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# MODELLING THE EVOLUTION OF SEASONAL INFLUENZA

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The human seasonal influenza virus is a major cause of morbidity, with an estimated 5 million cases of severe illness and 500,000 deaths worldwide. There are currently four influenza subtypes co-circulating around the world: the A/H1N1, A/H3N2, B/Victoria and B/Yamagata. Their complex dynamics is the subject of ongoing research activity.

The global circulation of influenza coupled to its continuous antigenic evolution causes it to escape the immunity built in individuals due to previous flu infections: vaccine do exist, but their composition must be decided six months in advance of season, and therefore their efficacy is strictly linked to our capability to correctly predict the antigenic evolution of each subtype.

We introduce a seasonal transmission model for specific influenza subtypes which uses a highly detailed description of the population demography, including age distribution and age-dependent contact heterogeneities. Using an ABC Sequential Monte Carlo algorithm and data on the incidence of reported laboratory cases, we use it to estimate several parameters of the influenza dynamics for different countries, including transmission coefficients, seasonality, recovery rate and, crucially, the rate of antigenic evolution at the population level.

Here we discuss results for the specific case of the United Kingdom, using data from the last 7 influenza seasons for the different co-circulating influenza subtypes.