Mathematical Virology in the Fight against Viral Infection

The Covid-19 pandemic has highlighted the need for novel antiviral strategies that also provide protection against newly emerging strain variants. Insights into the geometric principles underpinning viral geometry provide a key to uncovering the mechanisms by which viruses replicate and infect their hosts, and thus pave the way for the discovery of novel antiviral solutions. In this talk, I will demonstrate how an interdisciplinary approach, combining mathematical insights into virus architecture with stochastic simulations and experiment, has enabled the discovery of genome-encoded virus assembly instructions in many viral families, including major viral pathogens such as coronaviruses. These multiply dispersed sequence/structure motifs in the viral genome act collectively in regulating both its efficient encapsidation in the arms race against host defence mechanisms, and its timely release at the required time during the viral life cycle. The high degree of conservation of the motifs amongst strain variants makes them promising antiviral drug targets that protect against emerging strain variants. This assembly and genome packaging mechanism also explains the outcome of directed evolution experiments with a bacterial system that has been engineered to package its own messenger RNA as a platform for applications in virus nanotechnology. These results shed new light on the early stages of viral evolution and inform the design of protein nanocontainers for a host of applications, including vaccine design and gene therapy.