links to likely alternative frames which will have a good chance of making sense of the input. Each frame has slots for the kinds of information it expects to find and, until these slots are filled, they are likely to have default assignments. My frame for bedrooms, which will be evoked if you start to tell me what happened in your bedroom, has defaults for things like the size of the room, and the style of the bed. In the absence of specific information, I will simply assume the presence of a normal bed to supply the default. If you then say that ten people slept in your bed last night, I will expect them to have been very crowded. On the other hand, an earlier description of your particularly huge bed would have displaced the default and so have led to different inferences. As long as a particular frame is in charge, it coordinates the information that comes in, making inferences to connect what might otherwise look like unconnected bits of evidence, and calling on other frames with narrower expertise to work with details of the situation. In this way, frames supply an interpretive context and constitute their owner's model of the world.

Some critics regard the frame theory as a re-statement of ideas long current in philosophy and psychology. In fact Minsky explicitly disavows claims of formal precision for his theory, but it is oriented specifically towards computer models of cognition. Terry Winograd of Stanford pointed out various ways in which frames were suggestive of, but not merely equivalent to, a variety of other paradigms from artificial intelligence—scripts, patterns, decision trees, semantic nets, actors, and production systems. He suggested that frames share important characteristics with each of these, but that you miss part of the point of frames by limiting your perspective to any one. I see the frames concept not as a unified theory but as a vantage point for discussing the shortcomings of present systems and pointing to some of the properties that better cognitive models must have.

A workshop session on methodological issues considered the difficult problem of evaluating and comparing the contributions of different projects in the field. Two factors seem to exacerbate the situation. One is the notorious lack of perspicuity of large computer programs. The other is the fact that language is so inextricably involved with everything we do that it is hard to gain the perspective needed to see how a particular piece of work fits into the whole domain. W. A. Woods, of Bolt, Beranek and Newman, presented a particularly well-reasoned paper on this subject. He argued, among other things, the need for cognitively efficient representations—models whose explicit structure can act as a guide to understanding the theory they incorporate.

There was somewhat less than one might have expected in the way of new results reported at the meeting. Several people were in the process of working out some of the implications of their version of the frames idea. Roger Schank and his colleagues at Yale, for example, described initial work with a program which knows what to expect when it hears a story about someone going to a restaurant. A few sentences relating John's experience eating a lobster dinner will trigger off a variety of inferences about who cooked the lobster, how it arrived at John's table, that if he gave the waiter a large tip it was probably because he enjoyed the lobster, and so on. And Sheldon Klein, of the University of Wisconsin, passed out copies of a seven page murder story generated by his computer in nineteen seconds! But there was more emphasis on what people had been thinking about methods and paradigms than on what they had learned about language.

Motion of muscle proteins

from a Correspondent

THE dynamic behaviour of proteins—their rotation and internal flexibility—are important for many aspects of their biological function. This is particularly true in the actomyosin system of muscle, where these phenomena are intimately related to the mechanism of contraction.

In such a situation, it is obviously necessary to be able to study the behaviour of individual components of the system, and in practice this means they must be labelled in some way. Two such labelling techniques have been widely used over the last few years. In the first, the protein is labelled with a strongly fluorescent group; the time course of the decay of the anisotropy of the fluorescence after excitation with a short flash of polarised light can then yield a value for the rotational correlation time, τ_c, of the label. The second approach, known as spin-labelling, involves the attachment of a stable nitroxide free radical to the protein. The value of τ_c is obtained by careful analysis of the shape of the electron paramagnetic resonance (EPR) spectrum of the nitroxide. Both of these methods are at their best in the study of relatively rapid motions—those with correlation times shorter than a few times 10^{-7} s.

Recently a new EPR technique has been developed (Hyde and Dalton, *Chem. Phys. Lett.*, **16**, 568; 1972; Hyde and Thomas, *Ann. N.Y. Acad. Sci.*, **222**, 680; 1973) which promises to extend the application of the spin-labelling method into the time range 10^{-7}–10^{-3} s. This technique, known as saturation transfer EPR spectroscopy, depends upon the use of partially saturating microwave fields and out-of-phase detection to obtain a spectrum whose shape depends critically on the rate of rotational diffusion. The theory of the method is discussed by Thomas and McConnell (*Chem. Phys. Lett.*, **25**, 470; 1974); the maximum sensitivity to motion occurs when $\tau_c \sim 1/\omega_m \sim T_1$ ($\sim 10^{-5}$ s), where ω_m is the modulation frequency and T_1 the electron spin-lattice relaxation time.

This technique has now been applied to myosin and its interaction with actin (Thomas, Seidel, Hyde and Gergely, *Proc. natn. Acad. Sci. U.S.A.*, **72**, 1729, 1975). The spin label was attached to a thiol in the globular 'head' (subfragment 1) of the myosin molecule. The correlation time of the isolated subfragment 1 was 1.8×10^{-7} s, and for myosin this increased to 3×10^{-7} s. Thus there is only about a 40% decrease in τ_c when subfragment 1 is cleaved from myosin, although the molecular weight decreases by a factor of more than four. There must therefore be considerable internal flexibility in the myosin molecule; the same conclusion was drawn earlier from closely analogous fluorescence experiments by Mendelson *et al.* (*Biochemistry*, **12**, 2250, 1973). The saturation transfer EPR technique can also be applied to supramolecular complexes of myosin, which are essentially beyond the range of previous methods. Aggregation of myosin into filaments led to a ten-fold increase in correlation time, indicating that there was still considerable flexibility of the 'heads' of the myosin molecules. In contrast, addition of actin to either subfragment 1 or myosin led to a very substantial immobilisation of the label, giving a correlation time of 10^{-4} s. This indicates that the globular 'head' of myosin is essentially irrotationally bound to actin.

The saturation transfer EPR method shares two problems with the other labelling methods. Motion of the label relative to the protein to which it is attached will obviously lead to erroneously short values of τ_c for the protein. Though this does not seem to happen in the case of subfragment 1, it may limit the application of these methods to some systems. In addition, for a non-spherical protein, rotational motion cannot strictly be described by a single correlation time, and the value obtained will depend on the orientation of the label relative to the hydrodynamic axes of the protein. But notwithstanding the difficulties in precise quantitation, it is clear that this new method is a valuable addition to the armoury of the physical biochemist interested in supramolecular structure.