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How far back can biology's big data take us? "Can we model biology's beginnings?"

Modern Biology now claims to be a "big data" science. Unfortunately the term "big data" has a lot of associated hype these days. Clearly the science at the Large Hardon Collider at CERN involves big data, as does the astronomy with Hubble's deep field images. It is confluence of ever expanding genomic, structural and image data that supports such claims for modern biosciences. While the claims in the medical area will soon be justified; but the main concern is providing insight into the oldest and fundamental questions of the earliest evolutionary events. There have been, successfully reconstructs of the Phylogeny of major animal taxonomic divisions. For example, the phylogeny of the entire class Aves or Birds has just recently been published, pushing the origins back. 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 transnational system, current data is very suggestive of some early evens. Here we review the challenges of Big Data and its applications to biomedicine and evolution.

Biography

Temple Smith graduated with a Ph.D. in Nuclear Physics from the University of Colorado in 1969. Then did a National Institutes of Health (USA) postdoctoral fellowship under the direction of the mathematician, Stanislaw Ulam, and the molecular biologist, John Sadler. There he carried out a detailed analysis of the E. coli Lac operator mutations. In 1979, Smith was one of the founders of GenBank, initially at Los Alamos National Laboratory. There, he with Walter Goad developed a statistical mechanical model of the Lac operon system similar to those now being developed in system biology. Smith is a co-developer with Michael Waterman of the Smith-Waterman sequence alignment algorithm, underlying most DNA and protein sequence comparison methods today.

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