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AUTOMATIC OFF-LINE GENERATION OF DIGITAL TERRAIN MODELS

Abstract:

A procedure was conceived for the generation of D.T.M.'s from images digitised along epipolar lines. The corresponding objectives have been: minimum need for dedicated equipment, maximum efficiency in processing, and generation of a compressed D.T.M. grid.

The main stages are: compression and hierarchial structuring of the image data, their partitioning into suitable submatrices and further into segments, and matching of the conjugated segments through all hierarchial levels, i.e. by proceeding "from coarse" to "fine". By introducing suitable decision criteria, matching can be sequenced only to preselected pertinent pairs of conjugated segments. This allows an automatic adaption of the resulting D.T.M. grid to the local variability in terrain relief.

Automatic Off-line Generation of Digital Terrain Models

I. Introduction

The high potential of up-to-date digital means promotes their implementation in various fields. In photogrammetry, one of the problems of central interest concerns efficient acquisition of digital terrain model (D.T.M.) data. In this context, methods and means for fully automatic collection of D.T.M. data for medium and small scale applications are very important. Hence, the objective of this paper is to outline a method for generating D.T.M.'s automatically using a minimum of dedicated equipment and with a minimum of computational load. Moreover, the redundancy of D.T.M. data obtained should be substantially reduced.

The basic features of the method conceived are: the epipolar geometry (1), compressed and structured image data (2), sequential matching from coarse to fine (3), and predictive selection of D.T.M. points by applying the concept of Progressive Sampling (4). The operation is supposed to be off-line.

The entire operation can be strictly formalised and is therefore feasible for automation. This, however, does not restrict the flexibility of the method, which has a great capacity for adaption to different circumstances.

The paper outlines the different phases of the process, i.e. digitising images, data preparation, image matching and determination of parallax, and a predictive selection of pertinent D.T.M. points. The outline is followed by some general conclusions.

II. Digitising images

Analogue to digital (A/D) conversion is linked at one end with analogue sampling of the image data, and at the other end with the data compression and structuring. The two operations will now be considered in greater detail.

1. Digitising

In photogrammetry, the epipolar geometry represents a rational approach to sampling of conjugated images (1). For generation of D.T.M.'s, however, the sampling parameters should be specified rationally, as these specifications affect very substantially the quantity of the raw data, to be further processed (5).

In order to illustrate the order of magnitude of the data an example will be presented throughout the following paragraphs. The sampling intervals are $\Delta x = 40$ um and $\Delta y = 400$ um, whereby Δx represents the step size along the epipolar lines, and Δy the separation between the adjacent epipolar lines.

During image matching, one photograph may serve as the "master" and the other as the "slave". The model area can therefore be defined on the "master". In our example the left photograph will serve as the "master", and thus the dimensions of the corresponding model area M' are D'x and D'y (fig. 1).

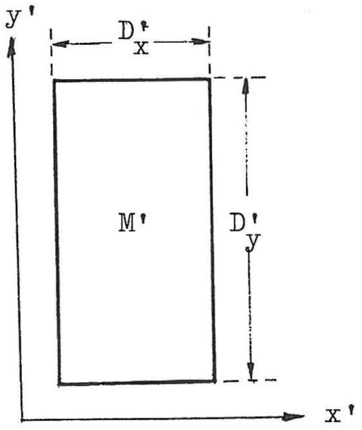

Fig. 1: Model area

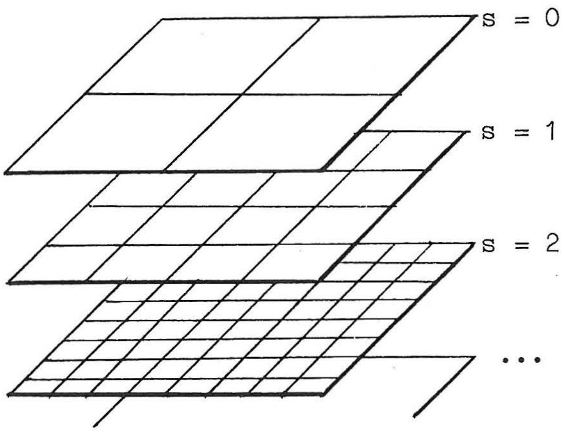

Fig. 2: Hierarchy of s-levels

2. Data structure

The desired structure is obtained as a by-product of the data compression, i.e. by applying the Laplacian operator successively to different densities of the raw digital data (2). In figure 2 the corresponding second differences

$$\delta_j = d_{j+1} + d_{j-1} - 2d_j$$

are symbolically represented by a hierarchy of the s-levels. Each lower level (increasing s) refers to a higher density of the raw data.

The second differences, δ, in these levels, which are smaller than a specified threshold, can be neglected. Hence, the δ-matrices, arranged in the s-levels, are incomplete, i.e. with many vacant elements.

In level s the sampling interval along an epipolar line is defined by

$$\Delta\xi_s = \Delta x . 2^{(s_{max} - s)}$$

where Δx is the interval of the original sampling, which corresponds to the level s_{max}.

In a given s-level the Laplacian operator can either be applied to individual pixel values or to average values of the adjacent groups of pixels (i.e. pairs, quadruples, etc.).

The sampling interval in the y-direction can be defined, similarly to $\Delta\xi_s$ by

$$\Delta\eta_s = \Delta y . 2^{(s_{max} - s)}$$

In table 1 the intervals $\Delta\xi$ and $\Delta\eta$ are tabulated for Δx = 40 µm, Δy = 400 µm and s_{max} = 4.

s	0	1	2	3	4
$\Delta\xi$	640	320	160	80	40
$\Delta\eta$	6400	3200	1600	800	400

Table 1: Sampling intervals (in µm) for data compression.

The number of pixels per epipolar line (within the model area) $n'_x = D'_x : \Delta x$ and the number of the epipolar lines per model $n'_y = D'_y : \Delta y$. Subsequently, the total number of pixels per model M'

$$n'_M = n'_x n'_y$$

i.e. in our example $n'_M \approx 1.25 \cdot 10^6$ pixels.

The corresponding area on the right photograph should be larger in order to accomodate for the differential geometric distortions (i.e. parallaxes). An estimate for $n''_M \approx 1.5 \cdot 10^6$ pixels is realistic for near vertical photography.

III. Data preparation

The compression and structuing of image data are, in essence, preparatory operations. Nevertheless, since these operations can be carried out on-line with the A/D conversion, they have been considered under the "digitising" stage.

The specific preparation for image matching concerns the partitioning of the σ-matrices, arranged in s levels, into sub-matrices (or patches) of suitable size for processing, and a further division of the sub-matrices into the target segments (for M') and the conjugated search segments (for M").

1. Sub-matrices

The partitioning of the model area (M' and M") into the sub-matrices can be on-line with data compression, or it may be performed in a separate stage. The structure of the sub-matrices is illustrated, for a few s-levels, in fig. 3. In the highest level (s = 0), a sub-matrix covers half of the model area M', whereas in the lowest level (s_{max}) the sub-matrices are very small. The location of a sub-matrix in level s is defined by the indices g'_s and h'_s.

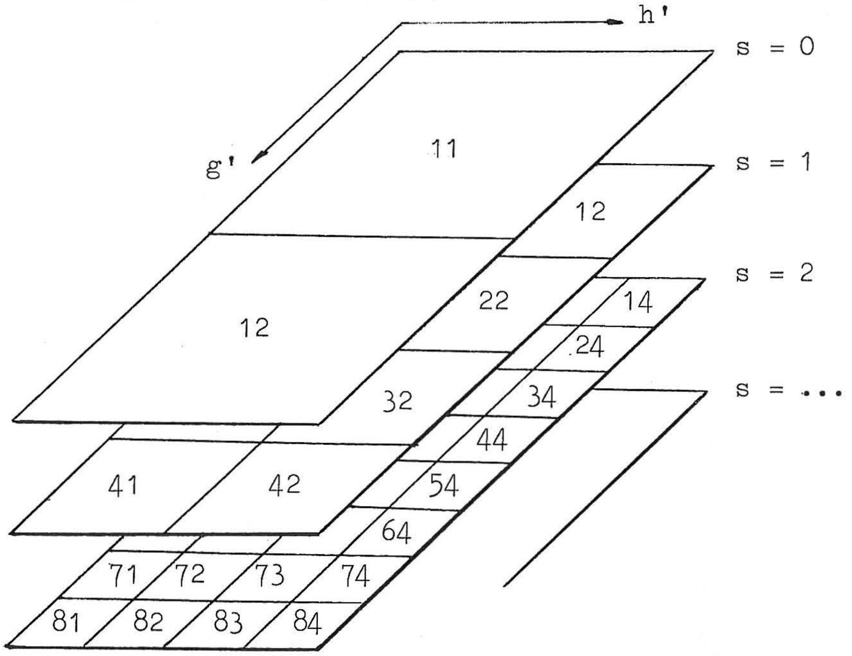

Fig. 3: Hierarchy of sub-matrices

In level s the number of sub-matrices is determined by $g'_{s\,max} \cdot h'_{s\,max}$ where

$$g'_{s\,max} = 2^{(s+1)} ; \quad h'_{s\,max} = 2^{s}$$

and the corresponding submatrix dimensions

$$m'_{sx} = D'_x \, . \, 2^{-s} \qquad m'_{sy} = D'_y \, . \, 2^{-(s+1)}$$

In table 2 the sub-matrix dimensions m_x and m_y are tabulated for s (0.4), and D'_x = 100 mm and D'_y = 200 mm.

m \ i	0	1	2	3	4
m_x	100	50	25	12.5	6.25
m_y	100	50	25	12.5	6.25

Table 2: Dimensions (in mm) of sub-matrices

The sub-matrices need not necessarily be square.

In level s the number of the sub-matrices

$$n_s = 2^{(2s+1)}$$

and subsequently, the total number of the sub-matrices in all levels

$$n_t = \sum_s 2^{(2s+1)}$$

i.e. in our example n_t = 682.

The δ-matrices of the right photograph can be similarly partitioned. However, provision has to be made for the extreme parallax differences. Therefor the dimension m''_{sx} of the conjugated "search" sub-matrices should be accordingly greater, and thus the adjacent sub-matrices have to overlap in direction of the epipolar lines. The amount of the overlap should be specified in accordance with the expected maximum geometric ("differential") distortion.
Prior to matching, each sub-matrix is further divided into small segments, i.e. the target segments for M' and the search segments for M".

2. Target- and search segments

The division of the sub-matrices into target (or search) segments is identical for all the s-levels. It is sufficient to consider here the target segments only; the considerations for the search segments are similar.

A row of δ-values in a sub-matrix can be segmented into equal groups of elements. The adjacent segments may join or they may overlap. In the case of joining segments, their length may be equal to the (average) spacing of the D.T.M. grid (in photo-plane) to be generated. According to (5) this corresponds with the separation Δy between epipolar lines (fig. 4). Consequently (in any s-level) the number of elements per target segment $n_p = \Delta y : \Delta x$ i.e. in our example n_p=10.

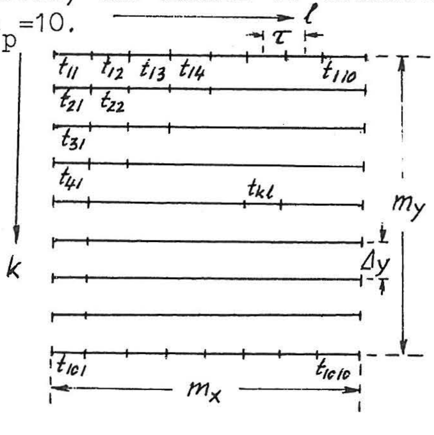

Fig. 4: Arrangement of segments in a sub-matrix

The location of a segment, within the sub-matrix is defined by the indices k and l, which refer to the rows (i.e. epipolar lines) and the columns of segments. The number of segments t per row m_x: $l_{max} = \mathrm{INT}\ |m_x : n_p \Delta\xi|$

and the number of rows per sub-matrix : $k_{max} = \mathrm{INT}\ |m_y : \Delta\eta|$

i.e. in our example $l_{max} = k_{max} = 16$.

The indices k and l are identical for the sub-matrices in all the s-levels. Thus the number of segments is in any sub-matrix $q_s = k_{max}\ l_{max}$

and subsequently the total number of segments in all s-levels (for M' or M")

$$q_t = q_s\ n_t$$

i.e. in our example $q_t \approx 1.77 \cdot 10^5$ segments.

The structures and thus the numbers of the target- and search segments are identical, though the search segments are longer and therefore they overlap.

For the case where the adjacent target segments are overlapping, the lay-out of the segments is as shown in figure 4, although the segments are longer. If their overlap is v-percent, the length of a target segment is

$$n_p = (1+v/100)\,\Delta y : \Delta x$$

The corresponding search segments are, obviously, accordingly longer. The partitioned and segmented image data form the input for image matching.

IV. Matching and parallax

A matching operation embraces several successive trials of fitting a target segment into the conjugated search segment. After each trial the target is virtually shifted for a step ($\Delta\xi$). If the data are hierarchically structured, matching is applied successively throughout all the s-levels, which implies the principle "from coarse to fine".

Matching can be applied either to all conjugated pairs of segments in all the s-levels or to the preselected pertinent pairs only. In the latter case the logic for sequencing of matching is more complex, but the computational load can be substantially reduced.

If matching is applied to all conjugated pairs of segments the number of matches equals the number of such pairs, i.e. in our example $q_t \approx 1.77 \cdot 10^5$. By supposing that on average five trials are needed per match, the total number of matching trials per model is about 10^6.

The matching operation is started in the upper level (s = 0) and proceeds gradually to the lowest level (s_{max}). The related segments in the neighbouring s-levels are linked by a two-dimensional hierarchial tree, which can be modeled by a simple recursive algorithm. The algorithm is used for the control of the matching sequence.

As already indicated, the number of matches can be substantially reduced by pre-selecting the pertinent pairs of the target and search segments. To this end, however, a suitable logic for automatic selection of the pertinent branches in the hierarchial tree, has to be devised.

1. Image matching

A matching trial can be interpreted as a superimposition of a target segment on the conjugated search segment (fig. 5). In order to estimate the degree of similarity, a search is made for the coinciding δ-pairs (each having the same polarity). All other coinciding pairs of elements do not contribute to the similarity. The degree of similarity can be quantified by using one of the following criteria:

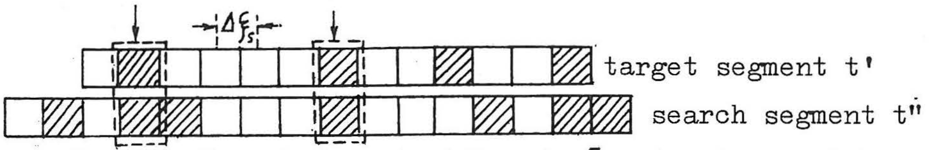

Fig. 5: Search for significant δ-pairs in a matching trial.

i. the number τ of significant δ-pairs.
ii. the covariance $COV = \sum_{\tau} \delta'\delta''$

The first criterion is very time-efficient, whereas the second one is sharper. Both criteria may be applied in combination, e.g. the number τ is used for all s-levels except in the lowest one (s_{max}) for which the covariance should be calculated.
The matching trials are repeated after each shift of the target segment over $\Delta\xi_s$, and a match is terminated after exceeding the maximum similarity estimate.

2. Parallax

In each s-level the corresponding epipolar partial parallax should be determined for all the successfully matched pairs of segments. A partial parallax Δp_s, in level s, is represented by the shift of the target segment from its initial position to that of the maximum similarity estimate. In general

$$\Delta p_s = \sum_n \Delta\xi_s$$

where n is the effective number of the shift intervals
At the lowest level (s_{max}) the accuracy can be increased by determining algebraically the maximum for the similarity, i.e. by means of fitting a parabola.

As matching proceeds from the highest to the lowest s-level, the partical parallaxes are accumulated: $p_s = p_{s-1} + \Delta p_s$
where the summation is along the branches of the two-dimensional hierarchial tree (figures 6a and b).
Differences between the partial parallaxes Δp_s of the adjacent target segments in level s reflect the relative geometric image distortions. These differences can be used for adaptive feedforeward control, i.e. for resampling the target segments (i.e. expansion or contraction) in the next lower s-level. This may replace the commonly applied iterative feedback control.

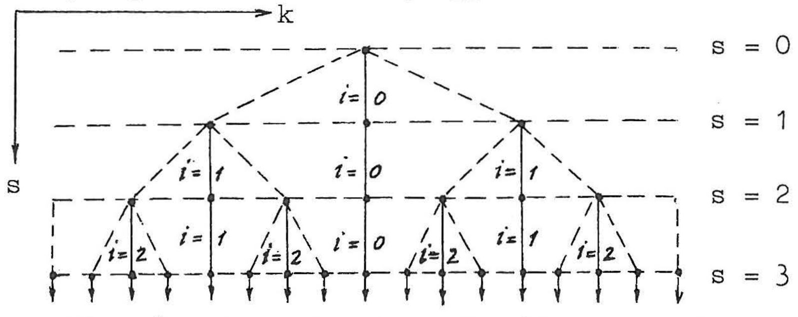

Fig. 6a: Tree structure for line segments.

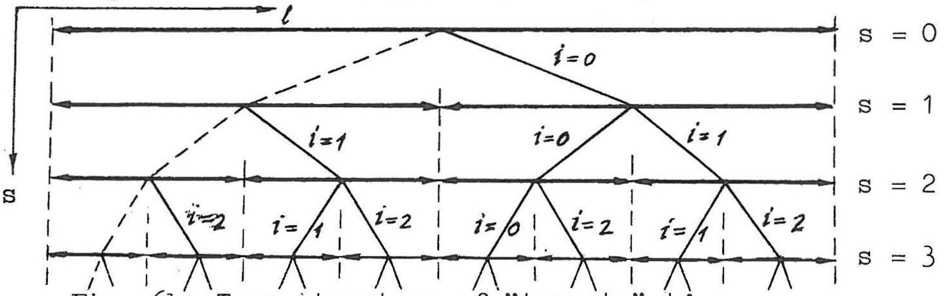

Fig. 6b: Tree structure of "targets" t'

V. Predictive selection

A predictive selection of conjugated segments is justified for two reasons, i.e. to reduce the computational load and to generate directly a compressed set of D.T.M. data.

Hereby the parallaxes are generated in several successive matching runs. In run i only selected branches pass through all the s-levels where $s \geqslant i$. In the zero-run ($i = 0$) parallaxes are determined for a sparse pattern of the target segments (in our example the grid spacing is 6.4 mm). These segments are positioned on the "most vertical" branches of the hierarchial tree from the level $s = 0$ downwards (figs. 6a, b). The parallaxes of these sparse locations are then analysed and subsequently new pertinent target locations (i.e. branches) in the level $s = 1$ are identified. These segments and the corresponding ones in the lower levels ($s > i$), which are linked with the "most vertical" branches of the tree, are used in the next matching run ($i = 1$). Then the new and the old parallaxes are analysed together, and new pertinent target locations (i.e. branches) in the level $s = 2$ are identified. Subsequently the matching starts in the level $s = 2$ and continues along the "most vertical" branches in the lower levels ($s > 2$). The same procedure is applied in the following runs and terminates either when no further target locations are pertinent or when the last (predetermined) matching run ($i_{max} = s_{max}$) is accomplished.

Figures 6a and b illustrate schematically the branches of the hierarchial tree. However, only the pertinent branches are used in the case of predictive selection. The logic for predictive selection is applied to the analysis of all the prallaxes after each matching run (except the last one). The analysis itself is similar to that applied in Progressive Sampling (4), which uses the Laplacian operator as the basic criterion.

For each triplet of adjacent segments the second parallax difference is calculated and compared with a specified threshold Th. If the threshold is exceeded, the tree should be branched further. Figure 7 illustrates a local densification for the case

$$\nabla_p^2 = p_{j+1} + p_{j-1} - 2p_j > Th$$

Thus in the next matching run the target segments 1 to 9, and those "most vertically" below in the lower s-levels, should be applied.

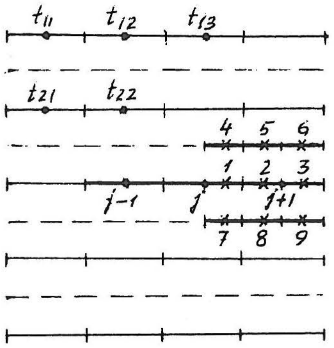

Fig. 7: Sub-matrix densification

Due to the predictive selection the sub-matrices of parallaxes thus obtained, are incomplete, i.e. having many vacant elements.
The structure of the overall process is shown, simplified, in fig. 8.

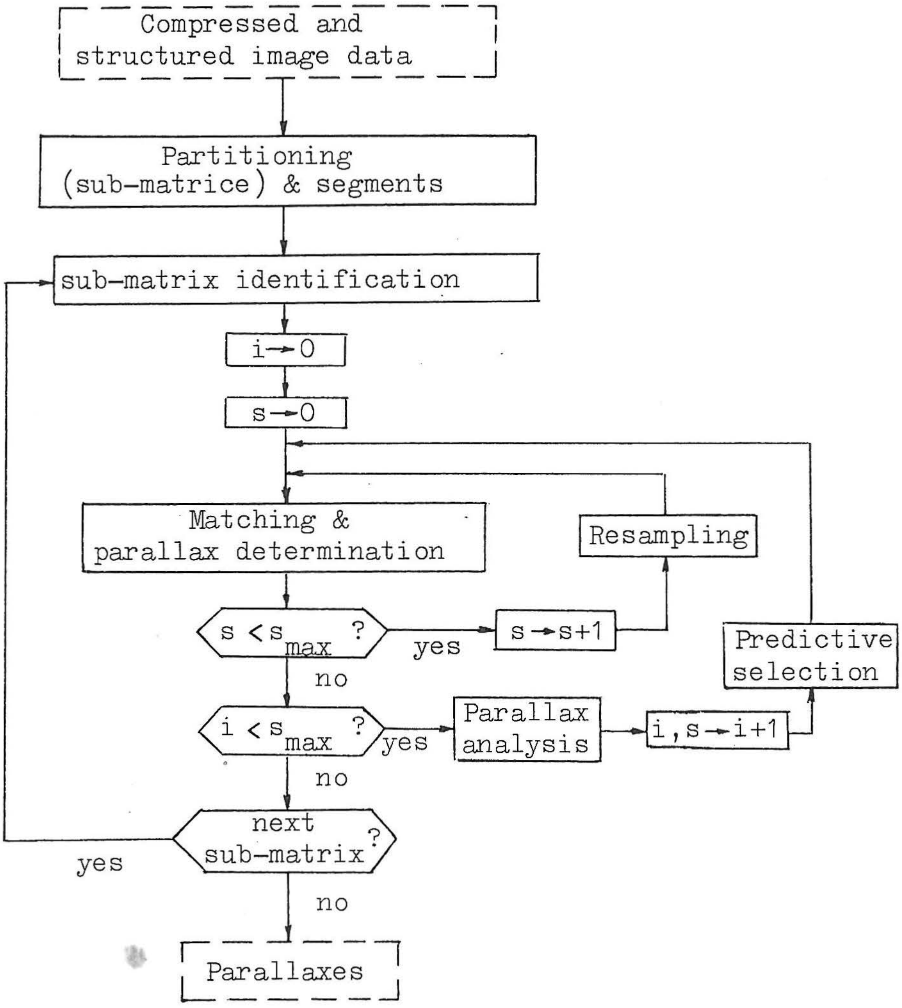

Fig. 8: Flow chart of the overall process.

As the location, x'y', of each matrix element is known, the conjugate locations x", y" can be calculated and subsequently the corresponding spatial locations in the model and/or in the terrestrial coordinate system can be determined.

VI. Conclusion

The off-line methods of digital image matching for automatic generation of D.T.M.'s are characterised by a minimum of dedicated equipment, and great flexibility with regard to the matching algorithms and corresponding strategies. The strategy should be well devised, and the procedures and data structures should be standardised. The standardisation concerns:
- sampling and A/D conversion
- compression and structure of data
- data partitioning into sub-matrices and segments
- matching procedure, i.e. criteria and strategy
- predictive selection of pertinent D.T.M. points.

The design of the method has been governed by the following basic objectives:

- to minimise the computational load
- to attain high accuracy and reliability
- to reduce redundancy of the resulting D.T.M. data.

Further improvements can be expected by refining the criteria pertaining to image matching and by improving the decision logic for predictive selection of the pertinent D.T.M. points.

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