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How far back can computation take us? “Can we model biology’s beginnings?”

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Modern Bioinformatics computational tools have allowed the reconstruction of some of the earliest evolutionary events. We have, for example, successfully reconstructed the Phylogeny of major animal taxonomic divisions. For example, the phylogeny of the entire class Aves or Birds has just recently been published. In general, this success has rested on two things: The fact that modern biology is a “big data” science with tens of thousands of full genome DNA sequences, and on the concept that what is widely common has been conserved over long time periods. The history for example of a programmed cell death regulation system, the Lifeguard gene family, has yielded information as far back as the divergence of plants and animals, and allowed the identification of a mutation shared by modern human and Neanderthals, but not other mammals. However most of the earliest events are still left to theory and hypothesis. Yet in the case of the DNA to protein translational system, current data is very suggestive of some early events. Here we review the Lifeguard and tRNA synthetase studies to show what data and computational methods were used, and what more is needed, in this big data era.

Biography

Temple F Smith, PhD, is one of the founders of bioinformatics and is currently Professor Emeritus at Boston University's Dept. of BioMedical Engineering. His research is focused on developing statistical and other computational approaches to the detection of syntactic and semantic patterns in DNA, RNA, and protein sequences, and applying them to functional and evolutionary problems. He has received the ISCB's 2007, Senior Scientist Award and has published over 200 reviewed papers.

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