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Strain dynamics and influenza drift

One of the most exciting current areas in infectious disease modelling is in bringing together the epidemic and evolutionary dynamics. Influenza drift is perhaps the most striking example of where the two processes must be considered together: epidemics give rise to new strains, which in turn permit new epidemics.

We will begin with a general introduction to models of multiple strains, and some of their challenges, both technical and in terms of capturing observed biological phenomena. In most population-based models of strain dynamics, the number of variables grows exponentially with the number of strains. We present two items of our recent work, each of which avoids this problem in one way or another:

1) The impact of evolutionary constraints on influenza drift: standard drift models assume influenza is free to mutate to escape host immunity. In practice, there may be some functional cost associated with these mutations, and this can be incorporated into a mathematical model. In contrast to unconstrained drift models, this system is bistable, exhibiting both drift-like patterns and single strain dynamics for the same parameter values. This raises some important questions for vaccination strategies.

2) Age-structure and immune history: although relatively simple assumptions about the acquisition of immunity capture well the general dynamics of influenza drift, recent outbreaks have highlighted the importance of considering the details of precisely how immunity is acquired by an individual over their lifetime. In particular, strains that infect us when we are young may be disproportionately important (e.g. through original antigenic sin), and the immune response may be weakened in the elderly.