

i.e. p/p 1-5.

Dear Fisher

The enclosed may interest you. If it is correct, mutation pressure is even more important than you thought. I have criminally mislaid your letter about linkage values, but think the following is right:-

If the linkage values are p, q, in the 2 sexes, and we have the following from back-cross & F<sub>2</sub> data:-

Statistic	Optimal value.	Amount of information
p	p <sub>0</sub>	I <sub>p</sub>
q	q <sub>0</sub>	I <sub>q</sub>
pq	r	I <sub>r</sub>
(1-p)(1-q)	c	I <sub>c</sub>

Then the logarithm of the likelihood,

$$L(p, q) = \text{const} - \frac{1}{2} I_p (p - p_0)^2 - \frac{1}{2} I_q (q - q_0)^2 - \frac{1}{2} I_r (pq - r)^2 - \frac{1}{2} I_c [(1-p)(1-q) - c]^2$$

$$\therefore -\frac{\partial L}{\partial p} = I_p (p - p_0) + I_r q (pq - r) - I_c (1 - q) [(1-p)(1-q) - c] = 0$$

$$-\frac{\partial L}{\partial q} = I_q (q - q_0) + I_r p (pq - r) - I_c (1 - p) [(1-p)(1-q) - c] = 0$$

So if p<sub>n</sub> be an estimate of p, q<sub>n</sub> of q, a better one is:-

$$p_{n+1} = \frac{p_n + \frac{I_r r}{I_p} q_n + \frac{I_c}{I_p} (1 - q_n)^2 - \frac{I_c c}{I_p} (1 - q_n)}{1 + \frac{I_r}{I_p} q_n^2 + \frac{I_c}{I_p} (1 - q_n)^2}, \text{ and similarly for } q_{n+1}$$

Hence starting with  $p_0, q_0$ , we iterate till they come steady, or we may use a judicious fake for  $p_1, q_1$ .

If I am wrong, I shall be very glad if you will let me know. I have not worked out the correlation of  $p$  &  $q$ .

I have also got a paper on inverse probability in the Proc Camb. Phil. Soc. to which I expect will rouse you in defence of Likelihood. This should be in the next number. If it contains a fallacy it is, I think, a new one. Wishart does not remember seeing it before.

I have also got a maximum likelihood solution of Hogben's problem in the current Journal of Genetics. This is now in Punnett's hands. In Hogben's terminology it is as follows:—

If there form a group of families, each containing at least one abnormal, and derived from normal parents, consists of  $n_s$  families of size  $s$  ( $0 < s < C+1$ ), and contains  $R$  recessives in all, then the most likely value of  $q$  (the proportion of normals in a family) is the real + root other than unity of:—

$$\frac{R}{1-q} = \sum_{s=1}^C \frac{s \cdot n_s}{1-q^s} \dots (1),$$

and the amount of information about  $q$  is

$$I_q = \sum \frac{s^2 q^{s-2} n_s}{(1-q^s)^2} - \frac{R}{q(1-q)^2} \dots (2)$$

the root of equation (1) being substituted. I hope this is O.K.

y

If not I can withdraw my paper, and you may  
proclaim the glorious verity.

Will you please return the evolutionary paper, which  
as you can see, is only a rough draft.