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Direct computerized translation of biological data into biological information is now feasible: The gains of digital signal processing-based bioinformatics techniques

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Obtaining biological functionalities such as pharmacological activities, disease processes, physiological and structural properties by analyzing the sequence information attributed to them has preliminarily been considered impracticable. This is because there are no known procedures that could be engaged in order to help uncover biological functionalities encoded in the sequence information. It has also been recognized that most biological functionalities of drugs consisting of alkaloids, flavonoids, Terpenes, steroids, etc could be expressed in one gene/protein or the other. For example, Multidrug-resistance transporter gene (MDR1) encoding genes for P-glycoprotein and CYP450, which play vital roles transport and metabolism of Antiretroviral agents have been identified. This MDR1 gene regulates the activity of some antiretroviral drugs. Similarly, anti-bacteria multi-drug resistance genes (MDR1 and MDR2) control the activities of Ciproxfloxacin (an alkaloid), Penicillin (a Beta-lactamase) and tetracycline (a polyketide), Gentamycin (an Aminoglycoside) antibiotics, etc. The same applies to anti-Malaria agents and others. In effect, activities of a wide range of therapeutic agents belonging to numerous groups could be read from one gene/protein they express. Furthermore, genes/proteins encoding therapeutic agents can provide as much information as the therapeutic agents. Direct translations of sequence information into biological functionalities were truly impossible until 1985 when researchers saw proteins/peptides as signals (numerical sequences) instead of piece of fish, meat, bowl of beans or an enzyme. This has opened up a novel area of research. As signals, proteins and peptides were analyzed using techniques that have help develop technologies like Radar, Image Processing and Speech Detector. This technique is called Digital Signal Processing (DSP).

This presentation demonstrates how biological functionalities could be translated directly from their sequence information using a DSP technique called Informational Spectrum Method (ISM) and two peptides VIPMFSALS and CAPAGFAIL. This technique has offered direct translation of sequence information into various bio-functionalities. It compared the efficacy of two anti-retroviral agents (Enfurvitude and Sifurvitude) as well as two starter materials (P18 and P32) for the designing of anti-malaria vaccines. It explained the HIV progression to AIDS. It identified the origins of HIV-1 non B subtypes that infected American soldiers on Foreign Service. It elucidated the molecular mechanisms to protection offered to the heart by Influenza vaccines as well as Emilins to Anthrax antigen. It calculated biological functionalities and has helped develop a biomedical device, Computer-Aided Drug Resistance Calculator. Based on the level of biological functionalities uncovered from sequence information using DSP procedures, it can be ascertained that it has now become feasible to obtain same results we get from clinical laboratories by analyzing sequence information involved. Because this approach is rational, it is recommended that it be fully exploited.

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