

AN ALGORITHM FOR MATCHING DISTORTED WAVEFORMS USING A SCALE-BASED DESCRIPTION

Hiroshi SAKOU, Haruo YODA, Masakazu EJIRI

Central Research Laboratory, Hitachi Ltd.,
1-280 Higashi-Koigakubo, Kokubunji,
Tokyo 185, Japan

ABSTRACT

In the process of visually matching two mutually-distorted waveforms, we first try to detect major corresponding points between them by observing their rough outlines. Then, we look for more detailed corresponding points from every division of the waveforms between the major points. This suggests that the human observer usually matches corresponding portions of the waveforms by observing them at different resolutions or viewscales. The matching algorithm proposed in this paper models this human matching process for distorted waveforms, by using a scale-based description. The algorithm is composed of two main parts; one is the method of matching each characteristic point of two waveforms at a certain scale factor, and the other is the method of controlling the matching, by which each waveform is divided into smaller portions at decreasing scale factors until the matching succeeds. The algorithm is also applied to matching of two-dimensional distorted shapes and to pattern-width measurement of semiconductor chip patterns obtained from a scanning electron microscope. The generality and practicability of this algorithm are confirmed through these experiments.

INTRODUCTION

Matching of two mutually-distorted waveforms or two-dimensional shapes is often a problem in the field of signal or image processing. This problem occurs not only in matching of images that are apparently distorted due to lack of data or difference in sampling pitch in digitizing, but also in matching of actually distorted object images or stereo images. There is a similar problem in recognition of hand-written characters and symbols on a drawing. In this case, the purpose of recognition is to estimate and classify each object by a number of characteristics detected from it. On the other hand, the purpose of matching distorted objects is to deduce the meaning of each of its portions by obtaining suitable corresponding points between two objects. That is, if one object pattern is regarded as a standard pattern such that the meanings of its portions are well-known, it is possible to deduce the meaning of every portion of the distorted object by this matching.

This paper discusses a matching algorithm for distorted waveforms using a scale-based description. The description uses loci of characteristic points (e.g. inflection points) of the scale-space image [1][2] expressed by a series of waveforms or shapes transformed by a series of Gaussian filters with various standard deviations (scale factors). Recognition of planar curves and two-dimensional shapes [3] is realized by using the hierarchical structures of their scale-space images. Scale-space image is analyzed theoretically [4]-[6] and some important properties are shown. These properties include the monotonous decrement of the number of inflection points with increment of scale factor and the existence of drastic change in the structure caused by a small distortion in the waveform. Due to this drastic change in structure, the typical algorithm based on the analysis of the hierarchical structure is not applicable to matching of waveforms with slightly larger distortion.

This paper proposes a matching algorithm for two mutually-distorted waveforms, each having partial differences in the hierarchical structure of its scale-space. This algorithm is applied to matching of two-dimensional shapes and to pattern-width measurement of semiconductor chip patterns obtained from a scanning electron microscope (SEM).

BASIC CONCEPT

In the human process of visually matching two distorted waveforms, we first try to obtain a number of major corresponding points between them by observing rough outlines characterized by the levels and positions of peaks and valleys, and the distances between them. Next, we look for more detailed corresponding points in each portion of the waveforms between the major points. That is to say, the human observer usually tries to match the waveforms, not by observing whole waveforms uniformly, but by observing every portion of them at different resolutions or viewscales. Therefore, we try to define a series of Gaussian filters with various scale factors for portions of each waveform to make two distorted waveforms almost the same shape.

The algorithm is composed of a control method for matching, which divides the waveform into smaller portions with decreasing scale factors, and a method of matching the portions expressed by a scale-based description. This concept is realized by combining these two methods.

MATCHING ALGORITHM

The scale-space representation of a waveform $f(x)$ is a series of transformed waveforms $g(x;s)$ processed to $f(x)$ by a series of Gaussian filters with various scale factors s . This transformation is expressed as follows;

$$g(x;s) = (1/\sqrt{2\pi}s) \int_{-\infty}^{+\infty} f(z) \exp\{-(x-z)^2/2s^2\} dz \quad (1)$$

Some transformed waveforms with selected scale factors for two mutually-distorted waveforms are shown as thin lines in Fig.1 (a)(b). The symbol \bullet in the figure denotes inflection points of each $g(x;s)$, and the symbol \circ denotes minimum or maximum points. It is well-known that $g(x;s)$ with a large s only maintain macroscopic characteristics of the original waveform, and when s decreases, the shape of $g(x;s)$ approaches that of the original. Therefore, even for two mutually-distorted waveforms, the transformed waveforms at some large s have almost the same profiles. However, even if matching is executed between the transformed waveforms at a large scale factor, the matching is too rough because the transformed waveforms lose the details of the originals. Therefore, it is important to decide suitable minimum scale factors with which the Gaussian filters make the two waveforms almost equal. Furthermore, these scale factors ought to depend on the degree of local distortion between each portion of the two waveforms.

The following sections discuss the method of matching characteristic points of two waveforms transformed with certain scale factors, and the control

method for the matching, by which each waveform is divided into smaller portions with decreasing scale factors.

The matching result for the waveforms in Fig.1 (a) and (b), using this algorithm, is shown in (c).

MATCHING METHOD

This section describes the method of matching the two waveforms $g(x;s)$ and $G(X;S)$ using scale factors s and S respectively. This matching method consists of two parts as shown in Fig.2. They are detection of characteristic points and calculation of the minimum total error for every combination of characteristic points.

Distortion occurs in both width and height of the waveform. Therefore, we define two distortion functions, H in width and V in height. These functions are assumed to be polynomials, $a_0 + a_1x + \dots + a_nx^n$ and $b_0 + b_1x + \dots + b_nx^n$, respectively. The distortion is regarded as the transformation of the point $(x_i, g(x_i;s))$ to the point $(H(x_i), V(g(x_i;s)))$. Thus, if we pick up the same number of points $(x_i, g(x_i;s))$ on one waveform as the points $(X_i, G(X_i;S))$ on the other waveform, matching for the distorted waveform is reduced to a problem of deciding coefficients of H and V and the combination of corresponding points which make both of the following square errors minimum;

$$d_0 = \sum |X_i - H(x_i)|^2 \tag{2}$$

$$d_1 = \sum |G(X_i;S) - V(g(x_i;s))|^2 \tag{3}$$

However, the number of points on the waveforms and their combinations are infinite because the waveforms is continuous. Therefore, we take finite characteristic points from the waveform, which satisfy the following equations;

$$d^m g/dx^m = 0 \tag{4}$$

$$d^m G/dX^m = 0 \tag{5}$$

These characteristic points, hereinafter called CPs, are maximum or minimum points where $m=1$ and inflection points where $m=2$. Suppose that there are k CPs on $g(x;s)$ and K CPs on $G(X;S)$, and we pick up h ($\leq \min\{k, K\}$) from each of them, making it possible to calculate coefficients of H and V such that square errors d_0 and d_1 are both minimum. Then, the least square error must be calculated for every combination of h CPs of the k and K CPs, considering agreement in polarity order. Polarity means the peak or valley where $m=1$, or the sign of the gradient where $m=2$. The best correspondence of h CPs between those of $g(x;s)$ and $G(X;S)$ is obtained when the following total square error [7] has the least value;

$$d = (w_0 d_0 + w_1 d_1) h^{-c} \tag{6}$$

where h varies in the range of $3 \leq h \leq \min\{k, K\}$, w_0 and w_1 are weights, and h^{-c} ($c \geq 1$) is the multiplier for the proper estimation of error value against the tendency for the errors d_0 and d_1 to decrease as h decreases.

Advantages of this matching method are;

- (1) Local CPs with extraordinary unmatched distortion function H and V have no significant influence on matching, because they are removed automatically from the best combination having the least error,
- (2) The best correspondence of CPs between waveforms and the coefficients of polynomials are obtained simultaneously.
- (3) If the degree of distortion can be predicted, it is possible to avoid recognition error by limiting the range of coefficients or the total square error.

The disadvantage of this method is that the combinatorial explosion of CPs reduces processing speed. Taking the polarity and order of CPs into consideration, the number of combinations of h CPs from k CPs is calculated by the summation of $r_0 = {}_{h_0}C_h$ and $r_1 = {}_{h_1}C_h$, where $h_0 = [(k+h)/2]$, $h_1 = [(k+h-1)/2]$ and $[\]$ is Gaussian parenthesis. For example, where $h=3$ and $k=5$ with polarity order $(+ - +)$, the number of combinations is 5, which is the summation of $r_0 = {}_4C_3 = 4$ with the polarity

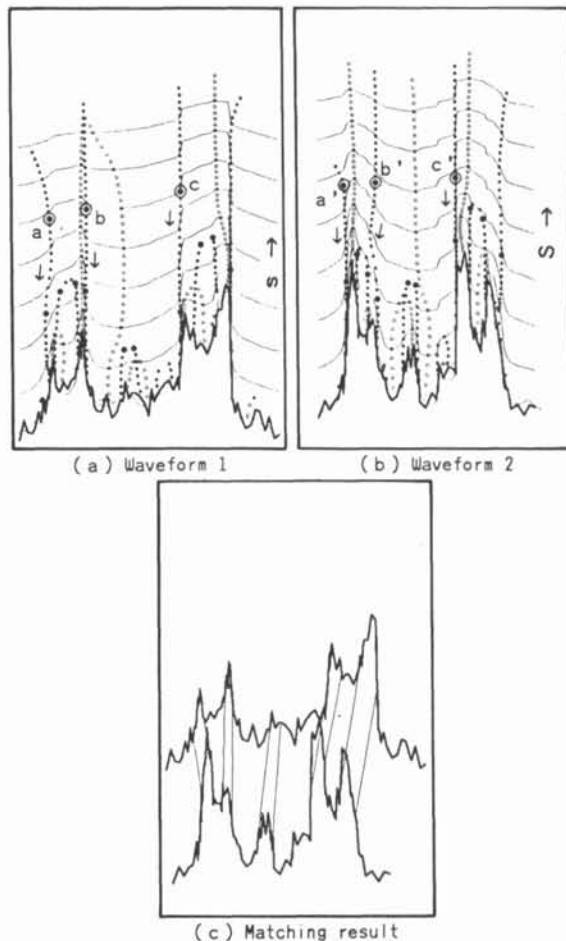


Figure 1. Matching process of one-dimensional waveforms.

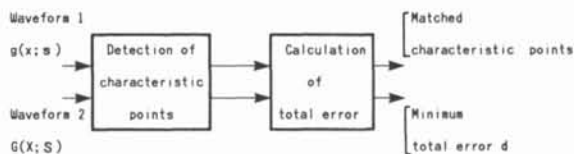


Figure 2. Outline of matching method.

order $(+ - +)$ and $r_1 = {}_3C_3 = 1$ with the polarity order $(- + -)$. Similarly, we denote the number of combinations of h CPs of K CPs on the other waveform as the summation of $r_0' = {}_{h_0'}C_h$ and $r_1' = {}_{h_1'}C_h$, where $h_0' = [(K+h)/2]$ and $h_1' = [(K+h-1)/2]$. Then, the number of combinations between the two waveforms is expressed by $r_0 r_0' + r_1 r_1'$. Therefore, the number of the total combinations M is calculated by $\sum r_0 r_0' + r_1 r_1'$, because h itself varies as stated before. This total number of combinations M explodes, as k or K increases. For example, M becomes 3 ($k=4$), 61 ($k=6$), 575 ($k=8$), 4178 ($k=10$) and 27710 ($k=12$), where $k=K$ and $3 \leq h \leq k$.

To cope with this problem, a coarse-to-fine control method is developed to handle only a few CPs. This method, which will be described in the next section, divides the original waveform into an increasing number of portions as the scale factor is decremented.

CONTROL METHOD

There are two typical cases of waveform distortion. One is where distortion is distributed almost equally over the entire waveform. The other is where distortion exists in a number of local portions. The former is caused mainly by differences in sampling pitch or amplifier-gain in obtaining waveform data. For this distortion, it is usually satisfactory to apply the matching method based on distortion functions with low-order polynomials. However, a problem occurs if this method is applied in the latter case: it is impossible to decide the corresponding CPs on the locally-distorted portion because the combination of CPs on the undistorted portion usually has a minimum total error. Though the matching method with high-order polynomials can be examined, its calculation usually demands much time. Therefore, we propose a control method which can cope with both this problem and the explosion problem described in the previous section.

In this method, the waveform is divided into a locally-distorted portion and a normal portion. The relationship between CPs on a divided portion of one waveform and CPs on that of the other waveform must be much simpler than the relationship between CPs on the entire waveform and the other entire waveform, thus making it possible to use lower-order polynomials. The division has the additional advantage of checking the number of CPs in the matching. This method controls the division and matching of each divided portion as follows;

(1) The first matching --- The matching between CPs on $g(x;s)$ ($x_s \leq x \leq x_e$) and $G(X;S)$ ($X_s \leq X \leq X_e$) is executed at every scale factor s and S by varying them from large to small values. The matching is stopped when both numbers of CPs on each waveform are just beyond a certain constant value N , and the corresponding CPs, (x_1, \dots, x_h) and (X_1, \dots, X_h) , and the scale factors s' and S' for minimum total error are obtained. Since it has been proved that the number of CPs such as inflection points increases monotonously as the scale factor decreases [4][5], the number of the scale factor at which the number of CPs exceeds N is zero or one. In the former case, the lower limits of scale factors, s_s and S_s are set at an appropriately low level.

(2) From the second to the n -th matching --- Matching of CPs on every portion of one waveform with CPs on corresponding portions of the other waveform is executed in the same way as in the first matching. Each portion is a part of a waveform between a pair of corresponding adjacent CPs, obtained at the first matching. Subsequent matchings are executed repeatedly in the same way until the scale factor attains the low limit.

The following program C-MATCH written in "C" program language realizes this matching control method. In the program, the definition of variables and transfer operations are omitted or abbreviated.

```
C-MATCH(S0,S1,X0,X1,s0,s1,x0,x1)
/* S0/S1 s0/s1 : range of each scale factor */
/* X0/X1 x0/x1 : range of each waveform */
{ /* step 1 : stop conditions */
  if(S1 == Ss){goto end;}
  if(s1 == ss){goto end;}
  /* step 2 : matching */
  for(s=s1,err0=9999; s >= s0; s--)
    { /* detection of xni (=CPs) and
      their number h on gi (=g(x;s)) */
      GETPOINTS(gi,x0,x1,k,xni);
      /* examination for number h */
      if(h >= N){goto next0;}
      for(S=S1; S >= S0; S--)
        { /* detection of Xni (=CPs) and
          their number K on Gi (=G(X;S)) */
          GETPOINTS(Gi,X0,X1,K,Xni);
          /* examination for number K */
          if(K >= N){goto next1;}
          /* detection of best corresponding CPs
            (xi and Xi), which has minimum total
```

```
error (err), among all combinations of
CPs (xni and Xni) */
/* number of corresponding CPs
   on each waveform : h */
MATCH(gi,k,xni,Gi,K,Xni,h,xi,Xi,err);
/* storing of all data, if minimum total
error is smaller than that of last
combination at s and S */
if(err < err0){s'=s; S'=S; Xni' <= Xni;
              xni' <= xni; err0=err; (1 ≤ i ≤ h)}
next1;}
next0:
if(err0 >= const){ /* err0 is too large */ goto end;}
/* step 3 : matching for every divided portion */
for(i=1; i <= h-1; i++)
  {C-MATCH(S0,S',Xni,Xni+1,s0,s',xni,xni+1);}
end;}
```

Step 1 in this program contains conditions to judge if the recursive calling is stopped, and if one of the conditions is met, the execution is returned to its parent program. In step 2, x^i (CPs) on the interval $[x_0, x_1]$ of one waveform $g(x;s)$ at the scale factor s , and X^i (CPs) on the interval $[X_0, X_1]$ of the other waveform $G(X;S)$ at the scale factor S are first detected by the subroutine GETPOINTS, and numbers h and K of the CPs are also examined to see if they exceed N . Then, the matching between x^i and X^i is executed by the subroutine MATCH, which uses the matching method explained in the previous section. Of these results, only those with the best corresponding CPs (x^i and X^i) having the least total error and scale factor s' and S' are stored. However, if the least total error is more than a constant value (const), the program decides that the matching between entire (or divided) waveforms is impossible due to large distortion. In step 3, a more detailed matching between portions $[x^i, x^i+1]$ and $[X^i, X^i+1]$ of waveforms, divided by the CPs obtained in step 2, is executed by the recursive calling of this program. The initial values of variables in this program are $S_s(S_0)$, $S_s(S_1)$, $X_s(X_0)$, $X_s(X_1)$, $s_s(s_0)$, $s_s(s_1)$, $x_s(x_0)$, $x_s(x_1)$.

The best corresponding CPs between entire original waveforms in the first matching are shown by the symbol ● in Fig.1 (a) and (b). The second matching between every corresponding portion of each waveform is executed for decreasing scale factors from s' and S' . These portions are the intervals from the starting point of one waveform to a in Fig.1 (a), from the starting point of the other waveform to a' in Fig.1 (b), a to b, a' to b', b to c, b' to c', c to the end of one waveform, and c' to the end of the other waveform. Though both ends of each portion move slightly as scale factors decrease, as shown by arrow-symbols in the figures, both ends of every portion at every scale factor can be easily obtained by considering the connectivity to both ends for the previous scale factor. The result of the second matching is shown by the slightly bigger symbols ● in the figures. The final correspondence between the two waveforms is shown in Fig.1 (c).

In this method, for large scale factors at which there are few CPs, first matching is executed on the entire waveform. On the other hand, for small scale factors at which there are many CPs, detailed matching is executed after the waveform is divided into portions having fewer CPs. Thus, one advantage of this method is that the number of total combinations of CPs on every portion at a certain scale factor is far less than the number of CPs on the entire waveform at the same scale factor. For example, in the matching of waveforms shown in Fig.1 (a) and (b), if N , the upper limit of CPs, is set to a large value, the matching between 10 CPs on each entire waveform must be executed and the number of total combinations M is 4178. However, if N is set to an appropriately small value, there can be only 4 CPs on each of 3 portions due to the division of waveform. Since the number of combinations of 4 CPs is 3, the number of total combinations becomes $9 (= 3 \times 3)$ and is about 1/460 of the former. Another advantage is that distortion functions with low-order polynomials can be used to match corresponding portions of two waveforms, because division reduces the complicated relationship between CPs of two

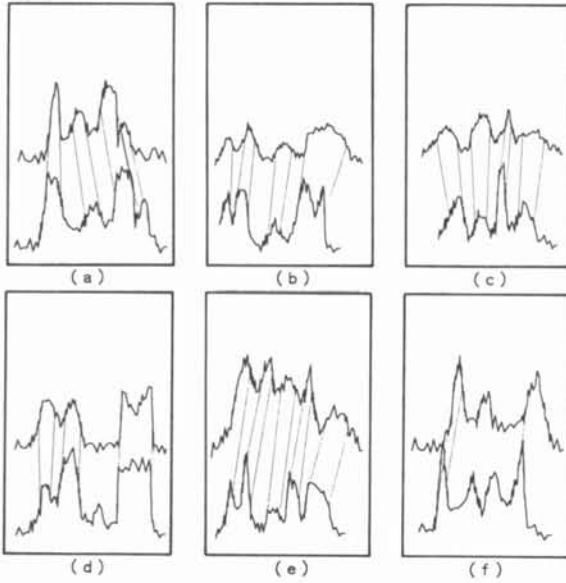


Figure 3. Matching results of some one-dimensional waveforms.

Table 1. Coefficients of polinomial and total error.

Items	(a)	(b)	(c)	(d)	(e)	(f)
Coefficient a_0	-7.5	1.0	6.0	0.0	-5.5	-5.0
Coefficient a_1	1.4	0.9	0.8	1.0	1.0	1.0
Total error d	1.7	2.1	3.1	3.4	5.2	6.8

entire waveforms to several simpler ones between CPs of corresponding portions. These advantages decrease the amount of calculation required: an important factor to realize high-speed processing. Furthermore, in this control method, except for the tracing of the ends of every divided portion, the matching between (divided) waveforms is executed independently at every scale factor by using the characteristics of position and height of each CP. That is the reason why this method is applicable to matching between each mutually-distorted waveform having partial differences in hierarchical structure of its scale-space representation.

Matching results for several pairs of mutually-distorted waveforms are shown in Fig.3 (a)-(f). These results confirm the usefulness of the matching algorithm for the waveforms, such as those which are entirely-extended or contracted as shown in (a)(c), the ones having peaks or valleys of different heights or at different positions as shown in (b)(c)(e), and ones to which peaks or valleys appear or disappear as shown in (b)(d)(f). In this experiment, we assumed the distortion functions H and V to be $a_0 + a_1x$ and $b_0 + b_1x$, respectively, and used parameters $m=2, w_0=3, w_1=1, c=2, N=6$. Coefficients a_0 and a_1 , and total error d obtained at the first matching are shown in Table 1, where symbols (a)-(f) correspond to those of Fig.3. The coefficient a_0 represents the positional error of the lower waveform compared with the upper one in Fig.3. Also, the coefficient a_1 represents the degree of extension or contraction. The total error d represents a degree of distortion that the distortion functions, which are first-order polynomials, can not express. These results seem to agree well with human judgment, and to show the validity of this matching algorithm.

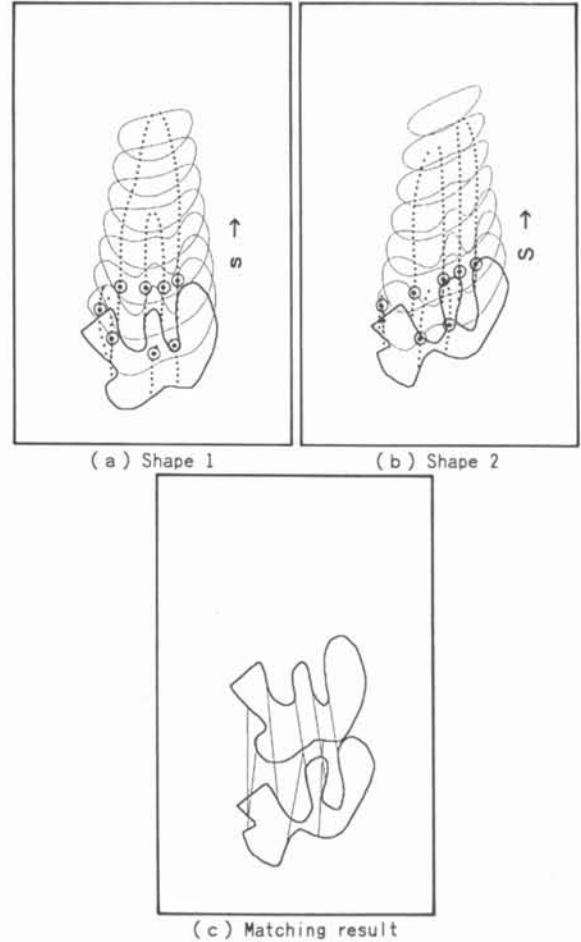


Figure 4. Matching process of two-dimensional shapes.

APPLICATION TO TWO-DIMENSIONAL SHAPES

It is possible to apply the matching algorithm explained in the previous chapter to any problem which can be reduced to the matching of one-dimensional waveforms. In this chapter, the algorithm is applied to matching between two mutually-distorted shapes, which are expressed by closed contour curves $p(x,y)$ and $P(X,Y)$, respectively. The curve $p(x,y)$ can be expressed in terms of two periodic functions $x=u(l)$ and $y=w(l)$, where the variable l is measured along the curve from a specified starting point. We can obtain the functions $u'(l;s)$ and $w'(l;s)$ by applying the Gaussian filter with a scale factor s to the original functions $u(l)$ and $w(l)$. The closed curves reconstructed by the functions $u'(l;s)$ and $w'(l;s)$ at certain scale factors are shown by thin curves in Fig.4 (a). The curves represent the original shapes macroscopically with a reasonable degree of accuracy depending upon each scale factor. Next, we define, as CPs, points with coordinates l_i where the curvature r is zero [3]. The curvature r is formulated by;

$$r = (\dot{u}'\ddot{w}' - \dot{w}'\ddot{u}') / (\dot{u}'^2 + \dot{w}'^2)^{3/2} \tag{7}$$

where $\dot{u}' = du'/dl, \dot{w}' = dw'/dl, \ddot{u}' = d^2u'/dl^2, \ddot{w}' = d^2w'/dl^2$.

We can similarly define two functions $U'(L;S)$ and $W'(L;S)$, and also CPs with coordinates L_i for the other closed curve $P(X,Y)$ as shown in Fig.4 (b). The square errors

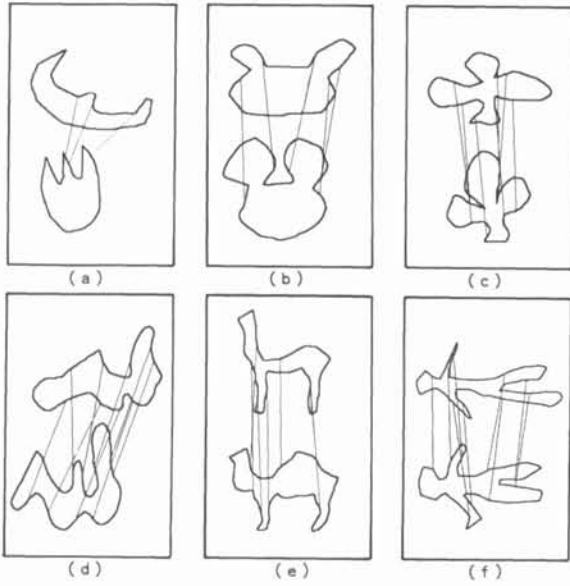


Figure 5. Matching results of some two-dimensional shapes.

in this case, corresponding to equations (2) and (3), are defined as follows;

$$d_0 = \sum |L_i - H(l_i)|^2 \quad (8)$$

$$d_1 = \sum |D(L_i) - V(d(l_i))|^2 \quad (9)$$

where $d(l_i)$ (or $D(L_i)$) denotes the distance between the CP with coordinate l_i (or L_i) and the centroid of the closed curve $p(x,y)$ (or $P(X,Y)$). Since the matching problem of shapes results in a one-dimensional problem, it can be solved by the algorithm described in the previous chapter.

The corresponding CPs obtained by the first matching are shown by symbol ● in Fig.4 (a) and (b), and the final result is shown in (c). This result shows directly that the algorithm can be applied to shapes, each having partial differences in the structure of its scale-space representation. Some results are shown in Fig.5. In this experiment, we assumed the distortion functions to be first-order polynomials, and used parameters $w_0=3$, $w_1=1$, $c=2$, $N=6$.

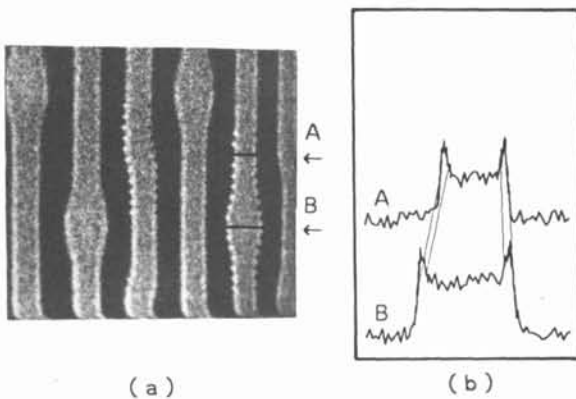


Figure 6. Matching result of SEM waveforms for pattern-width measurement.

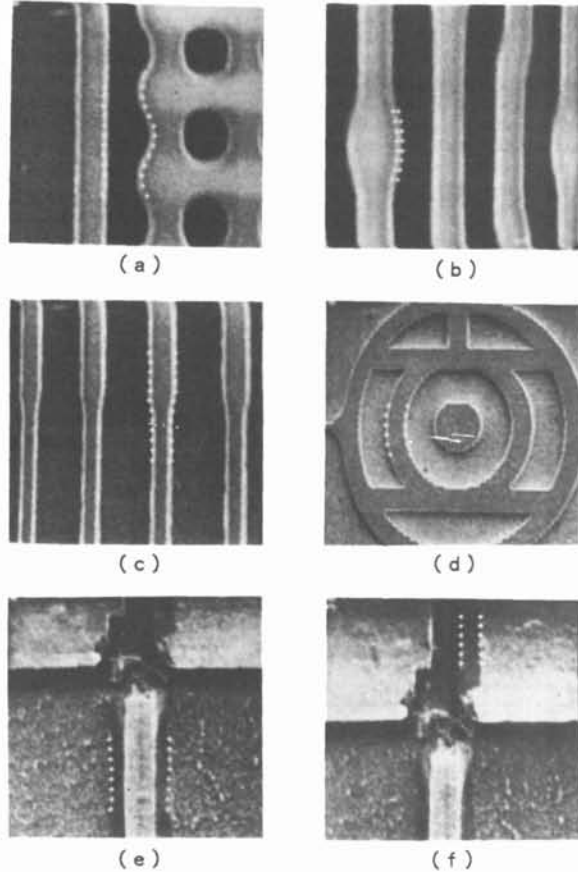


Figure 7. Matching results of SEM waveforms.

APPLICATION TO SEM WAVEFORM ANALYSIS

In this chapter, we apply the algorithm to matching between real waveforms of semiconductor chip patterns obtained from a SEM. Pattern-width measurement is an important inspection process in semiconductor production. Recently, SEMs have been increasingly used to observe the extremely fine patterns of semiconductor chips because the SEM image maintains its high resolution capability even at a high magnification power. One of the problems in realizing pattern-width measurement by means of a SEM is that the observed waveform is often distorted due to differing edge sharpnesses of semiconductor patterns and the charge-up effect of electrons. Therefore, the simple template matching method can not be applied to detect edges necessary to measure the pattern width. To overcome this problem, the proposed algorithm is used to match CPs on the template and object waveform, and we obtain each corresponding portion of two waveforms. The position of each edge necessary to measure the pattern width is calculated by a DP-matching method between a portion of object waveform and the corresponding portion of the template which contains the edges.

The pattern edges detected by this algorithm are shown by cross marks in Fig.6 (a). In this matching, the edges on wide-pattern portion B are detected correctly even though the waveform at the narrow-pattern portion A is used as a template. Fig.6 (b) shows the correspondence of CPs on each waveform. This result reveals that the algorithm can cope with fairly large distortion of waveform in the width direction. Results for other samples are shown in Fig.7.

Fig.8 shows the repeatability of pattern width as measured by this algorithm. This is a histogram of 100 measurements of the same portion on a semiconductor chip pattern. The degree of repeatability is 0.03 micrometers (at 3σ , for a pixel size of 0.04 micrometers). The average processing time for a matching using a 16-bit microcomputer is kept under 0.6 seconds by limiting the range of the scale factor variation and the number of times the waveform is divided. These results also confirm the practicability of the algorithm proposed in this paper.

CONCLUSIONS

A matching algorithm between mutually-distorted waveforms using a scale-based description is proposed. The algorithm is composed of the matching method and the control method of matching, summarized as follows;

(1) Matching method: The inflection points of a waveform transformed by a Gaussian filter with a certain scale factor (standard deviation) are regarded as characteristic points of the original waveform. The best correspondence of characteristic points between the waveforms is calculated by the least square error method assuming some distortion polynomials with unknown coefficients. In this method, all combinations of the characteristic points are examined to obtain a best match for the entire waveform without being influenced by local unmatched portions. A rough degree of the distortion can be estimated by analyzing the coefficients of the polynomials.

(2) Control method: This method controls the above matching process, by which each waveform is divided into smaller portions with decreasing scale factors until the matching succeeds. This division of waveforms checks the combinatorial explosion of characteristic points and the increment of the order of polynomials, thus minimizing the processing time for the matching. As a result, every portion of each waveform is matched with its best-suited scale factor.

The algorithm is also applied to matching of two-dimensionally distorted shapes and to pattern-width measurements of semiconductor chip patterns obtained from a scanning electron microscope. The generality and practicability of this algorithm are confirmed through these experiments.

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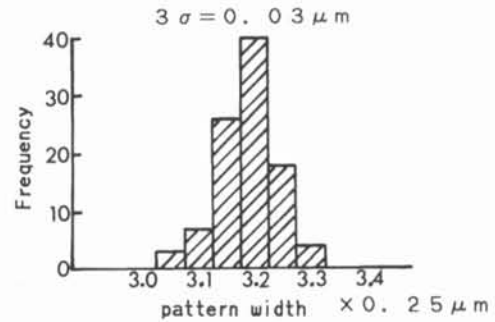


Figure 8. Repeatability of pattern-width measurements.

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