Keynote Talk

Genome Paleontology: Discoveries from Complete Genomes

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Our group has been developing new algorithms for the analyses of complete genome sequences, and using these algorithms to make a variety of biological discoveries in organisms ranging from bacteria to humans. The computational backbone of many of our analyses is a system that that can align DNA sequences of essentially any size, including entire human chromosomes, in just a few minutes on a large-memory computer. After a brief description of the algorithm, I will discuss several findings that emerged from comparisons of whole genome sequences.

First, we have used this system to align numerous bacterial genomes against each other, which has led to the surprising discovery that the genomes of a number of bacteria can be aligned in both directions; i.e., one of the genomes is globally similar at the DNA level to both the forward and the reverse strand of the other. When both alignments are displayed together, an X-shaped pattern is clearly visible. We have discovered X-alignments between the genomes of E. coli and V. cholerae, M. tuberculosis and M. leprae, and others. I will discuss the biological explanation of this phenomenon. Second, we looked at the model plant Arabidopsis thaliana and the human genome and found two very different pictures of large-scale ancient duplications. Third, our comparison of the human and mouse genomes demonstrates the remarkable similarity between these two organisms, which share some 95% of their genes. Finally, I will discuss our analysis and refutation of the claim that bacterial genes were laterally transferred into the human genome.

References

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