

## **HivStudy**

This is a method to study the phylogenetic relationships among complete genome sequences of different subtypes of viruses. The source codes of our method and datasets used can be downloaded from <https://github.com/myl446/HivStudy>

ComputerdistanceMatrix.java: This is a program for calculating the distance matrix of species.  
5596data.rar : This dataset contains 5596 pure subtype HIV sequences.

datacg1625.rar : This dataset contains 1625 Circulating Recombinant Form (CRF) HIV sequences.

PureSequences867.rar: This dataset contains 867 pure subtype HIV sequences.

This program needs to install JDK 1.7, eclipse-jee-mars-2-win32-x86\_64 to run.