hen erythrocytes. The mono-oleate fraction from ethylene glycol mono-oleate also produced changes in the structural organization of egg lecithin phosphatidylcholine liposomes resembling those produced by glycerol mono-oleate (cf. Howell *et al.*, 1972).

It seems from these experiments that a relationship may exist between the ability of some substances to alter the organization of the lipids of membranes in such a way as to lead to membrane fusion and their adjuvant activity. The effects of certain adjuvants may be at least partly on the membrane systems of macrophages (Asherson & Allwood, 1969). Conceivably cell fusion *per se* induced by some adjuvants may be important if cytoplasmic connexions between macrophages and lymphocytes (Schoenberg *et al.*, 1964; Clarke *et al.*, 1971) are of functional immunological significance.

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- Asherson, G. L. & Allwood, G. G. (1969) *Biol. Basis Med.* **4**, 327
 Clarke, J. A., Salisbury, A. J. & Willoughby, D. A. (1971) *J. Pathol.* **104**, 115
 Dresser, D. W. (1961) *Nature (London)* **191**, 1169
 Dresser, D. W. (1968) *Nature (London)* **217**, 527
 Gall, D. (1966) *Immunology* **11**, 369
 Howell, J. I., Ahkong, Q. F., Cramp, F. C., Fisher, D., Tampion, W. & Lucy, J. A. (1972) *Biochem. J.* **130**, 44P
 Lucy, J. A., Ahkong, Q. F., Cramp, F. C., Fisher, D. & Howell, J. I. (1971) *Biochem. J.* **124**, 46P
 Poole, A. R., Howell, J. I. & Lucy, J. A. (1970) *Nature (London)* **227**, 810
 Schoenberg, M. D., Mumaw, V. R., Moore, R. D. & Weisberger, A. S. (1964) *Science* **143**, 964
 Spitznagel, J. K. & Allison, A. C. (1970) *J. Immunol.* **104**, 119
 Westphall, O., Fischer, H. & Munder, P. G. (1970) *Proc. Int. Congr. Biochem.*, 8th. 319
 Younger, J. S. & Axelrod, V. (1963) *J. Immunol.* **90**, 1

DEMONSTRATION

Analysis of Enzyme Mechanisms and Metabolic Pathways

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Trial-and-error model building is frequently the best method of interpreting experimental results obtained from 'freeze-clamp' metabolite assays or from measurements of enzyme kinetics. Previously this type of work has been the province of specialist computer programmers; however, the present demonstration illustrates a computer model-building system that requires no programming knowledge and that is sufficiently versatile to handle any biochemical process that can be broken down into a sequence of partial reactions.

The model to be tested can be typed into the computer in ordinary chemical notation, for instance:

(where LDH stands for lactate dehydrogenase) and so forth, until the whole model has been entered with the steps in any order and without format restrictions. This section may be very complex with many different

enzymes, substrates and allosteric effectors. There are facilities for entering estimates of rate constants and for providing optional initial values for the concentrations of the intermediates.

The system responds either with a steady-state solution describing the flow of material between the intermediates in the model or with a time-course for the intermediate concentrations if this has been specifically requested or if no steady-state solution exists. This solution can now be compared with the experimental results and the necessary alterations made to the model before another test is made.

When used 'on line' the program is obeyed interactively, the results being typed out as these become available and a chance being given to modify the model while the system is running. The necessary differential equations are set up by the computer and solved automatically. The system chooses between matrix inversion for simple cases and numerical integration for non-linear or time-varying problems.

During the demonstration there will be opportunities for visitors to run problems of their own choosing. Please contact the author if you wish to save time by typing in large models before the demonstration. The maximum size for enzyme mechanisms is well over 100 intermediates; however, there is little point in testing such complex models without comprehensive experimental results. Large metabolic models can also be accommodated; however, for demonstration purposes such problems should not contain more than 20 different intermediate names.