As can be seen from Table 1, the segments II, III and IV contained the desired unsaturated C_{20} fatty acids. The total yield after the countercurrent distribution was 5.5 g (94%), of which 4.9 g (88%) were C_{20} acids. The 20:3 amounts to only 0.04% of the rapeseed oil. The C_{20} fatty acids can be further purified by silver nitrate thin layer chromatography.

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REFERENCES

Graphic Presentation of Computer-Derived Schlieren Lipoprotein Data

ABSTRACT
Computer produced graphs of lipoprotein spectra visually present a large amount of information and greatly facilitate error detection. Data derived from schlieren patterns in the analytical ultracentrifuge are fully corrected to standard conditions allowing valid comparison of serum lipoprotein concentrations and profiles. The computer program is flexible enough to provide appropriate representations for many types of spectra and several possibilities for comparison of data.

The computer analysis of schlieren photographs of serum lipoprotein distributions has been described in detail by Ewing et al. (1). This computer program yields numeric output fully corrected to standard conditions in terms of lipoprotein concentration of the original sample, allowing valid comparisons to be made from sample to sample. In addition, an analytic ultracentrifuge data acquisition system (2) provides the accumulated value of k_fomega^2(t)dt for the mean time of each schlieren photograph. These data permit more accurate schlieren analysis of very low-density lipoproteins, where

the precise equivalent up-to-speed centrifugation during the acceleration phase of the run is required. In order to extend and improve the computer analysis of lipoprotein distributions, a program has been written to present these data in graphic form, allowing rapid visual evaluation, comparison of samples and error detection.

The computer input data consist of lipoprotein concentrations for a series of standard flotation rate (S_f or F rate) intervals in the card format produced by the schlieren analysis program (1). Although the low-density analysis is presented here in terms of S_f values, the program is similarly used for high-density graphic analysis or for single frame analysis at any time, including the acceleration frame. The results from any frame may be plotted at any desired up-to-speed time value for ease of comparing data. The plotting program converts these S_f rates into appropriate linear dimensions and lipoprotein concentrations into areas equivalent to those of the corrected schlieren patterns, routinely presented at three times the concentration of serum. It then calculates frequent points along a best fit curve through the resulting histogram, from which the graph is subsequently plotted on a physical device. At the same time the program sums lipoprotein concentrations of the total pattern and specified subfractions (S_f 0-12, S_f 12-20, S_f 20-100 and S_f 100-400 in the standard low-density run), as well as determining the S_f rate where

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the maximum concentration occurs. The final steps are to draw a rectangle around each frame, with tick marks and frame boundaries which normally correspond to the template upon which the schlieren pattern was initially traced, label the plot and print standard interval lipoprotein concentration values. It is possible to plot several patterns on one frame, or to plot the mean or standard deviation, or both, of a group of cases.

At the present time we normally use an Sf rate scale identical to that of the 0', 6' and 30' up-to-speed (52,640 rpm) frame template used for tracing the enlarged schlieren patterns (Fig. 1). However, the montage of three frames (taken at different times required to include all the low-density lipoproteins) results in a discontinuous curve (Fig. 1 and 2a) representing what is essentially a continuous spectrum. In Figure 2b, a logarithmic scale has been chosen to achieve continuity across the entire Sf 0-400 lipoprotein spectra, avoiding discontinuities at the frame boundaries of Sf 20 and Sf 100. To accomplish this a variable k log (Sf + 5) is used to avoid negative values while preserving the relative widths represented by the individual schlieren frames. The usefulness of a similar logarithmic scale, which has been applied to β lipoprotein fractions (Sf 0-12), has been discussed earlier (3). This detailed theoretical analysis of distribution functions also includes corrections for both diffusion and concentration dependence. Another potentially useful scale using the square root of Sf rate would yield a scale nearly linear in particle diameter.

Although patterns may be compared visually or by plotting them on a single graph, small but significant differences still may be hard to detect. A modified version of the program subtracts the first pattern of a series from each subsequent one and plots the difference at specified magnification (Fig. 2d).

Figure 1 was drawn using a Cal-Comp plotter, which moves a pen about a segment of chart paper under computer control. To present a visually effective profile, the pattern has been shaded, producing a high quality figure. Since the Cal-Comp plotter is accurate to 1/100 in., it is therefore also useful in drawing master templates for tracing schlieren patterns from the film. However, the main disadvantage of the Cal-Comp plotter is that it is a relatively slow process requiring extensive operator intervention; thus, plotting on it, especially in any quantity, is expensive and subject to delays.

In contrast, the plots in Figure 2 were traced electronically on a cathode ray tube (CRT) and photographed on 35 mm film. This CRT system lacks the resolution and absolute dimensions given by the Cal-Comp, but it is rapid and requires only occasional removal of film. Rough 8 1/2 x 11 in. prints in any quantity usually are available on an overnight basis.

Logically there is one plotting program with an extra input routine to handle population means. It is written in Fortran IV for the