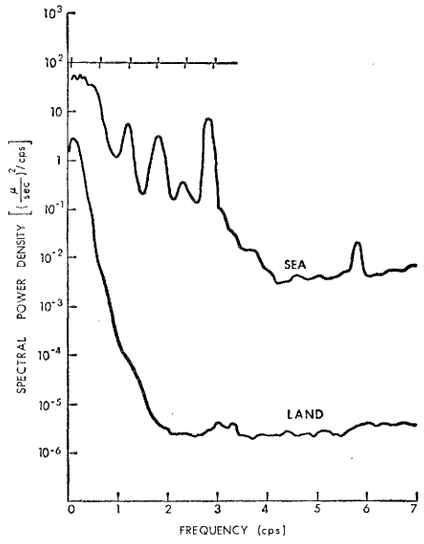

Fig. 11. Typical microseism noise spectra for the ocean bottom and for Oahu, Hawaii, 8 February 1963.

these waves in spectral peaks if the energy comes from a localized source. Pure Love waves, for example, would have no vertical component and would have a zero-degree or 180-degree phase difference between the two coherent, horizontal components. Pure Rayleigh or Love waves are rarely found, since modes are converted by scattering in the inhomogeneous earth, and more than one source may be active at any time. We are unable to regularly associate the energy in the microseism peak with either the vertical or the horizontal polarized surface waves that are commonly recognized at land stations, although either form of wave may contribute much of the energy on a given day. We find that near-vertical compressional waves in the water, which we call "organ-pipe" waves, can be responsible for some marked peaks in the low-frequency region.

The shape of the spectrum does not change markedly as we travel to mid-ocean, far from storms or shore lines. From that observation we conclude that high-frequency seismic background noise is generated locally, throughout the area of our stations in the Pacific Ocean. The most likely mechanism for generation of high-frequency energy is a statistical superposition of oppositely traveling surface-water waves. These standing waves will exert forces on the bottom, at half the wave frequency (*16*).

We have found good examples of all the currently accepted mechanisms of microseism generation. There is evidence for generation near shore, and in storms far from shore. We suggest that the normal, continual microseism background is a superposition of energy from many sources. The peak at a period of 6 to 8 seconds may be accentuated by the resonance of the 5-kilometer thick ocean wave guide, as well as by the predominant frequency of the surface waves.

Conclusion

With apparatus developed for ocean-bottom seismic recording, earthquakes have been observed, propagation velocities have been measured, microseism noise has been studied, and it has been determined that signal-to-noise ratios may allow the monitoring of bomb tests. But many more measurements will be needed before definitive remarks can be made about any of the phenomena.

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High-Speed Automatic Analysis of Biomedical Pictures

Robert S. Ledley

The biological and medical scientist has developed highly specialized and precise techniques for photographing structures, forms, and phenomena that occur in almost every field of biomedical research. Huge masses of material are accumulating at an ever-increasing rate, such as photomicrographs of chromosomes that relate to genetic diseases; photomicrograph sequences showing the dendritic structure of nerve cells; electron micrographs of muscle fiber structure and of DNA with bases containing radioactive heavy atoms; and films of x-ray diffraction patterns of biologically important molecules. Individual pictures hold a great wealth of precise numerical information, such as morphological and structural characteristics of lengths, areas, volumes, densities; from sequences of pictures quantitative results can be derived, such as kinematic and dynamic characteristics of trajectories, velocities, and accelerations.

The large-scale quantitative analysis of these pictures cannot be achieved by manual methods, because of the tedium, manual precision, and extensive time that is necessarily involved. Hence we have embarked on a program designed to enable such pictures to be analyzed

The author is president of the National Biomedical Research Foundation and instructor in pediatrics at the Johns Hopkins Medical School.

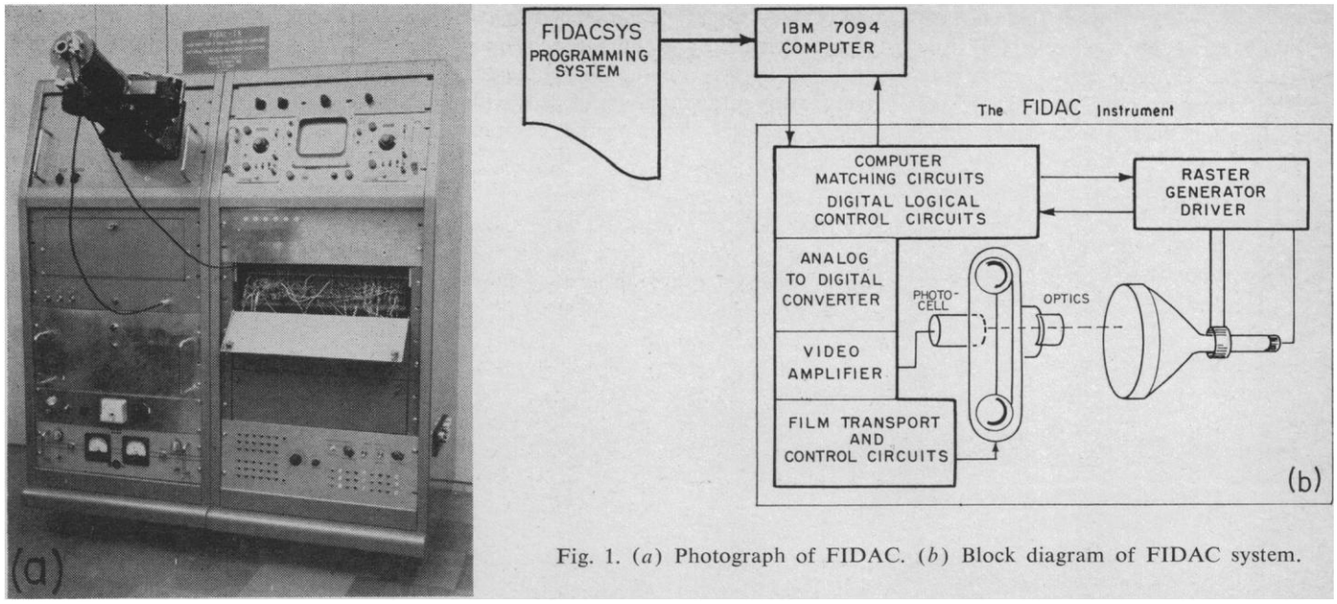


Fig. 1. (*a*) Photograph of FIDAC. (*b*) Block diagram of FIDAC system.

automatically by means of a digital computer. The technique described in this paper promises to open up entirely new fields of investigation in biological and medical research (*1*). There are two main steps in this technique: first, a scanning instrument called FIDAC (Film Input to Digital Automatic Computer) "reads" the picture on-line into the high-speed memory of a digital computer; second, a computer programming system, called FIDACSYS, "recognizes" the object to be measured and processes the quantitative data according to requirements of the particular biological or medical problem under consideration. The FIDAC system was designed specifically for the processing of biomedical pictures.

The FIDAC instrument is responsible in the first place for putting the picture into the computer's memory; it is an on-line computer-input device which can scan in real-time at very high speed and with high resolution with computer-program feedback control (see Fig. 1). FIDAC has (i) a high-speed scan of less than 0.2 second per frame, which makes possible the rapid processing of pictures for statistical analysis and screening purposes; (ii) a high resolution (greater than that of the optical microscope), enabling all information to be retained when it is scanning photomicrographs—that is, for a magnification of 1000 each 0.2 μ of the specimen is sampled by more than three points (*2*); (iii) the capability of real-time operation, enabling program control of the FIDAC by the computer—that is, when the processing of a film frame has been completed, the program signals the FIDAC to move automatically to the next frame; and (iv), direct input to the computer—this results in extreme flexibility, convenience, and economy of storage of the original data (*3*). During the scan, over 800,000 points per picture (1,000 × 800 point raster) are sampled in the black-and-white mode, one memory bit per picture point being used, or over 350,000 points per picture (700 × 500 point raster) are sampled in the eight-level gray mode, three memory bits being used (*4*). As a comparison, FIDAC can load the computer's core memory 10 to 50 times faster than can conventional magnetic-tape input units. In fact the speed of the scan and the number of points per picture that are sampled are presently limited not by the FIDAC device, but rather by the large-scale high-speed computer being used [that is, by the cycle-time and size of the magnetic core memory (*5*)]. The new generation of computers, with higher speed and larger memories, will be able to take further advantage of the capabilities of the FIDAC instrument (*6*). This resolution and scanning speed holds for 16-mm movie frames, 35-mm movie frames, and 35-mm slide frames.

The FIDACSYS Programming System

Once the picture is recorded in the computer's core memory, as a grid of points each with one of eight gray-level values (see Fig. 2), the computer analysis proceeds by means of the FIDACSYS programming system. This system consists of a large number of basic computer programs integrated with each other in different ways for different problems; in effect, the system constitutes a general pattern-recognition and analysis programming language.

To illustrate the basic concepts of our programming system FIDACSYS, its use in the analysis of chromosome photomicrographs will be described. This example represents an important application of the system in its own right, and I will begin by giving some background information about the chromosome-analysis problem.

The Chromosome Problem

Recently, there has been much active interest in the analysis of chromosomes in the metaphase stage of mitosis, when they appear as structures split longitudinally into rod-shaped chromatids lying side by side and held to one another by a constricted area called the centromere. Certain abnormalities in the number and structure of chromosomes are particularly evident at this stage and can be related to clinical conditions in animals and in man. For example, in man, mongolism and the Klinefelter and Turner syndromes have been correlated with chromosome aberrations (*7*).

The study of chromosomes by manual methods, however, requires a great deal of time—enlarged prints must be made from photomicrographs, and each chromosome must then be cut out from the print so that it can be aligned with the others for classification into the so-

called chromosome karyotype (see Fig. 3). With the FIDAC system, the time required for analyzing and classifying each chromosome can be radically reduced to about half a second per chromosome, or about 20 seconds for the full complement of human chromosomes. Here we use the computer for investigating large numbers of cells with respect to total chromosome complement counts, to quantitative measurements of individual chromosome arm-length ratios, densities, areas, and other morphological characteristics, and so forth.

By processing large numbers of chromosome sets and statistically analyzing the data, it is possible to give very accurate descriptions of the standard complement of chromosomes and individual chromosome variability for particular species. This statistical technique may be the only way to uncover small variations, which may prove important in relating chromosome karyotypes to diseases. For example, careful analysis of the chromosomes of individuals with myeloid leukemia, prior to the availability of automatic computer analysis, showed that the chromosomes characteristically lack a small portion of one arm; less obvious abnormalities may well be revealed by means of the computer.

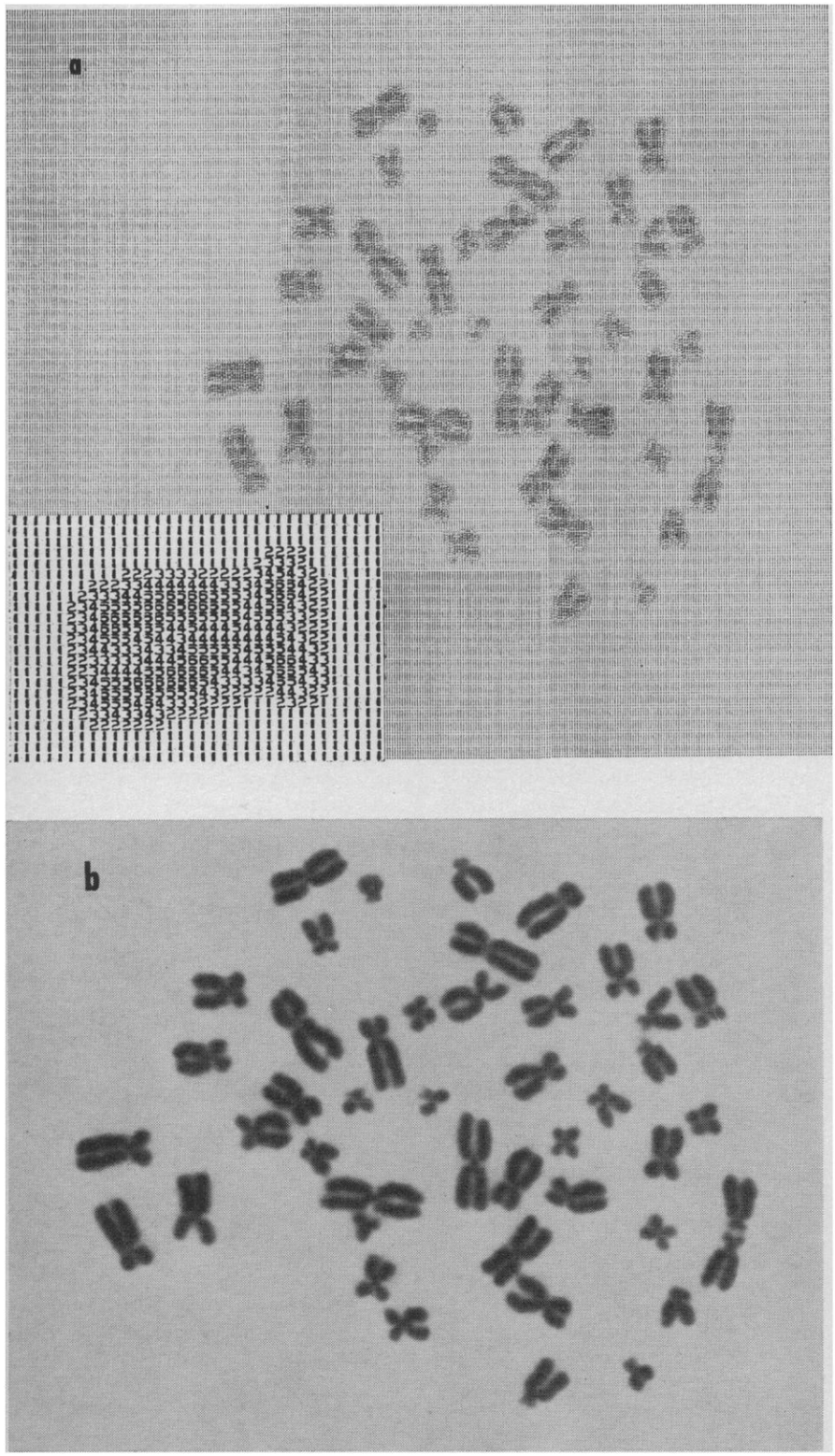


Fig. 2. Representation of chromosome photomicrograph in the computer's memory. (*a*) Actual computer print-out of picture (with detail inset) that has been put into the computer's memory in 0.2 sec by FIDAC. (*b*) The original photomicrograph.

Processing a Roll of Film by FIDACSYS

When a roll of photomicrograph film frames is ready for processing, the film is placed in the film transport unit of the FIDAC instrument, and the start button on the computer is pushed. Figure 4 illustrates the sequence of functions performed by the computer. After setting the frame count p to 1, the FIDACSYS (computer program) signals the FIDAC to scan the frame, and within 0.2 second the picture is in the computer's memory.

Next a spectrum is computed for the picture, giving the number of points with gray value 1, gray value 2, . . . , gray value 7. The 8th gray level is reserved for the erasing operation. From the spectrum the FIDACSYS can determine whether or not the picture is blank —that is, either all black or all white (or at least 98 percent black or 98 percent white). If the picture is all black or all white, the program signals FIDAC to move to the next frame. In this way blank frames or leader frames can be skipped automatically. If the frame is not blank, then the spectrum information can be used for other purposes, such as determining the proper *cut-off gray-level* value that indicates those gray values that represent points inside the chromosomes. For example, it may be determined that the cut-off level L should be chosen as the gray level such that 10 percent of the points have a gray value greater than L.

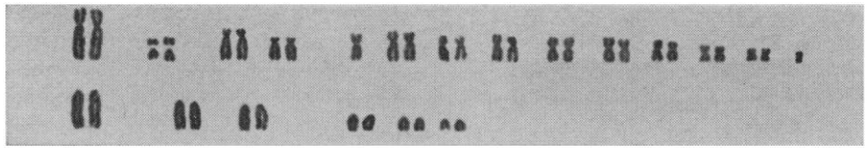


Fig. 3. A chromosome karyotype of an animal.

After every chromosome on the frame has been analyzed, the FIDACSYS program determines whether or not there is another frame on the film, and if there is, the FIDAC instrument is signalled to move to the next frame, and the process is repeated. If the predetermined number of frames has been processed, then the resulting information is statistically analyzed; for example, the distribution of the number of chromosomes in each cell is found, as are the distribution of chromosome arm-length ratios by group and the distribution of relative positioning of homologous chromosomes. Having completed the statistical analysis, the FIDAC system is then ready for another roll of film.

Processing the Objects of a Frame

In Fig. 4, the heavy-outlined box represents the actual processing of the pictorial information on a frame. Figure 5 represents the details of this process. The object count i is set to 1 and the process starts by the FIDACSYS performing an interval scan on the picture image in the computer's high-speed core memory. This is accomplished in effect by moving a "bug" across successive horizontal rows of the raster of picture points, "searching" for points with a gray level greater than the cut-off level. Such a point will be that of the next object to be processed.

If the search does indeed locate another object, then the object is processed by the FIDACSYS program. For our chromosome illustration, this processing consists of first making a determination of whether or not the object is truly a chromosome, and if it is, of determining the location, the length, the individual arm-lengths, the arm-length ratio, the overall length, and the area of the chromosome. Having completed the processing of the object, the FIDACSYS then goes on to search for the next object in the frame.

Eventually it will happen that all the objects have been processed, and no "next object" will be found. In such a case the "bug" will reach the end of the raster (that is, the lower right-hand corner) indicating that all objects have been processed. Then the results of the measurements made on the objects of that frame are evaluated. The evaluation of these results consists of pairing homologous chromosomes by criteria of overall length, of arm-length ratio, and of area; and then of placing each pair into one of seven groups or classes generally accepted for human chromosomes. A count of the chromosomes is also made; the total chromosome length for the frame is evaluated, and the fraction each chromosome contributes to this length is determined.

In Fig. 5 the heavy-outlined box represents the actual processing of the object. Figure 6*a* represents the details of this process. The first step in processing an object is to characterize its boundary. This is accomplished by having the "bug" trace around the boundary by following a constant gray-level contour at a level just greater than the cut-off level. This contour or *boundary* is analyzed in terms of successive *segments*, and characterized by a *boundary list* of measurements from which the "curvature" and "direction" for each segment can be determined. Since in the analysis of the chromosome illustration, the objects are considered conceptually as silhouettes, once the boundary list has been constructed, the image of the object is no longer required. To prevent the object's being counted or analyzed again, it is literally erased from the picture in the computer's memory.

From the boundary list, the so-called *basic parts* are determined, and then the *derived parts* are recognized to determine whether or not the object is indeed a chromosome. If it is a chromosome, then measurements on the object are made from the *derived-parts list*.

Boundary Analysis Approach

In Fig. 6*a* the heavy-outlined box represents the actual characterization of the boundary of an object. Figure 6*b* represents the details of this process. First the coordinates are recorded of the point at which the boundary of the object was entered, for this point marks the end as well as the start of tracing around the boundary. The boundary is traced in such a direction that the interior of the object is kept to the right of the "bug." The "next" boundary point is determined by looking clockwise around the "present" boundary point, starting from the "previous" boundary point (see Fig. 7). When a certain number N of boundary points (that is, a certain boundary length) has been traversed, a *segment* is defined.

The segment is then characterized by (i) the coordinates of its *center point*, (ii) the components of a *leading vec-*

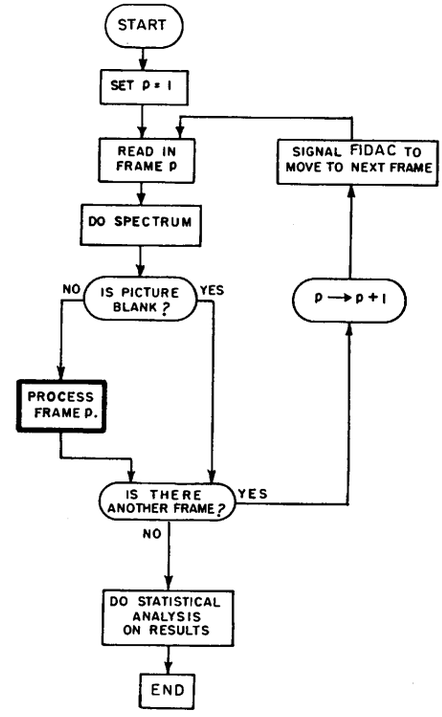


Fig. 4. Processing a film roll.

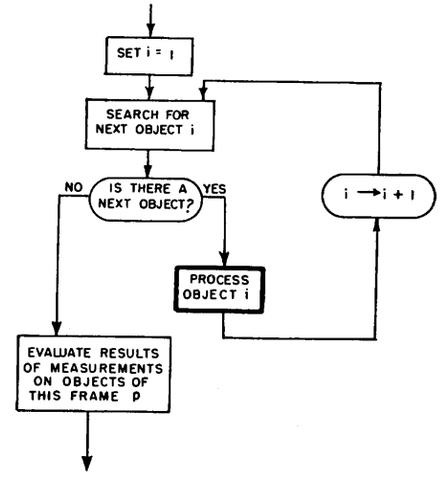


Fig. 5. Processing frame p.

Table 1. Sample syntax for submedian and telocentric chromosomes.

⟨arm⟩ : : = *B* ⟨arm⟩ | ⟨arm⟩ *B*|*A*	70 : : = *B*,70|70,*B*|*A*
⟨side⟩ : : = *B* ⟨side⟩ | ⟨side⟩ *B*|*B*|*D*	71 : : = *B*,71|71,*B*|*B*|*D*
⟨bottom⟩ : : = *B* ⟨bottom⟩ | ⟨bottom⟩ *B*|*E*	72 : : = *B*,72|72,*B*|*E*
⟨right part⟩ : : = *C* ⟨arm⟩	73 : : = *C*,70
⟨left part⟩ : : = ⟨arm⟩ *C*	74 : : = 70,*C*
⟨arm pair⟩ : : = ⟨side⟩⟨arm pair⟩ | ⟨arm pair⟩⟨side⟩	75 : : = 71,75|75,71
| ⟨arm⟩⟨right part⟩ | ⟨left part⟩⟨arm⟩	|70,73|74,70
⟨submedian chromosome⟩ : : = ⟨arm pair⟩⟨arm pair⟩	76 : : = 75,75
⟨telocentric chromosome⟩ : : = ⟨bottom⟩⟨arm pair⟩	77 : : = 72,75

tor, and (iii) the components of a *trailing vector* (see Fig. 8). The length of the segment chosen must be short enough so that the angle between the leading and trailing vectors becomes an approximation to the measure of the *curvature* of the segment. Then the vector sum of the leading and trailing vectors is approximately the tangent to the segment at its center point, and gives a measure of the *direction* of the segment. There are three parameters associated with a segment that are chosen to suit the particular problem under consideration: these are the segment length N, the arrow length A, and the distance D between centers of successive segments. Each boundary segment is analyzed successively, and a boundary *characterization list* is constructed until the original boundary entry point is reached again.

As each boundary point is traversed, its value is changed to the value "8" completely enclosing the object in the string of 8's. The erasing process becomes greatly simplified, for now only values on a row between 8's need to be erased. Holes in the object are discovered during the erasure procedure, and when found, their boundaries are characterized by segments. Hence erasing resolves two problems: it eliminates the possibility of analyzing an object more than once, and it locates any holes in the object. Islands within holes are found by filling in the holes, and holes within islands within holes are found by erasing, ad infinitum. However, only simple holes with no islands are found in chromosome applications.

Syntax-Directed Pattern Recognition

In Fig. 6*a* the two boxes with the heavy bar on the left side comprise the syntax-directed pattern-recognition portion of the FIDACSYS programming system. This approach to pattern recognition is based on some of my original work, and an introduction to the technique can be found elsewhere (*8*). Here I will briefly describe the method as applied to the recognition of chromosomes.

Consider a characterization of the boundary of an object in terms of five types of curves: a clockwise curve, type A; a relatively straight line, type B; a counterclockwise curve, type C; a notch, type D; and a wide clockwise curve, type E (see Fig. 9). Syntactical definitions of the different kinds of chromosomes can be made in such terms as these. A boundary is first characterized as a list of such curve types, as shown in Fig. 9*b*, and then the syntactical definitions are used to "build up" derived parts of a chromosome from combinations of these curve types. For example, the syntax for a submedium chromosome and a telocentric chromosome (see Fig. 9*c*) is shown in Table 1. The recursive definition

⟨arm⟩ : : = *B* ⟨arm⟩ | ⟨arm⟩ *B* | *A*

means that the generic concept *arm* is defined as being a *B* type followed by an arm, or an arm followed by a *B* type or an *A* type. In this notation the angular brackets ⟨ ⟩ indicate that a generic name is enclosed, the ": : =" means "is defined as being," and the "|" means

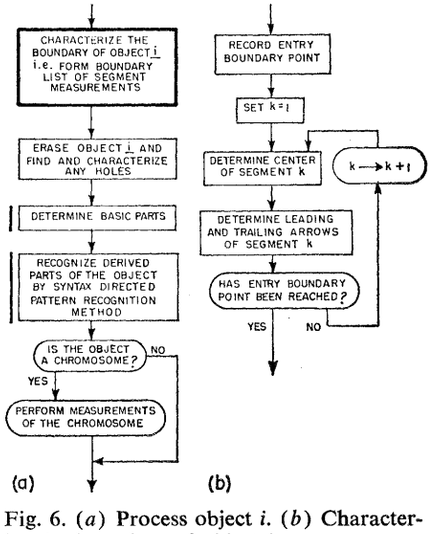


Fig. 6. (*a*) Process object *i*. (*b*) Characterize the boundary of object *i*.

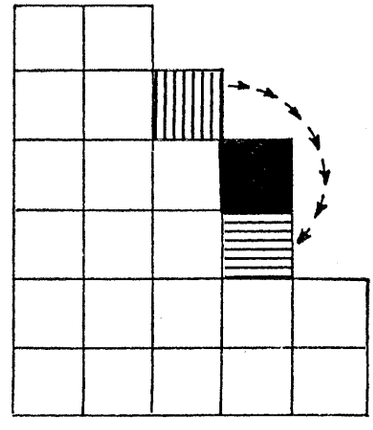


Fig. 7. The black box is the present boundary point; the vertically hatched box the previous boundary point; and the horizontally hatched box, the next boundary point.

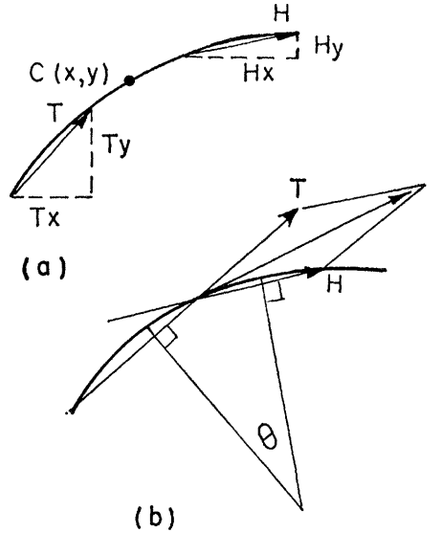
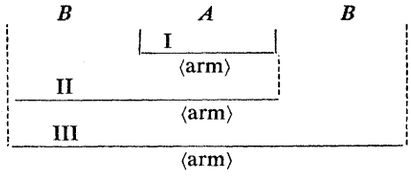


Fig. 8. (*a*) A segment illustrating the center of the segment $C(x,y)$, the trailing arrow components T_x and T_y, and the leading arrow component H_x and H_y. (*b*) The tangent vector $T+H$ and the angle $\theta = L/K$, giving $K = L/\theta$, where K is the curvature and L is the segment length (and θ is in radians).

"or." The definition is *recursive* in that it is used repeatedly. For example, consider Fig. 9*c*; our definition can be applied to the figure as follows:



where we first (I) identify the *A* type as an *arm*, and then build up the arm by repeated application of the definition to include (II) the *B* type on the left and (III) the *B* type on the right. Further consideration of these concepts can be found in (*8*). Figure 10 shows the building up of a submedian chromosome; the numbers on the brackets indicate the order of recognition.

The process is, of course, systematic, and is carried out by a special program in the FIDACSYS system called the MOBILIZER [which is directly analogous to the "translator" of automatic-programming-language translation (*8*)]. The mobilizer operates on a parts list for a particular object, and by using the generic syntactical description of various kinds of chromosomes "recognizes" the object as a chromosome or not a chromosome, and if a chromosome is recognized, as a particular kind of chromosome (see Fig. 11). Actually the mobilizer works with numbers: as shown in Table 1 the syntax can as well be written in terms of *level numbers*, where the numbers are assigned to the left-hand entities in the order in which they appear in the syntax. The basic parts, namely *A*, *B*, *C*, *D*, and *E*, are always considered to have number values less than any generic or "derived" part. Note that each syntax definition is given as a list of *alternatives*, and each alternative is made up of one or two *components*. Thus in the definition of the arm given above *B*, ⟨arm⟩ is the first alternative, ⟨arm⟩ *B* the second alternative, and *A* the third alternative. In the alternative *B* ⟨arm⟩, *B* is the left component, and ⟨arm⟩ is the right component.

The mobilizer starts with the first part of the object (see the arrow in Fig. 10), and looks through the syntax list for a matching part; if, say, only the left component matches, then if the right component has a level-number greater than the part of the object, an attempt is made to develop this part into the higher generic form. A simplified flow chart of the mobilizer is shown in Fig. 12, where the particular part being worked on is demarked by the *pointer*, and the syntactical alternative under consideration at any time is demarcated by the *locator*. A little reflection on the example shown in Fig. 10 in conjunction with Fig. 12 will make the details of this process clear.

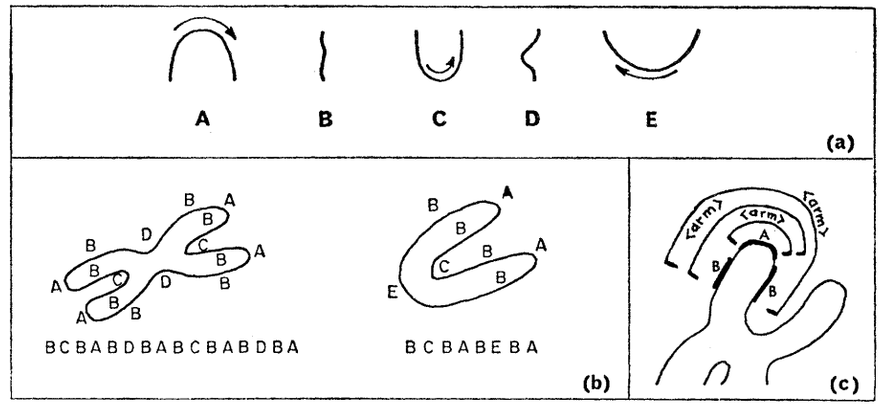


Fig. 9. (*a*) The basic types of curves used for the illustration in the text. (*b*) Illustration of submedian and telocentric chromosomes. (*c*) Short example used in text.

It should be pointed out that for the purposes of this paper the programming system FIDACSYS has been greatly simplified. Actually the system itself is vastly more complex than may appear from this discussion.

Although engineers often examine so-called neuron-net models, surprisingly

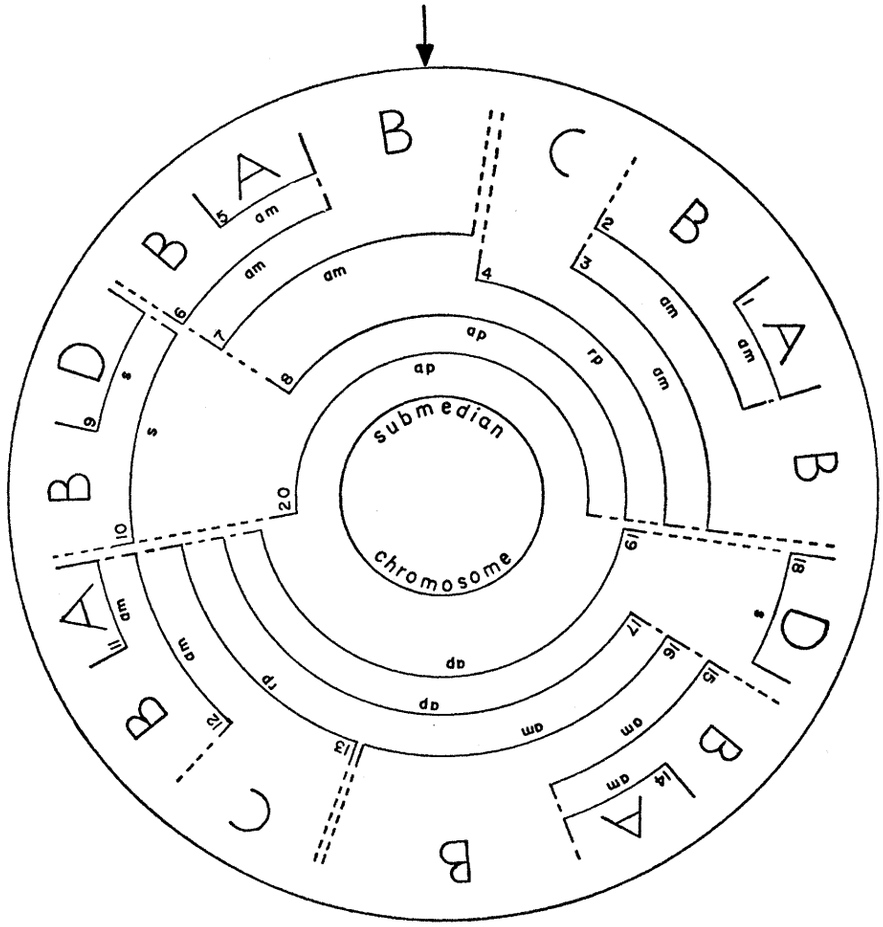


Fig. 10. Example of syntactical analysis or the build-up process followed in chromosome recognition. Here *am* stands for <arm>, *rp* for <right part>, *ap* for <arm pair>, and *s* for <side>.

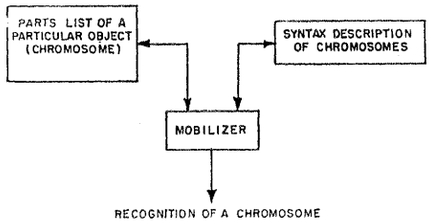


Fig. 11. Role of the mobilizer in recognizing a chromosome from a list of parts and a generic syntax description.

little is known about the actual connections between individual neurons, or about quantitative morphological characteristics of neurons. Utilizing the so-called Golgi staining techniques, neuron-anatomists, with great labor, have manually traced individual dendrite branches in three dimensions for a small number of cortical neurons, and have attempted to characterize the branching structure of the dendrite tree of such nerve cells (*9*). In this technique, successive sections of a cortex are photographed through the microscope as the plane of focus of the microscope is moved through the specimen in one-micron steps. Each such photograph then records that part of the nerve-cell structure that lies very nearly in the plane at the corresponding level, and the entire sequence of photographs contains the three-dimensional structural information desired.

The examination in quantitative detail of thousands of such cells is made possible by utilizing the FIDAC instrument to read such serial sections into the computer's memory for automatic analysis. The computer program is designed to distinguish dendrites (from blood vessels and axons) as follows: (i) a dendrite has small projections, called gemmules; (ii) there is a gradual tapering, or reduction in diameter, of the element distally from the cell body; and (iii) the branches of a dendrite are either of a "Y" type or are at right angles. On the other hand, a blood vessel is identified by its smooth surface, its relatively constant diameter, and its curved course. An axon also has a relatively smooth surface profile, has a relatively constant diameter over a relatively longer length, and has collaterals branching predominantly perpendicularly. The various individual dendrite fibers are identified in successive sections in a manner analogous to the identification of various individual aircraft on successive rotations of a radar scan. The locations of branch points are recorded, the distance between them is measured, and the number of branches is counted. The cells are then characterized as trees may be characterized, by their "bushiness," branching-structure features, distribution of bifurcations as a function of distance from the cell body, and so forth.

The use of a digital computer offers the possibility of analyzing quantitatively medical x-ray photographs. Such use of the computer would have many advantages; for example, the results of the analysis would presumably be more uniform than in conventional methods of examination, more stringent pattern-recognition requirements could be worked out, and the rate of examining x-rays might be significantly accelerated. Clearly, however, a great deal of research and development must be done before such a goal can be approached in the field of medical radiology. We felt it was best to begin with a relatively simple problem, though a significant one from a medical point of view, that of analyzing x-ray motion pictures (cineradiographs) of the action of the ventricles of the heart. When a soluble dye which is opaque to x-rays is properly injected into the blood stream by means of a catheter, the frontal projection of the blood mass in the ventricle, as recorded on the x-ray film, can be examined.

By means of the FIDAC instrument, successive frames of such x-ray photographs are put into the memory of the computer. A computer program analyzes the pictures for various quantitative characteristics of the opaque area formed by the blood in the ventricles. Each frame of the picture is of a different stage of contraction of the heart, and therefore an analysis of successive frames leads to information concerning velocities and accelerations associated with the contractile dynamics of the ventricles. With this technique, correlations are made between the rates and accelerations developed during ventricular contraction and various states of cardiac disease, such as valvular leaks, mitrol stenosis, and coronary heart disease. For each frame the computer program measures the projected area of x-ray opacity in the ventricle, the

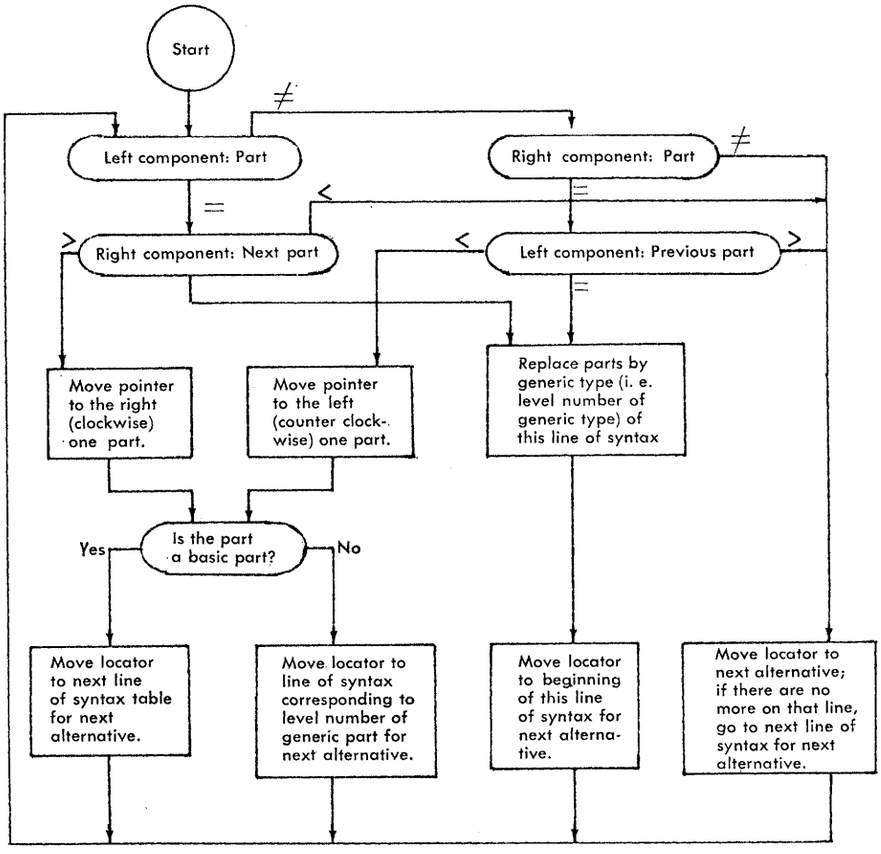


Fig. 12. Flow chart of the operations performed by the mobilizer. The *locator* normally moves from left to right, starting on a line with the leftmost alternative. The ":" represents "comparison" of *level numbers*.

lengths of the maximum and minimum diameters through the center of gravity of the opaque area, and the location of the lowest and most lateral points of the area. From these measurements, the rates and accelerations are computed from differences between the values measured in successive frames.

The FIDAC instrument and the FIDACSYS programming system are thus opening up new fields of investigation in the area of quantitative analysis of pictorial data. While the variety of applications to which the system may eventually be put cannot possibly be predicted now, it is evident that this tool may well bring numerous problems now occupying the minds of biomedical research scientists within reach of a solution (*10*).

References and Notes

1. R. S. Ledley, *Science* **130**, 1225 (1959).
2. When the specimen is seen at a magnification of 1000, the field has a diameter of about 50 μ. Thus 750 points across the field give about 750/50 = 15 points per micron on the specimen, or 3 points per 0.2 μ, where 0.2 μ is the optical resolution of a microscope at 1000 power.
3. The fact that FIDAC is on-line with the computer, with no intermediate magnetic-tape recording, means that pictorial data on film can be used; a single 100-foot roll of 16-mm film, which fits in a 3½-inch diameter can, contains 4000 frames and will record over 4 million bits of information; this would require over 50 conventional magnetic-digital tape reels, making a stack over 4 feet high.
4. We used the IBM 7094 computer equipped with a direct data channel.
5. The computer used has a memory cycle time of about 2 μsec and the core memory has 32,768 words of 36 bits each.
6. For example, the IBM 360 series computers can have up to five times the high-speed core memory and more than twice the speed of the computer presently used.
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11. A large team of biologists, physicians, engineers, and programmers are contributing to this work: F. Ruddle, Yale University; B. Migeon, The Johns Hopkins University; E. Ramon-Moliner, Laval University; G. L. Rasmussen, National Institutes of Health; E. Freis and G. Shugoll, Mount Alto Veterans Administration Hospital; and L. S. Rotolo, J. B. Wilson, J. Jacobsen, T. Golab, M. Ginsberg, and G. Cheng, National Biomedical Research Foundation. I am grateful to Drs. Robert E. Cooke and H. Van der Loos for their kind encouragement. The Goddard Space Flight Center also assisted this work. The work is supported, in part, by NIH grants GM 10789, GM 10797, and NB 04472 to the National Biomedical Research Foundation, and in part by a legacy of Loula D. Lasker, New York City.

Nuclear Magnetic Resonance Spectroscopy in Superconducting Magnetic Fields

F. A. Nelson and H. E. Weaver

The availability of superconducting wire which can carry current of many amperes in a very high magnetic field has made fields in excess of 50 kilogauss practical. The exploitation of these magnetic fields for high-resolution magnetic resonance spectroscopy provides exciting prospects for extending the range and sensitivity of this type of analytical instrumentation. The benefits include increase in chemical shift, with resultant simplification of the spectra of large molecules; greater resolution of broad resonance lines; increased Knight shift in metals; and an increase in signal-to-noise ratio.

Ever since the initial commercial development of nuclear magnetic resonance spectroscopy as an analytical technique in the early 1950's, considerable effort has been directed toward increasing the sensitivity and resolution of the type of spectrometer used in this method. This has resulted in the availability, over the last decade, of spectrometers operating at an ever-increasing resonance frequency, beginning with 30 megacycles per second (corresponding to a field intensity of 7050 gauss) with continual improvement in sensitivity, stability, and resolution. The attainment of these latter characteristics has required very high quality iron-core electromagnets and associated electronic stabilization circuits. It is now apparent that a field strength of 23.5 kilogauss (or 100 Mcy/sec, for protons) is the practical upper limit for such iron magnets. While it is too early to make accurate predictions of practical upper limits for field strength attainable with superconducting magnets, 100 kilogauss may be mentioned as a practical limit with some degree of confidence.

Since the original discovery in 1911 by K. Onnes that certain metals lose all measurable trace of electrical resistance at temperatures near absolute zero, it has been the dream of scientists to use those materials in the form of wire-wound solenoids to generate very high magnetic fields without continual expenditure of large amounts of electrical energy and the associated need for exorbitant amounts of coolant. These early attempts were frustrated by an unexpected incompatibility between the state of zero resistance and a certain maximum intensity of an applied magnetic field. It was quickly established that the magnetic field above which resistivity was restored was a field of only a few hundred gauss. This effect received more attention in the 1930's, when Meissner and Ochsenfeld established the interesting fact that a superconductor, when cooled below its transition temperature, spontaneously expelled a magnetic field from its interior, so long as the intensity of the applied field was below the critical value for the material. In other words, a superconducting metal, when cooled below its characteristic transition temperature, not only lost all measurable resistivity but assumed the magnetic susceptibility of a perfect (or very nearly perfect) diamagnet. This abrupt change in magnetic susceptibility with decreasing temperature, occurring simultaneously with

The authors are affiliated with the Analytical Instrument Division of Varian Associates, Palo Alto, California, in the Research Department.