Malaria transmission dynamics: A formal comparison of rival hypotheses

Anindya Bhadra

Abstract

Malaria is a major cause of death in developing countries and a lot of attention has been focused in recent years to the statistical modeling of the disease dynamics - still a major challenge for complicated vector-borne diseases. A model that is scientifically plausible tends to be too complicated and poses significant identifiability issues to the statistical fit. As such, most analyses so far have been restricted to relatively simpler and non-mechanistic models that are hard to interpret scientifically. In this talk, we describe a novel mechanistic coupled stochastic differential equation model of malaria transmission driven by Lévy noise, which is complex enough to capture the essential dynamics while maintaining the feasibility of data analysis. Our results, a comparison study of several nested statistical models fitted by the maximum-likelihood method, provide a systematic framework for the model selection and prediction problems. Our use of the iterated filtering technique allows us to fit and compare more complicated models that have been intractable so far.

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