

Dear Fisher

Bernstein- ~~gives~~ some data in his paper. As he was hunting for linkage rather than estimating it, his method is all right. He would doubtless send you a copy if asked.

I think at the next meeting of the human genetics committee there will be a fight about investigating ^{marriage} consins as such. If p^2 be the probability of getting a recessive genotype in a random mating population, it is raised to $\frac{p(1+15p)}{16}$, or $p^2 + \frac{1}{16}p(1-p)$ in

the offspring of first-cousin marriages. Hence you won't notice much if $p^2 > \frac{1}{209}$, when the frequency is doubled. Now, on the offspring of, say 1000 ^(cousin) marriages, will you probably spot anything unless $p^2 > \frac{1}{4000}$,

say. Do you consider it likely that there are many genes - recessive genes with clearcut effects where p lies between $\frac{1}{14}$ and $\frac{1}{60}$? If not the research is not worth undertaking.

Our marriage law is rather inconsistent from the eugenic angle. Thus for offspring of step-uncle x step-niece we have $\frac{1}{16}p(1+15p)$, for that of double first cousins $\frac{1}{8}p(1+4p)$; but the former is illegal, the latter not.

Yrs sincerely
JBSH.