A journey through structural bioinformatics

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Abstract

Trained as an electronics engineer, I was not particularly meant to conduct research in bioinformatics. However, a chance encounter with a professor of Bioinformatics made me discover the fascinating world of protein structures and realise that my expertise in computer graphics could allow me to explore it. This presentation reports the scientific and sometimes physical journey that I have made through the field of structural bioinformatics during the last 15 years. Starting from the study of the 3D properties of protein active sites, I then investigated the language of proteins and interactions between pairs of proteins. Eventually, I embarked on contributing to the 50-year-old challenge of predicting a protein's structure from its sequence alone. This has led to many adventures and publications, but at the end "it is not about the journey, it is about the people you meet . . . "

About the presenter

Jean-Christophe Nebel is a Professor of Computer Science in the School of Computer Science & Mathematics at Kingston University, London. He is also a Senior Fellow of the Higher Education Academy (SFHEA) and School Director for Research & Enterprise.

For more than 20 years, he has made original, theoretical, and applied contributions to pattern recognition and machine learning supported by multidisciplinary and international collaborations. Following the award of a M.Sc. (Eng.) degree in electronics, he completed a Ph.D. in parallel programming from the University of Saint-Etienne, France. As a postdoctoral researcher at the University of Glasgow, Scotland, he pioneered the world first experimental 3D television studio for which he became co-recipient, in 2004, of the A. H. Reeve Premium award by the UK Council of the Institute of Electrical Engineers. Since then, he has been an academic at Kingston University, London, where he has applied his expertise mainly to computer vision and bioinformatics. His achievements include: the generation of realistic 3D body motions guided by neuroscience models, the first stochastic context free grammar-based framework able to handle the complexity of the protein alphabet, a novel embedding-based dimensionality reduction method able to model any concept represented by multivariate sequences, the pioneer usage of common-sense reasoning for computer vision-based human action recognition, the meta-analysis of

gene variants, the enhancement of fragment-based protein structure prediction, the development of a game-theoretic approach to schedule electricity consumption in a smart grid, and the exploitation of deep convolutional networks for the study of honeybee's audio signals. In addition, he has recently introduced a genomics-inspired paradigm (vide-omics) for visual surveillance where videos are interpreted as the evolutionary record of a mutating image. Finally, he has contributed to the COVID-19 effort by applying game theory to enhance stock management of personal protective equipment.

Together with Prof. Malgorzata Kotulska, Prof. J-C.Nebel co-supervised a few M.Sc. and Ph.D. students, and shared research grants. He visited Wrocław University of Science and Technology several times, giving talks and teaching a Bioinformatics course for students of Biomedical Engineering.

More information at: www.kingston.ac.uk/staff/profile/professor-jean-christophe-nebel-43