

# Statistical Methods for Computational Biology

**Pr. 1** How do you model linkage disequilibrium in structure ?

**Pr. 2** How do you set  $K$  ?

**Pr. 3** Why is Metropolis/Hastings used to update  $\alpha$  ?

**Pr. 4** What is label switching and why is this not a problem ?

**Pr. 5** Give some examples of distance metric based methods in inference of population structure.

**Pr. 6** Sketch the EM (expectation-maximization) version of structure.

**Pr. 7** In a GWAS how does one correct for population structure.