

Multi-state Markov model for estimating HIV incidence from HIV surveillance data in France, 2008-2018

Charlotte Castel¹, Cecile Sommen², Yann Le Strat², Ahmadou Alioum^{3,4}

¹Oslo Centre for Biostatistics and epidemiology (OCBE), Oslo University Hospital, Oslo, Norvege

²Santé publique France, Direction Appui, Traitements et Analyses de données (DATA), Saint Maurice F-94415, France

³Equipe Biostatistique, Centre Inserm U1219-Bordeaux Population Health, Université de Bordeaux, F- 33000 Bordeaux, France

⁴Université de Bordeaux, ISPED, Centre Inserm U1219-Bordeaux Population Health, F-33000 Bordeaux, France

E-mail for correspondence: c.j.y.castel@medisin.uio.no

Abstract:

Thirty-five years after the discovery of the human immunodeficiency virus, the epidemic still going in France. Assessing the dynamics of the epidemic, through the estimation of incidence is a statistical challenge to guide HIV prevention strategies.

The main objective was to develop a method for estimating the number of new HIV infections. Knowing that HIV is mainly transmitted by undiagnosed HIV-positive individuals, we also estimated the number of infected people who are unaware of their HIV-positive status. Finally, the distribution of time between infection and diagnosis is estimated.

We used a non-homogeneous multi-state Markov model describing the progression of the HIV disease. We proposed a penalized likelihood approach to estimate the HIV incidence curve as well as the diagnosis rates. The HIV incidence curve was approximated using cubic M-splines and an approximation of the cross-validation criterion was used to estimate the smoothing parameter.

The method is first illustrated from a thorough simulation study, then applied to the HIV mandatory notification data. From the simulation study, theoretical value is comprise between the confidence limits of the estimated value for 9 years among 11 for the HIV incidence and all over for the HIV diagnosis for the period 2008-2018. From the HIV mandatory notification data, the obtained estimates are consistent with previous estimates using other approaches.

Our model is a new tool for estimating the HIV incidence giving more precise estimates that previous methods. The non-homogeneity of the Markov model allows to introduce changes in testing behavior over time which is not the case for other methods used currently in France.

HIV, incidence, multi-states Markov model, penalized likelihood, notification data