

Invited Paper presented at the
International Symposium
ADVANCES IN DIGITAL IMAGE PROCESSING
Bad Neuenahr, September 1978
to be published by PLENUM PRESS

DESY DV-79/01
March 1979

THE PROCESSING OF X-RAY IMAGE SEQUENCES

K. H. Höhne, M. Böhm, G. C. Nicolae
Institut für Mathematik und Datenverarbeitung
in der Medizin
Universitätskrankenhaus Hamburg-Eppendorf and

Deutsches Elektronen-Synchrotron DESY, Hamburg, FRG.

1. INTRODUCTION

Among the variety of image processing applications the analysis of x-ray data is of growing importance. Whereas in the past 10 years effort has been concentrated on the analysis of static pictures, there is an increasing interest on the part of physicians in extracting functional parameters from time-sequenced X-Ray pictures (angiography). An angiographic analysis (e. g. for the kidney) proceeds as follows: (see fig. 1). The physician applies a radio-opaque contrast medium to the kidney to be examined. The contrast medium propagates through the kidney vessels at the speed of circulation of the blood. The resulting scene, which is of constant morphology but varying intensity, is viewed by the image intensifier video system of the x-ray equipment. Usually the scene is assessed by estimating differences from image to image in order to get qualitative information about the blood dynamics. Potentially, however, the sequence contains spatially very differentiated quantitative information about the blood velocity or the filtration function

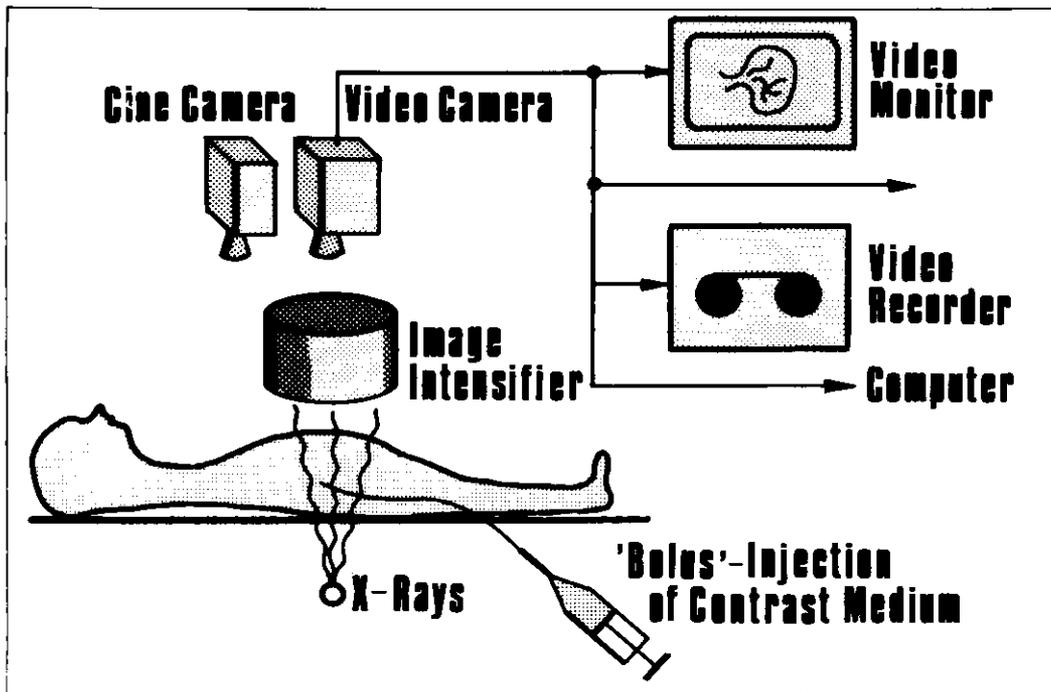


Fig. 1 Principle of angiography

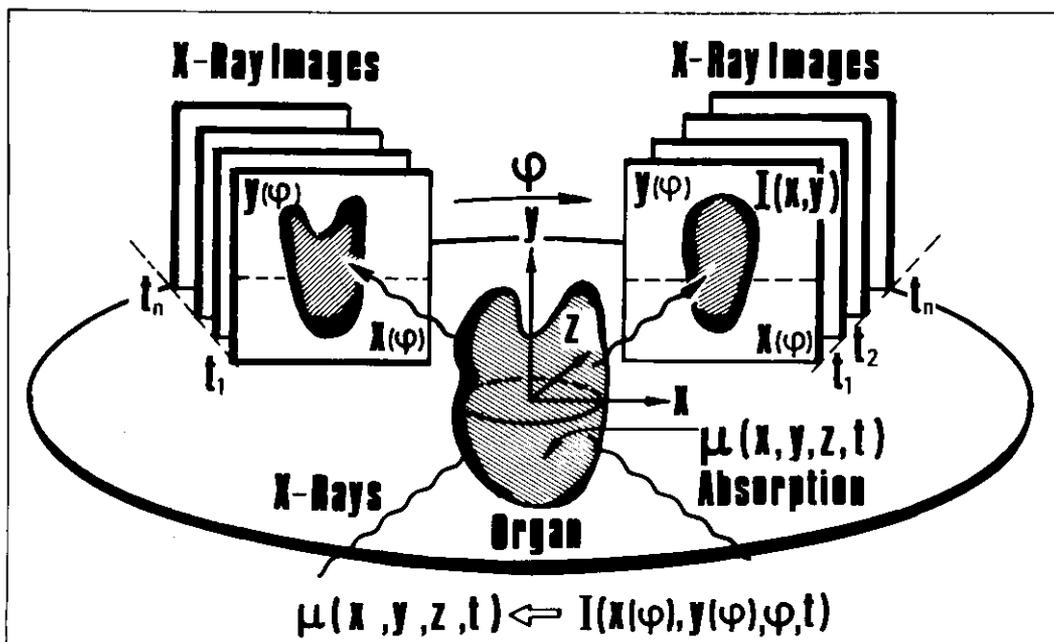


Fig. 2 Schematic diagram of image formation in radiology

of the kidney which cannot be extracted in sequential viewing by eye. Thus, it is desirable to use image processing tools to extract these parameters.

Before tackling this problem it is useful to look at the present situation of image processing in radiology. The ideal imaging technique in radiology would be one, which delivers the X-Ray absorption of the examined organ as a function of space and time. As illustrated in fig. 2 this could in principle be achieved by taking image sequences of the organ from several (typically 180) directions. Although, there are experimental setups proposed which allow the acquisition of such complete information (1), the involved amounts and rates of data are prohibitive for a clinical application in the near future. Consequently, we have to confine ourselves to subsets (see fig. 3) of the data which are specified on one hand by the technology, and on the other by the problem to be solved. The most simple subset is the conventional projection *radiograph*. The image formation process here is a single projection. Image processing procedures have concentrated on the automatic detection of size, shape and texture and the classification of these properties into diagnostic categories. Another procedure is that of *computer tomography*, producing maps of absorption values parallel to the X-Ray direction from a set of projections. The resulting images are assessed by the physician directly or, in some cases, processed in a way similar to what is done with conventional radiographs. Comparing these two main image processing techniques we find that the processing of conventional radiographs has no clinical relevance yet, whereas computer tomography is in wide-spread use. The reason for this is obvious. In the first case the image *interpretation* process has to be automated by appropriate algorithms. This has proven to present very complex problems. In the second case the *image formation* is done by the computer in a way which converts a non-interpretable data structure (the projections) into a pictorial structure (the computer tomogram) which the physician may interpret in a way he is used to. Although there are implementation problems, the algorithms for reconstruction are comparatively simple.

Since in our special application we are interested in the time course of a process we consider the subset of X-Ray data which contains one conventional projection as a function of *time*. Having in mind that better images or images containing new information are more helpful to the physician than automatic interpretation, we have concentrated our investigation more on the search for algorithms for image formation than for image interpretation.

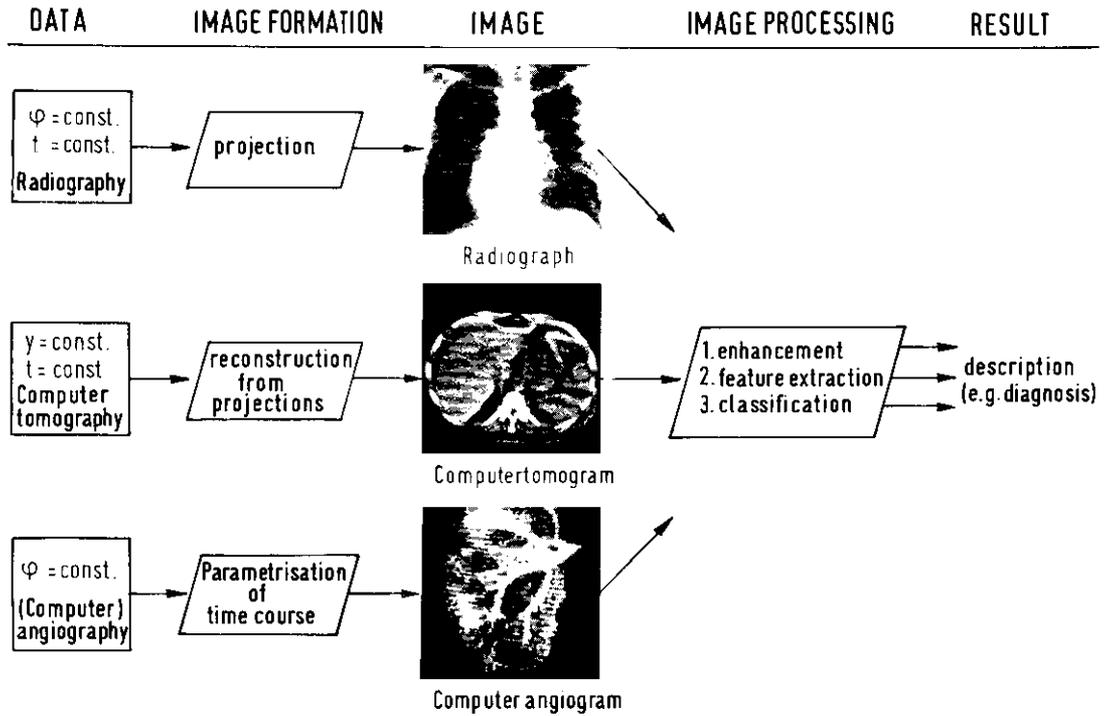


Fig. 3 Different scopes of image processing in radiology

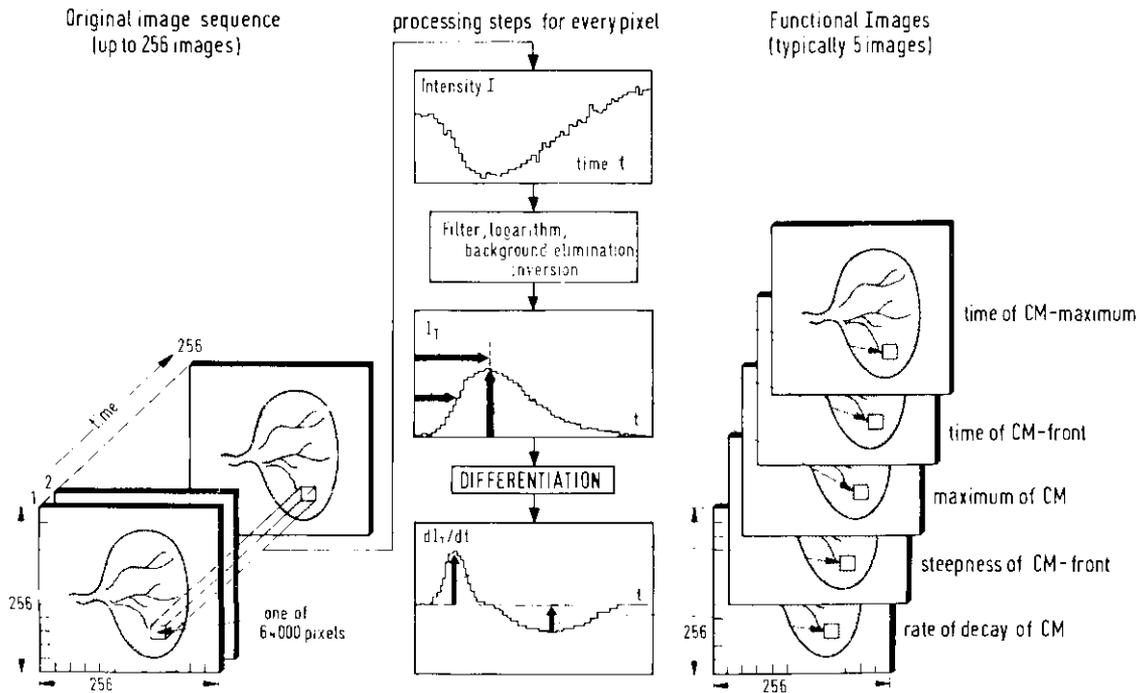


Fig. 4 Principle of computer angiography

Earlier approaches to the problem of the quantitative measurement of blood dynamics from an X-Ray image sequence used the technique of angiodesitometry (2 - 8). In the case of non-moving organs (e. g. the kidney) the time course of X-Ray intensity at one or several regions selected by the physician is registered. The analysis of the resulting curve yields parameters such as the velocity of the blood stream. For moving organs (e. g. the heart) the boundaries of the region of interest are determined first and thereafter the dynamic behavior of the parameter describing the region such as the area of a ventricle, is computed. Even in the simpler case of non-moving organs the angiodesitometry is far from clinical application for the following reasons:

- Unless advanced image processing tools are used the analysis procedure is too laborious for utilization in a clinical environment.
- If one nevertheless computes a parameter such as the blood velocity in a single vessel, one recognizes that there is
 - because of the complexity of the kidney function - no unique reference value to which it could be compared.
- If one therefore measures only relative differences for various regions of the same organ, one has the problem of comparing a large set of numbers, which especially at the high resolution of X-Ray images is prohibitive for a practical application.

Our approach to the problem of analysis of an X-Ray image sequence is based on the fact that an appropriate pictorial presentation of the parameters derived from the sequence is best suited for usefully combining the ability of the computer to do computations on large amounts of data with the ability of man to interpret complicated pictorial structures. The method, which we have named Computer Angiography (9, 10), is described in the following chapter.

2. COMPUTER ANGIOGRAPHY

2.1 Image Coding

As the picture sequence in general is highly redundant, it has to be compressed to have a manageable amount of data. Typically it consists of 128 frames of

256 x 256 pixels with 8 bit grey level resolution. It is now encoded in a way which is based on the fact that only the characteristics of the intensity variation with time contains the information the physician is interested in. Thus the following procedure is applied (see fig. 4): At any pixel the variation of intensity with time caused by the wash-in and wash-out behaviour of the contrast medium (CM) is considered. Its shape - in the case of the kidney a curve with a steep rise, a variable plateau and a slow decay - is now described in a first order approximation by features such as the *time of the CM-maximum*, *time of the CM-front*, *maximum of CM*, *steepness of the CM-front* and *rate of decay of the CM*. Instead of storing and processing the full length curve (128 bytes), we now have to process a vector of 5 bytes only for each pixel, which is a manageable size for a routine application. It will be shown in a later section that this coding scheme preserves at least the information the physician draws from the sequential viewing.

2.2 Visualization of Blood Dynamics by Functional Images

The decisive point of our approach for extracting more information than by sequential viewing is the following: Instead of presenting the physician a sequence of pictures as a function of time, we give him a set of static pictures, each of which describes *one* point of view of the dynamic behavior of the organ. This is achieved simply by presenting the feature matrices as grey tone or colour pictures. Thus, the image '*time of CM-front*' is representative for the blood velocity, whereas the image '*maximum of CM*' is representative for the blood perfusion. Fig. 5 shows a functional image of the type '*time of CM-front*' together with one frame of a conventional angiogram.

We recognize the following properties:

- *Formally* it is very similar to the conventional one.
Thus, the radiologist does not have to change his practice of interpretation.
- The *semantics* however, is completely different. It shows a survey of the blood speed during the observation time. In other words: it transforms functional information into static *morphological* information which can be assessed by the physician in a way he is used to.

- As a decisive advantage any background from overlaying tissue or from device inaccuracies disappears.
- As shown in fig. 9 (left) a quantitative analysis is possible by presenting the image in a colour code. Nevertheless, here too, the radiologist assesses the image from its morphological appearance.

Functional imaging has also been used in nuclear medicine (10 - 13) but has not reached clinical applicability yet. This seems to be due to the inferior spatial and time resolution.

2.3 Computation of Global Function Parameters

Functional images present *local* functional parameters, dependent on the morphology of the organ. From the data global parameters which do not depend on the morphology can also be derived. Fig. 6 shows as example the histogram of the parameter time of CM-front. From the time of the decay of the histogram in a simple way the transit time from the arteria into the cortex of the kidney can be computed.

2.4 Computation of Functional Histograms

The elements of a functional image represent only one parameter. The information which is contained in the combination of parameters is not used. Thus the optical presentation of two-dimensional histograms of pairs of parameters is a tool for visualizing patterns which could contain more detailed information on the organ function. These histograms can be considered as some kind of a second order functional image which, of course, no longer contains the morphology information the physician is used to. Suspicious regions, however, may be retransformed into the morphological picture. Fig. 7 shows as an example the histogram time of CM-front vs. time of CM-maximum for a kidney.

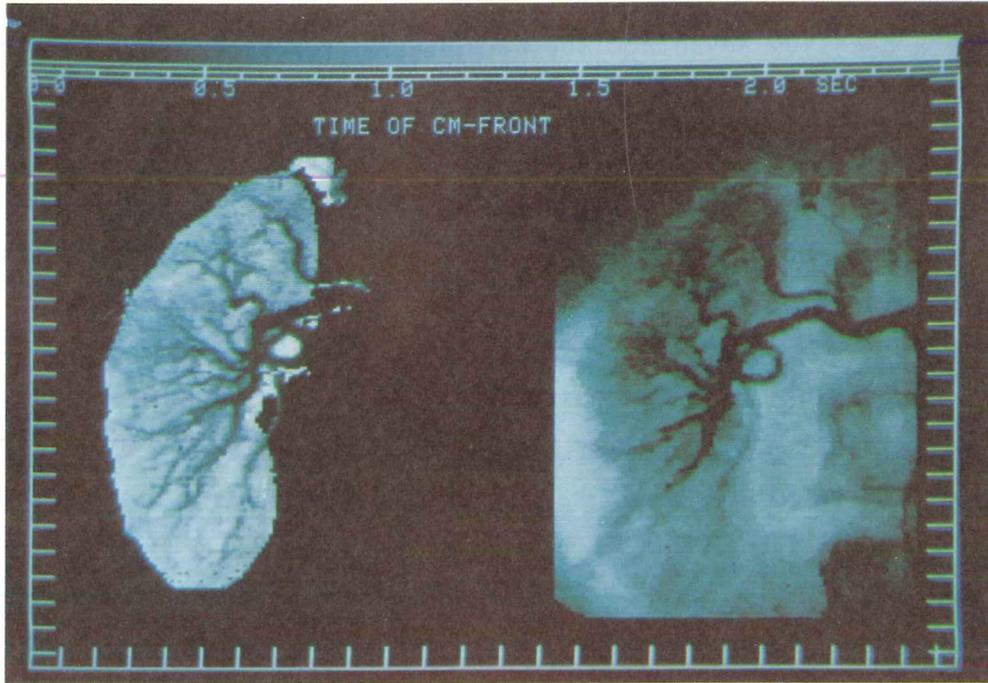


Fig. 5 Functional image 'time of CM-front' of a kidney together with one digitized frame of the angiogram

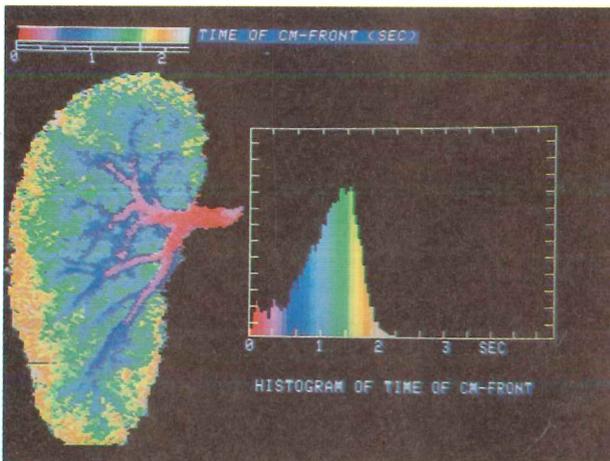


Fig. 6 Example of a histogram for one parameter

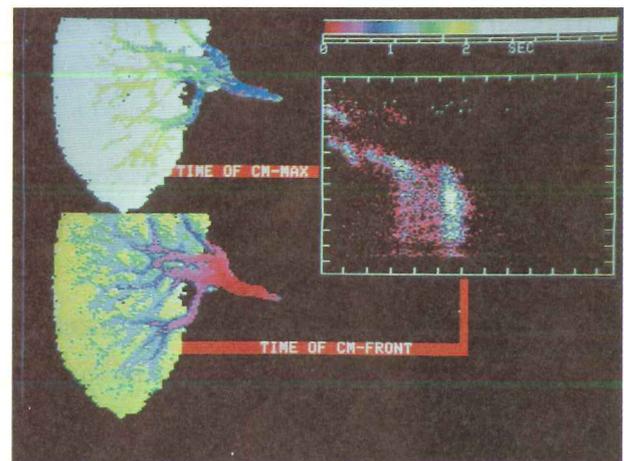


Fig. 7 Example of a histogram for two parameters

2.5 Classification according to Physiological Criteria

Should the investigation of the two-dimensional histograms, which is still done with the human eye, deliver promising results, the classification of the multi-dimensional parameter combination according to physiological criteria is to be considered. The projection of the classes (e. g. healthy or damaged tissue) into the morphological image may then lead to *refined functional images*.

3. IMPLEMENTATION

Except for the classification the algorithms are fairly simple. For a thorough test and a final utilization in a *clinical environment*, however, there are constraints concerning the hardware and software *implementation*. Clinical environment means that the users are not at all interested in image processing algorithms but need a quick availability of a medical result. Thus, one has to find hardware and software structures which are fast and hide complex internal structures from the medical user. In the following chapter we describe the implemented system, which we have named CA-1 (Computer Angiography System One).

3.1 System Hardware

Requirements. The requirements were that the system had to be fast, and that the *acquisition* of the picture series had to be performed at a speed allowing immediate analysis. As a consequence, we chose the video signal as input and aimed at a real-time digitization of the video information. Also the analysis had to be fast because it had to be carried out as an interactive process. A routine application of this technique is only possible if it is not time consuming. Furthermore, should the result of a processing step require the acquisition of a new data, it has to be available during the time the patient is still present. To meet these requirements, one must decide between two approaches. A pure real-time processing of multitemporal images as proposed by Kruger et al. (15, 16) has on the one hand the advantages that some simple algorithms are fast and no temporary storage of large amounts of data is necessary, which makes the system cheaper, but on the other hand it has the severe disadvantages that more sophisticated algorithms cannot be applied and that, after the image sequence has passed, all information which could not be obtained in real time is lost. Therefore we decided not to aim at a pure real-time processing. Instead we aimed at a high speed processing from stored data. One reason is that the time context necessary for our algorithms is too large. Another reason is that development and refinement of algorithms is much more difficult if they are implemented in hardware at a too early stage of research. In detail the following functions have to be performed:

- Picture data acquisition, storage, display and transfer of pictures (or regions of pictures) at standard video rates (50 frames/s, 10 Msamples/s)
- Picture data processing such as the computation of functional images at a speed allowing interactive analysis
- Suitable communication between user and system by
- adequate means of (graphic) command input,
- pictorial and graphic output which is fast enough for interactive use and animation of pictures.

Concept. Considering that the most urgently required features are flexibility and speed we chose for the realisation a multiprocessor structure (14) which is called Digital Video System (DVS). Fig. 8 shows the structure of the multiprocessor system. It consists of several dedicated microprogrammed processors which are connected through a high speed asynchronous bus (60 ns cycle time). The high speed bus dynamically switches data paths between pairs of processors and performs the process synchronization according to the preassigned priorities.

Image buffers. Two image buffers of 32k x 16 bits for digitized video images are used as common resources by all processors. The image sequence buffer presently being implemented serves for storage and retrieval of up to 4 million pixels (4 Mbytes). The memory control processor gives the user the possibility to access the memory on a picture by picture basis or orthogonally on a 'time course of pixel' basis. This decisively reduces the data reorganisation time for the analysis algorithms which generally work on the time course.

Real time digitizer. The Real-Time-Digitizer (RTD) performs the real-time acquisition, digitizing and storage of video images. In its design we aimed at a maximum data reduction immediately at acquisition time. It is achieved by the programmability of the acquisition parameters such as region of interest and time and spatial resolution. Thus, only limited regions are digitized with no more spatial and time resolution than necessary.

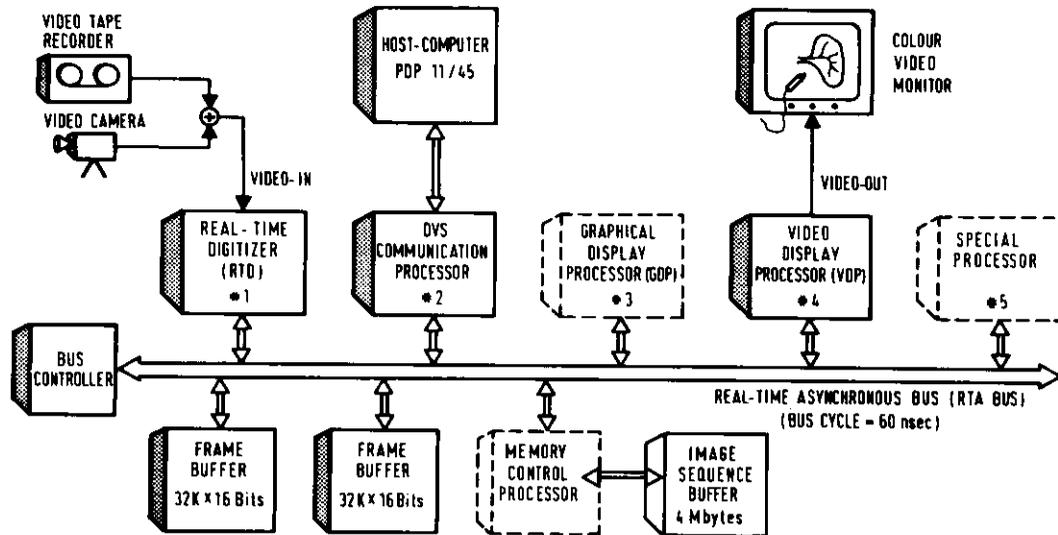


Fig. 8 Basic hardware structure of the system CA-1

The RTD contains three classes of instructions:

- Instructions controlling the acquisition format. The user can select any rectangular window with $0 \leq X \leq 255$ and $0 \leq Y \leq 255$ for the acquisition.
- Instructions controlling the spatial resolution (sampling rates of 5 MHz or 10 MHz) and the time resolution (up to 50 frames/s).
- Instructions controlling the destination of the digitized data.

Video Display Processor. The Video Display Processor (VDP) is used for the display of the data contained in the frame buffers or the color video monitor. To give an easily interpretable optical presentation of the different semantics of the data grey level transformation and/or colour coding is provided. Thus, the main feature of the VDP is its programmable real time processing facility, based on the technique of fast look-up tables. Monadic and dyadic operations are available. Monadic operations work on one of the frame buffers or the concatenation of both. A typical monadic operation is contrast enhancement. A dyadic operation takes the two frame buffers as operands. A typical application

is image subtraction. As the look-up tables can be updated up to 50 times/s a dynamic interpretation of the picture data is possible, which even allows the reconstruction of moving scenes from images containing time parameters. The VDP contains three classes of instructions:

- Instructions controlling the display format: any rectangular window with $0 \leq X \leq 255$ and $0 \leq Y \leq 255$ can be selected by the user.
- Instructions controlling the spatial resolution: (256 or 512 pixel/line).
- Instructions for filling the look-up tables (256 words 8 bits, 4096 words, 9 bits).
- Instructions controlling the data paths.

Video Tape Controller. For the long-term storage of image sequences a Video-Tape-Controller has been built which together with the Real Time Digitizer makes the video tape looking like a digital tape from which any image is addressable. Thus, about 350 scenes of 10 seconds each may be stored and retrieved.

The structure of the DVS is such that it is open to new processors. For instance algorithms tested in the host computer may be implemented in a special processor for fast execution. The system has now been successfully in operation since two years.

3.2 System Software

The main requirements which had to be met by the software implementation are one the one hand high efficiency, necessary to process in acceptable time the large amounts of multi-temporal image data and on the other hand enough flexibility to use the system in an interactive way.

Concept. In order to achieve these features we implemented an experimental dialog system called 'PROFI-11' (Processing and Retrieval of Functional Images on a PDP-11 Computer). To achieve flexibility PROFI-11 includes dialog features like immediate execution of single commands as well as execution of programs which have been edited before. User definable function-keys are

provided for frequently used commands or programs. Programs may be interrupted by an user-interrupt, e. g. to enter commands for inspection or modification of variables. Afterwards the program-execution may be continued. Efficiency was achieved by using the concept of a simple *table driven compiler* instead of a time consuming interpreter and by using an implementation language (SIMPL-11), which we had previously designed (17), which combines efficiency and machine-orientation of assembly languages with the advantages of control structures and data types as they are known from high level languages.

The system is partitioned into a frame (supervisor, table driven compiler, data definition facilities) and a set of problem oriented software processors. These processors, which are the largest part of the system, use the standard FORTRAN subroutine interface, so they may be used without the frame as libraries for stand-alone programs, or the processors may be incorporated into other frames, e. g. a dialog language for image processing (18) which has been implemented concurrently. This language shall also support interested but untrained physicians.

Data Definition and Data Types. The data definition facilities include, besides the basic data types INTEGER and VECTOR, the problem oriented data types COLOR, IMAGE and MULTIPLE IMAGE. To define the total size or to access subsets of images and multiple images we use the data types REGION (1-dim.) FRAME (2-dim.) and CUBE (3-dim.). For better readability the names of such objects are preceded by special signs (% for regions, = for frames, for cubes). E. g. the regions %X and %Y are defined by:

```
REGION %X, 100, 128.
REGION %Y, 50, 200.
```

A frame named XY may be composed of both regions by:

```
FRAME XY, %X, %Y.
```

Then an image, which shall be physically located in image buffer 1 (indicated by M1), may be defined by one of the following equivalent commands:

```

IMAGE TSTIMA, XY, M1
IMAGE TSTIMA, %X, %Y, M1
IMAGE TSTIMA 100, 128, 50, 200, M1.

```

During a session new data objects may be defined, old ones may be inspected via an ASK-command or dropped via a DROP-command. For suitable objects (e. g. frames) is also an interactive definition or alteration by trackball provided.

Operators. A large set of monadic and dyadic operators (including byte and word arithmetic with and without automatic scaling, bit-handling, I/O-operators) is implemented only once in a common operator pool which is shared by the operations on integers, vectors, images and multiple images. The execution speed of complex monadic byte operators is greatly increased by using the concept of computing only once a look-up table for the operator which is afterwards used as fast transformation map (e. g. for logarithmization of images). For image enhancement and analysis we use iterative neighbourhood techniques which have important advantages over pure local or sequential approaches. Pure local approaches are too sensitive to noise and the results of sequential approaches will often depend on the order on which the pixels are examined. All neighbourhood algorithms are implemented using a common program frame for effective fetching of operands and storing of results.

Specific Hardware Support. To achieve flexibility it is necessary that specific hardware requirements and restrictions are hidden from the user. E. g. the user may work with images which are physically located in one of the frame buffers in the same way as with images which are located in memory. Also it is not necessary to know how to fill the hardware look-up tables to perform a specific monadic or dyadic image operation. From any byte operator the corresponding look-up table may be derived automatically.

Manipulation (shifting, scaling) of tables for grey-level-transformation or pseudocolor-coding may be done interactively by trackball.

Database Facilities. To provide local database facilities, a simple relational data base system has been implemented. It is based on the file system and allows definition of new relations and offers the necessary selection, deletion, addition and update features. Because the involved data amounts

are small, all searches are purely sequential. For long-term storage the local database will be connected to a large relational database system (20), which we have implemented in parallel on an IBM 370/168 on top of the commercial linear data base system ADABAS.

Performance. PROFI-11 is implemented on a PDP-11/45 computer. For our application the average processing speed has been doubled by adding a cache-memory. The following examples shall give an impression of the system's execution times:

- *Monadic image operations:* To clear an image (256 x 256 x 8 bit) takes 0.25s. Logarithmization of such an image with explicit computation of the logarithm for each pixel takes 45 s. Using a software look-up table the execution time is only 1.7 s.
- *Dyadic and Neighbourhood operations:* Adding or subtracting two images (256 x 256 x 8 bits) takes 2.0s. A simple 3 x 3 smoothing algorithm needs 15 s. A more complex noise cleaning algorithm which takes into consideration which points of a 3 x 3 neighbourhood will probably belong to the same region (therefore sorting of neighbourhood is necessary) needs 21 s to execute.
- *Multitemporal images:* To compute a set of 4 functional images from a series of 128 images of an organ that fits into a 128 x 128 picture matrix takes 4 min. Most of this time is necessary for noise cleaning of the intensity versus time curves. We are presently investigating whether parameters could be found with comparable physiological meaning but less noise sensitivity.

4. APPLICATION

With the described method about 140 image sequences (120 kidneys, 20 livers) have now been examined. The following examples are to show that already in the present state results with clinical relevance are achieved.

Fig. 9 shows the functional images of the type 'time of CM-front' for a normal kidney (left) and a kidney with a nephrotic syndrome (right). At a first glance the absence of device dependent intensity inhomogenities and overlays is obvious, which leads to a clear presentation of the organ. The radiologist can immediately infer from the color distribution that the blood flow in the right kidney is delayed. By comparison with the color scale he even can quantify the delay. This diagnostically relevant information is not obtainable from the conventional angiogram. As these functional images represent 'time tables' for contrast medium propagation, the original sequence may be reconstructed from them and played back by the CA-1 system in real time (see fig. 10). The visual impression is nearly the same as from the original sequence. We, therefore, conclude that the main part of the information contained in the sequence is already represented in one single functional image.

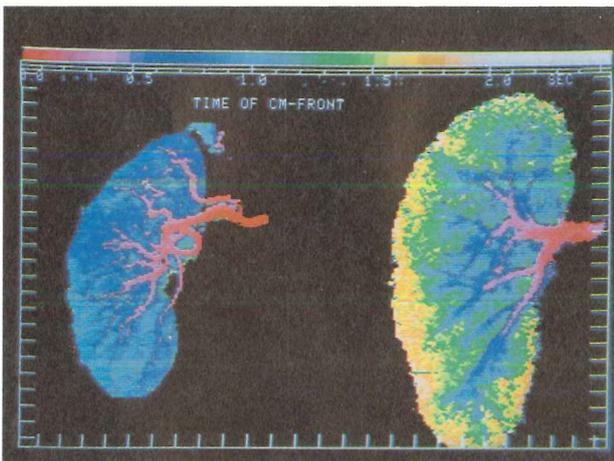


Fig. 9 Functional images of a normal and an abnormal kidney

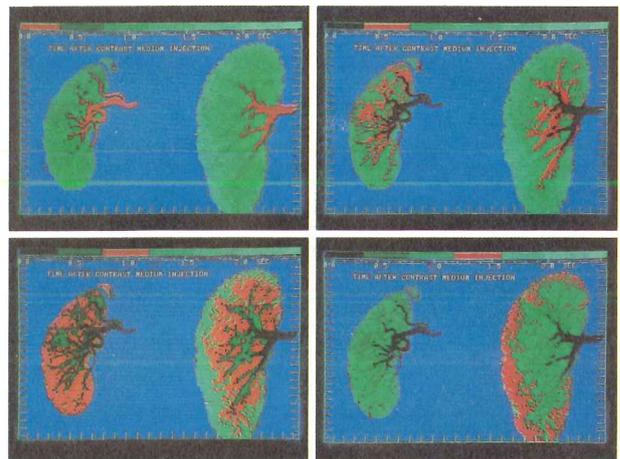


Fig. 10 Four phases of the real time reconstruction of blood flow

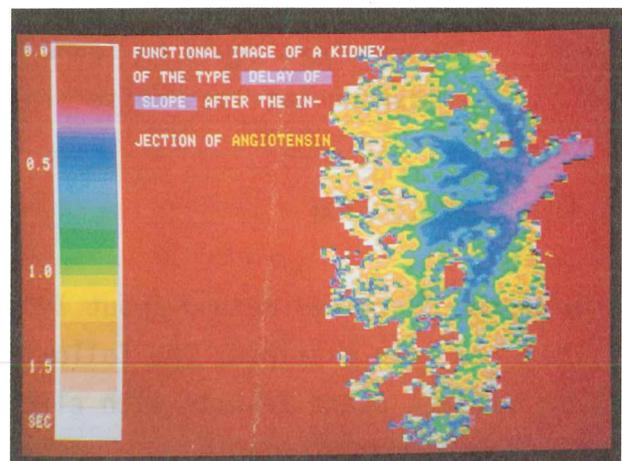
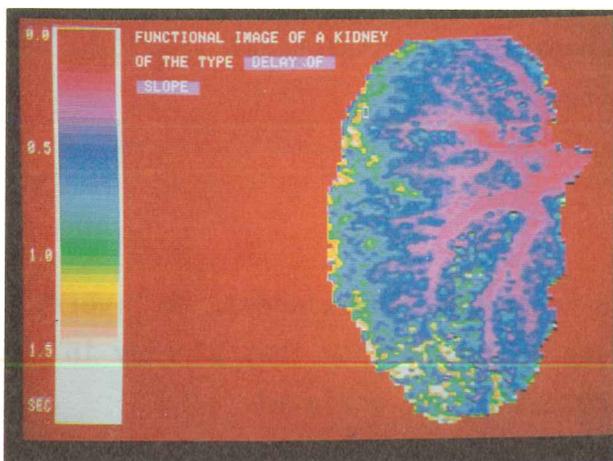


Fig. 11 Functional images 'time of CM-front' for a kidney before (left) and after the injection of angiotensin

Fig. 9 shows the functional images of the type 'time of CM-front' for a normal kidney (left) and a kidney with a nephrotic syndrome (right). At a first glance the absence of device dependent intensity inhomogeneities and overlays is obvious, which leads to a clear presentation of the organ. The radiologist can immediately infer from the color distribution that the blood flow in the right kidney is delayed. By comparison with the color scale he even can quantify the delay. This diagnostically relevant information is not obtainable from the conventional angiogram. As these functional images represent 'time tables' for contrast medium propagation, the original sequence may be reconstructed from them and played back by the CA-1 system in real time (see fig. 10). The visual impression is nearly the same as from the original sequence. We, therefore, conclude that the main part of the information contained in the sequence is already represented in one single functional image.



Fig. 9 Functional images of a normal and an abnormal kidney

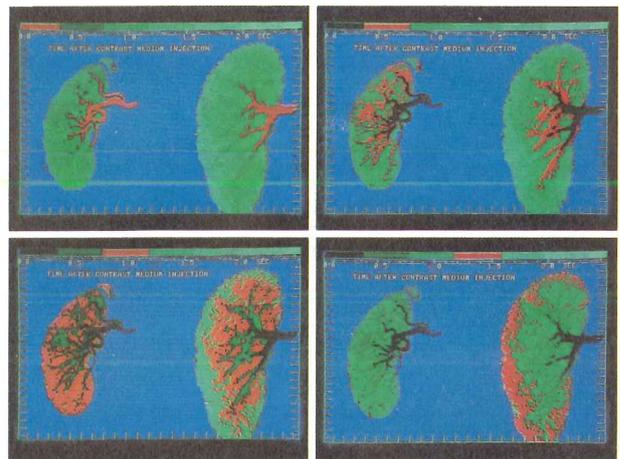


Fig. 10 Four phases of the real time reconstruction of blood flow

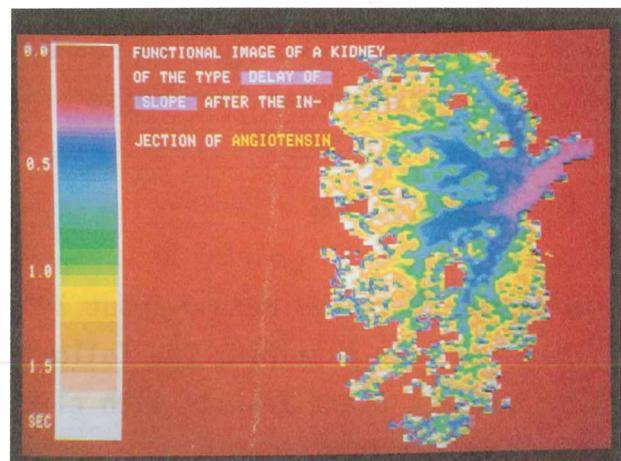
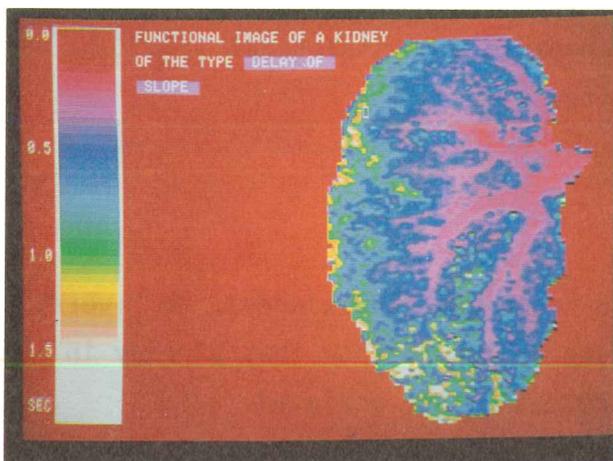


Fig. 11 Functional images 'time of CM-front' for a kidney before (left) and after the injection of angiotensin

(yellow-brown region) could be recognized earlier than by conventional methods. Fig. 14 is to demonstrate that even more complicated defects in the blood dynamics may be localized by the Computer Angiography. It shows a functional image 'time of CM-Maximum' of a kidney with a tumor covering nearly the whole organ. The yellow region in the center gives the impression that there is a region with delayed blood flow. The analysis of the x-ray intensity as a function of time in the suspicious region gives the result that this region describes a shunt between the arterial and the venous system. In this case the curve (fig. 15) shows a twin peak corresponding to the arterial and the venous flows respectively. The program, accidentally, interpretes this situation as a delayed arterial flow. We conclude that the refinement of the algorithms to recognize more special features such as the presence of twin peaks may lead to the localisation of abnormalities not visible at all in conventional angiograms.

The method is, of course, applicable to other organs such as the liver, the brain or the heart. Fig. 13 shows the functional image 'time of CM-front' of a liver before (left) and after the injection of Dilatol which is known to increase the blood flow. In the case of this patient, who was suffering from a liver cirrhosis it could be proven by the functional image that there was no significant influence on the blood flow.

5. CONCLUSIONS

It has been shown that the new method of Computer Angiography is an instrument for obtaining essentially more and better diagnostic information from angiograms of organs such as the kidney and the liver. Although the radiologist gets a new kind of information, he does not have to change his technique for interpreting images. The proven success of the described method supports our opinion that at the present state of medical image processing one most promising approach is to compute new images containing better information rather than to aim at the automation of the image interpretation, which is still best done by the radiologist.

REFERENCES

- (1) Johnson, S. A. et al., 'Bioimage Synthesis and Analysis from X-Ray, Gamma, Optical and Ultrasound Energy', 'Digital Processing of Biomedical Images' (K. Preston and M. Onoe Eds.), Plenum Press, New York 1976, 203.
- (2) Silverman, N. R. 'Videometry of Blood Vessels', *Radiology* 101 (1971), 697.
- (3) Silverman, N. R., M. Intaglietta, W. R. Tompkins, 'Renal Cortical Transit Times', *Radiology* 105 (1972), 25.
- (4) Rosen, L., N. R. Silverman, 'Application of Videodensitometry to Quantitative Radiological Measurement in Medicine', *Proc. of the Soc. of Photo Optical Instr.* 40 (1973), 69.
- (5) Vanselow, K., F. Heuck, 'Neue Grundlagen und Theorien zur Verbesserung der Angio-Cine-Densitometrie', *Fortschr. Röntgenstr.* 122 (1975), 453.
- (6) Epple, E., D. Decker, F. Heuck, 'Meß- und Auswerteverfahren der Röntgen-Cine-Densitometrie mit einer Datenverarbeitungsanlage', *Fortschr. Röntgenstr.* 120 (1974), 345.
- (7) Deininger, K. H., 'Angiographisch densitometrische Möglichkeiten zur Bestimmung der renalen Blutdynamik', *Med. Welt* 27 (1976), 1764.
- (8) Pieroth, H. D., E. Magin, M. Georgi, M. Marberger, 'Ergebnisse der kineangioidensitometrischen Nierendurchblutungsbestimmung', *Fortschr. Röntgenstr.* 126 (1977), 126.
- (9) Höhne, K. H., M. Böhm, W. Erbe, G. C. Nicolae, G. Pfeiffer, B. Sonne, 'Computer-Angiography - A New Tool for X-Ray Functional Diagnostics', *Med. Progr. Technol.* 6 (1978), 23.
- (10) Höhne, K. H., M. Böhm, W. Erbe, G. C. Nicolae, G. Pfeiffer, B. Sonne, E. Bücheler, 'Die Messung und differenzierte bildliche Darstellung der Nierendurchblutung mit der Computer-Angiographie', *Fortschr. Röntgenstr.* 129 (1978), 667.

- (11) Kaihara, S., C. Natarajan, D. Maynard et al., 'Construction of a Functional Image from Spatially Localized Rate Constants Obtained from Serial Camera and Rectilinear Scanner Data', *Radiology* 93 (1969), 1345.
- (12) Agress, H., Jr., M. V. Green, D. R. Redwood, 'Functional Imaging Methodology: Recent Clinical and Research Applications', *Proc. of the IVth Intern. Conf. on Information Processing in Scintigraphy* (1975), 1289.
- (13) Toyama, H., M. Ilio, J. Iisaka et al., 'Color Functional Images of the Cerebral Blood Flow', *J. Nucl. Med.* 17 (1976), 953.
- (14) Nicolae, G. C., K. H. Höhne, 'A Multiprocessor System for the Real-Time-Digital Processing of Video Image Series', *DESY-Report DV 78/2* (1978).
- (15) Kruger, R. A., S. J. Riederer, T. L. Houk, C. A. Mistretta, C. G. Shaw, J. C. Lancaster, 'Real-Time-Computerized Fluoroscopy and Radiography', A Progress Report, Preprint.
- (16) Kruger, R. A. et al., 'Preliminary Studies of Real-Time computerized Fluoroscopy Techniques for Non-Invasive Visualization of the Cardiovascular System', Preprint.
- (17) Pfeiffer, G., 'SIMPL-11 - eine einfache Implementationsprache für PDP-11 Rechner', *DESY-Report DV-76/2* (1976).
- (18) Pfeiffer, G. and K. H. Höhne, 'Improvement of Programming Efficiency in Medical Image Processing by a Dialog Language', *Proceedings of MIE 78, Lecture Notes in Medical Informatics, Vol. 1, Springer, New York, 1978.*
- (19) Erbe, W., B. Sonne, K. H. Höhne, 'Eine quantitative Bestimmung der Wirkung von Angiotensin auf die Nierendurchblutung', *Fortschr. Röntgenstr.* 130 (1979), in press.
- (20) Böhm, M., and K. H. Höhne, 'Aufbau eines Datenbanksystems nach dem Relationenmodell für die medizinische Anwendung', *Jahrestagung der GMDS, Göttingen, 1977 (in press).*