

RE-SEQUENCING A HISTORICAL PALM LEAF MANUSCRIPT WITH BOUNDARY-BASED SHAPE DESCRIPTORS

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ABSTRACT:

A stack of 66 historical Indian palm leaves, which were produced in the 8th Century AD, is kept in the Museum Rietberg, Zuerich. On the leaves, there are figures and a long poem, inscribed in ancient Sanskrit language and narrating a love story. The original sequence of the leaves was lost long time ago. At one point in history, the stack of the leaves was damaged by a mouse biting pieces off. Only the first 18 leaves have their pages numbered in Sanskrit language, but the rest of them got out of order. If it is assumed that the mouse chewed at the leaves in a regular manner, the geometry of the leaf perimeter, as left over after eating, should bear useful information to find the original sequence. After acquiring digital images of the leaves and a pre-processing phase, an inner boundary-tracing algorithm was applied to all leaves in order to segment them. The fundamental data used in this work are boundary coordinates of the leaves. In order to obtain quantitative shape similarity measures, two different Boundary Based Shape Descriptor algorithms were applied to the boundary data: Fourier descriptors and a rotation-translation invariant boundary intersection-based shape descriptor. Shape descriptors indicate the similarity of different leaves. These similarity measures among all of the leaf pairs were arranged in form of a symmetric square matrix. With this matrix and a threshold similarity value one can determine the most probable ancestor and successor leaves for a pointed leaf. In the final step, a Tree Search scheme that starts from the 18th (fixed) leaf and ends at the 66th (relaxed) leaf was established to generate the most probable sequence. Every node in the tree was defined as a leaf and branched to the most probable neighbor leaves. The similarity measures were expressed as costs of the arcs, which connect two nodes in the tree. The sequence which has minimum total path cost was proposed as the most probable original sequence.

1. INTRODUCTION

In the collection of *Museum Rietberg Zuerich* is an old palm leaf manuscript from India, consisting of 66 folios, inscribed on both sides. Originally, they had all the same dimensions and were once tightly bundled. On them are 100 erotic poems by a 8th century AD Sanskrit poet (by the name of Amaru) inscribed, many of which are illustrated with one or more pictures. The manuscript was prepared about 200 years ago to be kept as a bundle. All folios have a hole in the center through which a string was drawn to tie all leaves tightly between two wooden boards (Figure 1). However, the sequence of these poems is unknown (Fischer, 2002). The manuscript was kept for two centuries in an Indian library. Some time ago, a mouse did start to eat part of these folios. It is likely that at that time, the right sequence was still established, which was later lost, except at the beginning: Folios 1-18 are paginated and therefore their sequence is known. The mouse did not destroy the entire manuscript. She nibbled only about 5-10 % away from each leaf, mostly at the left side (Figure 2). If it is assumed that the mouse ate the leaves in a regular manner, the geometry of the leaf perimeter, as left over after eating, should bear useful information to find the original sequence.

Since the rest of the leaves does not give any information about the sequence, we must focus only the geometry of the harmed part in order to avoid irrelevant data. The holes in the center of the leaves constitute a base point that is approximately at the same position on the all leaves. After the pre-processing phase i.e. rectification, the harmed left parts were cropped from the full images, and saved as different image files. All processes were performed based on these cropped images.

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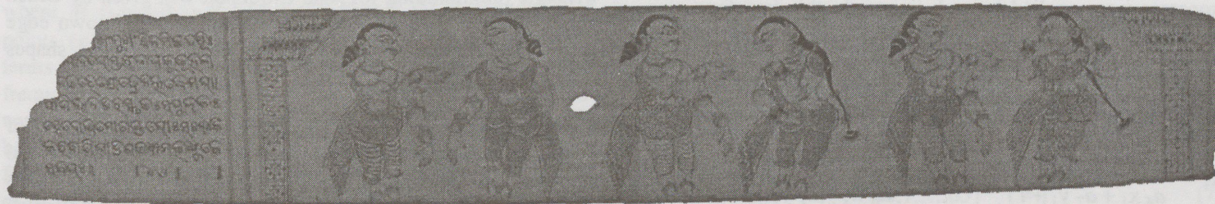


Figure 1: Front face of a leaf with hole for bundling up. Left perimeter side is damaged by the mouse.

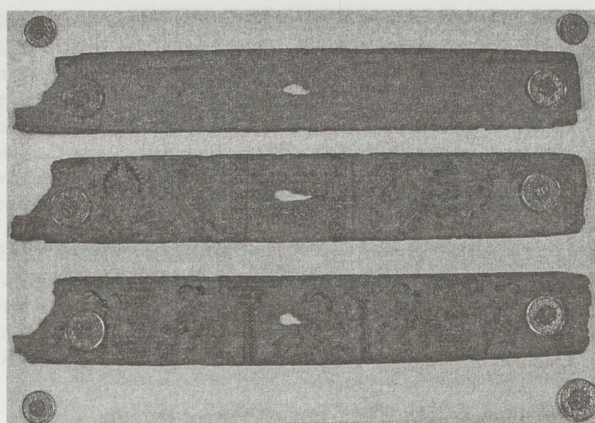


Figure 2: Left sides of the leaves, eaten by the mouse.

In the final step, a *Tree Search* scheme that starts from the 18th (fixed) leaf and ends at the 66th (relaxed) leaf was established to generate the most probable sequence. Every node in the tree was defined as a leaf and branched to the most probable neighbor leaves. The similarity measures were expressed as costs of the arcs, which connect two nodes in the tree. The sequence which has minimum total path cost was proposed as the most probable original sequence.

The paper is organized as follows. In the second section, the adopted methodology that is used to predict the most probable sequence is described. The methodology includes the rectification of the images, boundary tracing, shape description, and evaluation of the shape data using tree-search. The obtained results and the conclusions are given in the third section.

2. METHODOLOGY

2.1 Image Acquisition

The digital images of the leaves were acquired with a Sony DSC-F505 Cybershot CCD camera in free-hand mode at the Museum Rietberg Zuerich. The image size was 1600x1200 pixels, and the focal length was set at 7.1 mm, which is the widest-angle position for the camera. Three of the leaves, placed on an A4-sized white paper, were imaged in per image. The corners of the A4-sized page were used as reference points in the following rectification process, which will be described in the following section.

2.2 Rectification of the Images

Due to the varying orientation of the camera, perspective differences among the images occurred. Especially, the perspective effect due to the unstable *Omega* angle was observed in most images (Figure 3). In order to compensate this effect, *projective transformation* and *bi-linear resampling* processes were applied to each image. In this transformation, the corners of the A4-sized white page were used as reference points. Projective transformation parameters (a_i) were calculated using four common points according to the well known formula (Equation 1).

$$X_i = \frac{a_0 x_i + a_1 y_i + a_2}{a_6 x_i + a_7 y_i + 1}, \quad Y_i = \frac{a_3 x_i + a_4 y_i + a_5}{a_6 x_i + a_7 y_i + 1} \quad (1)$$

where $i = \{1, 2, 3, 4\}$. Then, the bi-linear resampling process was applied to obtain the corrected images (Figure 4).

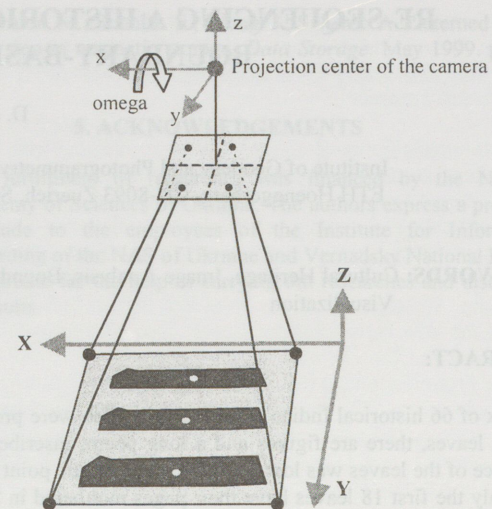


Figure 3: Imaging geometry and common points.

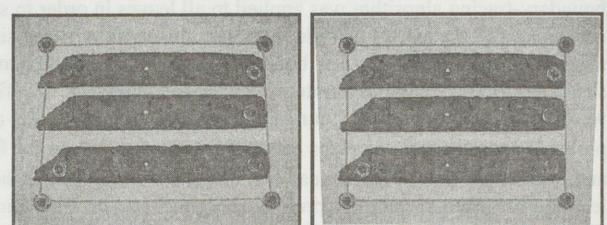


Figure 4: (left) raw image, (right) rectified image.

Radial distortion of the CCD camera was neglected because it is not relevant to our problem. After the projective transformation, each leaf in the images was cropped and saved as an image file. In the cropping process, the holes in the center of the leaves were assumed as the origin of the predefined 2D leaf coordinate system. This approach puts all leaves to the same alignment.

2.3 Boundary Tracing

Segmentation is one of the most important image analysis tasks. Its main goal is to delineate certain objects in the image and to distinguish them from irrelevant image parts. There are different segmentation methods according to their search strategies: thresholding techniques, edge based, region based, and hybrid methods. Edge based methods commonly use *edge detection operators* such as *Laplacian*, *Sobel*, *Kirsch*, *Marr-Hildreth*, and *Canny* operators. This is usually followed by other processing steps in order to combine edges into edge chains, for example *Hough transformation*. Some of the edge based segmentation methods need prior information about shape, such as *Snakes* (Kass et al., 1987) and graph searching or dynamic programming based *edge following* methods (Martelli, 1972, Furst 1986). A successful application of LSB-Snakes and dynamic programming for road extraction was given by Gruen and Li (1997). *Boundary tracing* is another well-known edge based segmentation method used to delineate closed shapes (Liow, 1991, Kovalevsky, 1992).

To generate the boundary-based descriptors, boundaries of every leaf must be delineated. Because of simplicity and suitability to our case, an *inner boundary tracing* method was adopted to segment the leaves from image background (Sonka, Hlavac, Boyle, 1993). Basically it comes in 4-connectivity and 8-connectivity modes. We opted for the 8-connectivity mode

because it generates better, less spurious results. The upper right corner of the all leaf parts was selected as starting point for the boundary-tracing algorithm. After the operation, inner boundary coordinates of every leaf were saved to an ASCII file. The developed software can generate boundary coordinates of the leaf images in a semi-automatic or fully automatic manner.

2.4 Fourier Descriptors

Fourier descriptors method is a 2-D boundary analysis method, based on Fourier analysis of the function derived from the boundary (Richard and Hemami, 1974, Zhan and Roskies, 1972, Persoon and Fu, 1977). The main advantage of the method is its invariance to translation, rotation and scaling of the shape to be described. Therefore, shape description becomes independent of the relative position and size of the object in the image space. One of the most popular implementation area of the Fourier descriptors is handwritten character recognition (Granlund, 1972, Cao et al., 1994). A classification of 2-D partial shapes using Fourier descriptors was given by Lin and Chellapa (1986). Another interesting implementation of Fourier descriptors in medicine was presented by Veropoulos et al. (1998). In this work, boundary tracing followed by Fourier shape descriptors was used to represent Tubercle Bacilli. In photogrammetry, the matching of area and line features with Fourier descriptors was proposed as a feature-based matching method by Tseng and Schenk (1992), Tseng et al. (1997).

Let us represent the boundary points as coordinate pairs; $(x_0, y_0), (x_1, y_1), \dots, (x_{N-1}, y_{N-1})$. Each coordinate pair can also be represented as a complex number. In this case, the x axis is treated as the real axis and the y axis as the imaginary axis of a sequence of complex numbers.

$$s(k) = x(k) + jy(k) \quad k = 0, 1, \dots, N-1 \quad (2)$$

This representation has one great advantage: It reduces a 2D to a 1D problem. The discrete 1D Fourier transform of $s(k)$ is:

$$a(u) = \frac{1}{N} \sum_{k=0}^{N-1} s(k) \exp[-j2\pi uk/N] \quad u = 0, 1, \dots, N-1 \quad (3)$$

The complex coefficients $a(u)$ are called the *Fourier descriptors* of the boundary. The inverse Fourier transform of the $a(u)$'s restores $s(k)$.

$$s(k) = \sum_{u=0}^{N-1} a(u) \exp[j2\pi uk/N] \quad k = 0, 1, \dots, N-1 \quad (4)$$

Instead of the full set of $a(u)$ coefficients only the first M coefficients can be used in the inverse transformation. The result is an approximation of $s(k)$.

$$\tilde{s}(k) = \sum_{u=0}^{M-1} a(u) \exp[j2\pi uk/N] \quad k = 0, 1, \dots, N-1 \quad (5)$$

where M is less than N ($M < N$). That is, the same number of points exists in the approximate boundary, but not as many terms are used in the reconstruction of each point. High frequency components represent fine details, and low frequency components determine the global shape. Thus the smaller M becomes, the more detail is lost on the boundary (Figure 5). A few Fourier descriptors can be used to capture the gross essence of a boundary. This property is valuable, because these coefficients carry shape information. Thus they can be used as the basis for differentiating between distinct boundary shapes (Gonzales and Woods, 1993).

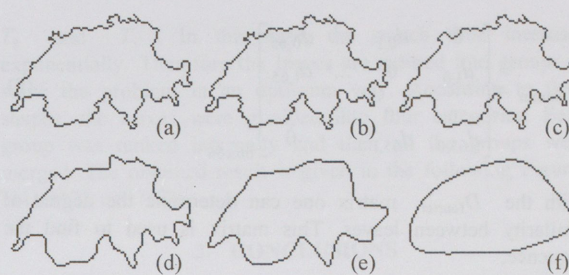


Figure 5: (a) original boundary with 708 boundary elements, (b), (c), (d), (e), and (f) are inverse Fourier transforms using 250, 150, 75, 25, and 10 coefficients, respectively.

In this application, Fourier descriptors of the boundary elements were calculated using 1D Fast Fourier transformation. Then, the Euclidean distance between the first 250 Fourier descriptors of the two different leaves is used as a shape similarity measure. The number of Fourier descriptors (250) used for calculation of the shape similarity measure was determined empirically (Figure 6). Also, these distance measures are aided by additional shape features (*area* and *dMax*) with proper weights (Figure 7).

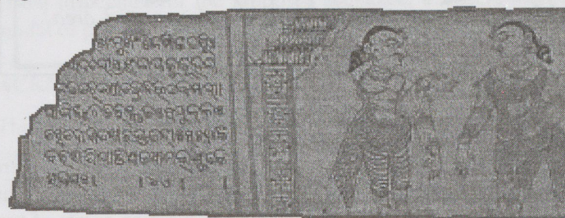


Figure 6: The original boundary has 1532 boundary elements. 250 Fourier coefficients (~16%) were used to capture the whole leaf part boundary.

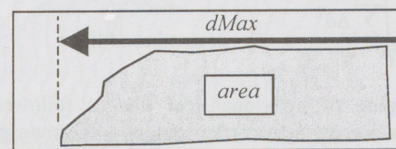


Figure 7: Additional shape features.

The Euclidean distance between the two vectors is calculated as:

$$v_{ij} = \begin{bmatrix} a(u_0)_i - a(u_0)_j \\ a(u_1)_i - a(u_1)_j \\ \dots \\ dMax_i - dMax_j \\ area_i - area_j \end{bmatrix} \quad P = \begin{bmatrix} 1 & 0 & \dots & 0 & 0 \\ 0 & 1 & \dots & 0 & 0 \\ \dots & \dots & \dots & \dots & \dots \\ 0 & 0 & \dots & W_{dMax} & 0 \\ 0 & 0 & \dots & 0 & W_{area} \end{bmatrix} \quad (6)$$

where vector v_{ij} is (252×1) , and weight matrix P is (252×252) . W_{dMax} and W_{area} are weights, determined empirically ($W_{dMax}=0.1$, $W_{area}=0.001$). This relates the different kind of parameters to each other. The Euclidean distance d_{ij} between the i -th and j -th leaves is

$$d_{ij} = \sqrt{v_{ij}^T P v_{ij}} \quad i, j = \{0, 1, \dots, 65\} \quad i \neq j \quad (7)$$

All Euclidean distances among the leaves were calculated, and an overall symmetric distance matrix was generated:

$$D_{\text{fourier}} = \begin{bmatrix} 0 & d_{0,1} & \dots & d_{0,65} \\ d_{1,0} & 0 & \dots & d_{1,65} \\ \dots & \dots & \dots & \dots \\ d_{65,0} & d_{65,1} & \dots & 0 \end{bmatrix}_{66 \times 66} \quad (8)$$

With the D_{fourier} matrix one can determine the degree of similarity between leaves. This matrix is used to find the sequence.

2.5 Spatial Boundary Intersection

Apart from the Fourier descriptors another shape similarity measure was also used. In this approach, boundaries of every leaf pair were intersected (Figure 8), and two features of the intersected area were calculated: *intersected area* and *standard deviation of the intersection distances* (in pixel unit).

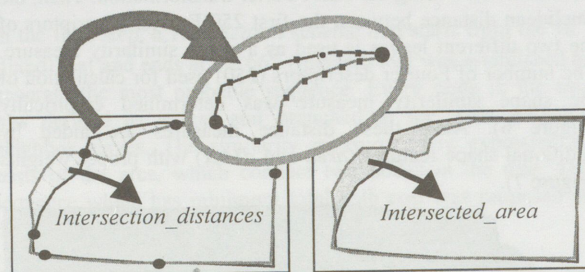


Figure 8: Intersection distances and intersected area.

The standard deviation of the intersection distances were calculated according to Equation (9). Start and end points of the inner lines were determined according to junction points of two boundaries (Figure 8). Equally spaced points were determined along both boundaries between the two junction points, and these points were linked as inner lines.

$$\text{int_dist} = \sqrt{\frac{\sum \Delta d^2}{n}} \quad n: \text{number of lines} \quad (9)$$

Since cropping of individual leaf images followed by the rectification process was carried out in a common coordinate system that is defined by the holes in center of every leaf, all leaves have the same alignment. These two different shape descriptors were merged to one value using proper weights (Equation 10).

$$dl_{ij} = \text{int_dist}_{ij} \cdot W_{\text{int_dist}} + \text{int_area}_{ij} \cdot W_{\text{int_area}} \quad i \neq j \quad (10)$$

$W_{\text{int_dist}}$ and $W_{\text{int_area}}$ weight values were determined empirically ($W_{\text{int_dist}} = 1.0$, $W_{\text{int_area}} = 0.002$). All dl_{ij} values among the leaves were calculated, and an overall matrix was generated.

$$D_{\text{intersection}} = \begin{bmatrix} 0 & dl_{0,1} & \dots & dl_{0,65} \\ dl_{1,0} & 0 & \dots & dl_{1,65} \\ \dots & \dots & \dots & \dots \\ dl_{65,0} & dl_{65,1} & \dots & 0 \end{bmatrix}_{66 \times 66} \quad (11)$$

Similar to D_{fourier} this matrix also gives useful metric information about the similarity of a leaf pair. In the processing steps it was observed that both matrices (D_{fourier} and $D_{\text{intersection}}$) give very similar results.

2.6 Evaluation of the Shape Data using Tree Search

In the evaluation step, D_{fourier} and $D_{\text{intersection}}$ matrices were used to generate the proposed sequence. These matrices can easily solve the *partial problems*: which leaves might be ancestor and successor for a pointed leaf in the sequence? But the *global problem* still remains: how can this information be evaluated efficiently in order to generate the full sequence? In the first attempt, a simple evaluation scheme (Figure 9) was designed.

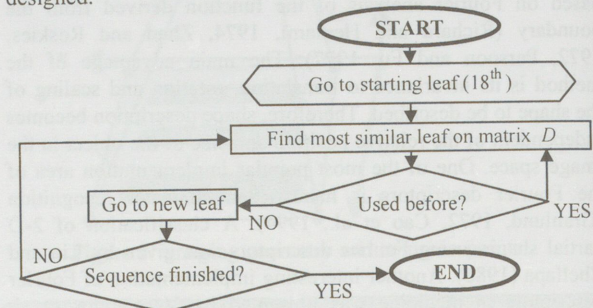


Figure 9: Implemented simple evaluation scheme.

Since the first 18 leaves were already fixed by the Museum, the algorithm started from the 18th leaf. Although it provides good results for the first 1st – 3rd quarter of the full sequence, some of the last leaves are slightly different with respect to their neighbor leaves on the sequence. The reason of the outcoming result was the one-way search strategy of the implementation. In order to develop a better evaluation scheme, a *tree search* method was adopted. One of the well-known application topics of tree search methods is *relational matching*. The more general matching scheme has been developed by computer vision researchers (Shapiro and Haralick 1987, Boyer and Kak 1988). Successful applications of relational matching in photogrammetry were given by Haala and Vosselman (1992), Zilberstein (1992), Cho (1996), and Wang (1996). Several examples of potential applications of tree search methods in digital photogrammetry were also given by Vosselman (1995).

Search *trees* consist of hierarchical *nodes* connected by *arcs*. Tree starts from a root node and descends into successor nodes in a branched structure. An ancestor node can only branch into possible successor nodes in order to keep the volume of tree in acceptable limits. In the case of relational matching, the problem is to match two primitive sets, namely relational descriptions. The primitives $p_i = \{p_1, p_2, \dots, p_n\}$ $p_i \in P$ of one relational description are called *units*, and the primitives of the description to be matched $q_i = \{q_1, q_2, \dots, q_m\}$ $q_i \in Q$ are termed *labels*. The number of units defines the depth of the tree. The best mapping of $P \rightarrow Q$ is the path with the lowest cost. In our example a tree search scheme that starts from the 18th (fixed) leaf and ends at the 66th (relaxed) leaf was established. The rings of the sequence chain are defined as *units*. Therefore, the number of *units*, namely depth of the tree, and the number of *labels* are the same (49). Every node in the tree was defined as a leaf and branched to the most probable neighbor leaves. The root node is the 18th leaf, which is the last leaf of the page numbered leaves. The similarity measures, calculated using shape descriptors, were expressed as the costs of the arcs, which connect two nodes in the tree. The implemented tree search method proposes the total path with minimum cost as the most probable sequence. Figure (10) shows a part of the designed tree search.

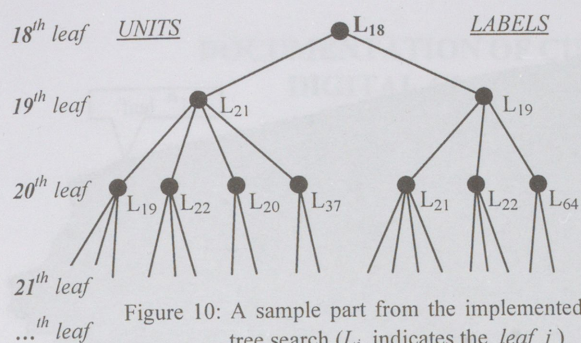


Figure 10: A sample part from the implemented tree search (L_j indicates the leaf j)

In the implementation phase, the number of allowed successor leaves for an ancestor leaf was defined according to two predefined rules (limits):

- Limit T_c : maximum count for allowed nodes
- Limit T_v : maximum value limit for shape similarity measure from matrix D_{fourier} or $D_{\text{intersection}}$

These two limits state that the number of successor nodes for an ancestor node cannot exceed the limit T_c , and the cost value for any arc cannot exceed the limit T_v . In tree search methods search time increases exponentially with the number of used combinations. These two limits reduce the combinations. Some leaves in the set have completely different shapes with respect to other leaves. This means that either none of the leaf might give a branch (arc) to these different shaped leaves or these extremely different leaves might not find similar leaf (leaves) as successor. To get rid of this problem one should relax the limits

T_c and T_v . In this case, the search time increases exponentially. Therefore the leaves are splitted into groups to solve the problem in an optimum way. According to their shapes, the leaves were grouped into four categories. Each group was ranked internally and then all the groups were merged. The obtained result is given in the following Figures (11), (12), and (13).

3. CONCLUSIONS

In this work, the missing sequence of the historical palm leaf manuscript was found by using shape descriptors. Two boundary-based shape descriptor algorithms were applied. Both of these shape description algorithms can find the most similar neighbour leaf for a pointed leaf successfully. The fundamental problem of this work is to establish the original sequence for all leaves using shape similarity information provided by the shape description algorithms. A tree search scheme was performed to achieve this task. The sequence, which has the minimum total cost, was proposed as the most probable sequence. An alternative method to the tree search method might be probabilistic relaxation. In this case, similarity measures provided by the shape description algorithms can be interpreted as probability of neighborhood. In order to provide a useful visual inspection for the proposed sequence, a texture mapped model of palm leaf manuscript was visualized and animated.

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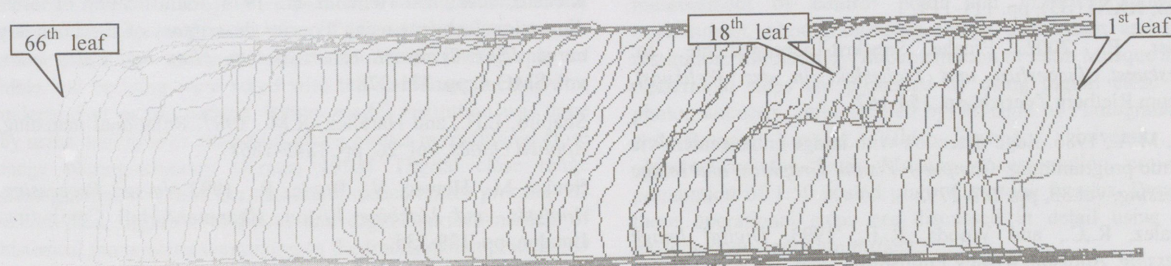


Figure 11: Orthographic view of the proposed sequence (constant shift: 15 pixels).

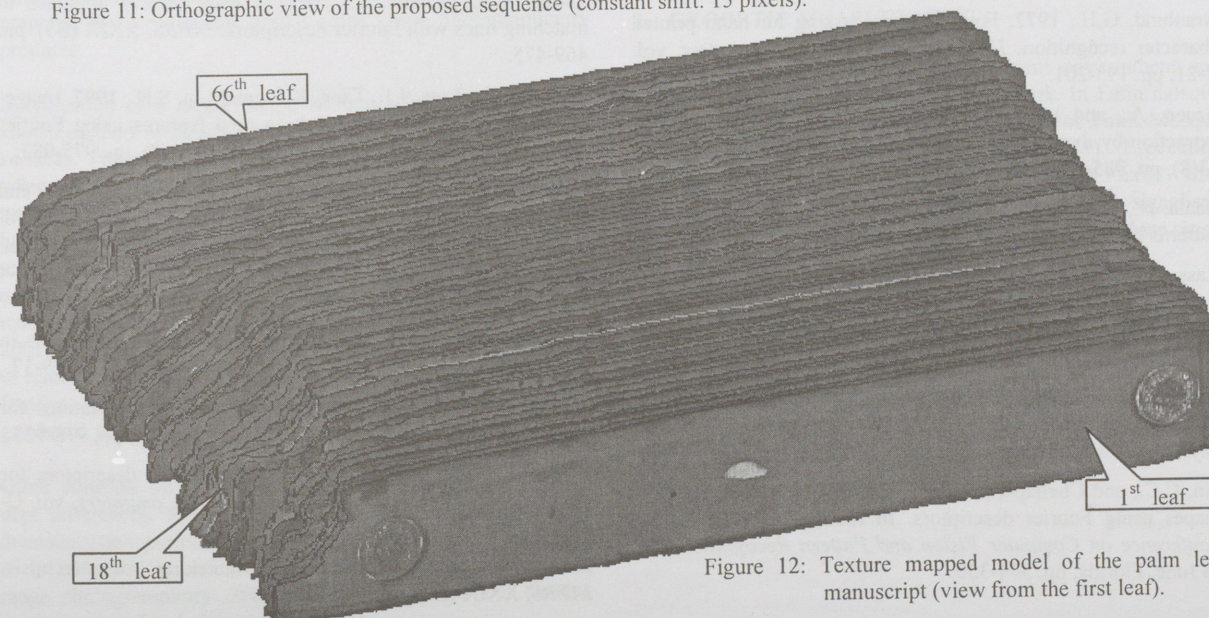


Figure 12: Texture mapped model of the palm leaf manuscript (view from the first leaf).

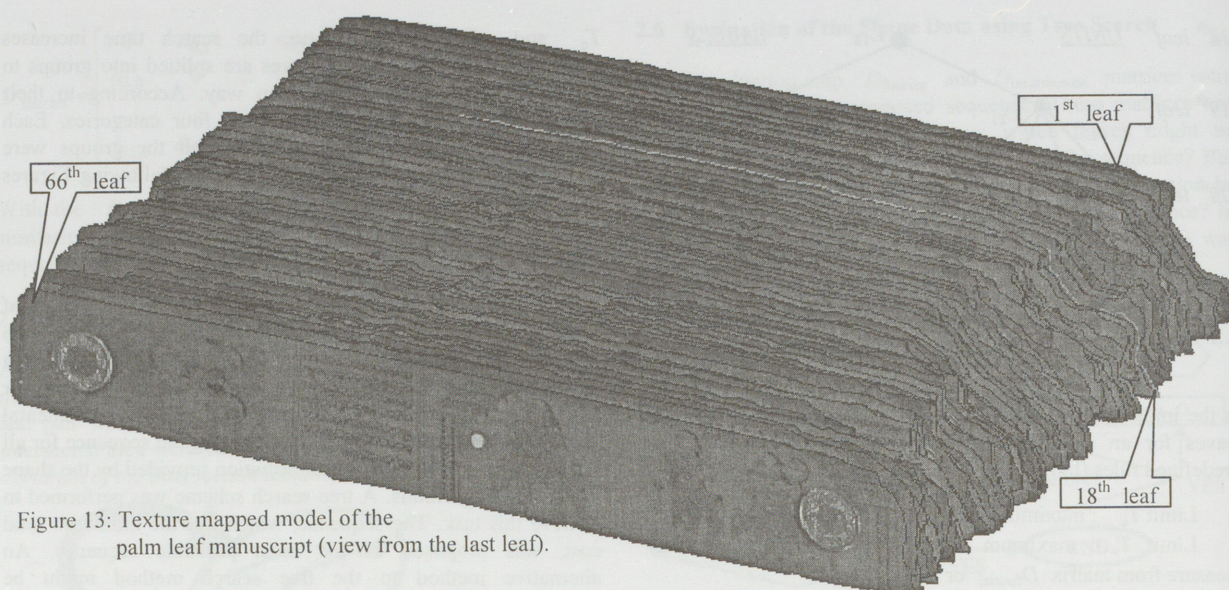


Figure 13: Texture mapped model of the palm leaf manuscript (view from the last leaf).

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