ESTIMATING THE RISK OF SECONDARY TRANSMISSION OF VCJD: A HIDDEN MARKOV MODEL APPROACH

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The cause of the epidemic of variant Creutzfeldt-Jakob Disease (vCJD) is widely believed to be transmission of the aetiological agent for Bovine Spongiform Encephalopathy (BSE) from bovines to humans. Epidemiological models were developed to assess the risk of vCJD to human health, and fitted to epidemiological data using back-calculation and simulation-based methods. Predictions from these models now suggest that large primary epidemics are unlikely in the UK and in France, the countries most exposed to BSE.

However, recent findings suggest a secondary vCJD epidemic is possible via human-to-human vCJD transmission via infected blood in transfusions and surgical procedures. In this study, we assess the risk to human health from inter-human vCJD infection. We develop a Hidden Markov Model to predict the epidemic size by fitting it to epidemiological data using maximum likelihood and Bayesian methods (MCMC).

Only focusing on inter-human transmissions related to blood transfusions, our results suggest large scale epidemics are unlikely in France or the UK as the estimated number of individuals who may potentially contaminate other humans is low.

Besides these epidemiological results, the method developed here appears as an efficient tool for assessing the risk linked to rare diseases and/or to diseases whose biology is poorly understood. Thus, that approach could be fruitfully generalised and used to assess the timely issue of the risk of epidemics related to emerging diseases.