一般シンポジウムS5 Evolutionary informatics in the era of sequence data deluge

時間 10:00-12:00

会場：コンベンションホールB
提案者：田村浩一郎(東京都立大学)・岩崎渉(東京大学)

シンポジウムの趣旨：

More and more sequence data are becoming available in molecular evolutionary studies thanks to the advanced sequencing technologies. To let researchers take full advantage of this "sequence data deluge" to gain insights into the origins, background, and rules of the evolution of genes and genomes, effective computational methods are strongly needed to overcome the computational cost and resolve the intrinsic complexities of genome evolution. In this symposium, we will focus on the frontiers of evolutionary informatics in the era of sequence data deluge.

講演者と発表タイトル

10:00-10:30 Sudhir Kumar (Institute for Genomics and Evolutionary Medicine, Temple University)
Accurate, efficient, and green computing in Big Data Phylogenetics

10:30-11:00 SAITOU Naruya* and Kirill KRYUKOV (National Institute of Genetics)
External Edge Elimination (3E) methodfor phylogeny construction

11:00-11:30 Koichiro Tamura (Tokyo Metropolitan University)
Dating the origin and evolutionary history of pathogenic viruses from massive sequences

11:30-12:00 Wataru Iwasaki (The University of Tokyo)
Evolutionary informatics for obtaining more knowledge from the sequence data deluge