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Book reviews

Biological Effects of Electromagnetic Fields (Mechanisms, Modeling, Biological Effects, Therapeutic Effects, International Standards, Exposure Criteria)
P. Stavroulakis (editor), Springer Verlag, Heidelberg, Berlin, 2003, ISBN 3-540-42989-1, xv+ 793 pages, € 149.00

This book presents a collection of more practical results and, together with the books *Biological and Health Effects from Exposure to Power-line Frequency Electromagnetic Fields* by H. Takebe et al. (lOS Press, 2001) and *Magnetobiology—Underlying Physical Problems* by V. Binhi (Acad. Press, 2002), provides a complete coverage of our present knowledge on electromagnetic and electric field effects mostly in the ELF region.

The five main topics dealt with are (A) Mechanisms of action of EMFs on biological systems, (B) Mathematical modeling of EMF absorption in biological systems, (C) Field computations and measurements, (D) Biological effects of EMFs (ELF and RF), and (E) Therapeutic effects of electromagnetic fields.

In part (A), the chapter "Theoretical considerations for the biological effects of electromagnetic fields" by Panagopoulos and Margaritis favors the free ions' forced-vibration mechanism over irregular channel gating, where a single ion displacement is able to generate about 30 mV in membrane potential. However, for 'cell-free' PEMF effects, it should be modified in the sense of Binhi's 'interference bound ions model' (see chapter 4 in Binhi's book mentioned above). In the chapter by Pilla, time varying models and signal to noise calculation, and also static magnetic fields with respect to clinical applications, are discussed. Liboff emphasizes the experimental evidence for the 'ion cyclotron resonance model' and lists the observed enhancing and inhibitory effects on bone healing, rat behavior, diatom mobility, cell cultures, neurons, and plants in valuable tables.

Methods for evaluating specific absorption effects (SAR), dosimetry of mobile phones, transmission lines, environmental fields, and magnetic rail systems are discussed in all chapters of parts (B) and (C), which comprise 300 pages.

In part (D), Henderson et al. review examples of signal transduction on the cellular level, such as proliferation, apoptosis, gene expression, tumor promotion, and enzyme cascades. Due to quite different conditions, the numerous results are hardly comparable, and a presentation in the form of tables as done by Liboff would be advantageous. In the short section 5.2.2.3, "Gene expression", a reference to several papers by Goodman et al. dealing with transcription and translation of HL-60 cells is missing. The brief chapter by Blank and Goodman on biomedical applications is restricted to the generation of stress proteins besides electron transfer, and mentions the possibility of effects on gene expression. In the comprehensive chapter by Tuncel about the effects of electromagnetic fields on the immune system, the risks of cancer promotion (leukemia, breast cancer), DNA damage, chromosomal aberrations, induction of cytological markers, and immune system impairment (calcium efflux, melatonin reduction) are ruled out. The detailed section on transcription comprises also contradictory results, which urgently need to be clarified. Section 5.4.1.1.6, "What can we do in future: many questions and problems", presents basic hints for further research.

Panagopoulos and Margaritis describe in detail the effect of ac magnetic fields (inductive coupling), pulsed electric fields (capacitive coupling), and 900 MHz RF modulated and non-modulated fields combined with thermal stress on the reproductive capacity of *Drosophila melanogaster*, showing that the three types of treatment have quite different effects. Effects of RF treatments on embryos (fertilized chicken eggs) and rats (tabulated results) are also presented in two additional chapters.

In part (E), the largest chapter by Chang et al. mentions 396 references on "applications of therapeutic effects of electromagnetic fields" and deals extensively with bone healing, osteoporosis (including characteristic micrographs) besides controlling osteoclasts, tumor necrosis factor-α, interleukin-1β, and prostaglandin-E2. Several studies on multiple sclerosis, neurological disorders, tendinitis, and venous ulcers are mentioned, but promising results on tumor therapy recently published by Markov, Tofany, Veyret, and others are missing.

Of considerable interest are "world health organization criteria for EMF health risk assessment" by Jonston, and also the diagrams showing danger levels of EMF exposure for the working and the general population besides prevalent international exposure criteria.

The 'state of art' is taken into account until 2001. However, since frequently the same topic (e.g., cyclotron resonance, signal transduction, transcription, or apoptosis) is treated independently in different chapters (but based on the same references), a subject index would be highly desirable. On the one hand, this book makes the opting for PEMF applications possible, on the other hand, it proves to be a valuable source of information for all life scientists.

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Bioinformatik. Methoden zur Vorhersage von RNA- und Proteinstrukturen (Bioinformatics. Methods for RNA and protein structure prediction)

G. Steger, Birkhäuser Verlag, Basel-Boston-Berlin, 2003, ISBN 3-7643-6951-5, €44.86 + VAT

In the early days of the development of predictive algorithms for molecular biology (when the term bioinformatics was not yet coined), approaches related to either 3D structures or sequences seem to have developed at a comparable speed [see, e.g., the following landmark papers from the 1960s and 1970s: Levitt, *Detailed molecular model for transfer ribonucleic acid*. Nature 224 (1969) 759-763; Needleman, Wunsch, *A general method applicable to the search for similarities in the amino acid sequences*. J. Mol. Biol. 48 (1970) 443-453; Chou, Fasman, *Prediction of protein conformation*. Biochemistry 13 (1974) 222-245; Chothia, *Structural invariants in protein folding*. Nature 254 (1975) 304–308]. Later on, there was a strong shift towards sequence analysis and a preference for informatics methods accompanied by a more or less phenomenological view of the field leading to the notion of bioinformatics and to its emergence as an independent discipline. More recently, the scope of this field has broadened again including constituents such as sequence analysis, structural bioinformatics, network analysis, but also methods from theoretical biophysics and still other fields. From a methodological point, we need a combination of informatics approaches with methods from other fields, making the notion of computational biology very likely more appropriate than bioinformatics. A widely used workaround to this terminology problem is to adopt a relatively broad view of bioinformatics without worrying too much about the precise meaning of the term.

Structural biology has experienced fast developments within recent years. The number of experimentally known 3D structures of proteins and nucleic acids has dramatically increased. Currently (July 15, 2003), we know the 3D structures of 19,631 proteins, 918 protein-nucleic acid complexes and 1205 nucleic acids. The latter two groups comprise 654 structures that contain RNA. Furthermore, various structural genomics projects have been started aimed at the structure determination of all proteins for a given species. Even though the output from these projects in terms of new structures is not yet very impressive, this will certainly change within the next few years. Also, RNA structural biology has come of age, the most recent highlight being the atomic structures of the small and large ribosomal subunits. Moreover, five rounds of the structure prediction contest CASP have been performed. All these developments can be expected to have great impact on structure prediction methods. Hence, a book on structure prediction that describes the current status of this field is highly welcome.

The book by Steger has 16 chapters, with 7 of them devoted to RNA and the remaining 9 to proteins. DNA is not taken into account. Both, the RNA and protein parts of the book start with an introduction to secondary and 3D structures, and then describe algorithms and methods for structure prediction. A methods chapter on structure determination is included in the RNA part. It describes RNA-specific methods such as chemical probing, but also methods, in particular NMR spectroscopy and X-ray crystallography that are relevant to proteins as well. On the other hand, Circular Dichroism and Fourier-Transform Infrared Spectroscopy are not mentioned. There is also a special chapter on cooperative equilibria of RNA.

The major part of the book is devoted to structure prediction methods and here there is a strong focus on secondary structure prediction. This is actually one of the strengths of this book. The algorithms are described in great detail and supplemented with practical examples. On the other hand, RNA or protein secondary structure is of course only one part of the story. Unfortunately, the 3D aspects of structure prediction are not adequately covered. In the RNA part 3D structure prediction is completely missing. For example, the program Mc-Sym should have been mentioned here. There is almost no mentioning of the very influential RNA structure models generated by the Westhof group (except for references in Chapter 1.1.4). Also SCOR, the RNA analogon to the structural classification of proteins (SCOP), is not described.

In the book's protein part, a few 3D structure prediction methods, such as modeling by homology, threading, and folding by molecular dynamics simulations are briefly discussed. However, again as compared to the very detailed secondary structure prediction parts (ca. 60 pages) they are too short (ca. 30 pages) and some topics that are believed to be a must in a protein structure prediction textbook are not mentioned. Examples are statistical potentials, the CASP competition and target selection for structural genomics projects.