Bayesian evidence synthesis for surrogate endpoints in precision medicine
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Precision medicine research identifies subgroups of the population, for example defined by genetic biomarkers in oncology, to which targeted therapies can be delivered successfully, reducing time and cost of drug development process. Use of surrogate endpoints, which require shorter follow-up time to measure the treatment effectiveness compared to a final clinical outcome, can further expedite decisions about licensing and reimbursement of new therapies ensuring their timely delivery to patients. Such decisions can be made based on prediction of the treatment effect on the final (often long term) clinical outcome from a short term surrogate endpoint. Therefore, knowledge of appropriate surrogate endpoints is crucial to deliver targeted therapies to patients early. There are, however, challenges in identifying reliable surrogate endpoints which may be due to complexity of the relevant data structure. Bayesian multivariate meta-analysis methods, developed by the supervisors, provide flexible approach to modelling correlated outcomes including surrogate endpoints.

The aim of this project is to build on the models developed in our papers (Statistics in Medicine 2013; 32:3926-3943, 2016; 35:1063–1089.) to model complex association patterns between surrogate and final outcome. The PhD student will develop Bayesian hierarchical meta-analytic methods to model the relationship between the correlated endpoints tailored to specific data structures, including information on the biomarker, in different clinical settings in cancer. The project will also explore modelling of different sources of evidence (from both randomised and observational studies) by the use of appropriate Bayesian techniques.