Research Highlight: A Fast Program for Verification of Phylogenetic Network Models

Work of Professor ZHANG Louxin

Genetic material is transferred in a non-reproductive manner across species more frequently than commonly thought, particularly in the bacteria kingdom. On one hand, extant genomes are thus more properly considered as a fusion product of both reproductive and non-reproductive genetic transfers. This has motivated researchers to adopt phylogenetic networks to study genome evolution. On the other hand, a gene's evolution is usually tree-like and has been studied for over half a century. Accordingly, the relationships between phylogenetic trees and networks are the basis for the reconstruction and verification of phylogenetic networks. One important problem in verifying network models is determining whether or not certain existing phylogenetic trees are displayed in a phylogenetic network. This problem is formally called the tree containment problem. It is NP-complete even for binary phylogenetic networks. Zhang Louxin and his students designed an efficient method for solving the tree containment problem for arbitrary phylogenetic network on the basis of the so-called reticulation-visible property of phylogenetic networks.

Reference:

A.D.W. Gunawan, B.X. Lu, L.X. Zhang, "A Program for Verification of Phylogenetic Models". Bioinformatics, 32 (2016): i503-i510.