## Instructions for running the R script plot\_ms\_trees\_single\_pop.R

There are lots of ways of running R. The simplest for this example (but not necessarily the easiest way to learn R, which is probably via the package RStudio) is to use the Windows installation of R that is available on all the university machines. Even if you are on a Mac you can connect to this with Remote Desktop (look at ITS instructions for this). So I am assuming that here.

1) Download the R script from Blackboard. Put it in a folder in your myfiles (O: drive) system.

2) Choose Programs -> Rgui in Windows (NB not R by itself)

3) In R choose Packages -> Set Cran Mirror, and choose e.g. Bristol (but not Bristol https)

4) Packages -> select repositories, and accept the default it suggests

5) Packages -> select packages, choose ape and also choose phyclust

6) Then choose File -> Change dir and navigate to the folder in your myfiles system containing the plot\_ms\_trees.R file.

7) type: **source(“plot\_ms\_trees\_single\_pop.R”)** into the R console window. With luck you should get a plot.

If there are any problems send me an email. If there is something generally wrong with these instructions I’ll modify them and send an announcement.

If you are feeling brave, then you can try to familiarise yourself with R and with ms (and necessarily the phyclust package which contains ms) and use this as a framework for doing more stuff – i.e. generate sequences and calculate some of the quantities we are learning about in the lectures.

For a 2-deme model with migration I have an additional R script “plot\_ms\_trees\_mig.R”, which you can try running as above. It will produce a genealogy for samples taken from both demes, with the tips coloured by deme of origin.