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Bayesian inference and model selection for stochastic epidemics and other coupled hidden Markov models (with special attention to epidemics of Escherichia coli O157:H7 in cattle)

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Tuesday, 3rd May, **2 p.m.**
D202 Seminar room, School of Engineering, 2nd Floor

Abstract: Model fitting for epidemics is challenging because not all of the information needed to write down the likelihood function is observable, for example the times of infection and recovery are not usually observed. Furthermore, the data that are available from diagnostic tests may not be perfectly accurate. To make things even more difficult, most of the interesting epidemiological questions are best expressed as model selection problems and so fitting just one model is not sufficient to answer them. Instead we must fit a range of different models, each representing an important epidemiological hypothesis, and then make meaningful comparisons between them.

I will describe how to overcome (most of) these difficulties by rewriting the epidemic model as one or more hidden Markov models. These approaches will be illustrated with an application to Escherichia coli O157:H7 in cattle. Joint work with Panayiota Touloupou, Bärbel Finkenstädt Rand, Pete Neal and TJ McKinley.

More info: http://www2.warwick.ac.uk/fac/sci/wcpm/seminars

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