

## Assignment 1b

During the first computer class session each student downloads fastPHASE from <http://stephenslab.uchicago.edu/software.html> to their home directory/laptop and performs a test with simple example data.

The data which is planned to be analysed by fastPHASE will be retrieved from HapMap-database (<http://hapmap.ncbi.nlm.nih.gov/>) which, in addition to already haplotyped data includes raw genotype data that you can download either for a complete chromosome in one file (Bulk Data Download) or a subset of this (via HapMap Genome Browser).

As quite many students in the course already are familiar with HapMap, and it is useful to work in groups – at least to some extent, the advise is that you form groups ( 5-6 students in a group) with such a composition that at least one member is familiar with HapMap.

Each group takes a part of a human chromosome. Handling even the smallest of chromosomes in their entirety is not recommended due to the computation time involved in phasing the genotypes.

By familiarizing with the fastPHASE manual you are supposed to edit the data into a correct form. During the first week a group is supposed to get preliminary results to be presented in the second computer class session, during which the Assignment 1b will be planned further. The preliminary results need not be submitted to the student page.

On the basis of the preliminary results it will be decided whether each group member continues working with the whole chromosome part or only a smaller part of that. Results are supposed to be submitted until the 4<sup>th</sup> computer class session.