290 Teaching biochemistry to students trained in chemistry

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During recent decades biochemistry and molecular biology have entered the curricula of many non-biology specialties like chemistry (including chemical engineering), biotechnology, food technology, and forestry. Students of these have a strong background in chemistry, physics and mathematics and little knowledge of biology. Chemistry students want to understand the molecular basis of life from the point of view of chemistry. They want to know, for instance: how the basic laws and rules of chemistry are followed in biochemistry; how the coefficient of performance of living cells can be calculated and how it compares with that of man-made engines; why the electrons of hydrogen (during dehydrogenation) ìpreferì to go to NAD instead of to FAD, ubiquinone or cytochromes which are known to have much higher chemical affinity for them, etc. Answering these and other unexpected questions that arise during lectures is a challenge for most teachers who have been trained in biology. Besides a good knowledge in chemistry it needs also new approaches in the methodology of teaching biochemistry to chemists. It is not difficult to convince a chemist that the law of mass action is also a basic law in biochemistry. Due to the reversibility of enzyme reactions, the law of mass action is also a driving force of all biochemical processes and their precise regulation. The coefficient of performance of a living cell can be calculated roughly by the ATP molecules generated during the complete oxidation of glucose and the energy of a P-O-P bond in ATP (7200 kcal/mol). The value thus obtained, amounting of about 40%, is much higher than that of all man-made engines (15-30%). The hydrogen electrons pass over FAD, ubiquinone and cytochromes and go to NAD because of the enzymatic character of the oxidative dehydrogenation reactions, etc.

291 Teaching Biochemistry and Molecular Biology: new approaches for students with a poor background in Chemistry

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University teaching in Biochemistry and Molecular Biology (B&MB) has to adapt to the rapid changes of the global/local societal environment and the school curriculum. During the last 10 years, the transition societies from Central and East Europe had to adapt to new approaches regarding the content (what and how much) and methodology (by which means) of Molecular Biosciences, these being interdisciplinary areas linked to the 'core knowledge' in Chemistry.
My presentation is focused on the following key aspects in order to achieve an efficient and effective teaching of B&MB for students:
- what constitutes 'poor background' and sufficient basics for Chemistry in relation to Biochemistry Core
- how, in a short time, to bridge the 'gap of knowledge' in Chemistry, within a flexible framework of B&MB curriculum
- qualitative and quantitative relations between 'information and formation' during the teaching and laboratory practice in B&MB,
- a necessary balance between theoretical knowledge and experimental skills for different levels: undergraduates (BSc) and post-graduates (MSc, PhD)
- how acquired knowledge is assessed during university training: criteria for entrance, first cycle (B+2), second cycle (B+4) of undergraduate studies
- which are the specific needs (core skills) of potential employers for BSc, MSc graduates in B&MB, linked directly to their expertise in Chemistry (theory, practice)
Direct information will be given regarding the teaching curricula and the above-mentioned aspects for one particular group of students. All the aspects are discussed in the actual political/economical/social context, with emphasis on how a teaching system can rapidly adapt to European Community standards and needs and to a more flexible society where the market has changed from a centralized, rigid structure to a flexible capitalist system.

292 Do Students Really Understand Metabolism the Way We Think They Do?

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Numerous reports have described teaching approaches aimed at improving student understanding of metabolism. By contrast, few reports have focussed on assessing the nature of student understanding of metabolism and identifying related conceptual and reasoning difficulties. Questions on the effect of irreversible inhibition of a specific enzyme in a pathway revealed two related difficulties, termed "essential nature" and "localized reasoning". In the former students think that the inhibited reaction will continue normally, while in the latter they suggest that the inhibited reaction will have no effect on the functioning of the rest of the pathway. In parallel coupling with ATP cleavage, in glycolysis, some suggest that ATP is not an essential substrate in the reaction but merely supplies energy to speed it up. Others indicate that ATP cleavage will occur independently of the other reaction. In oxidative phosphorylation, some think that the electron carriers occur as a fixed repeating sequence in the membrane and do not need to collide to transfer electrons. On inhibition of electron transport some suggest that electron carriers will respectively accumulate or deplete, before or after the point of inhibition. On uncoupling some are confused as to whether ATP synthesis and/or electron transport can continue independently. In this paper we shall describe these difficulties and discuss how this type of research can lead to improved understanding of metabolism.

293 Genomic Perspectives of Microbial Metabolism and Regulation

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In the traditional view of the structure-function relationship, a molecular function is attributed to a single protein or a single gene. In contrast, the complete set of genes encoded in the genome is a starting point toward understanding a new level of structure-function relationship; namely, the relationship between a network of interacting molecules and a higher-level function representing a systemic behavior of cellular processes. The network prediction would not be possible without the knowledge of actual networks in living cells. The primary objective of KEGG (Kyoto Encyclopedia of Genes and Genomes) is to organize a reference database for such knowledge. In addition, we have been developing graph algorithms and practical software for network prediction. We consider the genome as a one-dimensionally connected graph with genes as its nodes. We also consider a combined set of various networks of interacting molecules as another graph with gene products as its nodes. Then, the network prediction involves a conversion from the genome graph to the network graph with the help of additional graphs resulting from functional genomics experiments. We have developed an algorithm to detect correlated clusters in multiple graphs, which is especially useful to integrated different types of data and to expand current knowledge of networks. The result of our database and algorithm developments is the actual network predictions for various cellular processes, including metabolism, membrane transport, signal transduction, and cell cycle, for all the organisms with completely sequenced genomes. These predicted networks provide insights into the overall architecture of biological systems and also possible solutions to experimental discrepancies in specific problems.