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Commentary

Genome Annotation and Comparative Genomics

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DESCRIPTION

Annotation is the process of identifying genes and other biological properties in a DNA sequence in the context of genomics. Because most genomes are too huge to annotate by hand, and because there is a need to annotate as many genomes as possible now that sequencing speed is no longer a limitation, this process must be automated. The fact that genes have distinguishable start and stop areas allows for annotation, however the exact sequence found in these regions varies between genes.

The nucleotide, protein, and process levels of genome annotation are the three levels of annotation.

A key part of nucleotide-level annotation is gene discovery. The most successful methods for complex genomes combine into gene prediction with sequence comparison with other organisms and expressed sequence databases. Genome sequencing can also be linked to other genetic and physical maps of the genome using nucleotide-level annotation.

Protein-level annotation's primary goal is to attribute function to the genome's products. For this form of annotation, databases of protein sequences, functional domains, and motifs are useful. Nonetheless, half of the predicted proteins in a new genome sequence are thought to be useless.

The purpose of process-level annotation is to understand the function of genes and their products in the context of cellular and organismal physiology. The inconsistency of words employed by different model systems has been one of the roadblocks to this level of annotation. The gene ontology consortium is assisting in the resolution of this issue.

The team at The Institute for Genomic Research, which accomplished the first complete sequencing and study of a free-living organism's genome, the bacterium Haemophilus influenzae, published the first description of a comprehensive genome annotation system in 1995. Owen White created a software method to detect all protein-coding genes, transfer RNAs, ribosomal RNAs (and other locations), and make early functional designations. Most modern genome annotation systems work in a similar way; however algorithms for analyzing genomic DNA, such as the GeneMark software, which was trained and used to locate protein-coding genes in Haemophilus influenzae, are always changing and improving.

Following the human genome initiative's goals after its conclusion in 2003, the National Human Genome Research Institute in the United States launched a new project. The encode project is a collaborative data collection of the functional elements of the human genome that uses next-generation DNA-sequencing technologies and genomic tiling arrays, technologies that can generate large amounts of data at a lower per-base cost while maintaining the same accuracy and fidelity.

While sequence similarity (homology) is the primary basis for genome annotation, other features of sequences can be utilized to predict gene activity. In reality, because protein sequences are more informative and feature-rich, most gene function prediction algorithms rely on them. Tran's membrane segments of proteins, for example, are predicted by the distribution of hydrophobic amino acids. External information, such as gene (or protein) expression data, protein structure, or protein-protein interactions, can be used to predict protein function.

The establishment of correspondence between genes (otology analysis) or other genomic properties in different organisms is at the heart of comparative genome analysis. These intergenomic maps allow researchers to follow the evolutionary processes that led to the divergence of two genomes. Genome evolution is shaped by a slew of evolutionary events operating at diverse organizational levels. Point mutations alter individual nucleotides at the most basic level. Large chromosomal segments go through duplication, lateral transfer, inversion, transposition, deletion, and insertion at a higher level. In the end, complete genomes are involved in hybridization, polyploidization, and endosymbiosis processes, which typically result in fast speciation. The complexity of genome evolution presents a wide range of algorithmic, statistical, and mathematical challenges for developers of mathematical models and algorithms, ranging from exact, heuristics, fixed parameter, and approximation algorithms for problems based on parsimony models to Markov chain Monte Carlo algorithms for Bayesian analysis of problems based on probabilistic models.

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