

## **Research Highlight: How to see clusters in an evolutionary network**

### **Work of Professor ZHANG Louxin**

Genomic studies indicate that extant genomes are more properly considered to be a fusion product of random mutations over generations and genetic material transfers between individuals of different lineages. This has motivated biologists to use networks to model genome evolution. A fundamental algorithmic problem arising from verification of evolutionary networks is to decide whether a set of genomes appears as a cluster in some tree displayed in an evolutionary network.

Although this cluster containment problem was introduced a decade ago, there has been little progress in developing fast algorithms for it on arbitrary evolutionary networks. Recently, Gunawan, Yan and Zhang presented a fast method for solving the cluster containment problem at the Annual European Conference on Computation Biology held at Athens in September, 2018. This program was developed on the basis of a linear-time transformation from the small version of the cluster containment problem to the Satisfiability problem that are widely studied in computer science.

#### **Reference:**

Yan H, Gunawan AD, Zhang L. S-Cluster++: a fast program for solving the cluster containment problem for phylogenetic networks. *Bioinformatics*, 34, No. 17 (2018): 680-686.