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Estimating historic disease trends from cross-sectional data using combined diagnostic tests

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Purpose: We show how to estimate the historic trend of incidence in a population from cross-sectional diagnostic test data collected at a single point in time. We combine two or more quantitative diagnostic tests operating at different time scales, and their test kinetics to estimate the time since infection for the individual, and the historic incidence trend in the population as a whole.
Methods: We used simulated data based on either the UK 2007 bluetongue epidemic, or a situation similar to endemic bovine TB as in the UK. Data were analysed in a Bayesian MCMC framework and inference compared to the simulation parameters.
Results: For bluetongue we found that using a cross-sectional sample of 20 positive animals taken 14 days after the start of the epidemic, tested for viral load and antibody levels, we were able to reconstruct the trajectory of the outbreak up until that point (R^2 of 0.85 compared to the true trend). Further, for bovine TB, a sample of 100 positive animals tested for bacterial load and antibody response would be enough to determine whether the incidence trend up until sampling had been steady, increaseing, or decreasing, with estimated slopes to within 10% of the true values.
Conclusion: We have developed a Bayesian approach that can estimate the historic trend of incidence from cross-sectional samples, without relying on ongoing surveillance. This could be used in endemic settings to evaluate changing disease trends; or in epidemic settings to inform outbreak response.
Relevance: The described approach is generic, applicable to a wide range of human, livestock and wildlife diseases. It can estimate trends in settings for which this is not possible using current methods, including for diseases or regions lacking in surveillance, to recover the pattern of spread during the initial “silent” phase once an outbreak is detected, and for emerging infections. Being able to estimate the past trend of disease from single cross-sectional studies has far-reaching consequences for the design and practice of disease surveillance in all contexts.