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Within-host evolution of viruses and epidemiological implications

Within-host adaptation and evolution of viruses during chronic infections is a common phenomenon: consider, for instance, the appearance of drug resistant HIV in a treated patient. In this talk I will describe mathematical techniques for analyzing viral evolution and show, in some simple cases, how insights from these models can be applied to understand changes in viral strain at the population level.

This is joint work with Jennifer Hubbarde, Colleen Ball and Michael Gilchrist.