. Need to find the scenarios where an exact SMI can be substituted by an approximation;
- SMI counts the number of standard deviations of MI, it might act as an exact p-value for MI. p-values quantifies the statistical significance of MI and this might sometimes interfere with the effect size of MI.

E.g. SMI=25.4 (25.4 standard deviations away from mean). Is this closer to an *effect size* or an assessment of *statistical significance* ? \Rightarrow need of trade-offs between importance of statistical significance and effect size.

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Thank you.

Questions?

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Code available online: https://sites.google.com/site/icml2014smi/

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