

Guest lecture

Data integration and visualization of phylogenetic trees

Guangchuang Yu, Ph.D.

Guangchuang Yu is a Professor of Bioinformatics at Southern Medical University, Guangzhou, China. He is broadly interested in bioinformatics, metagenomics and molecular evolution. He has contributed 10 Bioconductor packages including GOSemSim, ChIPseeker, clusterProfiler, treeio and ggtree.

Phylogenetic trees are increasingly used in various biological studies to investigate associated data in an evolutionary context. For instance, influenza virus has a wide host range, diverse and dynamic genotypes and characteristic transmission behaviors that are mostly associated with the virus evolution. Such information can be interpreted in phylogenetic context to help identifying evolutionary patterns. Data integration extends and broadens the applications of phylogenetic trees, especially for comparative studies. We developed two Bioconductor packages, treeio and ggtree, for phylogenetic tree data integration and visualization.

This talk will introduce these two packages, including parsing tree data from various file formats, mapping external data to tree structure, tree visualization and annotation, especially for associated data.

Date: 24 January 2019

Time: 14:00 — 15:00

Place: BMB Seminar room

Hosts: Thomas K. Doktor and Veit Schwämmle, BMB, SDU.