method employs a combination of Principal Component Analysis (to reduce the dimensionality of the space of output statistics), Latin Hypercube Sampling and sequential Approximate Bayesian Computation (to explore the parameter space in a time-efficient manner) and multivariate emulation (to interpolate output statistics for regions of the parameter space that have not been sampled explicitly).

A9 HIV subtype diversity across geography and transmission groups in Maryland

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The distribution of HIV subtypes within a local epidemic can provide insight into social dynamics underlying transmission patterns and inform treatment and prevention strategies. Subtype B predominates in most US regions, but non-B infections are increasingly evident in Maryland and large-scale examinations of subtype diversity are lacking. In 2014, Maryland HIV case surveillance began systematically collecting HIV genotypic sequence data to identify outbreaks and transmission patterns. We used sequences collected through 2015 to examine geographic and transmission group distribution associated with different HIV subtypes. HIV-1 pol sequences were aligned with Los Alamos HIV Database subtype reference sequences and subtyped using HIV-TRACE at a distance cutoff optimized for accurately identifying subtype B data (5 per cent). Non-B sequences were subsequently classified using the REGA HIV-1 Subtype Tool. All sequence subtypes were matched to data within the HIV case surveillance database for descriptive analysis. HIV sequences were available from 7,045 individuals between 2004 and 2015, ~20 per cent of all persons living with HIV in 2015. Subtype B accounted for 95.7 per cent of all sequences overall and 90.2 per cent of those from persons diagnosed in 2014. The most common non-B subtypes were subtype G, C, A, and D, and a variety of circulating recombinant forms. The proportion of non-B sub-types increased from 0 to 2 per cent of new annual diagnoses prior to 2000 to 7 to 9 per cent after 2010, particularly in the Central and Suburban regions. The highest frequency of non-B (4.3–25.5 per cent) was seen in five counties across the state. In contrast, <1 per cent of sequences from Baltimore City were non-B. Those with subtype B were 27.6 per cent heterosexual, 27.6 per cent people who inject drugs, and 25.2 per cent men who have sex with men (MSM). Non-B subtypes were primarily heterosexual (60.6 per cent), with increasing proportion among MSM after 2006. The large number of non-B subtypes likely reflects immigration patterns to the DC area. Non-B HIV is increasingly moving outside of DC and has been identified in some MSM and IDU cases. Increasing HIV viral diversity, including the potential for subtype recombination, across the state of Maryland poses challenges for clinical and preventive response and suggests geographic and social dimensions of HIV transmission patterns that require further examination.

A10 Using the molecular epidemiology of HIV transmission in New South Wales to inform public health response: Assessing the representativeness of linked phylogenetic data

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New South Wales has the largest number of people living with HIV in Australia, estimated at 11,500 and is undergoing a revolution in HIV prevention with the rollout of pre-exposure prophylaxis to 4,000 high-risk individuals. The recently established statewide HIV drug resistance database contains 9,982 sequences from 2004 to 2015 and has coverage of over 80 per cent of the HIV infected population. To allow enhanced analysis of these sequences, data linkage was performed on the HIV notifications database, which contains demographic data of all newly notified infections dating back to 1981. The aim of this study was to determine the representativeness of linked sequences compared to those that were unlinked using epidemiological and phylogenetic methods. Duplicate sequences per year were excluded. Deterministic linkage was performed using two by two namecode, date of birth, sex, and postcode. Differences in demographics were assessed between linked sequences and public health data for the state, using a chi-squared test for comparison of proportions. Sequences were aligned using MUSCLE, and phylogenetic inference using RaXML. Comparison of substitution rate, diversity, skyline plots, and cluster characteristics was made between linked and unlinked sequences. Only 2,843 (28 per cent) sequences were linked to HIV notification data. With the exception of 2011, the proportion of early infections in linked data was not significantly different to unlinked data from 2010, 2012 to 2015. Other demographics data were comparable. Between 2004 and 2007 there was a difference in the proportion of identical sites (23.5 vs. 8 per cent $P < 0.02$), while pairwise identity was not significantly different. For sequence data from 2008 to 2015, there was no significant difference in the proportion of identical sites, pairwise identity, or GC content. Despite the low proportion of sequences linked to notifications data, the epidemiological characteristics were representative of the HIV infected population in New South Wales. Phylogenetic analysis showed that the linked data were sufficiently representative to proceed with further cluster analysis to investigate the impact of public health interventions in this state.

A11 The 1988 Elista outbreak and the epidemiology of HIV subtype G in Russia

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One of the first major outbreaks of HIV-1 in Russia happened in Elista in 1988. About 270 patients, mostly children, were nosocomially infected with HIV subtype G in seventeen hospitals in 1988–1989. The infection was mainly transmitted between