

Estimating the basic reproduction number from arrival time data

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Background:

The basic reproduction number R_0 is interpreted as the average number of secondary cases generated by a single primary case. It has been used to predict the cumulative incidence and to calculate the required vaccination coverage, playing important roles in epidemiological modeling and public health interventions. This study aimed to develop a new method to estimate R_0 from the arrival time of an emerging infectious disease.

Method:

A metapopulation model was constructed by connecting multiple populations with migration rate of host. For an exposition, we investigated the early epidemiological datasets of influenza A(H1N1) in 2009, analyzing the dataset governing the time of first importation of an infected individual in each country from North America.

Result:

During the initial growth phase, the linearized system gives the geometrically distributed probability of arrival that contains R_0 as one of parameters. We show that a rapid importation mirrors large R_0 .

Conclusion:

R_0 of a single population at the source is estimated from the arrival time. The proposed method is applicable to a broad range of emerging infectious diseases.

*Mini-Symposium: Modelling migration and associated importation events of infectious diseases