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CRiSM Seminar
Wednesday, November 2
1pm – MB0.07

Joining Bayesian submodels with Markov melding

Integrating multiple sources of data into a joint analysis provides more precise estimates and reduces the risk of biases introduced by using only partial data. However, it can be difficult to conduct a joint analysis in practice. Instead each data source is often modelled separately, but this results in uncertainty not being fully propagated.

We propose to address this problem using a simple, general method, which requires only small changes to existing models and software. We first form a joint Bayesian model based upon the original submodels using a generic approach we call "Markov melding". We show that this model can be fitted in submodel-specific stages, rather than as a single, monolithic model. We also show the concept can be extended to "chains of submodels", in which submodels relate to neighbouring submodels via common quantities.

We illustrate the approach using examples from an A/H1N1 influenza severity evidence synthesis; integrated population models in ecology; and modelling uncertain-time-to-event data in hospital intensive care units.

Time permitting, I may also discuss ideas relating to Bayesian "cut distributions", a completely different notion of modular Bayesian modelling.