Genomic positioning systems for DNA and the tree of life

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Abstract

Geographic information systems represent the modern version of the scientific revolution ushered in by the introduction of now standard Cartesian coordinates and analytic geometry in the 1600s. They provide a universal means of communication and computation in a unified system that makes possible identification, comparisons and validations of geographic position, previously unattainable on a global scale. In this talk, the author propose an analogous coordinate system for the far more complex genomic biosphere based on the concept of "genomic" distance enjoying the geometric properties characteristic of geometric distance. The system has several properties: It is universal (applicable to any genome, known or unknown), feasible (computable for every given genome), zoomable (adaptable precision to various scales of resolution) and, more importantly, capable of revealing important functional and structural features of a given genome relative to other genomes. After a brief sketch of the foundations and contrast with earlier approaches, the author illustrate how these two latter features make possible a number of applications in various omics areas, such as molecular phylogenetic, universal genetic marker generation and classification, and comparative whole-genomic analyses on a common framework that may reveal significant commonalities in hitherto disparate taxonomies and procedures. Time permitting; some potential applications will be sketched in some detail, including applications of interest in Transcriptomics, such as molecular systematics, the Tree of Life, and Next-Generation Sequencing.

Biography

Max H Garzon is a Professor of computer science and bioinformatics at University of Memphis. He has Co-authored over 150 books, book chapters, journal and refereed conference publications. The main theme of his research is biomolecule- based computing and applications to areas such as bioinformatics, nanotechnology, self-assembly, semantic indexing and data mining. He is on the editorial board of several journals in these areas, including the International Journal of Genomic Medicine. He has served as TPC and Organizer of many scientific conferences and professional meetings in these areas. He has been a Visiting Professor and guest Scientist at a number of research institutions around the world.