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CORRESPONDENCE

Popper and the naked emperor

Science can be thought of as being based on verification/falsification. G. Prathap[1] and P. S. Moharir[2] have discussed the epistemology of Karl Popper. The present author is reminded of a story in English where a contrived verification is indicated. A presumably popular story: 'Emperor is Naked' relates to the weakness of verification as a valid source of knowledge. An evaluation of Popper by Frolov[3] is given at the end.

Science can be thought of as being based on verification and falsification. Falsification as the sole basis of science is formulated by Karl Popper. There is a story in English which seems to ridicule a contrived verification. The story may be retold as follows: There was an emperor who was crazy about new dresses. All the tailors in his empire were fed up by their emperor's insatiable desire for new dresses. A tailor claims to have received cloth from heaven and makes dress from the cloth. The tailor states that it can be seen by all pious citizens. The emperor supposedly wears the clothes and moves about. In the midst of silence of the elderly citizens, a child cries 'Emperor is naked'.

I. Frolov[3], agreeably from a Marxist viewpoint, gives the following account of Popper: Popper, Karl Raimund (b. 1902): Austrian philosopher, logician and sociologist. Popper opposed his conception of critical rationalism to logical positivism, despite the fact that he was influenced by the latter. He substituted the principle of falsification for the principle of verification, and the principles of organic connection between the theoretical and the empirical levels of knowledge for narrow empiricism and inductivism propounded by logical positivists. Popper maintains that all scientific knowledge is of a hypothetical character and is subject to errors. However, his conception of growth of scientific knowledge encountered considerable difficulties which stemmed from making an absolute of the principle of falsification, from his denial of objective truth of scientific knowledge, from relativism in interpreting its growth and conventionalism in treating the fundamentals of knowledge. In social philosophy, Popper criticized Marxism and historism, rejected the existence of objective laws of social development and upheld bourgeous reformism. His main works: *Logik der Forschung* (1935), *The Open Society and Its Enemies* (1945), *The Poverty of Historicism* (1957), *Conjectures and Refutations* (1963), *Objective Knowledge* (1972).

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NEWS

A novel method for the structural characterization of biopolymers

The topic of molecular conformation and conformational analysis is about four decades old. Chemists could perhaps claim to have had remarkable insights into shapes of molecules long before the foundations of the electronic theory of molecular structures were established by physicists; the inspired six member ring structure of Kekule for benzene (1865) and the proposal of zig-zag non-planar configuration for cyclohexane by Hermann Sachse in 1890 (not

accepted for a long time) are classic examples. It was only after 1950, particularly due to the pioneering work of Barton, Hassel and others that the foundations of conformational analysis were laid. The concept of conformation or conformational analysis is concerned with the different three-dimensional forms that can be assumed by molecules whose atoms are free to rotate around one or more single bonds in the structure. It is strange that prior to the work of Barton and others, no one apparently appreciated the point that there is a strong relation between conformational arrangement and chemical reactivity. When it comes to macromolecules we do find traces of their implications in the study of the shapes of macromolecules deduced from light scattering by Debye[2] and collaborators implying torsional rotation along single bonds in the chain. More explicitly Flory and coworkers[3] used the angle (torsional) ϕ in the four successive carbon atoms of a typical chain in polymer statistics. In the case of biopolymers, particularly proteins, two independent angles of rotation, namely ϕ, ψ were used by Ramachandran and coworkers[4] for the first time to characterize the folding of backbone atoms. This was extended soon to specify orientation of side chain groups[5]. It is interesting that almost at the same time similar torsional representations and characterization were adopted for other biopolymers also, such as nucleic acids[6] and polysaccharides.

It may be recalled that the early sixties also saw the first protein structures from single-crystal X-ray work. Although in the initial stages most protein crystallographers were content with tracing C^{α}-skeletal chain and its three-dimensional fold, the conformational angles ϕ, ψ were found to be very helpful to identify wrongly placed atoms particularly through the known allowed and disallowed regions of the ϕ, ψ mapping. A constant pair of ϕ, ψ values at successive sites uniquely characterize a helical structure. They are also of use in model building, refinements and other aspects of structures.

With the steady progress of protein structure solution, the detailed atomic coordinate data for several proteins started accumulating and more specific methodologies for extracting specific types of information on the 'fine structure' came to be developed. The (ϕ, ψ) mapping is found to be not entirely adequate in all situations. The distance map[7] is one directly based on C^{α} coordinate set. These could lead for example to locating regions of specific secondary structural characteristics.

In this context the use of (virtual) bond angle, torsion angle and distance parameters involved in a set of four consecutive C^{α}-skeletal atoms was pointed out[8] which led to characteristic angle (θ) for secondary structural regions. Other related parametrization for helical analysis also became available[9]. In the case of nucleic acid structures, particularly DNA, specific set of parametrization to bring out local features and distortions has been proposed and used in recent years[10]. The torsional representation for other biopolymers (and also polymers) is extensively in use in the recent decades.

In a paper recently published in the *Journal of Biomolecular Structure and Dynamics* Srinivasan *et al.*[11] proposed a generalized method of characterizing a given biopolymer in terms of essentially a single angle parameter. In principle the method can as well be adopted for any linear polymer. Their method of approach is based on a well-known principle in rigid body mechanics that given a pair of identical rigid bodies (rigid skeleton of atoms in the context of molecular structures) in space in any arbitrary orientation, one can be brought into congruent superposition on the other by involving only six parameters, namely, three which correspond to translation vector τ of centre of mass of one to the other and a single angle* of rotation (Φ_i) for superposition about an axis and direction cosines l, m, n**. For an ideal polymer in which the monomer units are rigid groups, in principle $(n-1)$ such (Φ_i) angles relating successive monomeric groups will define the three-dimensional fold. It may be noted that Φ_i angle has a complete −180° to +180° range and is the most important of all the parameters. The projection of t on l, m, n, provides the s_i vector which is useful in practical delineation of the folding behaviour. As may be anticipated, in ideal helical regions, Φ_i coincides with helical twist angle (also s with rise). However, the real interest here is that even in non-helical regions Φ_i, t (and s) have real significance, since they uniquely characterize the relative position of successive units.

They have demonstrated the use of these in the case of proteins and nucleic acids. In the former case the rigid space fraction could be the set of residue group $(C^{\beta}-C^{\alpha}_{C'}-N)$ (R unit) or the peptide plane $(C^{\alpha}-\underset{H}{N}-\overset{O}{C}-C^{\alpha})$ (P unit) leading to the two possible units for scanning.

The problem of choice of units in the case of nucleic acids is not that simple. They have however indicated, in the case of both a DNA and tRNA how the Φ_i angles behave using [P, C1' N1(9)] as the unit.

Unlike the case of (ϕ, ψ) representation where the behaviour as a function of residue number is not normally available, the Φ_i as a function of residue number acts as a fingerprint of the 3-D fold of backbone groups. It is of course possible to represent the twin angle ϕ_i, ψ_i as a chain plot, i.e. as a function of residue number, but the advantage in the new methodology is that only one angle is adequate.

Besides $\Phi_i(i)$ chain plot which delineates, different secondary structural regions, the method also helps one to trace the s_i vectors, succession of which defines the 'axoid', a term coined by the authors.

They have demonstrated the use of the axoid in tRNA and Dickerson's dodecamer (CGCGAATTCGCG). The axoid comparison also leads to interesting possibilities of quantification of structural and conformational homologies in proteins. One advantage of the method appears to be its generality. A set of atoms from the monomeric group can be chosen appropriately. This becomes necessary since, in real polymeric structures, the monomers

*Normally the six parameters are three Eulerian angles plus three for translation of C M It can be readily shown that the three Eulerian angles (through product matrices) reduce to a single rotation angle

**Although the total number of parameters is seven (called Cayley-Klein seven parametric representation) the equation of constraint $l^2+m^2+n^2 = 1$ reduces this to six effectively

need not be rigid, but are actually quasi rigid. They seem to emphasize this point for the first time since other methodologies currently available in the literature, particularly for the characterization of non-regular forms of nucleic acid structures, seem to lay less importance on this aspect. It is thus possible to expect that characterization can be different depending on which unit is used, for example phosphate group alone or sugar group alone or even in combination etc. Bases suffer from quasi-rigidity, they point out, and hence require special care in the current methodology. This flexibility in the choice of unit enables, for instance, to look at results (in the case of nucleic acids) for double strand (DS-mode), and single strand (SS-mode) superpositions as well leading to possibly interesting variations.

By way of contrast a few remarks may be presented here relating to proteins which are valid *mutatis mutandis* to other biopolymers as well. The ϕ, ψ are body-fixed internal parameters. The Φ_s methodology depends, however, on the choice of appropriate rigid fraction and then extracting a single angle Φ_s, through the rotation about an axis in space and not body-based. But the relation is firmly established and leads to, in the case of proteins, for example, a reduction from two to one angle parameter relating one unit to the next. The normal ϕ, ψ information content is now loaded into a single bond Φ_s. As may be expected Φ_s now has its own allowed and disallowed regions for biomolecular structures. A further study of this, as pointed out by them, is likely to lead to simplified approach to knowledge based-model building and prediction algorithms. Since any dipeptide now needs only one angle Φ_s to characterize the relative orientation, a full data bank build-up on all possible (400) amino acid–amino acid interactions from protein data banks would act as the core of the required knowledge base. Extensive use of the model is likely to prove its worth in future, not merely in characterization but as an effective tool in analysis of fine structures of biopolymers as deduced from single crystal X-ray data.

It is learnt from the authors that those who wish to have a copy of the computer program may write to Prof. R. Srinivasan, Department of Crystallography and Biophysics, University of Madras, Madras.

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A report on National Seminar on Recent Developments in Mathematics*

Contemporary mathematics plays a dominant role in popularizing science, engineering and many topics in social sciences. Recognizing its importance, a three-day National Seminar on Recent Developments in Mathematics was organized at the Department of Mathematics, Karnatak University, Dharwad from 16 to 18 December 1993.

The technical sessions covered important topics: physiological fluid dynamics (two sessions), general analysis of nature of solution of differential equations (three sessions), Ramanujan's contributions to the theory of elliptic functions, Lie algebra and Lie groups and its applications, Hadamard matrices, global domination, etc. in graph theory, univalent functions, Hall's conjecture on starlike functions, and non-continuous transformations (six sessions).

In a keynote address, T. J. Pedley (Leeds, UK) summarized the mathematical modelling of blood flow, breathing and bioconvection.

Bahulyan (NIO, Goa) presented the applications of fluid dynamics principles in three-dimensional circulation in ocean. P. C. Sinha (IIT, Delhi) presented the models in operation to study coastal oceanography. P. S. Kulkarni (IISc, Bangalore) gave a

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