Bayesian spatial modeling for prospective ID surveillance: with application to Seasonal influenza

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Venue | Natural science building B117, Hanyang university

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Abstract

Bayesian modeling of infectious disease behavior can be carried out at a variety of scales. Commonly, for human disease, aggregation leads to counts of infectives available in small areas over time periods. While it is possible to trace network contacts for infections from serology, it is often the case that only crude counts of infectives over time periods are available. In that case, modeling of the dynamic of the disease must rely on count models. SIR or SEIR models are often assumed for this and dependence on previous counts or counts in neighborhoods is often assumed.

In prospective surveillance the focus is on prediction of future events so that detection of change is carried out as early as possible. To this end it is possible to specify a Bayesian space-time (ST) model in a variety of ways to allow for detection of changes.

In this talk there are two foci: First, I will address the issue of endemic and epidemic model components and whether single component model are better in prospective surveillance. This will be addressed by examining the role of posterior functional measures SCPO and SKL in early detection of risk changes when different models are assumed. Second I will examine the use of different computational platforms (McMC versus SeqMC) which could be employed when sequential estimation is required in prospective surveillance scenarios. I will use an example from South Carolina where county level 2004-2005 flu season data is available. This consists of counts of C+ laboratory notifications for flu for counties within the state.

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