# Modelling SEIR infectious disease with time delay using deterministic cellular automata

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Epidemiology being a cornerstone of the public health, deals with the incidence and pervasiveness of diseases in large populations. An uncontrolled epidemic can be disastrous and can lead to pandemic circumstances. Moreover, the delay of an infectious disease is crucial when aiming to predict its potential and spreading patterns [1]. In this work the advancement of SEIR (susceptible - exposed - infected - recovered) epidemic spread with time delay is analyzed through a two-dimensional cellular automata model [2]. The time delay corresponding to the infectious span, primarily, includes death during the exposed period in due course of infection. The progress of whole system is described by SEIR transition function complemented with significant factors including inhomogeneous population distribution, birth and disease independent death rates. Further, to reflect more realistic population dynamics some stochastic parameters like population mobility and connections at spatial level are also considered.

Two key behavioral patterns of disease dynamics is found based on delay patterns: changes in delay effect over time and changes of performance across delays, at any time. The critical value of delay, afar which there is notable variations in spread patterns, is computed. We reveal the role of the basic reproduction number and its association with some spatial characteristics of the model. The overall scenario makes instinctive biological perception that if the exposure period is too long to transfer to the infectious, then the infectious population will experience low survival and, as a result, the infection eventually dies out in future generations, exemplifying the positive role of time delay to control disease progression in an infected host.

## References

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