humankind – and by the rapid emergence of a new society, the *information society*'. What is thus central to the book is that in the post-industrial transition (characterized by free-markets, private investments and high mobility), human resources, culture and knowledge as well as ecological services should be the backbone of development, and that tourism needs to be mainstreamed into the development process. The book also premises that deprivation is largely a reflection of lack of access to information.

The book is an outcome of an international symposium organized in September 2000 at Port-Cros, a Mediterranean Island. The Port-Cros Symposium was launched by the TotalFinaElf – a Corporate Foundation for Biodiversity and the Sea. The papers presented and discussed during this symposium are edited under seven sections, including an epilogue, and 28 chapters. Additionally, the book has a Foreword, Prologue and Preface that very lucidly introduce the scope of the book.

Despite the broad title of the book, the contents largely reflect the status of biodiversity and how tourism might affect and be affected by it in coastal areas and islands. Throughout the book, the different authors repeatedly draw attention to the adverse side effects and dangers of tourism, including erosion of indigenous knowledge. Apprehensions about the negative impact that the tourism industry could specifically have on local communities are addressed in chapter 2. In elaborating guiding principles that would ensure sustainable tourism, the possibility of 'ill-planned' tourism causing further inequality of wealth and power, changing gender relations and conflicts within communities is also discussed. The positive aspects of 'well-planned' tourism discussed are merely possibilities with little hard evidence. Even chapter 21 titled 'Information technologies and grassroots tourism: Protecting native cultures and biodiversity in a global world' is largely theoretical.

A global education programme is suggested as one means of addressing the negative impact. And herein lies the inherent contradiction – if large, pristine areas have been preserved due to the conservation culture of local rural or tribal communities, what information or education programmes are we envisaging for them? Empowerment, decentralization, involvement of all stakeholders in the planning processes are other strategies that are proposed as possible means to minimize negative impacts. But as it emerges in all the case studies, ecological systems seem far less complex to manage than social systems!

Tourism can provide for biodiversity conservation. IT can enhance the quality of tourism. Yet how exactly the three can be integrated has not been brought out with even one concrete example. Whereas we are not qualified to analyse the situation in nature preserves in other parts of the world where tourism is popular, we can discuss the Gulf of Mannar scenario discussed in the book. Linking eco-tourism and biodiversity conservation in the Biosphere Reserve with pilgrimage is adding just another murky dimension. The case of extensive habitat loss due to the annual pilgrimage to Sabarimala and the selective removal of macaques in Tirumala – Tirupati to make the area 'conducive' to visitors, for instance, do not readily encourage adding one more dimension to the already complex issue that is discussed in the book.

Ethnic strife in Sri Lanka, had, at least for a while, heavily interfered with pilgrimage (and tourism) in the Gulf of Mannar area. Here, the role that information played has proved negative to the tourism industry. Moreover, much before the Gulf was declared a National Park and Biosphere Reserve, many were aware of its rich biodiversity – the much-cited 3600 species! This attracted tourists of a different kind – students of biology, on specimen collection tours, who swarmed the area year after year. These students were all 'well informed' and they kept the information alive over the years! Is there any information on the impact these study tours had on the 3600 species that might be used to educate the future generations?

And although not in the main body of the text, the prologue does try to drive in the oft-cited dictum of Mahatma Gandhi: 'Nature provides for everybody's needs, but not for everyone's greed'. The line between need and greed is relative. In strict ecological terms, need could mean something like migration in birds and other animals. Tourism, however, unduly imposes one more dimension of human pressure on the earth's resources.

The complexities of ecosystems and biodiversity are far less understood for us to suggest avenues that lead to their conservation, particularly when there is little hard evidence. While the many approaches, statements and results developed and shown in this book seem to sound a positive note, at least in principle, tourism per se, as the closing section of the book admits, should be a driving force behind cultural exchange and understanding among different cultures and identities. This book is a good beginning. But there is still a long way to go.

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Biophysics. Vasantha Pattabhi and N. Gautham. Narosa Publishing House, 22 Daryaganj, Delhi Medical Association Road, New Delhi 110 002. 2002. 253 pp. Price: Rs 295.

Writing a text book is an onerous job which if done well can mould the professional characters of budding students for whom a good teacher in the classroom and a good text book outside can become captivating experiences. Such a milieu can nurture wholesome students who are creative, critical, methodical and decisive. This book written by Vasantha Pattabhi and N. Gautham is the distillate of the teaching experiences of two eminent professors of Biophysics. The book is meant to address the biophysical needs of students of biochemistry, molecular biology and medicine. Beginning with the laws of physics and chemistry, the book making a journey through separation techniques, physico-chemical techniques to study biomolecules, spectroscopy, Light and electron microscopy, X-ray crystallography, NMR spectroscopy, molecular modelling, Macromolecular structure, energy pathways in biology, Biomechanics and Neurobiophysics, concludes with a chapter on the origin and evolution of life.

My journey through the book has been a mixed experience. At first glance it appeared to be a pleasant book. I derived inspiration from a description of the

widely different group transfer potentials of ATP (–7.3) vs glucose-6-phosphate (–3.3). Release of a proton uniquely during the hydrolysis of ATP pulls the reaction towards greater hydrolysis since the intracellular pH is kept buffered at ~ 7. On the other hand, absence of proton release in the hydrolysis of G-6-P fails to provide an ATP like chemical drive for its hydrolysis. On asking what the steady state concentration of ATP in cells is, the present book says 'Under standard conditions, ATP^{4-}, ADP^{3-}, and HPO_4^{2-} will be present at concentrations of – 1.0 M while the hydrogen ion concentration – is only 10^{-7} M'. Are we to assume that ATP^{4-} in a cell would be of the order of 1.0 M? Among the opening statements to the chapter 'Energy pathways in biology' is this: 'When work is being done by living systems no temperature change takes place and hence these systems must spend their energy in some other form…'. This statement is difficult to digest since even when a warm blooded animal runs a hundred meters in seven to eight seconds, the warming can be felt and measured.

I was amused by the statement 'The central paradigm of biophysics, indeed of physics in general is structure → function' (chapter 10) and wondered if it is not more appropriate to consider the structure → function relation to be a central paradigm of science itself. I have seen examples of rifts between intentions and their expressions in the book: (a) 'During – these different functions the nucleic acid molecules have different 3-D structures' (p. 144) when the intention was to say 'The respective nucleic acids which perform these different functions, viz. transcription, translation, ribosomal architecture and ribozyme have characteristic three-dimensional structures'. (b) 'The determination of possible reverse turns is more complicated since each residue has a propensity value for its occurrence at each position of the reverse turn' (p. 136) when the intention was to say '… has a different propensity value for its occurrence at each of the four positions in a reverse turn'. (c) 'Ribosomal RNA molecules which form a part of the ribosome, are long nucleotides' (p. 158) implying 'polynucleotides' which alone can be long!

The example of a glass of hot water on a table has been considered as a closed system since 'energy, but not matter, can be exchanged between the glass and the room' (p. 15). However unless water is kept in a sealed vessel, not only will heat energy leave the glass, but water molecules would also evaporate out from the glass. I was surprised to see in the definition statement 'A dose of one rad can increase the temperature of one gram material by 2×10^{-6}K' (p. 22), the absence of the name of the material which will receive the rad.

I have found statements in the book which have profound implications in biology, but which have nevertheless been mentioned in a matter of fact way. Thus 'In RNA the pyrimidine thymine is replaced by uracil' (p. 146), I was saddened to see no desire to talk to the students on why biology chose to distinguish RNA from DNA not only by replacing a ribose in the former by a deoxyribose in the latter but also by tinkering with the structure of thymine such that it becomes uracil. Likewise it has been said (p. 151) 'Fibers at much lower humidity produced another pattern, with sharper spots and therefore a higher degree of order. They were called the A type patterns…'. Here no indication is given about how humidity controls DNA structure and if local humidity gradients can exist in chromatin.

Examples of neglect for accuracy can be seen in (a) figure 10.3 that shows three of its five carbon atoms as C2′. As a result the description of a glycosidic bond 'between C1′ atom of sugar and either N9 atom of purine or N1 atom of pyrimidine' finds no affirmation in the figure. (b) Table 10.1 has A for Å and the two grooves can be seen written in the horizontal plane for no reason or rhyme. The book has no dearth of misspelt words (loose for lose; shap for shape; gluteraldehyde for glutaraldehyde; could for cloud) and strange expressions (five peptides for pentapeptides; organelle for organ). In the conversion of NAD to NADP, a phosphate is shown attached to the adenine base of NAD (figure 11.40) when it should truly be bonded the 2′ hydroxyl of the pendant ribose moiety. It is good to remember that the distinction between a C-P (phosphonate) and an O-P (phosphate ester) bond is phenomenal and not trivial. The legend to figure 11.3 correctly describes it as 'resonance forms of orthophosphate' while the text refers to it in the context of ATP's hydrolysis. Examples of repetitiveness can be seen in (a) figure 4.9 showing IR stretching modes in carbon dioxide. However only the first two rows are needed since all others are mere repetitions of the same; figure 9.7 ('The C^{α} atoms of lysozyme') shows the same figure which is shown in figure 9.6 as well. Equally disturbing is an empty quarter on p. 156. The page caption of the chapter on molecular modelling (pp. 131–143) is NMR spectroscopy! Figure 10.32 shows parallel and antiparallel beta sheets in schematic and 3-D representations respectively when both should have been shown in one and the same representation. The statement 'Other factors which stabilize the tertiary structure… include salt bridges… between oppositely charged amino acids, such as Glutamic acid and Aspartic acid' (p. 169) is bizarre since Glu and Asp are both acidic and carry the same charge! Figure 14.6 shows β-D-ribopyranose, a pentose ($C_5H_{10}O_5$) as a hexose ($C_6H_{12}O_6$)! In 'Mirror inversion…, as it would require the presence of d-amino acids' (p. 171), 'd' should be 'D'. In 'ninhydrin, which binds only to amino acids and proteins' (p. 27), 'binds' should be 'reacts'. 'lectins (specificity for cells and macromolecules containing N-acetyl-α-galactosylamine)' (p. 31) gives the false notion of all lectins having a single specificity. Likewise 'Concanavalin A (specificity to glycoproteins) is incorrect since glycoconjugates that lack terminal α-D-mannosyl or α-D-glucosyl residues will not bind Concanavalin A. 1,6-diamino hexane and 6-aminohexanoic acid have been mentioned as examples of hydrophobic and hydrophilic spacers respectively (p. 31). This is strange since both kinds of spacers share the same hexamethylene arm and differ in having two amino groups vs an amino and a carboxyl group at the two termini. However following conjugation with matrix on one side and a ligand on the other, both linkers should end up having amide linkages which will confer identical polarities for all practical purposes.

The amount of SDS that binds to a protein has been mentioned as ('1.4 g per g of amino acid)' (p. 35). This should be 1.4 g/g of protein. In 'Even differences in pH of the order of 0.01 are enough to separate the molecules' (p. 35), 'pH' should be 'I pH'. In 'Biological macromolecules have molecular weights of the order of 10,000 daltons' (p. 37), 10,000 should be 'tens of thousand'. In 'chromophores… have rather low quantum yields and very short radioactive life

times' (p. 67), 'radioactive' (a nuclear phenomenon!) should be 'radiative'. Figure 8.8 shows an H–C–C–H system but its legend has described it as an H–C–H system. Figure 9.4 legend: 'A thermal ellipsoid representation of a molecule of thermal vibration of each atom, indicating the extent' ought to be 'An ellipsoid representation of thermal vibrations of each atom in a molecule'. In describing the Z type structure of 5′-CGCGCGCG-3′, it has been said (p. 151) 'CD and UV absorption studies indicated a change in the helical sense from right handed to left handed'. While CD certainly can, it is not clear how UV absorption studies would distinguish between DNAs of opposite handedness. 'mRNA molecules have varying lengths, depending on the code they carry' (p. 158) is misleading since mRNAs of the same lengths can carry different codes depending on their respective sequences. In 'carbon atoms have a valency of four and in amino acids this valency is satisfied by an amino group, a carbonyl group, a hydrogen atom and a side chain. The only exception – is – Proline' (p. 161), 'carbonyl' should be 'carboxyl'. The way in which Proline stands apart is not indicated and the structure of Proline (figure 10.25) which could have been helpful is itself flawed: it is showing an amino instead of the desired imino group for Proline! Retinal and retinol have been described as isomeric (p. 221). However aldehydes and alcohols with different molecular weights cannot be isomeric. I was puzzled to read 'when rhodopsin absorbs a photon, it undergoes a change in its electrical state, which is passed on as a membrane potential' (p. 223) and suspect that 'electrical state' should be 'conformation'. While ascending chromatography has solvent at the bottom from where it rises to the top, the descending chromatography has it the other way round (figure 2.3). However the descending chromatography figure shows the solvent not only at the top but strangely also at the bottom. Figure 11.3 shows four resonance forms of orthophosphate of which three represent HPO_4^{2-} and the fourth represents HPO_4^{3-}. This last resonance form looks improbable since it shows a negative charge on the phosphonium oxygen. Likewise the resonance form in which the phosphonium oxygen is protonated and carries a positive charge looks strange. I wish the book gave supporting evidences to convince the readers that the structures drawn indeed exist or that there are reasons to think that they may exist.

Table 10.1 describes A DNA as the one in which the major and minor groove depths at 13.5 and 2.8 Å respectively are quite different. Against this, B DNA is the one in which the major and minor groove depths at 8.5 and 7.5 Å respectively are nearly the same. However an analysis of these features in 'Biochemistry' (Mathews, Van Holde, 1990, p. 105) is just the opposite. It says, 'In the B helix there are two quite different grooves, called the *major* and the *minor* grooves. In the A helix the two grooves are more nearly equal in depth'.

The elucidation of Chou Fasman rules for prediction of protein secondary structures has left many stones unturned. For instance, while the normalized propensity values for amino acid residues are given, the basis of normalization has not been indicated. The α-helix propensity values have been given as 1.53 (Gln) > 1.17(Glu). Against these, in *Principles of Physical Biochemistry*, (Prentice Hall, N. Jersey, 1998) by K. E. van Holde, W. Curtis Johnson and P. Shing Ho (p. 163) these values are 1.12 (Gln) < 1.44 (Glu). The table of propensity values has listed the residues in a random order which is neither alphabetical nor in order of the secondary structural propensity of the residues. The greatest difficulty is encountered in the example of an 18 residues long peptide sequence for which a structure has been predicted. (Figure 9.2). This figure shows the average values of the propensities for 6 residues long window settings. But it is not clear which six residues are to be chosen and why. It would have been invigorating to have mentioned the observation of Minor and Kim (1996) who have shown that an undecapeptide dubbed the 'chameleon' sequence folds as an alpha-helix when in one position but as beta sheet when in another position of the primary sequence of the IgG-binding domain of protein G. Also missing is the perspective of the prion phenomenon which abounds with hypotheses that the infectious prion is converted from its non-infectious cellular form (PrPC) by means of an (Alpha)-helical to (Beta)-sheet conformational change. Even PolyLysine is known to change its secondary structure as a function of pH. However with the limited knowledge given in the chapter, I wonder if the student will be able find directions in the world of proteins, which has a penchant for not having any straight roads.

With reference to magnetic vs chemical equivalence (p. 123) it has been proposed that while magnetically equivalent atoms are chemically equivalent too, the chemically equivalent ones need not always be magnetically equivalent. What is not apparent is the reason why magnetic non-equivalence does not always result in chemical non-equivalence. The example of difluoroethylene (figure 8.9b) in which the two protons are chemically equivalent but magnetically non-equivalent is deceptively simple. Since the book does not disclose the proton or fluorine NMR spectrum of this simple looking molecule, students who are curious will be shocked to see in Harald Gunther's *NMR Spectroscopy* (II edition, John Wiley & Sons 1995, p.43 and p. 185) that well resolved proton NMR spectra of difluoroethylene have twenty lines!

I found it amusing to see in the structures of NAD/NADP (figure 11.4b), some bonds like the P–O–P to be disproportionately long. These appear to have become elongated so as to accommodate the nicotinamide and the adenine without a steric clash! However since both steric clashes and abnormally long bonds are contrary to reality, the drawing must be illogical. Inability to draw a molecular structure in a fashion consistent with normal bond lengths and angles should ordinarily navigate us to a more precise drawing. But that is not the case here. Figure 10.26 shows the two N–H bonds of NH_2 to be unequal in length. In the structures of Luciferin and its derivatives (figure 13.18), the C–S or the C=N bond lengths in one half of the molecule are different from the bond lengths of the same bonds in the adjacent half.

In my critique of the book I must not forget to mention that having read the book I have felt educated. I congratulate the authors for accomplishing the arduous task and wish they write more commendable books on Biophysics.

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