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Compositional order of proteins, a novel perspective on evolution

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The existence of compositional bias in some protein sections is well-known. Moreover, phenomena of amino-acid runs, tandem repeats, and repeats of large motifs have been noted in the literature. Their variants are known to be linked to disease in human. All these features can be labeled as Compositional Order (CO). They have been recently studied with a novel methodology in a unified manner. This allowed us to correlate the corresponding proteins (including a quarter of the human proteome) with functional annotations. Moreover, comparative genomic studies have led us to the conclusion that CO characteristics can distinguish between major evolutionary kingdoms (vertebrates, invertebrates, plants, fungi and prokaryotes) ranking them according to a CO richness measure. The latter can be viewed as representing a macroevolutionary stamp on the proteome. It suggests that major macroevolutionary events may involve novel CO generation during the creation of entirely novel species.

Biography

David Horn has served as Professor of Physics at Tel Aviv University from 1971 until his retirement at 2005. He has held various administrative positions including Vice Rector of TAU (1980-1083), Dean of the Raymond and Beverly Sackler Faculty of Exact Sciences at TAU (1990-1995) and first Director of the Adams Super Center for Brain Studies at TAU (1993-2000). His research interests have concentrated on Theoretical High Energy Physics until about 1990, followed by Neural Computation until about 2005, after which he switched to Bioinformatics. In addition to pursuing active research he serves as chairman of the Advisory Committee for Research Infrastructures for the Israel Planning and Budgeting Committee.

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