

Netview: Application Software for Constructing and Visually Exploring Phylogenetic Networks

Kirill Kryukov

kkryukov@lab.nig.ac.jp

Naruya Saitou

nsaitou@genes.nig.ac.jp

Division of Population Genetics, National Institute of Genetics / Department of Genetics, Graduate University for Advanced Studies, Mishima 411-8540, Japan

Keywords: phylogenetic network, neighbor-joining method

1 Introduction

Reconstructing evolutionary history of a group of species is a major task in biological study. Many methods exist for reconstructing such history, or phylogeny, but most of them are based on an assumption that evolution of given gene family can be represented as a tree. However some families of genes may have alternative historical structure that cannot be represented as a tree. Such history can result from events such as recombination, gene conversion and horizontal gene transfer, and require not tree but network for accurate representation. Parallel substitutions are also sources of non-tree networks. For the purpose of understanding such history we developed a program Netview, which enables constructing phylogenetic network based on the sequence data.

2 Netview

Netview uses following approach to construct a network: First, it constructs a NJ-tree [1] for provided set of sequences, using nucleotide difference distance matrix (Fig. 1). Then every nucleotide site position of sequence data is analyzed to check if it is compatible with the NJ-tree constructed. Sites that show incompatible partitioning configuration, are then listed for user's selection. When the site is selected by user, the initial NJ-tree is morphed into a network by splitting its nodes into two planes (Fig. 2). Two planes correspond to the sequence partitioning pattern, obtained from the given nucleotide site position. Tree nodes are assigned to the planes, according to the partitioning pattern of selected nucleotide site. Structure constructed in this way is no longer tree, but network, which is positioned in a 3D space. Netview program then enables user to view the network from different angles.

Netview has following features to support constructing and exploring phylogenetic networks:

1. Rotating network around any of 3 axes.
2. Shifting network structure to the left, right, upward or downward.
3. Zooming in and out
4. Take screenshot of current view.
5. Changing to another partitioning pattern, taken from different nucleotide position. The network is reconstructed based on the same initial tree.

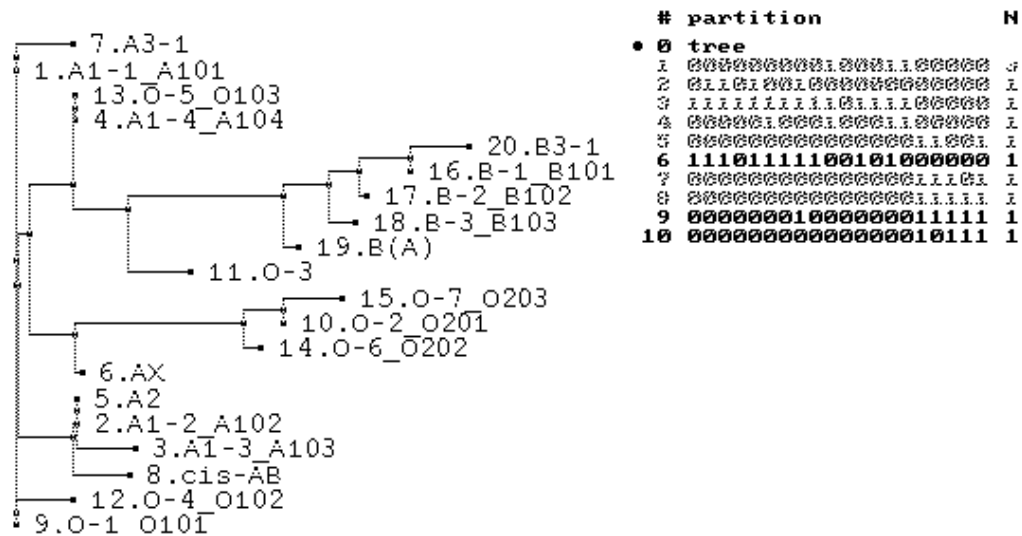


Figure 1: Initial NJ-tree used as a basis to build the network. On the right hand there is a table of partitioning patterns (designated with binary characters) that are present in the sequence data. Partitions 1-5, 7, and 8 are compatible with the NJ tree, while partitions 6, 9, 10 are not. (Example sequences are from [2])

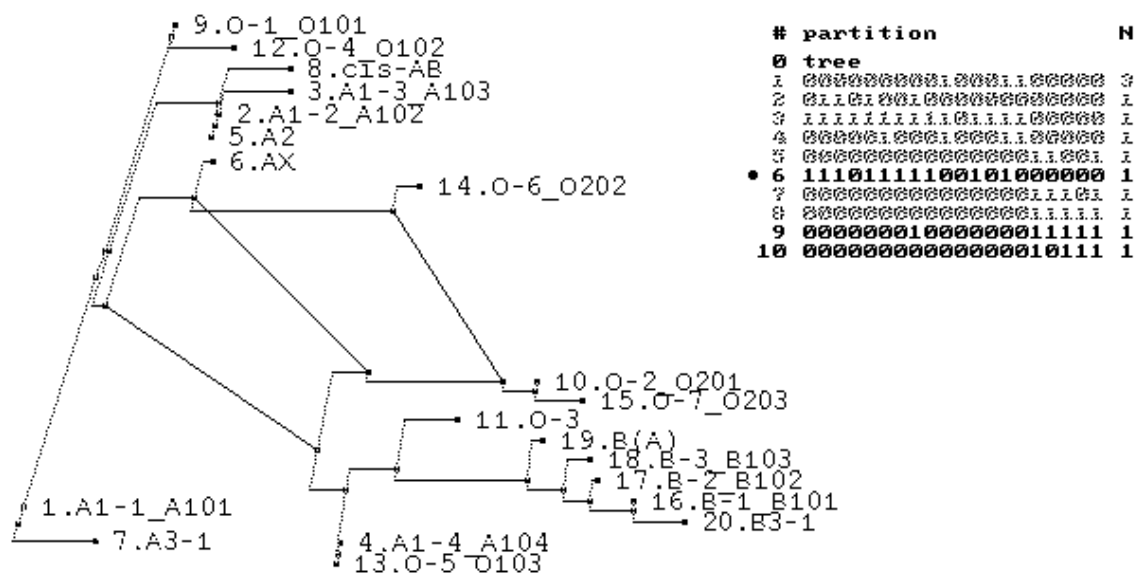


Figure 2: Example phylogenetic network, produced with Netview. Partition no. 6 was chosen.

Netview is written in C and its source will be open. Currently only a windows version exists, but it is written in a way making it easy to port the program to other OS, like Linux or MacOS. Netview can accept sequence data with FASTA-format or ClustalW multiple alignment format. The latest version of Netview is available from the program web-site [3].

References

- [1] Saitou, N. and Nei, M., The neighbor-joining method: a new method for reconstructing phylogenetic trees, *Molecular Biology and Evolution*, 4:406-425, 1987.
- [2] Saitou, N. and Yamamoto, F.-I., Evolution of primate ABO blood group genes and their homologous genes, *Molecular Biology and Evolution*, 14(4):399-411, 1997.
- [3] <http://esper.lab.nig.ac.jp/netview/>