

Something to think about

- What if the data look like this: n individuals, typed at two loci, all heterozygous at both loci. (ie all 01,01).
- What is the MLE for the haplotype frequencies?
- Conditional on this MLE, what are the diplotype distributions for each individual?
- What is the Bayesian solution?
- What kinds of problems might we expect to come across in MCMC? (especially for large n).