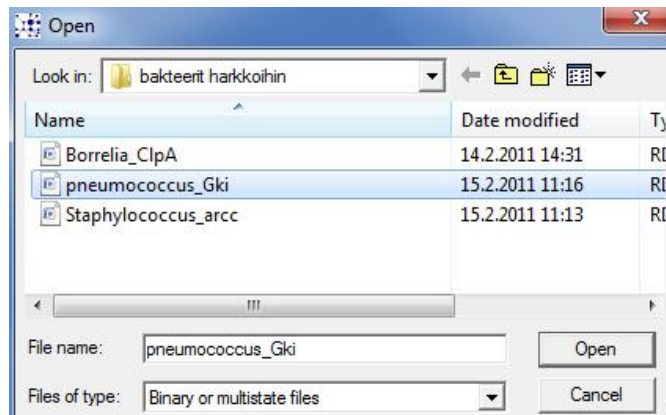# PRACTICAL INSTRUCTIONS FOR USING THE NETWORK-SOFTWARE

■ The algorithms are explained in the paper "Median-joining networks.pdf" in course webpage. Very much used especially in human population histories (explained in lecture).

■ The program Network4.6 is freely downloadable from http://www.fluxus-engineering.com/sharenet.htms. Some additional add-ons by charge, for example the required datafile format, rdf (which I have construcetd for you by using another program, Dnasp5).

■ The fileformat rdf includes the variable sites only plus some definitions (a typical haplotype-file).

■ Save the rdf-file from your email. It need not be in Network-folder.

■ All information given here is in the manual (in course webpage) in more detail.

■ Datafile here

■ Choose "import rdf-file",

   ■ "DNA-nucleotide data"
   ■ "continue"
     to your own folder

and open the rdf-file you plan to use.

■ Now you are here.

■ The necessary steps are to "save"

and

"exit"

■ You are ready to proceed to "Calculate network", choose "network calculations" → "median-joining" and open your datafile, "calculate network", save your file as Name.out and proceed to "draw network".

■ Now you are here, choose your name.out-file (notice the options here)

■ You get the drawing…

■ The red numbers are the mutations at specific sites… (see the editing facilities)

■ For example, H_1 (the first sequence in the file, which is one bacterial isolate, has "descendants" around it, many of which differ from it by one nucleotide change (at sites shown by numbers), some are more distantly related.