

Assignment 4

Group work, like assignment 3

To be ready for presentation Tue 13. Dec.

Analysis of molecular genetic variation within and between populations

- Collecting data from a HLA-gene, DRB1, from human populations:
<http://www.pypop.org/> → “data files” <http://www.pypop.org/#popdata> → Population data files “<http://www.pypop.org/popdata/>” and then you can look at worldwide frequency maps and from “Index of population datasets” you can collect information of the alleles and their frequencies in various populations.
 - If you work alone, you choose 5 populations
 - Two student –group choose 10 populations
 - Three or more student –group choose 15 populations
- Allele sequences are given as a separate file (they can – probably – be collected also from the same source as population information, but I didn´t find how...) to work with

You can choose between two software: DnaSP and Arlequin.

Both are easily downloadable to your own computers; both are in C128 computers, but DnaSP does not work there.

Answer the questions:

- Nucleotide diversity within populations and differences between populations. The two programs use a bit different terminologies. If you use Arlequin, make AMOVA (analysis of molecular variance).