contact with the refractory walls, life of the linings should be increased and not diminished) and whether the process is genuinely continuous. If the process has to be stopped to change the composition of the steel produced, much of its advantage would be lost. There is, too, the problem that the process has so far produced only plain carbon steel, and has not been used for alloy steels.

Animal Sonar

THE international symposium on animal sonar held at Frascati, Italy, under the auspices of the North Atlantic Treaty Organization, the United States Office of Naval Research, and the United States Air Force, brought together for the first time workers in this and related fields from member countries of the North Atlantic Treaty Organization. A feature of the symposium was the opportunity for an exchange of views between biologists, engineers and physicists, and it was so organized that the participants were able to study the main contributions in advance.

It rapidly became clear from the discussions that, although life scientists working on animal sonar had been in contact with sonar engineers over a long period, there had been insufficient exchange of information. Biologists tend to know too little about the advanced physics and systems engineering involved in the work of sonar engineers, while the engineers often lack the biological knowledge to take advantage of the information available about animal sonar. These difficulties have in the past tended to decrease the usefulness of experiments with animals. Such experiments need considerable preparation: the animals must be trained to carry out simple tasks, and the training may take many months. Unless the relevant physical processes are taken into account when the experiment is being planned, the results will be far less useful than they might otherwise have been.

Indeed, despite the extravagant claims of some early workers, animal sonar seems to obey the same laws as do artificial systems. The animal differs from the machine, not in its ability to transcend the laws of physics, but in its ability to adapt, and in the greater storage capacity of its neural system. The animal is also a single integrated system and takes its own decisions. The closest approximately to this aspect of animal sonar that can be achieved with a machine is to link a man to a machine so that he can take decisions. This is the approach used in the portable sonar outfits now issued to some blind persons, and the information obtained as a result of the use of such outfits has given a useful insight into the mode of action of animal sonar. Sonar engineers are probably trying to incorporate some of the animal adaptability into their machines, but they are reluctant to talk about this aspect of their work in public.

The symposium was less successful in its attempt to relate the processing of sonar signals in the animal brain to the systems used in engineering. This is scarcely surprising: neurophysiology is still far from the type of complex model used in systems engineering. Cross-fertilization of ideas will undoubtedly stimulate both sides even in this difficult corner of the field. The symposium seems to have broken the ice separating the disciplines concerned with sonar, and some beneficial effects of the thaw should be evident at the next gathering.

Ribonuclease Structure—Some Implications

from a Correspondent in Molecular Biology

THE solution of the ribonuclease structure at a resolution of 2 Å by Harker and his collaborators, as reported in *Nature* last week (Kartha *et al.*, *Nature*, **213**, 862; 1967), is clearly an event of unique importance and interest. Of all enzymes, ribonuclease has been the most intensively studied, and its structure is probably that which has been awaited most impatiently by protein chemists, physical chemists and enzymologists alike. The schematic illustration of the chain outline shown in the article gives only a small portion of the information which is expected shortly to emerge, but some interesting conclusions may already be drawn, particularly in connexion with predictions based on chemical evidence.

The active site, as identified by Kartha *et al.*, lies in a deep cleft between two wings of the molecule. There is remarkably good agreement with chemical evidence, due notably to Moore, Stein and co-workers (who also determined the sequence of amino-acids in the molecule). Two histidine residues, his-119 and his-12, were found to be necessary for activity and sterically related; thus, for example, the alkylation of either by a suitable reagent was prevented by the alkylation of its partner. These residues are indeed seen to flank the active centre cleft. Another residue which was unambiguously shown by Hirs in 1962 to be required for activity is lys-41, which appears at the third surface of the cleft opposite the two histidines. There is also some evidence for the involvement of lys-7 and indeed it has been shown that lys-7 and lys-41 can be joined by a bifunctional cross-linking reagent. With a minimum of hindsight it can be seen that other more equivocal identifications of active residues in the literature now appear to be wrong. Suggested mechanisms, of which a number have been put forward, will have to await critical examination until electron density maps of the enzyme with a bound substrate analogue have been obtained.

It is interesting to note that the segment corresponding to the *S*-peptide of Richards stands away from the molecule, almost over the cleft. This peptide (residues 1–20) can be split off by hydrolysis of a single peptide link with subtilisin. It will recombine non-covalently with the remainder of the enzyme molecule (*S*-protein) to give an active product. It was shown by Anfinsen and co-workers that residues 16–20 are in fact largely dispensable for binding and activity, but that 14 and 15 are required for proper binding. It is gratifying that residues 16–20 in the model appear to form a loop barely in contact with any other part of the protein, whereas in the region of residues 14 and 15, non-covalent interactions are likely.

The α-helix content of ribonuclease is low, 17 per cent being apparently an upper limit. This agrees well enough with optical rotatory dispersion measurements, which give values around 15 per cent. No β-conformation is present.

The appearance of the ribonuclease structure necessarily represents, among other more important consequences, a day of reckoning for those bold enough to have offered three-dimensional structures based only on indirect evidence. Such structures do not appear to have fared well. The most recent, by Hammes and Scheraga, has features in common with reality (apart