Supplement S1 Seropositivity thresholds from mixture models

Standard methodologies for seropositivity were usually based on control groups, from which a threshold for seropositivity was obtained by adding three standard deviations to their mean antibody titre (Dye *et al.*, 1993). Nevertheless, this method was prone to be biased and misclassify seropositive and seronegative individuals because it is not robust to small changes in antibody titres that can emerge from seasonality and/or small variations in laboratory assay performance (Bretscher *et al.*, 2013). To overcome the likelihood of misclassification, a novel method based on a finite mixture model has been proposed to determine a more sensitive threshold for seropositivity based on the distribution of titres, measured via optical density in a spectrophotometer, in a population exposed to a pathogen (Bretscher *et al.*, 2013; Stewart *et al.*, 2009). Basically, the finite mixture model assumes the statistical distribution ($f(x)$) of antibody titres, or optical densities, (x) in an exposed population to be a mixture of the distribution of titres from positive ($P(x)$) and negative individuals ($N(x)$) according to the following equation (Bretscher *et al.*, 2013; Stewart *et al.*, 2009):

$$f(x) = \pi(P(x)) + (1-\pi)(N(x)) \tag{S1.1}$$

Where π is the proportion of titres belonging to each category. Maximum likelihood estimates for the means and standard deviations of P and N distributions can be estimated and a threshold for seronegativity can be estimated as the mean of the distribution with the smallest mean (i.e., that of the negative individuals) plus three standard deviations (Stewart *et al.*, 2009). Parameters for the finite mixture model were estimated with the command normalmixEM() of the library mixtools in the statistical package R version 3.0.1.

References

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