A Complete Probabilistic Model for the Quick Detection of Dissimilar Binary Images by Random Intensity Mapping

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Abstract: - In this paper we present the *Probabilistic Matching Model for Binary Images* (*PMMBI*), a model for the quick detection of dissimilar binary images based on random point mappings. The model predicts the probability of detecting dissimilarity between any pair of binary images based on the amount of similarity and number of random pixel mappings between them. Based on the model, we show that by performing a limited number of random pixel mappings between binary images, dissimilarity detection can be performed quickly. Furthermore, the model is image size invariant; the size of the image has absolutely no effect on the dissimilarity detection quickness. We give examples with real images to show the accuracy of the model.

Key-Words: - image matching, probabilistic model, binary image, image similarity.

1 Introduction

Image matching rises frequently in the field of image processing under many topics such as, image registration, template matching, image retrieval, image classification, …, etc. These methods are either feature-based methods, that rely on extracting image features and then matching them, or area-based methods (aka intensity methods), based on comparing image intensity values directly. Since binary images, have only two intensity levels, a limited amount of scene detail is present in the image, rendering feature-based methods impractical, and area-based methods become a more practical approach.

Binary image matching is most commonly accomplished by calculating the correlation between the images [1] or simply by subtracting the two images [2]. These methods, as well as all methods presented in the literature require some type of similarity criteria to be evaluated over the entire images. Hence, these methods are image-size dependent; as image size increases, so does processing time. With modern day applications demanding higher image resolution resulting in higher image sizes (> 50 Mega-pixel images) in many fields such as robotics, industrial applications and medical surgery, traditional image-size based methods, such as correlation, can become quite slow in processing such huge images, even with the speed of today's computers. The dependency of matching techniques on image size is a topic which unfortunately has not been properly addressed.

In this paper we present a probabilistic matching model for binary image matching, called the *Probabilistic Matching Model for Binary Images* (*PMMBI*). The model predicts the probability of detecting dissimilarity between any pair of binary images with any level of similarity as a function of the number of random pixel mappings between them. By randomly mapping image points and using this model, the following unique advantages are immediately achievable,

1. Dissimilar images can be detected quickly without the need to process the entire image. Even images that are highly similar and near-duplicate can be amazingly detected by only comparing a minute fraction of the total size of the images.

2. Detecting dissimilarity is image size invariant; the size of the image has absolutely no effect on the dissimilarity detection process nor its quickness. Images of size, say 100 gega-pixels are processed just as fast as 10 kilo-pixels images.

3. By measuring the dissimilarity detection quickness, image similarity can be estimated to a good degree without the need to process the entire image. Hence, with the aid of the model, matching can be performed magnitudes faster than employing traditional matching techniques that require comparing the entire images.

This paper is organized as follows: following this introduction, section 2 points out related literature, section 3 reviews related work that is necessary for the understanding of the work presented. Section 4 presents the main theme of this paper and introduces the probability model. We show how quickly dissimilarity can be detected using a few random mappings. Section 5 presents a discussion of tests conducted on real images, which show the accuracy of the model. We finally conclude in section 6 and discuss where our future research is directed.

2. Related Literature

Image correlation is the most widely used method for image matching. Much research has been devoted to improving image correlation techniques [3] [4] [5] [6]. Other area-based methods have also been developed based on a variety of principles; minimizing image intensity co-occurrences [7], Hausdorff distance [8], Haar-like binary features [9], mathematical morphology [10], as well as many other techniques, e.g. [11] [12]. However, all of these methods are image size dependent and require that the entire images be processed for matching.

3. Related Work

In this section, we review some earlier developed concepts that are necessary for the understanding of the work presented. We review the definition of similarity between images, and how images are categorized based on it. We then review the γ similarity measure that is used in our work as an index for image similarity. Finally, we summarize how dissimilarity detection is measured.

3.1 Similar and Dissimilar Binary Images

The closeness between two binary images is based on a pixel-to-pixel comparison between the binary images. Image closeness is categorized as either *similar* or *dissimilar* images [13] as follows:

- *Similar Images* (*S*): For images to be similar, the two images must be the same. They are of two types; either *exact* or *inverse*:
  - o *Exact Images* (*E*): The two images are exactly the same; they have the same intensity values at all corresponding pixels.
  - o *Inverse Images* (*I*): The two images are the inverse of each other, as they have the compliment intensity values at all corresponding pixels.

- *Dissimilar Images* (*R*): The two images are different and this can only be true if they are not similar; i.e. neither exact nor inverse. *Dissimilar images* are of two types:
  - o *Distinct-dissimilar Images* (*D*): The two images are ideally different (as measured by γ below).
  - o *Quasi-dissimilar Images* (*Q*): The two images have concurrences between them at some pixels, but not all pixels. These images are also referred to as *Quasi-similar images*.

This categorization of binary images is the basis on which the probabilistic model discussed in this paper is based upon.

3.2 The γ Binary Similarity Measure

The *binary similarity measure* (γ) measures the amount of similarity and concurrence between two binary images [14]. Formally stated: given two images **u** and **v**, γ is defined as,

$$\gamma(\mathbf{u},\mathbf{v}) = |1 - 2P_o((Z = \mathbf{u}\oplus\mathbf{v}) = z)|, \quad z \in \{0,1\} \qquad (1)$$

where $\oplus$ is the *exclusive-or* operation and $P_o()$ denotes the probability mass function of the image intensities (i,e. the normal image histogram). As a result, $0 \leq \gamma \leq 1$, and hence values of γ correspond to,

- $\gamma = 0$ for *distinct-dissimilar* images
- $0 < \gamma < 1$ for *quasi-dissimilar* images
- $\gamma = 1$ for *similar* images

In practice, image pairs with $\gamma < 0.01$ are assumed to be $\gamma \approx 0$, and thus are considered to be *distinct-dissimilar* image pairs. Furthermore, image pairs with $\gamma > 0.99$ are termed as near-duplicate images.

3.3 Measuring Mapping Performance

The *Mapping Detection Number* (*MDN*) is defined as the number of mappings required to detect a pair of images as being dissimilar. Furthermore, MDN_{DC} notation is used to denote *MDN* at a specific detection confidence (*DC*) value. For example,

$MDN_{0.90} = 5$ implies that 5 mappings are sufficient to detect dissimilarity with 90% confidence.

4. The Probabilistic Matching Model for Binary Images

Many probabilistic models have been successfully applied to many areas of robot and computer vision, such as image comparison [15], image retrieval [16], image categorization [17], image tagging [18], image registration [19], image fusion [20], image segmentation [21], object tracking [22], and road extraction [23].

The *Probabilistic Matching Model* (*PMM*) [13] showed that detecting dissimilarity between *distinct-dissimilar* binary images can be performed quickly by randomly selecting points and comparing them. More importantly, it showed that there is no need to compare the entire images to detect dissimilarity. The model predicts the probability of detecting dissimilarity between any pair of binary *distinct-dissimilar* images by the pth random mapping by the following formula,

$$\Pr(p) = \Pr(\gamma = 0, p) = 1 - \left(\frac{1}{2}\right)^{p-1} \quad p = 2, 3, \ldots \tag{2}$$

The *Probabilistic Matching Model for Binary Images* (*PMMBI*) that we introduce here is a generalization of *PMM* that can be applied to any pair of binary images, not just *distinct-dissimilar* image pairs. The model can be summarized by the following equation which predicts the probability of detecting dissimilarity between any pair of binary images by the pth random mapping as a function of the amount of similarity (γ) between the images,

$$\Pr(\gamma, p) = 1 - \left(\frac{1}{2}\right)^{p}\left((1+\gamma)^{p} + (1-\gamma)^{p}\right) \tag{3}$$

or

$$\Pr(\gamma, p) = 1 - \left(\frac{1}{2}(1+\gamma)\right)^{p}\left(1 + \left(\frac{1-\gamma}{1+\gamma}\right)^{p}\right) \tag{4}$$

$$0 \le \gamma \le 1 \text{ and } p = 2, 3, \ldots$$

It is important to note that p is a discrete variable and γ is a continuous variable. Since the probability of detecting dissimilarity function, Pr(), is a measure of the confidence in detecting dissimilarity, it is also referred to as the *Detection Confidence* (*DC*). Furthermore,

- For distinct-dissimilar images (*D*), implies $\gamma = 0$ and thus (3) degenerates to,

$$\Pr(D, p) = \Pr(\gamma = 0, p) = 1 - \left(\frac{1}{2}\right)^{p-1} \tag{5}$$

which agrees with the expression of *PMM* and (2).

- For similar images (*S*), i.e. $\gamma = 1$ and hence (3) degenerates to,,

$$\Pr(S, p) = \Pr(\gamma = 1, p) = 0 \tag{6}$$

i.e., when images are similar, then there is no possibility of detecting dissimilarity between them, regardless of the number of mappings performed.

Several curves of $\Pr(\gamma, p)$ versus p for different values of γ are shown in Fig. 1. All curves of $\Pr(\gamma, p)$ start from a value of zero at $p = 1$ (no possibility of detecting dissimilarity on the 1st mapping) and approach unity for large p; as more mappings are performed, dissimilarity is surely to be detected (provided that $\gamma < 1$). Also noticeable is that all the curves quickly reach high probability values, indicating quick dissimilarity detection by using only a few mappings, e.g. $\Pr(0.4,7) > 0.9$ and $\Pr(0.8,22) > 0.9$.

Fig. 2 shows curves of $\Pr(\gamma, p)$ versus γ at different iso-p (constant p) curves. For any iso-p curve, *DC* decreases with increasing γ. As the value of p increases, the *DC* value also increases at any value of γ. This is an informative plot; e.g. it shows that detecting dissimilarity on the 2nd mapping is possible for all $\gamma < 1$; in particular the possibility is 50% for distinct-dissimilar images and decreases as γ increases. It is surprising to observe that even for near-duplicate image pairs ($\gamma \ge 0.99$), such as those shown for the *Leena* images of **Fig. 3**, that the possibility of "getting lucky" and detecting dissimilarity on the 2nd mapping –even though minute– still exists! Note that according to *PMMBI*, 200 mappings are required –on average– to detect dissimilarity for images with this level of similarity.

Fig. 4 shows curves of p versus γ for several *DC* values. For an iso-*DC* curve, p increases with increasing γ; the rate increases with higher values of γ. Higher *DC* values require more mappings at a given value of γ than lower *DC* values.
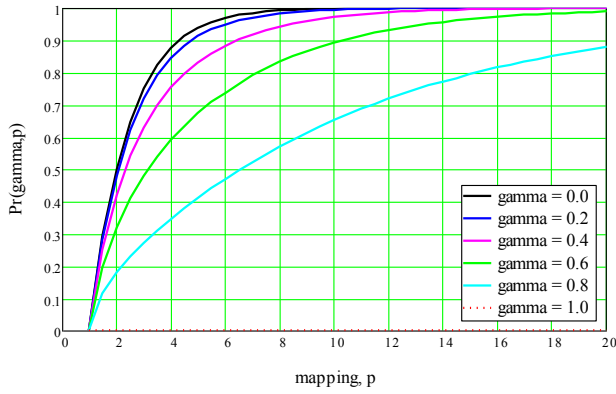
Fig. 1. Pr(γ, p) versus p for several iso-γ curves.
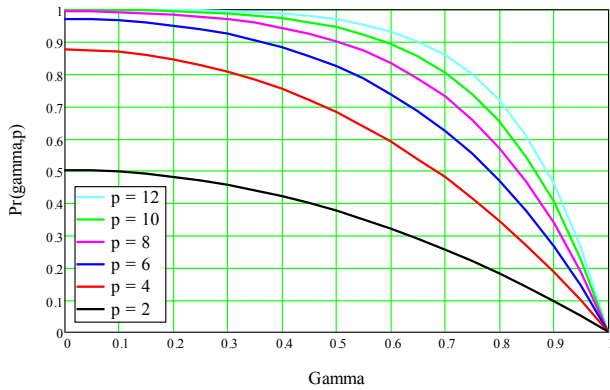

Fig. 2. Pr(γ, p) versus γ for several iso-p curves.

Fig. 3. Highly similar near-duplicate binary images of *Leena* ($\gamma = 0.99$). The difference image is also shown.
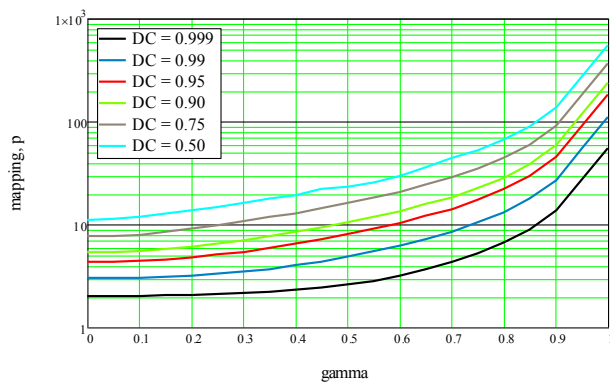

Fig. 4. p versus γ for several iso-*DC* curves.

4.1 The Probability Mass Function

Pr(), in essence, is a cumulative distribution function in the variable p of the probability mass function, denoted by $P_D(p,\gamma)$, of the number of mappings required to detect dissimilarity which is given by,

$$P_D(\gamma, p) = \left(\frac{1}{2}\right)^p \left((1-\gamma)(1+\gamma)^{p-1} + (1-\gamma)^{p-1}(1+\gamma)\right)$$

$$p = 2, 3, \dots \infty \text{ and } 0 \le \gamma < 1 \quad (7)$$

P_D, similar to Pr(), is a bivariate probability density function in the variables p and γ; as before, p is a discrete variable with values $p > 1$ and γ is a continuous variable in the range [0,1]. Fig. 5 shows plots of $P_D(p,\gamma)$ as a function of p for values of $\gamma = 0.0$, 0.5 and 0.9.

For distinct-dissimilar images (*D*), $\gamma = 0$ and thus,

$$P_D(D, p) = P_D(\gamma = 0, p) = \left(\frac{1}{2}\right)^{p-1} \quad (8)$$

It can be seen that most of the weight of $P_D(D, p)$ is at the low values of p concentrated in the first few terms. For example, the first four non-zero terms encompasses more than 93% of the total probability mass function $P_D(D, p)$:
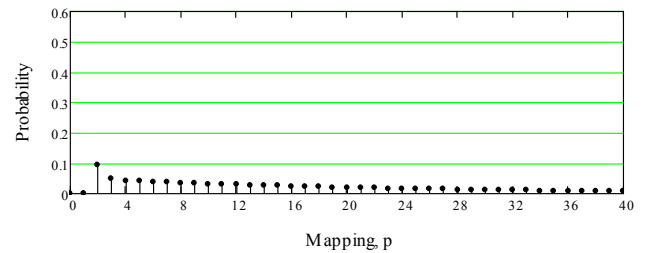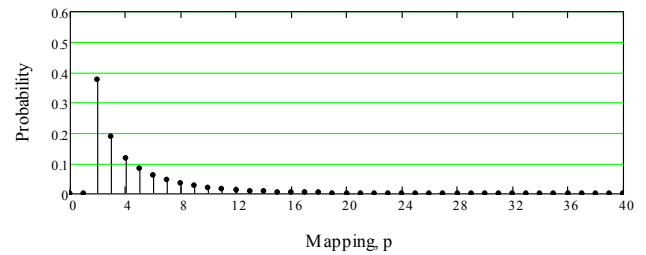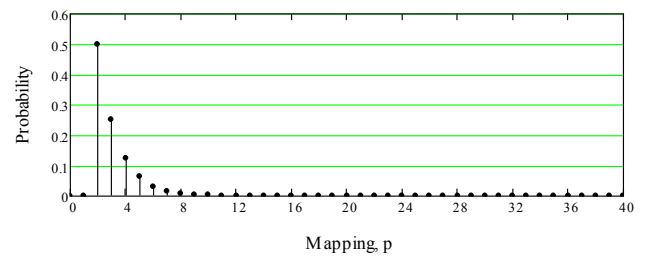

Fig. 5. $P_D(\gamma,p)$ as a function of p for different values of γ; from top to bottom $\gamma = 0.0$, 0.5 and 0.9.

$$\sum_{p=2}^{5} P_D(D, p) = \Pr(D,5) = 0.938 \qquad (9)$$

As the value of γ increases, the weight of the $P_D(D, p)$ terms becomes more evenly distributed, as shown in the plots for $\gamma = 0.5$ and $\gamma = 0.9$.

4.2 The Expected Value and Variance of p

The expected value of p, expressed as $E[p(\gamma)]$, is the mean number of mappings required to detect dissimilarity, denoted by $p*$, for any given γ. It can be stated as a function of γ and is given by,

$$p* = E[p(\gamma)] = E(\gamma) \qquad (10)$$

which can be shown to simplify to,

$$p* = \frac{4}{1-\gamma^2} - 1 \qquad 0 \leq \gamma \leq 1 \quad (11)$$

The variance of p is given by,

$$V(\gamma) = \frac{2(8 \cdot \gamma^2 - \gamma^4 + 1)}{(1-\gamma^2)^2} \qquad 0 \leq \gamma \leq 1 \quad (12)$$

A plot of $E(\gamma)$ and $V(\gamma)$ is shown in Fig. 6. $E(\gamma)$ increases slowly for low γ, but increases rapidly at higher γ values. $V(\gamma)$ also increases as γ increases, but at a quicker rate than $E(\gamma)$.

When the images are highly similar and near duplicate, γ is close to unity, and thus $(\gamma + 1) \cong 2$. Then from (11), $p*$ can be approximated by,

$$p* = E(\gamma) \approx \frac{2}{1-\gamma} \qquad \gamma \cong 1 \quad (13)$$

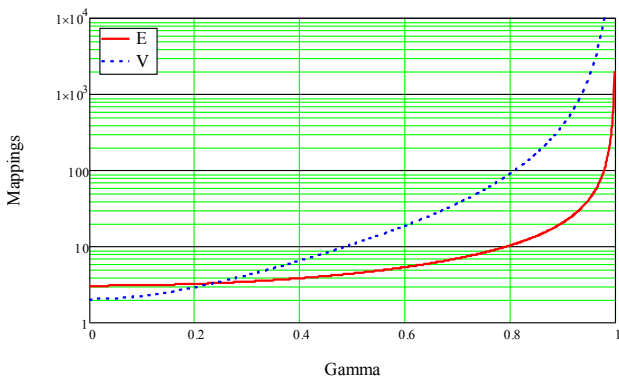Using this approximation produces an error < 2.5% for $\gamma > 0.705$, and an error < 1% for $\gamma > 0.809$.

Fig. 6. Plots of $E(\gamma)$ and $V(\gamma)$.

When the images are highly dissimilar and γ is small, then from (11), $p*$ can be approximated by,

$$p* = E(\gamma) \approx 3 \qquad \gamma \cong 0 \quad (14)$$

Using this approximation produces an error < 2.5% for $\gamma < 0.137$ and an error < 1% for $\gamma < 0.087$. (14) also implies that this is the lowest possible expected mapping. This should not be incorrectly misinterpreted that 3 point mapping is the lowest possible number of mappings required to detect dissimilarity; we have already shown above that 2 point mappings are possible for all image pairs, provided that $\gamma < 1$.

4.3 Matching with *PMMBI*

By measuring how quickly dissimilarity can be detected between image pairs and using *PMMBI*, the similarity (γ) between them can be estimated to a good degree. In such cases, several dissimilarity detection trials should be repeated and the mean value can be used as the value of $p*$. Then (11) can be used to estimate the amount of similarity, γ, between the images (see [24]). As a result, using the *PMMBI* model, matching can be performed magnitudes faster than employing traditional matching techniques that require comparing the entire images.

5 Discussion

Fig. 7 shows the images of the *Reduced KU-ME128B* binary image set that was used for testing the probability model. The set consists of 12 128x128 binary images of different scenes. The similarity values between all image pairs for this set are in the range of $0.002 \leq \gamma \leq 0.669$, with a mean value of 0.231 and a standard deviation of 0.161. Since *PMMBI* is based on random mapping and every mapping trial will produce a different *MDN* outcome, matching of each pair of images was repeated 1,000 times to obtain consistent and meaningful statistical results. The resulting $MDN_{0.50}$, $MDN_{0.90}$, $MDN_{0.99}$ and $MDN_{0.999}$ are plotted as a function of γ in Fig. 8. The theoretical iso-*DC* curves for 0.50, 0.90, 0.99 and 0.99 are also plotted in the figure for comparison. **Table 1** summarizes the dissimilarity detection mapping error statistics. Examining the discrepancy between the model's prediction and empirical results we observe the following:

Fig. 7. The *Reduced KU-ME128* binary image set.

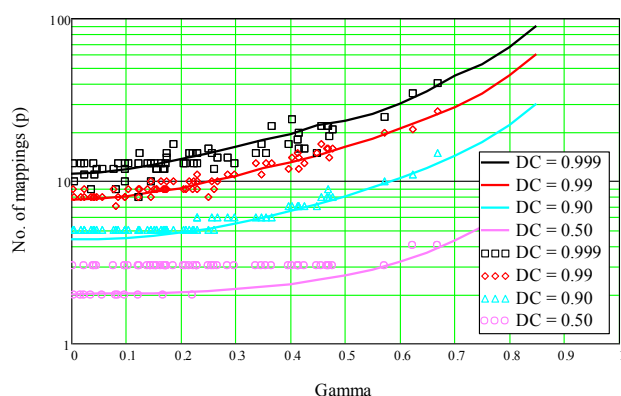| Table 1: *Mapping Results Statistics for the Reduced KU-ME128 binary image set*				
		Mapping Error		
DC	**Correlation**	**Max**	**Mean**	**Std. dev.**
0.500	0.839	1.000	0.629	0.391
0.900	0.989	2.185	0.455	0.353
0.990	0.986	2.464	0.675	0.530
0.999	0.956	6.868	1.502	1.359

Fig. 8. Plots of MDN_{DC} versus γ for DC = 0.50, 0.90, 0.99 and 0.99. The theoretical DC curves are also shown.

- All MDN_{DC} values have a high correlation (0.839 – 0.989) with the theoretical DC values as predicted by (7).

- The mean mapping error between predicted and empirical data is very small with less than one mapping for all DC values, except for $MDN_{0.999}$ which has a higher mean error value of ~1.5 mappings, which is expected

due to the larger expected value for p at higher DC values.

The results exemplify the high accuracy of the model in predicting how fast dissimilarity can be detected.

6 Conclusion

In this paper we have presented a probabilistic model for the quick detection of dissimilarity between binary images. The model is based on randomly mapping points between two images. The model predicts the probability of detecting dissimilarity between binary images as a function of the similarity between images and the number of mappings between them. The model shows that dissimilarity can be detected fairly quickly when the images are highly dissimilar, requiring only a few mappings between the images. As the images become more similar, more mappings are required to detect similarity, but still a small fraction compared to comparing the entire images. Even near-duplicate images require an average of 200 mappings regardless of image size. The model's invariance to image size is a unique feature of the model that gives it its strength, particularly when the images are huge. Testing with real images produced dissimilarity detection results close to that predicted by the model, showing the accuracy of the model.
Our future work will focus on showing how *PMMBI* can be used efficiently for template matching and image registration. We will also focus on developing a similar probabilistic model for greyscale images.

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