Discrete Distributed-SEIR Epidemic Models Outperform Continuous Counterparts in Fitting Ebola Data

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An important extension of SEIR epidemiological models is the so-called Erlang distributed delay model [1-3]. Here we develop a general discrete-time analogue of the continuous-time Erlang model, taking the novel approach of identifying diseases subclasses that represent *the number of days individuals have left before they transfer from the current disease class to the next in the chain* (i.e. E to I and I to R). This permits the exponential, Erlang, and Uniform distributed-delay models, among others, to be directly implemented as special cases. Beyond comparing our discrete time Erlang formulation to corresponding continuous time Erlang formulations in fitting models to data from the recent Ebola outbreak in West Africa, we compare simulation output among the discrete Erlang, Exponential and Uniform cases and demonstrate that our discrete Erlang formulation produces the best fitting models.

References

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