

LFSC 520

Week 7: Genetic Variation in Populations

Excise Notes

### **Nucleotide diversity**

1. Go to web site: <http://www.ub.es/dnasp/> and download DNasp 4.0, install it in your PC.
2. Download files Xq13.all.fas
3. Open DNasp, open file all.fas. Then click “Analysis” in tool bar. Calculate the nucleotide differences and nucleotide diversity for the sequences in the file all.fas
4. Click Data → Define Sequence Sets → choose following for Africans  
5 – 12, 23 – 27, 34, 57 – 58, 63 – 69  
click “Add new Sequence Set” → save as a set with your name, e.g. Africans  
Then choose following for non-Africans  
1 – 4, 13 – 22, 28 – 33, 35 – 56, 59 – 62  
click “Add new Sequence Set” → save as a set with your name, e.g. Non-Africans
5. Click Analysis → “nucleotide divergence between populations”

Neutrality test

1. Open DNasp, open file, then click “Analysis”, choose Fu and Li’s Tests

### **Haplotype inference**

1. Go to web site: <http://www.stat.washington.edu/stephens/software.html> and download Phase2.1, window version.
2. Go to DOS Command Prompt, find the path, and open Phase program
3. Type in the following command: phase phase.input.txt phase.output.txt
4. Open the results file in phase.output.txt

### **Haplotype network**

1. Go to web site: <http://www.fluxus-technology.com/sharenet.htm>, download NETW4109.exe
2. download file xq13.rdf
3. Open Network program → click “Data Entry” → choose “Binary data” in the popup box → click “Continue” button → choose the file “xq13.rdf” → Edit file and save → close program
4. Click “Calculate Network” → Choose “Median Joining” → Open file → choose file “xq13.rdf” → click “Calculate network” → calculate and save to “xq13.out” → close program automatically
5. Click “Draw Network” → open file → choose “xq13.out” → choose by instructions → have fun!