

1. MLE of Allele Frequency. Suppose you have the following alleles and their respective counts:

0 - 600

1 - 200

What is the maximum likelihood estimate of the frequency of the 1 allele?

Select from the following options and justify briefly in the box why you choose your answer.  $\,$ 

(a) 0.1

(b) 0.75

(c) 0.9

(d) 0.25

(G) = 200 = 2

by derivation in class

## 2. MLE question of Haplotype Frequency.

Suppose you have the following haplotypes and their respective counts:

1001 - 300

1101 - 1200

0.011 - 400

0101 - 100

What is the maximum likelihood estimate of the haplotype 1101?

Select from the following options and justify briefly in the box why you choose your answer.

(a) 0.1

(b) 0.25

(c) 0.6

(d) 9/2

By derivation

D= frequery 1200

~ = <del>3</del>

3. Trio Phasing. Suppose you have the following trio with the genotypes as below

Parent1 = 122102 Parent2 = 011120 Child = 112011



Assume there is no recombination. What is the phase of the child in this trio?

Select from the following options and justify briefly in the box why you choose your answer.

(a) 011001, 101010

(b) 111001,001010

(c) 01/1001, 111010

(d) 10010, 001010

	4. Clark's algorithm.						
	Suppose you have the following genotypes:						
Λ	AGHAA AGAAA						
/	GAGHA AGIGAA						
	HHGHA						
1							
	HHHHA GAGGA						
7	Perform Clark's algorithm, starting from the first genotype, what is the						
	final haplotype(s) that were adden to your known set.						
	Select from the following options and justify briefly in the box why you						
	choose your answer.						
	(a) AAAAA )						
	(b) GGGA						
	(c) AGAAA						
	(d) AGGAA						
	(d) NGG/M						
	1						

## 5. Haplotype phasing with the EM algorithm.

Suppose you have genotypes  $G=\{01210,10222,00110\}$ . Perform one round of the EM algorithm for haplotype phasing (assume that the haplotypes are equally probable  $p_1=p_2...=p_n=1/n$ ). After one round of EM, what haplotype(s) have the highest estimated probability?

Select from the following options and justify briefly in the box why you choose your answer.



(b) 00100,00111,00010,00000

(c) 10111,00111,00110,00100

(d)	10111,00111,00100	•
	/	

01210	01100	0.72 0.52 0.52 0.52	
60222	10111	0.5	
001100	00100	0.25	() ()
	00110	0.72	

## 6. Likelihood optimization

Consider the likelihood function of the haplotype frequency estimation problem with no missing data. In this setting, the parameters are the haplotype allele frequencies  $p_1,\ldots,p_n$ , satisfying  $\sum_{i=1}^n p_i=1$ , and  $p_i\geq 0$ , and the data is the haplotype counts  $c_1,\ldots,c_n$ , and let  $c=c_1+\ldots+c_n$ . We showed in class that the likelihood function  $L(p_1,\ldots,p_n)$  satisfies

$$\log L(p_1,\ldots,p_n) = \sum_{i=1}^n c_i \log(p_i)$$



Assume we are running a gradient ascent with projections algorithm, and we start from the guess  $p_1^{(0)}=p_2^{(0)}=\ldots=p_n^{(0)}=\frac{1}{n}$ . Let  $p_1^{(1)},\ldots,p_n^{(1)}$  be the next point that the algorithm reaches. Which of the following is true:

(a) There is  $\epsilon > 0$  such that for every i, j we have  $p_i^{(1)} - p_j^{(1)} = (c_i - c_j)\epsilon$ .

(b) There is  $\epsilon > 0$  such that for every i, j we have  $p_i^{(1)} - p_j^{(1)} = (c_j - c_i)\epsilon$ .

There is  $\epsilon > 0$  such that for every i we have  $p_i^{(1)} = (c_i - \frac{c}{n})\epsilon$ .

(d) There is  $\epsilon > 0$  such that for every i, j we have  $p_i^{(1)} + p_j^{(1)} = \frac{2}{n} + (c_i + c_j)\epsilon$ .

Select from the above options and justify briefly in the box why you choose your answer.

$$\frac{\partial}{\partial x} = \left( \frac{C_1}{R_1}, -\frac{C_2}{R_2} \right)$$

$$\frac{\partial}{\partial x} = \left( \frac{C_1}{R_2}, -\frac{C_2}{R_2} \right)$$