



Figure S1: Strain tree of influenza A (H3N2). This sample tree is constructed by maximum parsimony from coding sequence of the HA1 domain of 1971 strains occurring between 1969 and 2007 (other equiprobable trees differ only in peripheral branches). The observed HA1 sequences appear as external nodes. The horizontal coordinate D of a node is its mutational distance from the root of the tree. The trunk of the tree, i.e., the single lineage connecting past and future on time scales beyond the coalescence time, is marked by a thick line. The year of occurrence of all sequences (colored dots) is estimated from their D value for inferred sequences on internal nodes (see *Methods*). The sequences of a given year are seen to be clustered around their average D value (colored lines), which increases by about 5.6 mutations per year.