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# Modelling, data analysis and model evaluation of symptomatic and asymptomatic dengue infection

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ABSTRACT

BACKGROUND: With relatively simple epidemiological models of susceptible-infected-recovered SIR-type including reinfection, one can investigate the interplay between notified severe disease and asymptomatic infection and its role in disease pattern.

OBJECTIVES: The objective of this study is to test such models on its performance on some of the best currently available time series data.

METHOD: In this same modelling framework further effects of multi-strain interaction for primary versus secondary infection up to multi-compartmental four-strain models are investigated, leading in wide parameter regions to complex dynamics, including deterministic chaos as skeleton of the stochastic system, which easily can describe all observed qualitative features of the present dengue data. In such cases new parameter estimation techniques suitable for only short time predictability have to be used. The statistical tools have to go beyond classical methods implemented in statistical software packages.

RESULTS: These models of increasing complexity can now be evaluated on empirical data, due to recent advances in the analysis of epidemiological stochastic processes (Fokker-Planck description, semiclassical approximation, also called WKB or eikonal approximations, etc.), leading to computational likelihood functions and their Bayesian description, including Bayes factor for model comparison.

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CONCLUSIONS: A testable set of models with increasing complexity in dynamic behaviour is presented and statistical tools for the evaluation on empirical data, present and future, are given. Extension to spatially explicit stochastic systems are shown.

KEYWORDS: Dengue fever modeling, Parameter estimation and evaluation, symptomatic versus asymptomatic infection as accidental pathogenicity

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