Dear Fisher,

The enclosed may interest you. If it is correct, mutation pressure is even more important than you thought. I have crumingly 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 $F_2$ data:

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Optimal value</th>
<th>Sum of information</th>
</tr>
</thead>
<tbody>
<tr>
<td>$p$</td>
<td>$p_0$</td>
<td>$I_p$</td>
</tr>
<tr>
<td>$q$</td>
<td>$q_0$</td>
<td>$I_q$</td>
</tr>
<tr>
<td>$pq$</td>
<td>$r$</td>
<td>$I_n$</td>
</tr>
<tr>
<td>$(1-p)(1-q)$</td>
<td>$c$</td>
<td>$I_c$</td>
</tr>
</tbody>
</table>

Then the logarithm of the likelihood,

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

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

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

So if $p_n$ be an estimate of $p$, $q_n$ of $q$, a better one is:

$$p_{n+1} = p_n + \frac{I_q (q_n - q_0)}{I_p} + \frac{I_c (1-q_n)}{I_p} (1-q_n) - \frac{I_c C}{I_p} (1-q_n), \quad \text{and only for} \quad q_{n+1}$$

$$1 + \frac{I_n (q_n - q_0)}{I_p} + \frac{I_c (1-q_n)}{I_p} (1-q_n)$$
Hence starting with $p_1, q_1$, we try to tell the same story, 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 $p$ and $q$.

I have also got a paper on inverse probability in the Proc Camb. Phil. Soc. to which I expect will raise you in defence of Likelihood. This should be in the next number. If it contains a fallacy it is, I think, a new one. Wiener 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 Emmett's hands. In Hogben's terminology it is as follows:

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

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

and the amount of information about $q$ is

$$\Gamma_q = \sum \frac{s^2 \cdot q^{s-2} \cdot n_s}{(1-q^s)^2} - \frac{R}{q(1-q)^2} \quad (2)$$

the root of equation (1) being substituted. I hope this is OK.
If not, I can withdraw my paper, and you may proceed the glorious venture.

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