A MEASURE OF DEPENDENCE BETWEEN DISCRETE AND CONTINUOUS VARIABLES

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Abstract. Mutual Information (MI) is an useful tool for the recognition of mutual dependence between data sets. Different methods for the estimation of MI have been developed when both data sets are discrete or when both data sets are continuous. The MI estimation between a discrete data set and a continuous data set has not received so much attention. We present here a method for the estimation of MI for this last case based on the kernel density approximation. The calculation may be of interest in diverse contexts. Since MI is closely related to Jensen Shannon divergence, the method here developed is of particular interest in the problem of sequence segmentation.
1 INTRODUCTION

Mutual Information (MI) is a quantity theoretically based on information theory (Cover and Thomas (2006)). Since MI between two independent random variables (RV) is zero, a non-null value of MI between the variables gives a measure of mutual dependence. When analyzing two data sets $X$ and $Y$ (assumed to be the realization of two RV) MI may give us a measure of the mutual dependence of these sets. Although MI may be straightforwardly calculated when the underlying probability distributions are known, this is not usually the case and only the data sets are available. So MI must be estimated from the data sets themselves. When $X$ and $Y$ are of discrete type MI may be estimated by substituting the joint probability of these variables by the relative frequency of appearance of each pair $(x, y)$ in the sequence of data Grosse et al. (2002); Ré and Azad (2014). For real valued data sets (or of discrete type with many possible values) the estimation of MI is more difficult since relative frequency or binning are not efficient methods. Alternative proposals when both data sets are of continuous type have been made Steuer et al. (2002).

Estimation of MI between a discrete RV and a continuous one has not been so extensively considered in spite of being a problem of interest in diverse situations. For instance, we could compare the day of the week (weekday-weekend, discrete) with traffic flow (continuous) quantifying this effect. In a different context, we might wish to quantify the effect of a drug (given or not, discrete) in medical treatments (epilepsia continuous data).

In this paper, we propose a method for estimating MI between a discrete and a continuous data set based on the kernel density approximation (KDA) Silverman (1986) for estimating the probability density function (PDF) for continuous variables. For the discrete variable, we make use of the usual frequency approximation Grosse et al. (2002); Ré and Azad (2014). To complete the calculation of MI it is necessary to calculate an integral. This calculation is approximated by sample average.

MI between a discrete and a continuous RV may be identified with a weighted form of Jensen Shannon divergence (JSD) Grosse et al. (2002), a measure of distance between two (or more) probability distributions. JSD is of particular interest in the problem of segmentation of sequences. In this case, the discrete variable is identified with the segment in the sequence and the distance between the conditional probabilities of the sequence variable is calculated.

Our proposal is an alternative method to that proposed by Ross (2014) based on the nearest neighbour method. We find our proposal more suitable for instance in the problem of sequence segmentation since it would not require a reordering of the sequence.

In the Methods section, we present the approximations in the calculation of MI: KDA and sample average. A test of the performance of our proposal is given in the Results section by numerical experiments. In the Discussion section, we consider the results obtained and the application of the method to the sequence segmentation problem.

2 METHODS

We present in this section our proposal for estimating MI based on the KDA estimator of a PDF. To calculate MI we start from a sequence of data pairs $(x, y)$ where $x$ is a discrete variable and $y$ a continuous one. We assume that these data are sampled from a joint probability density
\( \mu(x, y) \), although unknown at first. From the joint PDF we define the marginal probabilities

\[
p(x) = \int_{-\infty}^{\infty} dy \mu(x, y)
\]

\[
\phi(y) = \sum_x \mu(x, y)
\]

The MI between the RVs \( X \) and \( Y \) is expressed in terms of these PDFs as

\[
I(X, Y) = \sum_x \int_{-\infty}^{\infty} dy \mu(x, y) \ln \left[ \frac{\mu(x, y)}{p(x) \phi(y)} \right]
\]

Note that if the variables \( X \) and \( Y \) are statistically independent then \( \mu(x, y) = p(x) \phi(y) \) and in this case \( I(X, Y) = 0 \). In this way a value of \( I(X, Y) \neq 0 \) gives a measure of the mutual dependence of the variables. We may rewrite \( I(X, Y) \) in terms of the conditional PDFs

\[
\mu(y \mid x) = \frac{\mu(x, y)}{p(x)}
\]

as

\[
I(X, Y) = \sum_x p(x) \int_{-\infty}^{\infty} dy \mu(y \mid x) \ln \left[ \frac{\mu(y \mid x)}{\phi(y)} \right]
\]

### 2.1 Kernel density approximation

To carry out the calculation in (4) it would be necessary the knowledge of the conditional PDFs. As was already mentioned these densities are assumed unknown and they have to be estimated from the sequence itself. Here we make use of the KDA Silverman (1986), summarized in the following.

Let us assume a sequence of \( n \) values sampled from a PDF \( f(y) \). The estimated value \( f_a(y) \) at a particular value \( y \) is given by

\[
f_a(y) = \frac{1}{nh} \sum_{j=1}^{n} K\left( \frac{y - y_j}{h} \right)
\]

Here \( y_j \) are the values in the sampled sequence. The kernel function \( K(y) \) must only satisfy the normalization condition

\[
\int_{-\infty}^{\infty} dy K(y) = 1
\]

and \( h \) is a smoothing parameter that avoids spurious fine structure. In this paper we are using a Gaussian kernel with the reported optimal bandwidth in Steuer et al. (2002)

\[
h_o \simeq 1.06 s_m n^{-1/5}
\]

with \( s_m^2 \) the variance of the sample.

To estimate the conditional PDFs in (3) we consider separately each subset of pairs with a particular value \( x \). For each subset we approximate the conditional PDF in (3) as

\[
\mu_a(y \mid x) = \frac{1}{n_x h_o} \sum_{j=1}^{n_x} \exp \left[ -\frac{(y - y_{jx})^2}{2h_o^2} \right]
\]
Here $n_x$ is the number of data pairs with the particular value of $x$. The sum is carried over the values of $y$ in this subset. The marginal probability of $X$ is approximated by

$$p_a(x) = \frac{n_x}{n} \quad (9)$$

and the marginal probability density of $Y$ by

$$\phi_a(y) = \sum_x p_a(x) \mu_a(y \mid x) \quad (10)$$

We illustrate the KDA with an example: let us consider the Gaussian joint probability distribution $\mu(x, y)$ with two possible values of $x$

$$\mu(x = 1, y) = \frac{1}{3} \frac{1}{\sqrt{2\pi}} \exp \left[ -\frac{y^2}{2} \right]$$

$$\mu(x = 2, y) = \frac{2}{3} \frac{1}{\sqrt{2\pi}\sigma_g} \exp \left[ -\frac{(y - y_m)^2}{2\sigma_g^2} \right] \quad (11)$$

with the marginal PDF for $y$

$$\phi(y) = \frac{1}{3} \frac{1}{\sqrt{2\pi}} \exp \left[ -\frac{y^2}{2} \right] + \frac{2}{3} \frac{1}{\sqrt{2\pi}\sigma_g} \exp \left[ -\frac{(y - y_m)^2}{2\sigma_g^2} \right] \quad (12)$$

We sampled 1000 pairs from this distribution for two different values of $y_m$ and from these pairs we made an estimation of the conditional PDFs by the KDA. In figure 1 A and B we plot the probability functions in (11) and (12) for two values of $y_m$ and the corresponding approximations.

![Figure 1: Kernel density approximation. KDA for the PDFs in Eq (11) and (12) for two different values of $y_m$ and with $\sigma_g = 1$. Solid lines: PDF; dashed lines KDA. A: $y_m = 1$. B: $y_m = 5$.](image-url)
2.2 Sample average approximation

Habiendo aproximado las densidades de probabilidad, para completar el cálculo en (8) debemos obtener el valor de las integrales. Reconocemos en estas integrales el valor de expectación

\[ \langle \ln \frac{\mu_x (y)}{\phi (y)} \rangle = \int_{-\infty}^{\infty} dy \mu_x (y) \ln \left[ \frac{\mu_x (y)}{\phi (y)} \right] \]

que podemos aproximar por el promedio sobre la muestra en el segmento (Steuer et al., 2002)

\[ \langle \ln \frac{\mu_x (y)}{\phi (y)} \rangle \approx \frac{1}{n_x} \sum_{j=1}^{n_x} \ln \left[ \frac{\tilde{\mu}_x (y_j)}{\tilde{\phi} (y_j)} \right] \]

Notar que aquí la suma está restringida a los valores en el subconjunto \( x \).

Sustituyendo todas las aproximaciones obtenemos finalmente

\[ \tilde{D} [\mu_1, \mu_2] \approx \frac{1}{n} \sum_{x=1}^{2} \sum_{j=1}^{n_x} \ln \left[ \frac{\tilde{\mu}_x (y_j)}{\tilde{\phi} (y_j)} \right] \]

3 RESULTS

We test the performance of our proposed method by considering numerical experiments. In the first place we consider two distributions \( \mu (x, y) \): the Gaussian distribution in (11) and an uniform distribution

\[ \mu (x = 1, y) = \frac{1}{3} [\Theta (y + 0.5) - \Theta (y - 0.5)] \]

\[ \mu (x = 2, y) = \frac{2}{3} \frac{1}{a} [\Theta (y + y_m + a/2) - \Theta (y + y_m - a/2)] \]

Here \( \Theta (y) \) is the step function

\[ \Theta (y) = \begin{cases} 0 & \text{for } y < 0 \\ 1 & \text{for } y > 0 \end{cases} \]

From each distribution we generated 100 data sets sampling 1000 \( (x, y) \) data pairs with different values of \( y_m \), the mean value of the distributions, or of \( \sigma_g \) or \( a \) respectively. We estimated the MI, \( I (X, Y) \), from each set by the method described in the previous section. Since we are sampling the data pairs from known distributions we are also able to calculate MI from its analytical expression. In this way we may compare the results obtained from the approximation with the corresponding analytical results. These results are included in Fig. 2 for the Gaussian distribution and in Fig 3 for the uniform distribution respectively. We include the average value of MI over the 100 data sets for the different values of the parameters and the bars correspond to the standard deviation in each set. In addition we calculated the MI for samples of statistically independent variables to establish a significance value for the MI of the dependent variables. The analytical value in this case is
Figure 2: **MI estimation for Gaussian distribution.** For the Gaussian distribution in (11) the dots represent the MI average value of 100 data sets of 1000 \((x, y)\) pairs each with the bars indicating the standard deviation of each set. The black line is the analytical value of MI. A) in function of mean value \(y_m\). The inset shows the distribution of MI for a particular value of \(y_m\) for a dependent and an independent set. B) changing \(\sigma_g\) in the inset the same plot but in log-log scale to highlight the MI value for independent sets.

Figure 3: **MI estimation for uniform distribution.** For the uniform distribution in (16) the dots represent the MI average value for 100 data sets of 1000 \((x, y)\) pairs each, with the bars indicating the standard deviation. The black line is the analytical value of MI. A) in function of mean value \(y_m\). B) changing \(a\).

We consider the effect of the size of the sample repeating the experiment with the Gaussian distribution for different values of \(n\), the number of data pairs in each set. We again generated 100 data sets of \(n\) data pairs each. The results are included in Fig 4 for three sets of parameters. As can be appreciated there is a slight overestimation of MI for small values of \(n\).

Finally we considered an usual situation when there is only one sample of data pairs. We sampled 1000 pairs from the distributions in (11), in (16) and from the exponential distribution

\[
\mu (x = 1, y) = \frac{1}{3} e^{x} (-y) \Theta (y)
\]

\[
\mu (x = 2, y) = \frac{2}{3} \frac{1}{2} e^{x} (-y/2) \Theta (y)
\]

(18)

For each sample we estimated MI by the approximate method developed. These values are included in table 1.
Figure 4: MI estimation for Gaussian distribution. For the Gaussian distribution in (11) the dots represent the average value of 100 data sets for different number of \((x,y)\) pairs with the bars indicating the standard deviation. The dashed lines are the analytical values of MI for the different sets of parameters.

To set up a significance value for each sample we proceeded in the following way: we generated 100 data sets of 1000 pairs of independent variables, the discrete values were sampled from the distribution

\[ p(x) = \frac{n_x}{1000} \]

with \(n_x\) the number of times that the value \(x\) appears in the original sequence and the continuous values were sampled from the Gaussian distribution

\[ \mu(y) = \frac{1}{\sqrt{2\pi s}} e^{\exp\left[-\frac{(y-m)^2}{2s^2}\right]} \]

independently of the value of \(x\). Here \(m\) is the mean value in the original sequence and \(s^2\) the variance.

We calculated the MI for each data set and then the MI mean value and its variance. These results are also included in table 1. It can be appreciated a clear difference between the MI of the dependent values and those of the independent sequences.

Table 1: MI and significance value.

| PDF     | MI    | Significance Value |
|---------|-------|--------------------|
|         | mean  | st. dev.           |
| Gaussian| 0.6359| \(4.5 \times 10^{-3}\) | \(1.8 \times 10^{-5}\) |
| Uniform | 0.1429| \(4.5 \times 10^{-3}\) | \(1.8 \times 10^{-5}\) |
| Exponential | 0.0718| \(4.5 \times 10^{-3}\) | \(1.9 \times 10^{-5}\) |

MI of the sampled dependent sequences (see text) and the corresponding significance values computed from the independent sets.

4 DISCUSSION AND CONCLUSIONS

We have presented a method for estimating MI between a discrete and a continuous data sets. The numerical experiments described in the previous section show a good performance of this
method. This can be appreciated in Figs 2 and 3 where the analytical results are compared with the approximate method showing a good agreement. It can be appreciated a slight underestimation of MI in Fig. 3. This may be attributed to the kernel selection we have made. This fact will be addressed in future research. Nevertheless approximate MI calculation is a reliable tool for dependence detection between discrete and continuous data sets. The quality of the approximation depends on the size of the sample, as could be expected, being better for larger samples as is shown in Fig. 4. In any case the analytical value is within the standard deviation interval. This interval is reduced as \( n \), the size of the sample, increases. The method can also give an estimation of a significance value as described in the previous section. This is important when deciding the dependence between the data sets. MI may be identified with a weighted JSD, an entropic measure of distance between probability distributions Grosse et al. (2002)

\[
D = H \left( \sum_x \pi_x \mu_x(y) \right) - \sum_x \pi_x H \left( \mu_x(y) \right) \tag{21}
\]

where, for continuous range RVs,

\[
H \left( \mu_x(y) \right) = -\int \mu_x(y) \ln \mu_x(y) \tag{22}
\]

is Gibbs-Shannon entropy of the probability densities and \( \pi_x \) denotes the weights of each density. MI coincides with JSD identifying the weights \( \pi_x \) in (21) with the marginal probability \( p(x) \) in (1) and the PDFs \( \mu_x(y) \) with the conditional probabilities \( \mu(y|x) \) in (3). JSD was used by Grosse et al. Grosse et al. (2002) to develop an algorithm to partition a non-stationary sequence of discrete RVs into stationary subsequences. With the method we have presented here for MI calculation this algorithm may be extended to the problem of sequence segmentation of continuous RVs. The calculation does not require a reordering of the sequence as it would be necessary for instance with the nearest neighbour method Ross (2014). Research along this line will be published elsewhere.

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