Local responses to local epidemics for national impact need advanced spatially explicit tools

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See related paper on page 1467

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Effective programmatic responses to HIV epidemics require targeting the right people, in the right places, at the right time, in the right ways. We now have proven intervention strategies to prevent HIV acquisition for both concentrated and generalized epidemics. One limitation in achieving effectively targeted interventions is that average national HIV prevalence masks subnational variations. Although most tools currently used to estimate incidence and prevalence do not adequately capture this heterogeneity, new sources of geographical program data are becoming available to supplement traditional surveillance data, including population-based surveys, sentinel surveillance, and case reporting data. This makes it increasingly possible to account for epidemiological heterogeneity when producing HIV epidemic estimates. As it is time-consuming and expensive to collect detailed spatial data, it is important to get maximum benefit from available data.

The Subnational Estimates Working Group of the HIV Modelling Consortium offers an assessment of geospatial methods for producing and visualizing spatially precise estimates of HIV prevalence [1]. They used statistical validation approaches to compare the leading approaches and found that all methods produced broadly similar results. Of these, the 'Bayesian geostatistical' approach was found to have the best statistical performance and provided useful uncertainty estimates, at a cost of having the greatest complexity to implement [1]. This assessment suggests that the Bayesian geostatistical approach should be generalized for different settings, with different data types and data availability, and integrated with programmatic data routinely to allow efficient and finely tuned spatial estimates. Most importantly, any of these methods should be applied to better inform the targeting of current responses. The Bayesian geostatistical method should be applied where additional geographical data can supplement standard epidemiological data, and there is evidence of sufficient heterogeneity in the epidemic that large potential benefits could be realized by even small improvements in estimation accuracy. When these conditions do not hold, given the significantly increased data and methodological requirements of this method compared to kernel density estimation and only a modest advantage in accuracy, the simpler method may be preferable.

The methods considered by Anderson, Hallett, and others are suited to the generalized epidemic settings of southern Africa where detailed spatial information is most needed. But for concentrated epidemics, further consideration is needed, particularly as reliable surveillance data for key population groups can be notoriously difficult to obtain. Because these groups are likely to be more spatially concentrated in larger cities, the use of interpolation techniques that assume a more homogenous spread across subnational administrative units may not be finely grained enough. Furthermore, epidemics can have both concentrated and generalized transmission, often in the same area, as in much of West Africa. These epidemics can also be geographically mixed, with concentrated epidemics occurring in some areas and generalized epidemics occurring in others, as in Indonesia. There is much more work to be done to produce reliable estimates

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of HIV prevalence and incidence at local levels in such settings. However, available data readily reveal broad geographical epidemiological characteristics in concentrated and mixed settings, for example, more than 70% of India's HIV/AIDS burden among its 29 states is concentrated in four southern states (Andhra Pradesh, Karnataka, Maharashtra, and Tamil Nadu) and four north-eastern states (Bihar, Gujarat, Uttar Pradesh, and West Bengal) [2]; 69% of Pakistan's epidemic among people who inject drugs is in four cities (Faisalabad, Hyderabad, Karachi, and Lahore) that account for 19% of the total population [3]; 70% of new infections in Thailand come from 33 out of 76 provinces [4]; whereas in Kenya, nine counties with the highest burden account for 54% of new infections but only 24% of the Kenyan population [5]. Resource allocation tools [such as Goals, Optima, and the AIDS Epidemic Model] have clearly shown that there has generally been considerable mistargeting of resources in concentrated settings, namely a need to shift more resources toward ART and proven prevention programs for key populations [6]. If these approaches can be applied in the broad administrative regions of known greater burden, then considerable impact will likely be achieved [7,8] before needing to assess more finely grained spatial burden. However, in a generalized setting it is essential to make use of detailed geographical data for a more targeted programmatic response.

To identify and target the right people in the right places, mapping methods such as those assessed in the study can provide a more detailed picture of the HIV burden down to the local level. However, it is important to keep in mind that the inputs to such models are historical estimates of HIV burden. As such, these methods may help to show the geographical variation in HIV prevalence but are not especially effective for identifying areas of rapidly increasing HIV burden. The primary data source used by the reviewed geospatial methods is the Demographic and Health Survey, conducted around every 5–10 years. Strung together over time, this can be useful for gauging broad historical changes in the epidemic, but programmatic responses would benefit from more temporal data. As the authors suggest, further model development, particularly in the use of ancillary data, would be useful to help national decision makers plan more locally targeted responses to local epidemics for greater epidemiological impact.

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Conflicts of interest

There are no conflicts of interest.

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