is determined not only by his type of sexual activity and frequency of partner acquisition, but also by the probability of his selecting a seropositive partner (5), which is measured by the weighted seroprevalence of HIV in the community. Hence, we have demonstrated (by an empirical analysis) that an individual's choice of sex partner can be an important risk factor for HIV infection (5). These findings illustrate that, because sexual network data are rarely collected, a high-risk individual may be misclassified as a low-risk individual. Our statistical analyses have also revealed that individuals who have a high rate of partner acquisition also have periods of time in which the rate is low (6). Our results concerning sexual networks (which determine the probability of selecting a seropositive partner) and temporal variability suggest that it might often be impossible to identify all of the high-risk individuals. Furthermore, we have also shown that (even when a risk group is identified) the membership of the risk group is not stable over time (7). The problems of risk group identification and risk group instability mean that, in practice, a targeted vaccine program could be extremely ineffective.

Rida *et al.* also suggest that our parameter estimates are based on little or no data. We disagree. Our analysis was specifically designed to investigate the potential effects of prophylactic vaccines in San Francisco. Consequently [as described in our report (*1*)], we obtained analytical results and parameter estimates from data from the San Francisco Young Mens Health Study (SFYMHS), a large, multistage probability sample of gay men conducted in 1993 in San Francisco (*8*). The sampling design of the SFYMHS provides a population-based estimate of HIV infection and sexual behaviors; consequently we believe that our parameter estimates are reliable and have external validity.

We do not believe that we have used our model to paint a bleak picture for HIV vaccines. We would like to stress that (as we pointed out) it is possible to eradicate HIV without any vaccine if the current levels of risk behavior can be reduced to certain (specified) levels. Mathematical models have great utility as epidemiological tools for evaluating the potential effects of HIV vaccines. We believe that models should be used to explore the possible outcomes before the real world is used as an experimental system.

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Corrections and Clarifications

In Claire O'Brien's News & Comment article "Priority initiatives squeeze science" (10 Feb., p. 782), David Porteous was incorrectly described as head of the Medical Research Council's (MRC's) Human Genetics Unit. He is head of the Molecular Genetics Section of the MRC's Human Genetics Unit.