

Supplementary Information

Title: Graph-Guided Multi-Task Sparse Learning Model: a Method for Identifying Antigenic Variants of Influenza A(H3N2) Virus

Running title: Multi-task Learning Model For Influenza Vaccine Strain Selection

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Supplementary Tables

Table S1. Numerical evaluation of the prediction performance of the multi-task learning (MTL) methods (including the GG-MTSL, $l_{1,2}$ norm regularized MTL and $l_{1,\infty}$ norm regularized MTL), and the single task learning methods (including Lasso and Ridge regressions). The running time, rooted mean square error (RMSE), accuracy, sensitivity, and specificity are evaluated.

Method	RMSE	Accuracy, %	Sensitivity, %	Specificity, %
GG-MTSL (training time: 2 minutes)				
2009	0.5495	78.32	44.90	95.99
2010	0.5959	68.73	52.11	94.80
2011	0.9994	80.90	84.78	66.17
2012	1.4209	97.07	97.04	100.0
2013	0.8613	98.20	97.85	78.26
2014	0.9092	93.15	94.26	88.28
2015	1.1416	81.58	78.00	93.36
2016	0.8457	86.44	89.59	79.92
Average	0.9154	85.55	79.82	87.10
$l_{1,\infty}$ norm regularized MTL (training time: 32 minutes)				
2009	1.2662	72.90	57.27	88.24
2010	1.2679	72.85	63.13	82.05
2011	1.1008	95.50	95.86	95.32
2012	1.189	91.50	78.64	97.25
2013	1.1265	85.15	67.87	94.83
2014	1.1024	85.32	70.35	93.70
2015	1.1028	85.27	70.06	93.70
2016	1.1019	85.20	69.73	93.70
Average	1.1572	84.21	71.61	92.35
$l_{1,2}$ norm regularized MTL (training time: 29 minutes)				
2009	1.2612	72.94	56.38	89.18
2010	1.2636	73.06	64.06	81.58
2011	1.1865	92.42	95.98	90.68
2012	1.1676	91.01	78.64	96.54
2013	1.1195	85.21	68.23	94.72
2014	1.0984	85.39	70.19	93.90
2015	1.0983	85.34	69.90	93.90
2016	1.0978	85.30	69.75	93.84
Average	1.1616	83.83	71.64	91.79
Lasso (training time: 1.5 minutes)				
2009	1.4428	69.62	41.76	96.94
2010	1.4721	68.21	37.16	97.61
2011	2.0900	95.69	96.30	95.39
2012	2.0737	91.69	78.68	97.51
2013	1.6881	84.22	59.69	97.96
2014	1.4662	84.59	64.02	96.10
2015	1.4588	84.53	63.66	96.11
2016	1.4550	84.53	63.50	96.07
Average	1.6433	82.89	63.10	96.71
Ridge (training time: 0.5 minutes)				
2009	2.1098	53.42	5.94	100
2010	2.1185	51.36	0.00	100
2011	1.6329	96.08	94.72	96.75
2012	1.8990	92.08	77.96	98.39
2013	2.0767	84.48	59.14	98.66
2014	1.9285	84.51	59.23	98.66
2015	1.9299	84.45	58.83	98.66
2016	1.9220	84.41	58.44	98.66
Average	1.9521	78.85	51.78	98.72

Table S2. The selected residues and their scores computed by the product of the local coefficients, \bar{w}^{local} , and the PIMA score (i.e., the antigenic distance contribution in terms of units) for 50 different tasks performed on influenza A(H3N2) viruses collected from 1968 through July 2016.

Task 1 1968–1979		Task 2 1969–1980		Task 3 1970–1981		Task 4 1971–1982		Task 5 1972–1983	
Residue	Score								
145	0.1092	145	0.1075	145	0.1079	145	0.1061	137	0.1111
137	0.0709	137	0.0867	137	0.0955	137	0.1061	145	0.0995
278	0.0551	278	0.0642	278	0.0671	278	0.0706	278	0.0754
193	0.0478	193	0.05	193	0.0509	158	0.0567	158	0.0566
83	0.0254	158	0.0351	158	0.0422	193	0.0513	193	0.0442
155	0.0238	83	0.0271	62	0.028	62	0.0374	62	0.0424
78	0.0237	62	0.0226	83	0.0274	83	0.0256	172	0.0297
275	0.0218	189	0.0213	189	0.0229	172	0.0255	189	0.026
158	0.021	155	0.0198	155	0.0161	189	0.0241	160	0.0247
189	0.018	275	0.0164	172	0.0151	160	0.0217	83	0.0206
62	0.0164	78	0.0164	260	0.0145	260	0.0195	260	0.0193
122	0.0145	174	0.013	174	0.0141	54	0.0163	54	0.0185
174	0.0119	260	0.0121	160	0.0122	174	0.0145	133	0.0174
159	0.0107	122	0.012	275	0.012	133	0.0139	174	0.017
144	0.0081	172	0.0107	53	0.0115	53	0.0127	53	0.0152
53	0.0077	159	0.0104	159	0.0106	155	0.0111	156	0.0102
		53	0.0102	54	0.0098	159	0.0093	213	0.0101
		160	0.0084	122	0.0098			50	0.008
		54	0.0071	78	0.0097				
		217	0.0065						
Task 6 1973–1984		Task 7 1974–1985		Task 8 1975–1986		Task 9 1976–1987		Task 10 1977–1988	
Residue	Score								
137	0.1169	137	0.1097	137	0.0787	124	0.0685	124	0.1215
145	0.0869	145	0.0654	144	0.0445	144	0.0666	144	0.0852
278	0.0713	158	0.0568	62	0.0444	159	0.0496	159	0.082
158	0.0597	278	0.0533	158	0.0435	163	0.0469	163	0.0748
62	0.0481	62	0.0503	172	0.0335	137	0.0429	173	0.0424
172	0.0345	172	0.0367	159	0.0314	173	0.0367	248	0.0354
193	0.0338	160	0.0261	173	0.0289	248	0.0351	155	0.0247
160	0.0277	144	0.025	248	0.0286	62	0.0257	156	0.0231
189	0.0248	133	0.0236	124	0.026	156	0.0256	137	0.0209
54	0.0214	193	0.023	160	0.0232	158	0.0243	186	0.0191
133	0.0209	54	0.0227	133	0.0231	172	0.0229	133	0.0167
260	0.0203	173	0.0196	163	0.023	133	0.0197	213	0.0143
174	0.0197	248	0.0196	174	0.0217	174	0.0194	189	0.0113
53	0.0163	174	0.0195	54	0.0206	160	0.0167	158	0.0096
83	0.0128	260	0.0192	145	0.0204	54	0.0139	172	0.0094
156	0.0128	189	0.0191	156	0.0199	193	0.0125	193	0.0089
213	0.0125	156	0.017	193	0.0197	262	0.0115	174	0.0086
262	0.0097	159	0.0159	260	0.0145	213	0.011	62	0.0085
		53	0.0148	278	0.0132	260	0.0078	160	0.0084
		213	0.0144	213	0.0122	307	0.0077	307	0.0079
		124	0.0122	262	0.0119	155	0.0075	262	0.0071
						67	0.0058	219	0.0068
						138	0.0047	54	0.0056
						189	0.0045	138	0.0055
						217	0.0032	67	0.0054
						53	0.0031		
						186	0.0031		
						50	0.0029		
Task 11 1978–1989		Task 12 1979–1990		Task 13 1980–1991		Task 14 1981–1992		Task 15 1982–1993	
Residue	Score								
124	0.1588	124	0.1428	193	0.113	193	0.1978	193	0.1884
159	0.0846	159	0.075	124	0.0987	121	0.1166	135	0.1195
155	0.0628	155	0.0604	135	0.0857	135	0.0784	189	0.0791
163	0.06	82	0.0581	121	0.079	124	0.0451	121	0.0662
82	0.0547	83	0.0581	145	0.0581	145	0.0416	158	0.0461

Task 46		Task 47		Task 48		Task 49		Task 50	
2002–2013		2003–2014		2004–2015		2005–2016		2012–2016	
Residue	Score								
158	0.6048	158	0.6048	158	0.5993	158	0.5911	159	0.3456
145	0.3163	145	0.3163	145	0.3171	145	0.319	311	0.3311
173	0.2223	173	0.2223	173	0.2192	173	0.2143	138	0.2337
189	0.211	189	0.211	189	0.2069	278	0.2072	160	0.1881
278	0.2072	278	0.2072	278	0.2064	189	0.2063	142	0.1612
45	0.1381	45	0.1381	45	0.1386	45	0.1391	5	0.1285
144	0.115	144	0.115	144	0.1152	144	0.1156	144	0.1188
199	0.1005	199	0.1005	199	0.0997	199	0.1005	225	0.1163
53	0.0958	53	0.0958	53	0.0948	53	0.0949	62	0.0604
198	0.095	198	0.095	198	0.0874	198	0.087	214	0.0449
280	0.076	280	0.076	280	0.0783	280	0.0769	31	0.0404
140	0.0731	140	0.0731	140	0.0717	140	0.0682	83	0.0354
142	0.0543	142	0.0543	142	0.0544	142	0.0546	122	0.0316
213	0.0535	213	0.0535	213	0.0541	213	0.0542	53	0.0312
223	0.0483	223	0.0482	223	0.0403	223	0.0393	124	0.0279
156	0.0287	156	0.0287	156	0.0276	156	0.0273	140	0.0243
260	0.0274	260	0.0274	260	0.0261	260	0.0267	156	0.0109
57	0.0221	57	0.0221	57	0.0221	57	0.0219	78	0.0104
230	0.0209	230	0.0209	230	0.0212	230	0.021	198	0.0087
312	0.0179			312	0.019	312	0.0189	219	0.0085
225	0.0173			225	0.018	225	0.0169	193	0.0084
62	0.0159			62	0.0155	62	0.0145		
				214	0.013	214	0.013		
				192	0.0124	192	0.0124		
				193	0.0097	212	0.01		
				78	0.0091	78	0.0092		
				212	0.0084				

Supplementary Figures

Figure S1. Overview of sequence and serologic data used in this study of influenza A(H3N2) virus variants. A) Distribution of HA sequences in each year, 1968-2016; B) HI titer data generated by using turkey erythrocytes without neuraminidase inhibitor (left panel), guinea pig erythrocytes without neuraminidase inhibitor (middle panel), and guinea pig erythrocytes with neuraminidase inhibitor (right panel). Most entries in these matrices are missing values (indicated by dark blue). The effective HI titers mainly locate close to the diagonal region (the antigen and sera are sorted according to the time). The $\log_2(\text{HI titers})$ are shown in colors, from red (high titer) to blue (missing [Miss] values).

Figure S2. Optimization of parameters in the machine learning models. (A) The model performance versus the parameter λ in matrix completion. (B) The model performance versus the parameter ϕ in multi-task feature learning. (C) The model performance versus the parameter α in multi-task feature learning. (D) The average number of selected residues per task versus the parameter ϕ . (E) The number of the union of the selected residues in all tasks versus the parameter ϕ . RMSE, rooted mean square error.

Figure S3. The 3D structure of the HA protein with identified key mutations colored. Different colors indicate that the identified key mutations belong to different antibody binding sites (ABS) A-E and regions outside the ABS.

Figure S4. Clusters of influenza A(H3N2) virus antigenic variants in antigenic cartography. The antigenic clusters were generated by using spectral clustering. Due to the imbalance of the virus samples, the entire datasets were split into three parts with respect to the time periods 1968-1992 (**A**), 1992-2009 (**B**), and 2009-2016 (**C**). A total of 16 antigenic clusters were generated: HK68, EN72, VI75, TX77, SI87, BE89, BE92, WU95, SY97, FU02, CA04, BR07, PE09, TX12, SWZ13, and HK14. Red crosses indicate the position of pandemic influenza strain A/Hong Kong/1968(H3N2) and vaccine strains determined by World Health Organization collaborative centers; markers with white face and black edge indicate the center of each cluster.