The majority of emerging infectious diseases are zoonoses. Given that the line list is available on Dryad, we estimated the contribution of spillover to secondary transmission of influenza using a statistical framework. We found that the spillover hazard was persistent in all datasets, although the posterior distributions had higher uncertainty. The estimated value of $R_0$ was close to 1 in the three largest outbreaks reported for influenza, although the posterior distributions had higher uncertainty. In all three datasets, the estimate of $R_0$ was below 1, and the credible interval for the estimation of $R_0$ was very wide. The statistical framework we present has substantial potential value for public health. First, the approach can be applied to any outbreak of a spillover infection similar to influenza A, and gives a useful upper bound for $R_0$. The framework could be improved by considering time series with a mean of 33 observed cases (the average number of observed cases with serial interval of 3 days rather than 9.6 days). Overall, for these three outbreaks, we estimated that 13% (1%–32%) of human-to-human cases may have been confirmed if additional data on each case’s location was available. As was the case with full reporting, the $R_0$ estimates were improved when more information about the hazard was included in the model. Yu H, Cowling BJ, Feng L, Lau EH, Liao Q, Tsang TK, Peng Z, Wu P, Liu F, Fang VJ, Zhang H, Li M, Heesterbeek JA. A brief history of $R_0$ and a recipe for its calculation. Acta Biotheor. 2002;50(3):189–204.