

Design and reverse engineering of natural and synthetic biological systems

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This decade has seen an explosion in the use of engineering approaches to build synthetic biological systems. However, as the complexity and the demand on such systems increase, the need for new theoretical understanding and modelling methods is becoming more pronounced. While DNA synthesis methods have progressed rapidly our ability to design systems has lagged behind and indeed it has been noted that the complexity of the systems constructed in the last decade has reached a plateau. Synthetic biology increasingly relies on mathematical modelling to understand and predict the behaviour of potential designs. Often when systems are implemented, their behaviour is not how the modelling indicated. Thus our inability to fully understand models at the systems level has undoubtedly hindered progress. Faced with this considerable uncertainty on the the underlying biochemical processes the rational design of systems, that may also be stochastic in nature, is a major challenge. In this talk I will discuss methods for the reverse engineering of biological systems with an emphasis on the use of statistical methods including Approximate Bayesian Computation (ABC). I will then introduce a new design framework for synthetic biology that exploits the advantages of Bayesian model selection and argue that the difference between inference and design is that in the former we try to reconstruct the system that has given rise to the data that we observe, while in the latter, we seek to construct the system that produces the data that we would *like* to observe.