

## **Using a database and a prior for the estimation of structural evolution and recombination**

Leonardo de Oliveira Martins<sup>1</sup>, Teruaki Watabe<sup>2</sup> and Hirohisa Kishino<sup>1</sup>

1. Graduate School of Agricultural and Life Sciences, University of Tokyo

2. Center of Medical Information Science, Kochi University

Sequence evolution drives the adaptive evolution through phenotypic change. Because of its relatively simple life cycle, viral populations give us unique opportunities to quantify and to predict the fitness of the sequence evolution. To understand the cost of the escape from the immune system, we developed a knowledge-based binding ability of a protein complex. The change in the binding ability of the spike protein with the host receptor and the binding ability with the antibody determines the ability of the escape from the antibody and the reduced infectivity. Recombination plays an essential role in viral evolution through genome reorganization. We developed an algorithm to calculate the distance between tree topologies that expresses the number of recombination events. Our Bayesian hierarchical model penalizes the recombination distances between the neighboring segments and estimates the distribution of the recombination break-points along the genomes and the patterns of recombination events.