## The mathematical relationship between $\rho_{diff}$ value calculated using genotype information and LD calculated from allelic information

Let <sup>*a*</sup> and <sup>*b*</sup> be random variables for alelle from loci *A* and *B* where  $a \in \{-1, 1\}$  and  $b \in \{-1, 1\}$  and the observed haplotype frequency is shown in Table 1. Table 1: Two haplotype observed frequency

$$\begin{array}{ccc} A_1 & A_2 \\ B_2 & x_{21} & x_{22} \end{array}$$

We denote allele frequency from loci A and B as in Table 2.

Table 2: Estimated allele frequency

$$\begin{array}{cccc} A_1 & A_2 & B_1 & B_2 \\ p_1 & p_2 & q_1 & q_2 \end{array}$$

Given that the loci A and B are independent, expected haplotype frequency is determined by

$$x_{11} = p_1 q_1$$
  

$$x_{12} = p_1 q_2$$
  

$$x_{21} = p_2 q_1$$
  

$$x_{22} = p_2 q_2$$

Linkage disequilibium (LD) is defined as the deviation of the expected haplotype frequency and the definition of LD is given in Table 3.

	$A_1$	$A_2$
$B_1$	$x_{11} = p_1 q_1 + D$	$x_{21} = p_2 q_1 - D$
$B_2$	$x_{12} = p_1 q_2 - D$	$x_{22} = p_2 q_2 + D$

Let us compute the covariance of haplotype from two locus. The covariance is defined by Cov(a, b) = E[ab] - E[a]E[b]

From Table 1, E[ab] calculation is shown in the following equation:

$$E[ab] = -1 \times -1 \times x_{11} + -1 \times 1 \times x_{21} + 1 \times -1 \times x_{12} + 1 \times 1 \times x_{22}$$

$$= x_{11} - x_{21} - x_{12} + x_{22}$$

and E[a]E[b] is given by

$$\vec{E}[a]E[b] = (-1 \times p_1 + 1 \times p_2)(-1 \times q_1 + 1 \times q_2)$$

$$= p_1 q_1 - p_1 q_2 - p_2 q_1 + p_2 q_2$$

It follows that the haplotype covariance is

$$E[ab] - E[a]E[b] = x_{11} - x_{21} - x_{12} + x_{22} - (p_1q_1 - p_1q_2 - p_2q_1 + p_2q_2)$$
  
=  $(x_{11} - p_1q_1) - (x_{21} - p_2q_1) - (x_{12} - p_1q_2) + (x_{22} - p_2q_2)$ 

From the relationship between observed haplotype frequency and LD in Table 3, we have

$$E[ab] - E[a]E[b] = (x_{11} - p_1q_1) - (x_{21} - p_2q_1) - (x_{12} - p_1q_2) + (x_{22} - p_2q_2)$$
  
= D - (-D) - (-D) + D  
= 4D

which is the relationship between covaraince and LD.

Next, we consider genotype correlation. Let  $S_1$  and  $S_2$  be random variables of SNP1 and SNP2 respectively with the values of  $S_1 \in \{-1, 0, 1\}$  and  $S_2 \in \{-1, 0, 1\}$ . The observed genotype frequency is given Table 4.

Table 4: Genotype observed frequency

	$A_1A_1$	$A_1A_2$	$A_2A_2$
$B_1B_2$	$f_{21}$	$f_{22}$	$f_{23}$
$B_2B_2$	$f_{31}$	$f_{32}$	$f_{33}$

If two genotype locus are independent, the expected frequencies are given in Table 5. Table 5: Genotype expected frequency

	$A_1A_1$	$A_1A_2$	$\overline{A_2A_2}$
$B_1B_1$	$p_1^2 q_1^2$	$2p_1q_1^2$	$p_2^2 q_2^2$
$B_1B_2$	$2p_{1}^{2}p_{1}q_{1}$	$4p_1p_2q_1q_2$	$2p_{2}^{2}q_{1}q_{2}$
$B_2B_2$	$p_1^2 q_2^2$	$2p_1p_2q_2^2$	$p_{2}^{2}q_{2}^{2}$

Since 
$$S_1, S_2 \in \{-1, 0, 1\}$$
, the covariance of two SNPs is computed by

 $E[S_1S_2] = -1 \times -1 \times f_{11} + -1 \times 1 \times f_{13} + 1 \times -1 \times f_{31} + 1 \times 1 \times f_{33}$ =  $f_{11} - f_{13} - f_{31} + f_{33}$ 

and

$$E[S_1]E[S_2] = (-1 \times p_1^2 + 1 \times p_2^2)(-1 \times q_1^2 + 1 \times q_2^2)$$
  
=  $p_1^2q_1^2 - p_2^2q_1^2 - p_1^2q_2^2 + p_2^2q_2^2$ 

and, hence

$$E[S_1S_2] - E[S_1]E[S_2] = f_{11} - f_{13} - f_{31} + f_{33} - (p_1^2q_1^2 - p_2^2q_1^2 - p_1^2q_2^2 + p_2^2q_2^2)$$
  
=  $(f_{11} - p_1^2q_1^2) - (f_{13} - p_2^2q_1^2) - (f_{31} - p_1^2q_2^2) + (f_{33} - p_2^2q_2^2)$ 

Again, using the relationship in Table 3, we have

$$E[S_1S_2] - E[S_1]E[S_2] =$$

$$(f_{11} - (x_{11} - D)^2) - (f_{13} - (x_{12} + D)^2) - (f_{31} - (x_{21} + D)^2) + (f_{33} - (x_{22} - D)^2)$$

In conclusion, we have shown that the relationship between LD and correlation between haplotype of two locus is given by

$$Cov[ab] = 4D$$

Moreover, there is a relationship between covariance of two SNPs with  $\{-1, 0, 1\}$  representation and LD as shown in the following equation.

 $Cov[S_1S_2] = (f_{11} - (x_{11} - D)^2) - (f_{13} - (x_{12} + D)^2) - (f_{31} - (x_{21} + D)^2) + (f_{33} - (x_{22} - D)^2)$