Tables

Data/Information used	Method category	Predicted outputs	References
S	P, ST	C	Bush et al. [1]
S	P	C, AA	Steinbruck and McHardy [2]
S	P, ST, R	C	Luksza and Lassig [3]
S, H	P, ST	C, AA	Steinbruck et al. [4]
S, H, PR, O (Physicochemical Properties)	P, R	C	Suzuki [5]
S	P	C	Neher et al. [6]
S,(H), PR	P, ST	C, AA	Klingen et al. [7]
E (Infection Rates)	R	O (Influenza Peaks)	Shaman and Karspeck [8]
S	O (Information Theory)	AA	Xia et al. [9]
S,H	P, ST	AA	Steinbruck and McHardy [10]
S, H, PR, O (Physicochemical Properties)	ST	AC	Du et al. [11], Liu et al. [12], Peng et al. [13], Peng et al. [14]
PR, O (Physicochemical Information)	ST	AA	Suzuki [15]
S, H	ST	AA	Cui et al. [16]
S, H	P, ST	O (Antigenic Map)	Bedford et al. [17]
S, H	ST	AA	Ren et al. [18]
S, H, PR	P, O (Graph Theory)	AA	Kratsch et al. [19]
S, H	P, ST	AA	Neher et al. [20]

Table 1: Recent computational methods predicting antigenicity-altering sites, future predominant lineages or vaccine strains for human influenza A viruses.

S: Viral Sequences; H: HI Assay Data; (H): Derivative of HI assay data (e.g. antigenic patches); PR: Protein Structure; E: Epidemiological Information; P: Phylogenetics and Population Genetics; ST: Statistical Methods; R: Epidemiological Models; C: Lineages/Clades; AA: Amino Acids; AC: Antigenic Cluster; O: Other.