An ensemble-based design of experiments to reduce uncertainty in dynamic systems

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Model-based discovery in biology is an iterative process that integrates wet-lab experiments, *in silico* analysis, optimisation, and design of experiments. Most modelling studies in the literature involve the creation of an accurate model of the system, defined by a set of equations and parameter values that describe important or interesting behaviour of the system. There are many challenges in performing the iterative model-based discovery. The bottlenecking step is typically encountered during the estimation of unknown kinetic parameters from experimental data. Indeed, the estimation of kinetic parameters by fitting model simulations to biological data is usually ill-posed: there often does not exist a single (best-fit) solution to the data fitting problem, but rather one can find an ensemble of parameters that can fit the data equally well. The parameter estimation issue describes only one type of uncertainty in the mathematical modelling of biological systems, while there are other factors that contribute to model uncertainty, including structure uncertainty. In practical applications, it is often desired and necessary to reduce model uncertainty by performing additional experiments and gathering new data. I will present an ensemble-based strategy that (1) infers the ensemble from existing data; and (2) determines the optimal experiment to perform next in order to reduce the uncertainty by employing the ensemble as *a priori* information.