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Verification of Hypotheses generated by Case-Based Reasoning Object Matching

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Abstract. Case-based reasoning object-matching is the methods at choice when the objects can be identified by case models. The result of the matching process will be many hypotheses for the true shape of the objects. These hypotheses must be verified in a hypothesis-verification process. We review in this paper what has been done so far and present our hypothesis-verification rules. The rules get evaluated and the results are shown in the images and the achievements are discussed. We consider two different hypothesis-verification rules, one is based on set-theory and the other one is based on statistical measures. Finally, we describe the results achieved so far and give an outlook about further work.

Keywords: Case-Based Reasoning Object-Matching, Hypothesis-Test Verification, Set Theory, Statistical Measures

1 Introduction

Case-based object-matching [1] is the methods at choice when the objects can be identified by case models. These case models can be learnt from the raw data by case mining [2]. For the case-matching procedure, we need a proper similarity measure that depends of the case model description. In our case, the case models are object contours such as round, ellipse-like, or more fuzzy-like geometric figures. The chosen similarity measure in this work is the cosine-similarity measure [3]. The properties of this similarity measure have been described in detail in [3]. The case matcher takes the case models and matches them against the objects in the image. In case the similarity measure is high the found contour will be marked in the image. Often the matcher does not bring out only one contour for an object, instead of the matcher fires several times at slightly different spatial positions in the image for the same object. These multiple matches must be evaluated after the matching in a hypothesis verification procedure.

The aim of this hypothesis-verification procedure is to obtain only the considered object.

We describe in this paper what kind of hypothesis verification methods we have developed and tested on our image database. The state-of-the-art of hypothesis verification methods is described in Section 2. In Section 3 we describe the hypothesis generation and the problems concerned with it. In Section 4 we describe kinds of hypothesis-verification based on Set Theory. We give results in Section 5. Hypothesis-verification rules based on statistics and results are given in Section 6. Finally, we summarize our work in Section 7 and we give an outlook to further work on improvements of the matching results.

2 State-of-the Art

The aim of the hypothesis verification is to decide whether a match can be accepted as correct or not. Therefore, hypothesis verification is closely related to the object recognition process. In literature we can find different approaches for this process. Grimson and Huttenlocher [1] as well as Jurie [2] and Kartatzis et al. [3] refer to features in the form of points or line segments. The common target of all these researchers is to find the best pose for the detected data features. However, all papers follow different strategies: Grimson and Huttenlocher [1] focus on the question how random matches can be prevented. They developed a formal means for finding the fraction of model features that must be evaluated in order to ensure that the match occurs only with a given probability at random. The derivation of this fraction is done in three steps whereas the type of feature, the type of transformation from model to image and a bound on the positional and orientationally error are known. First for every pairing of a model feature to data feature the set of transformations is determined. This set defines a volume in the transformation space. In the next step the probability of a common point of intersection between l and more volumes is calculated. This probability corresponds to match of at least l pairings of model and image features. Last a second probability that describes that l or more volumes will intersect at random, is used to specify a threshold for the fraction of model features that must be evaluated at least in order to ensure that the probability of a random match is lower than a given value.

The aim of the research of Jurie [2] is to find the pose of the model features that best matches the data features. The pose hypotheses are generated by correspondences between the model and the data features. Early researches propose to evaluate only some correspondences to find an initial pose hypothesis P that is refined by iteratively enlarging the number of correspondences. Jurie [2] describes that this way of hypothesis generation and verification is not optimal. Therefore, the paper suggests the opposite approach: A pose space is generated from different model-data-pairings. A “box” of the pose space is computed including the initial position P that is large enough to compensate the data errors. If the distribution of model-data-correspondences is Gaussian, the maximal probability of the object to be matched is determined. Then the box can be refined. The process repeats until the “box” only contains one pose.

A simpler method of model-based pose estimation and verification is described in Shahrokni et al. [4]. They deal with the automatic detection of polyhedral objects. Hypotheses are generated by the knowledge-based connection of corners and line segments. The model and the transformed hypotheses are evaluated with the method of

the least squares. The best hypothesis minimizes the sum of squared differences between the model and the transformed hypothesis.

Katartzis et al. [3] discuss the automatic recognition of rooftops, which are characterized by lines and their connections. After detecting the line segments in the image, they are grouped in a hierarchical graph. The highest level of the hierarchy contains closed contours. Every node of the graph is assigned a value that on the one hand assigns the saliency of the hypothesis and on the other hand represents the likelihood of the presence of a 3D-structure, which depends on domain-specific knowledge. Based on the hierarchical graph is defined a Markov Random Field (MRF). By maximization of the posterior probability of the MRF for the concrete graph a consistent configuration of the data is found.

In general, the verification process for object hypotheses based on line segments is a widely discussed field.

An approach that totally differs from the discussed ones is given in Leibe et al. [7]. The heart of the described object recognition system is a database with different appearances of parts of the object that should be recognized. Additionally, an “Implicit Shape Model” is learnt to combine the parts to a correct object. If multiple objects are in the image, then some hypotheses may overlap each other so that a verification step is required. The method follows the principle of Minimal Description Length (MDL) that is borrowed from the information theory. The description length of a hypothesis depends on its area and the probability that the pixels inside the hypothesis are no object pixels. The description length of two overlapping hypotheses is generated in the same way. From the resulting values is concluded whether two overlapping hypotheses refer to two objects or only to one.

3 Hypothesis Generation and Problems

3.1 Hypothesis Generation

In this Section, we want to give you an overview about the model-based object recognition method that we use to generate our hypotheses. The method is extensively discussed in Perner and Buehring [8].

A model-based object recognition method uses templates that generalize the original objects and matches these templates against the objects in the image. During the match a score is calculated that describes the goodness of the fit between the object and the template.

We determine the similarity measure based on the cross correlation by using the direction vectors of an image. This requires the calculation of the dot product \tilde{l}_k between each direction vector of the model $\vec{m}_k = (v_k, w_k)^T$, $k = 1, \dots, n$, and the corresponding image vector $\vec{i}_k = (d_k, e_k)^T$:

$$\tilde{l}_k = \langle \vec{m}_k, \vec{i}_k \rangle = \vec{m}_k \cdot \vec{i}_k = (v_k \cdot d_k + w_k \cdot e_k), \quad k = 1, \dots, n \quad (1)$$

Note that the dot product \tilde{l}_k (see Equation 1) takes also into account the length of the vectors \vec{m}_k and \vec{i}_k . That means that \tilde{l}_k is influenced by the intensity of the contrast in the image and the model. In order to remove this influence, the direction vectors are normalized to unit length by dividing them through their gradient:

$$l_k = \left\langle \frac{\vec{m}_k}{\|\vec{m}_k\|}, \frac{\vec{i}_k}{\|\vec{i}_k\|} \right\rangle = \frac{\vec{m}_k \cdot \vec{i}_k}{\|\vec{m}_k\| \cdot \|\vec{i}_k\|} = \frac{v_k \cdot d_k + w_k \cdot e_k}{\sqrt{v_k^2 + w_k^2} \cdot \sqrt{d_k^2 + e_k^2}}, \quad k = 1, \dots, n \quad (2)$$

The score l_k (see Equation 2) considers only the directions of the model and the image vector, i.e. it is invariant against changes of the contrast intensity. We can get the angle between the direction vectors by determining the value of l_k . Therefore, we can conclude that the value of l_k ranges from -1 to 1. The vectors \vec{m}_k and \vec{i}_k have the same direction if $l_k = 1$, the vectors are orthogonal if $l_k = 0$ and both vectors have opposite direction if $l_k = -1$. In the rest of the paper we say that the value of l_k is the *local similarity score* of the two direction vectors \vec{m}_k and \vec{i}_k .

Usually, we are mainly interested in the similarity score between the complete model and the image. We want to define this *global similarity score* s_1 between the model and the image as the mean of all local similarity scores:

$$s_1 = \frac{1}{n} \sum_{k=1}^n l_k \quad (3)$$

Just like the local similarity score l_k the global score s_1 is invariant against illumination changes and it ranges from -1 to 1. In case of $s_1 = 1$ and $s_1 = -1$ the model and the image object are identical. If $s_1 = 1$ then all vectors in the model and the corresponding image vectors have the same direction. If $s_1 = -1$ then all the vectors have exactly opposite directions, that is only the contrast between the model and the image is changed.

In general, we have to subdivide between global and local contrast changes. If the contrast between the model and the image is globally inversed, then all the model and image vectors have opposite directions. If the contrast is locally inversed, then only some model and image vectors have opposite direction. With some little modifications the similarity measure s_1 becomes invariant to global contrast changes (see Equation 4) and local contrast changes (see Equation 5), respectively.

$$s_2 = \left| \frac{1}{n} \sum_{k=1}^n l_k \right| \quad (4)$$

$$s_3 = \frac{1}{n} \sum_{k=1}^n |l_k| \quad (5)$$

In contrast to range of s_1 , the values of s_2 and s_3 are non-negative.

The aim is to store only one model for objects with similar shapes of different scale and rotation. Therefore, a transformed model must be compared to the image at a location. The value of $\arccos s_2$ indicates the mean angle between the model and the image vectors.

3.2 Kinds of Hypothesis Verification based on Set-Theory

The matching process determines each possible match between the image pixels and the model. In the following we consider the found object as a hypothesis. To each hypothesis is assigned a matching score based on the similarity measure s_3 .

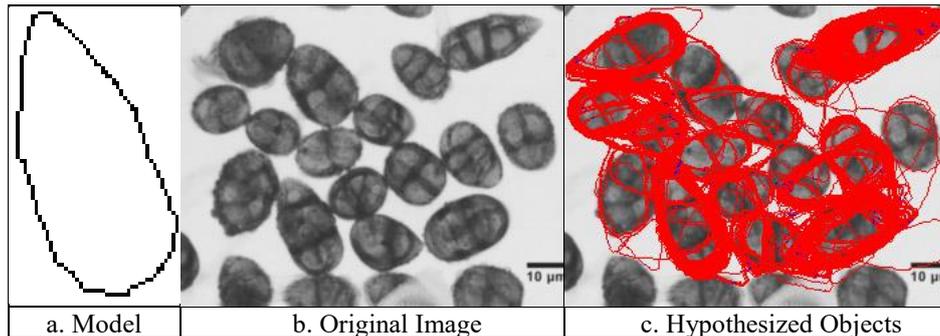


Fig. 1. Contour Model, Original Image and Hypothesized Objects

From the observation in Figure 1 we can see that the models often match the same object, i.e. we have a superimposition of models. All the hypotheses in this image have scores greater than 0.8 . Now we need to find a rule which allows us to remove determines the similarity between the model and the image pixels. It can range from 0 to 1 whereas the value of 1 says identity and the value of 0 dissimilarity. By defining a threshold for the score, we can exclude hypotheses. This is the simplest hypothesis verification process. If the threshold is set to 0.8 then 734 hypotheses remain. They are shown in Figure 1 false hypotheses. The hypotheses in this case overlap, touch or are inside of each other. From that we can develop special relationships of the hypotheses.

The definition of the relationships is based on two hypothesized objects A and B . $S(A)$ is the set of all image pixels that are inside the contour of the object A including also the image pixels of the contour. Equally, $S(B)$ is the set of all image pixels inside the contour of object B including all image pixels of the contour. We want to distinguish between three relationships that are described in Table 1.

4 Results

This Section focuses on the reduction of initial hypotheses.

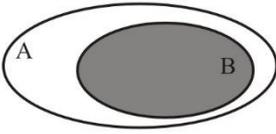
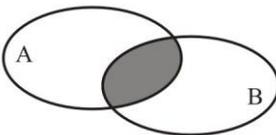
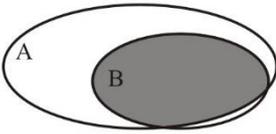
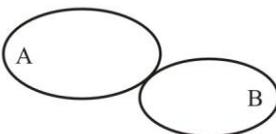
4.1. The relationship “Inside”

In this Section we want to investigate in the relationship “inside” (Table 1a). Given a sorted list¹ of hypotheses, we first extract the hypothesis pairs that fulfil the relationship

¹The matching process lists all matched objects sorted by the scale whereas objects with the same scale are sorted by the rotation.

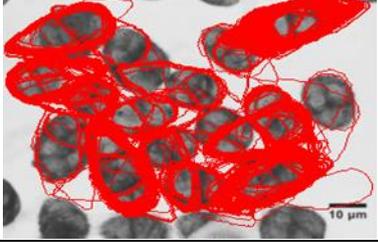
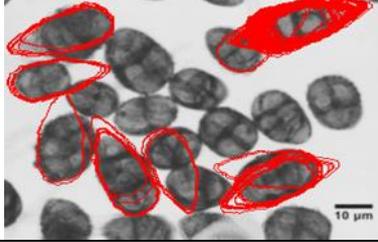
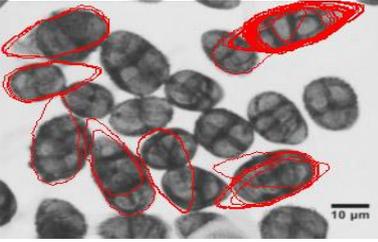
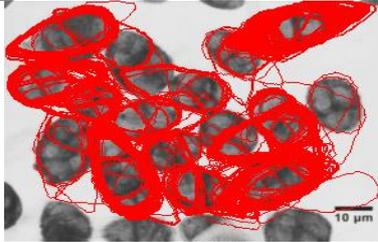
“inside” (see Figure 2b). From the 734 hypothesized matches we can create 138 hypotheses pairs that fulfil the relationship inside, i.e. one of both hypotheses is totally overlaid by the other. Note that these pairs are only based on 136 different hypotheses. Thus, we conclude that some hypotheses with high area overlay more than one smaller hypothesis. In other words, we can say that most of the hypotheses are involved in more than one pair.

Table 1. Relationships between two Hypotheses

Relation	Figure	Description
a. Inside		We say that the set $S(B)$ is <i>inside</i> the set $S(A)$ if all elements that are included in the set $S(B)$ are also included in the set $S(A)$, i.e. $S(B) \subset S(A)$ and there is $S(A) \cap S(B) = B$ and $S(A) \cup S(B) = S(A)$.
b. Overlapping		We say that the sets $S(A)$ and $S(B)$ <i>overlap</i> each other if they have some equal elements, i.e. $S(A) \cap S(B) \neq \emptyset, S(A) \cap S(B) \neq S(A)$ and $S(A) \cap S(B) \neq S(B)$.
c. Almost Inside		We say that the hypothesis B is <i>almost inside</i> the hypothesis A if almost all elements of $S(B)$ are also elements of $S(A)$, i.e. $S(A) \cap S(B) \neq \emptyset, S(A) \cap S(B) \neq S(A)$ and $S(A) \cap S(B) \neq S(B)$ and $ S(A) \cap S(B) \approx S(B) $ and $ S(A) \cup S(B) \approx S(A) $. This relation is a special case of the relation “overlapping”.
d. Touching		We say that hypotheses A and B are <i>touching</i> if their contours $C(A)$ and $C(B)$ have some equal elements, whereas the equal elements are neighbored. Touching Hypotheses are a special case of overlapping hypotheses. But it is also possible that two sets are touched, and one set is inside the other set.

For the reduction process we rule that the hypothesis with the higher matching score remains while the other hypothesis of this pair is removed. Since the removed hypothesis often is a partner in more than one pair, for some hypotheses there will be no other correct “inside” partner. That is in practice that the number of hypotheses pairs may decrease for more than one pair. We want to illustrate this fact based on Figure 2: We obtain a reduction of 67 hypotheses (Figure 2a and 2d) if we successively remove the “inside” partner with the lower score. Considering the hypotheses that are used to create correct “inside” pairs (Figure 2b) and their remaining partners (Figure 2c), gives a reduction by 95 hypotheses.

The matching process lists all matched objects sorted by the scale whereas objects with the same scale are sorted by the rotation. Determining the number of common pixels of every pair of hypotheses we conclude to their relation. In Section 4 we analyse the generated hypotheses using the defined relationships.

	
<p>Fig. 2a. Hypothesized Matches (734 Hypotheses)</p>	<p>Fig. 2b. Hypothesis Pairs that fulfils the Relation “inside” (138 Pairs based on 136 Hypotheses)</p>
	
<p>Fig. 2c. Remaining Hypotheses after removing the Hypotheses with lower Score (41 Remaining Partners)</p>	<p>Fig. 2d. Remaining Hypotheses after applying the “Inside”- Criterion (667 Hypotheses)</p>

From Figure 2a and 2d we can see that the total number of hypotheses is only reduced by about 10 %. Since this reduction does not significantly simplify the hypothesis verification process we investigate in the relation “overlapping” (see Section 3.2).

4.2 The Relationship “Overlapping”

In this Section, we concentrate on the relationship “overlapping”. Although we could not significantly reduce the number of hypotheses by applying the relationship “inside” we work with the reduced number of hypotheses (see Figure 2d). For presentation purposes we first only consider the 41 remaining hypotheses of the “inside” pairs which are shown in Figure 3 (compare to Figure 2c). At the end of this Section we extend our investigations to the complete set of hypotheses.

Note that the hypotheses are concentrated in some regions of the image (see Figure 3). It seems that many hypotheses are slightly transformed (shifted or twisted) with respect to other hypotheses. This means that the intersection area of two overlapped hypotheses A and B has approximately the same size as the area of the hypothesis A and the hypothesis B respectively. We express this fact with the condition (6):

$$|S(A) \cap S(B)| \geq t|S(A)| \quad \text{AND} \quad |S(A) \cap S(B)| \geq t|S(B)|, \quad t \in [0,1] \quad (6).$$

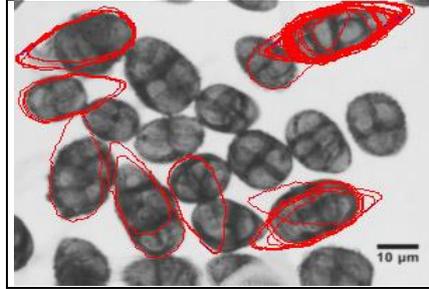


Fig. 3. Basic Hypotheses

We restrict the size of the intersection area with respect to the size of the hypothesis area by the value t . If two hypotheses fulfil the Condition (6) we say they overlap each other. As well as in the discussion of the relationship inside, we assume that the best match for an object has the highest score. From two overlapping hypotheses we therefore remove the hypothesis with the lower matching score. In the first part of Figure 4 the remaining hypotheses are given when we use the overlapping condition (6) and varying the thresholds t of the minimal common hypotheses area.

Since the condition (6) mainly combines hypotheses with comparable size, we replace the “AND” with “OR” (7). Then we repeat the test with the new condition (7). The results are given in the second part of Figure 4.

$$|S(A) \cap S(B)| \geq t|S(A)| \quad \text{OR} \quad |S(A) \cap S(B)| \geq t|S(B)|, \quad t \in [0,1] \quad (7).$$

C	$t=0.95$	$t=0.9$	$t=0.8$	$t=0.67$
(6)				
	28 Hypotheses	19 Hypotheses	14 Hypotheses	9 Hypotheses
(7)				
	19 Hypotheses	13 Hypotheses	9 Hypotheses	8 Hypotheses

Fig. 4. Applying the Relationship “Overlapping” with different conditions and degrees of common area to some selected Hypotheses (C = Condition)

As we can see from Figure 4 the number of hypotheses is as fewer as lower the threshold of the minimal common hypotheses area is. As we expected more hypotheses are removed with the second condition (7). Therefore, we take the condition (7) using

the threshold $t=0.67$ for applying the “overlapping” relation to all remaining hypotheses of the “inside” relation (Figure 5).

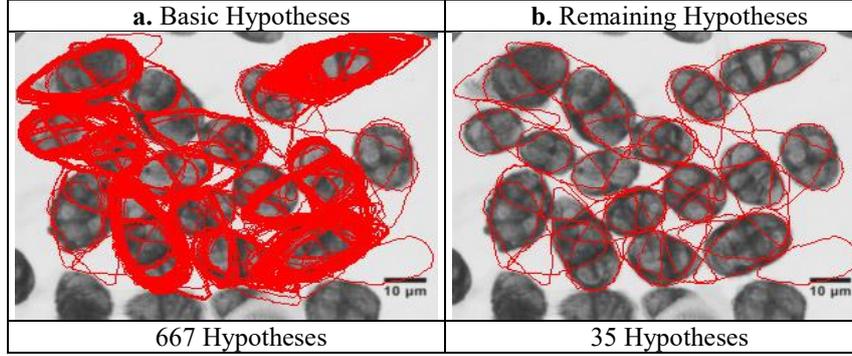


Fig. 5. Applying the Relationship “Overlapping” with Condition (7) and the Threshold $t=0.67$ after the Relationship “Inside”

From Figure 5 we can see that the applied criterion reduces the given hypotheses to about 5%. To improve the performance of the reduction process we used the described rule also to all hypothesized matches. We obtain the same result as if we remove some hypotheses with the “inside” relation. Therefore, we conclude that the first step in each hypothesis verification process should be the reduction of hypotheses using “overlapping” relation defined with condition (7) and the common area threshold $t = 0.67$. From each pair of overlapped hypotheses, the hypothesis with the lower matching score is removed.

5 Statistical Reduction of the Hypotheses

The method for hypothesis reduction that is described in Section 3.2 shows very good performance. One of the main weaknesses of this method is the arbitrary fixed threshold of common area. In this Section we want to discuss some more possibilities of hypothesis reduction based on statistical measures.

5.1 Common Statistical Measures

To determine the distribution of the matching scores that range from 0.8 to 1 , we generate a histogram by subdividing the range into non-overlapping classes with a class width of 0.05 . The number of hypotheses within each class is displayed in Figure 6.

From the Histogram in Figure 6 we cannot conclude to any distinct distribution because we only investigate in a part of the score space. Nevertheless, we can determine the mean μ_s and the standard deviation σ_s of all scores. In order to optimize the threshold, we develop a criterion for removing some hypotheses based on the mean and the standard deviation (8):

$$s_i < \mu_s + f \cdot \sigma_s \Rightarrow \text{delete hypothesis } i, \quad i = 1, \dots, h \quad (8).$$

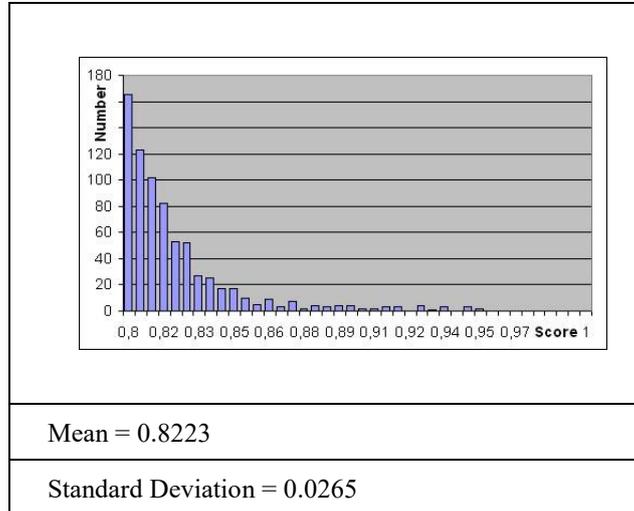


Figure 6. Histogram, Mean and Standard Deviation of the Hypothesis Scores

The number of hypotheses is denoted by h . Figure 11 shows the remaining hypothesized objects applying various factors f to the 734 hypotheses shown in Figure 1c:

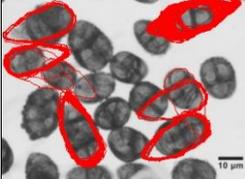
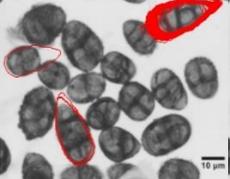
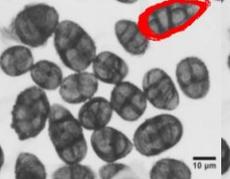
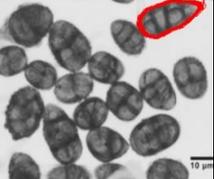
a. Hypotheses which Score mean $> (f=0)$	b. Remaining Hypotheses applying $f=1$	c. Remaining Hypotheses applying $f=2$	d. Remaining Hypotheses applying $f=3$
			
236 Hypotheses	78 Hypotheses	39 Hypotheses	23 Hypotheses

Figure 7. Remaining Hypotheses Applying Condition (9) with various Factors f

From Figure 7 we can see that the number of hypotheses can be reduced significantly if the threshold for the matching score is increased. Since we expect high scores if the model matches an object very well, we will obtain as more hypotheses for one object as better the model matches the object. The results reported in Figure 7 verify this assumption.

Remember that the matcher tolerates object occlusion and touching until 20% if the score threshold is 0.8. The described method for hypotheses reduction increases the threshold for accepting a match as a hypothesis. In the consequence it removes also hypotheses of objects which are occluded or touched. If we want to consider also such objects, we must not reduce the hypothesized matches based on Equation (8).

5.2 Hypotheses Reduction by the Evaluation of the Local Score

For each hypothesis we can store, during the matching process, the number of model pixels that have the same local contrast as the corresponding image pixel. In the following we denote this number with c_{same} . Remember that the model and the image pixel have the same local contrast if their dot product is positive. Otherwise their local contrast is inverted. To measure the quality of the hypothesis we determine, with respect to the number n of model pixels, the fraction of contour pixels of the hypothesis that have the same contrast as the model. Depending on the global contrast between the model and the hypotheses we should accept very high and very low values of this fraction. Given a threshold t the minimal fraction of the same contrast for acceptance, we determine the remaining hypotheses based on Condition (9):

$$t < \frac{c_{i,same}}{n} < (1-t) \Rightarrow \text{remove hypothesis } i, \quad t \in [0,0.5], i = 1, \dots, h \quad (9)$$

Figure 8 shows the remaining hypotheses using different values of the threshold t .

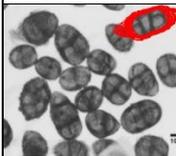
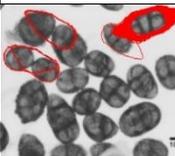
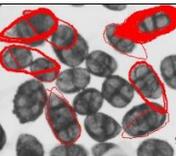
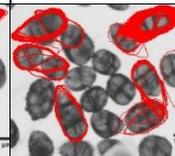
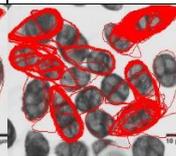
a. $t = 0.1$	b. $t = 0.15$	c. $t = 0.2$	d. $t = 0.25$	e. $t = 0.33$
				
62 hypotheses	107 hypotheses	181 hypotheses	266 hypotheses	412 hypotheses

Figure 8. Remaining Hypotheses Applying Condition (9) with different Thresholds t

It is strange that hypotheses which seem to match the object well are earlier removed than hypotheses which include some background. Figure 8 shows this phenomenon for the hypotheses of two selected objects in the image based on the threshold $t = 0.25$. Each image in Figure 8 shows a labelled hypothesis whereas red parts display negative local contrast and blue parts positive local contrast. Below each image the relative fraction of negative local contrast is given (blue parts of the contour).

Because of these unexpected results we ask if the approach of the differentiation between positive and negative local contrast is correct. The power of the similarity measure that we use is its invariance to local contrast changes, that is, we eliminate the influence of the sign of the local score by summing up the absolute amount of the local scores. On the other side we exactly evaluate the sign if we calculate the score of binary contrast changes (see Fig. 9).

Figure 10 shows the same hypotheses as Figure 9, but now pixels which local score higher than 0.9 or lower than -0.9 are marked blue. The other parts are red. Below the images the relative fraction of pixels with high local score (>0.9) is given.

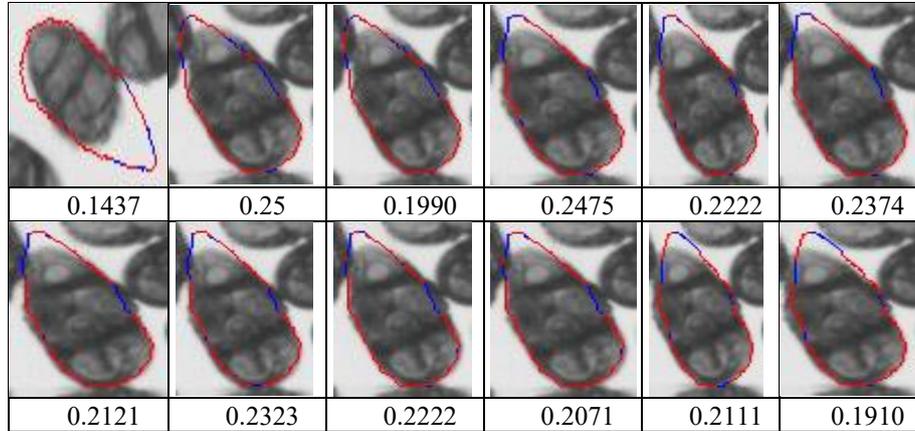


Fig. 9. Results for binary contrast changes for different Hypotheses

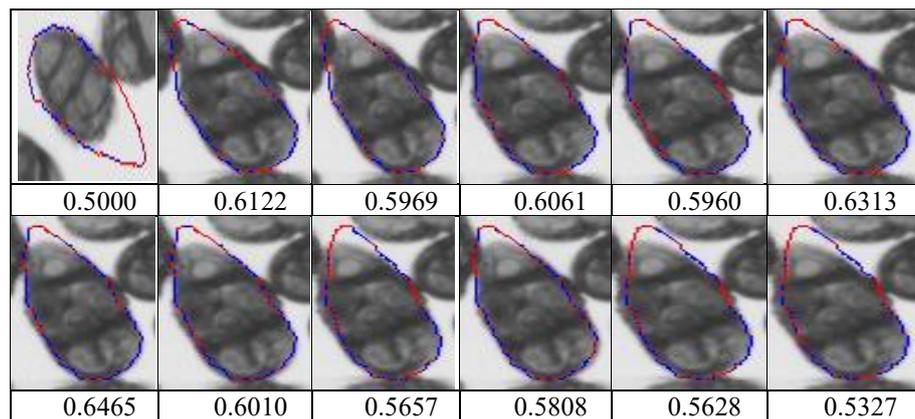


Fig. 10. Results for local score higher than 0.9 and lower than -0.9

Note that the fraction of high local scores depends on the threshold that defines a pixel with „*high local score*“. As higher as the threshold is as lower is the value of this fraction.

Like the experiment we carried out for the binary contour based on contrast changes (see Figure 8) we now create the binary contour for all hypotheses as described above by thresholding the local scores at the value 0.9 . Then we remove the hypotheses which relative fraction of high local scores is lower than (a) 0.6 (b) 0.66 and (c) 0.75 . The results are given in Figure 11.

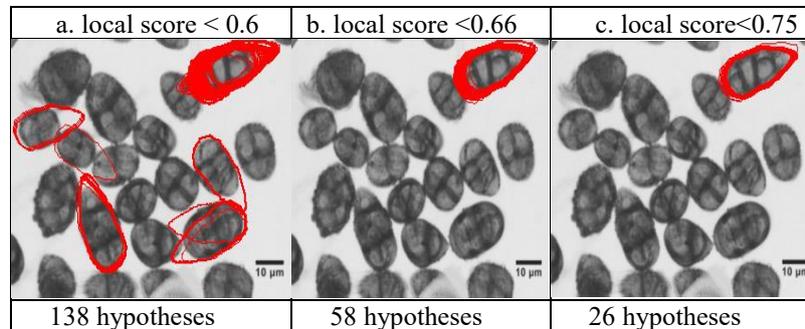


Fig. 11. Results for different local scores

From Figure 11 we can see that this method is another possibility to reduce the number of hypotheses. Since the hypotheses around the object in the right upper corner have high similarity scores most of these hypotheses remain.

6. Conclusions

In this paper we have described our hypothesis verification process for our case-based reasoning shape-object matching procedure. We have described the hypothesis-generation process in brief and the problems concerned with it. Then we described the kinds of hypothesis verification we have developed for our matching procedure. Results are given for the different rules. Finally, we introduce some statistical measures for hypothesis reduction and give results. The final results show good performance, but we can still think of some other verification measures that will further improve the results. These verification measures will be based on grouping the hypotheses, evaluation of the local similarity, and the background fraction of the found objects. This work is left for a further paper that will finish the hypothesis-verification work and will give a good summary about the work.

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