Supplementary Text:

Emergenet: Fast Scalable Pandemic Risk Estimation of Influenza A Strains Collected In Non-human Hosts

Kevin Wu¹, Jin Li¹, Timmy Li¹, Aaron Esser-Kahn^{2,3}, and Ishanu Chattopadhyay^{1,4,5}★

¹Department of Medicine, University of Chicago, IL, USA ²Pritzker School of Molecular Engineering, University of Chicago, Chicago, IL, USA ³Committee on Immunology, University of Chicago, Chicago, IL, USA ⁴Committee on Genetics, Genomics & Systems BioloScalegy, University of Chicago, IL, USA ⁵Committee on Quantitative Methods in Social, Behavioral, and Health Sciences, University of Chicago, IL, USA

SUPPLEMENTARY METHODS: NOTES ON Q-DISTANCE & SUPPORTING RESULTS

The *q-distance* is a pseudo-metric since distinct sequences can induce the same distributions over each index, and thus evaluate to have a zero distance. This is actually desirable; we do not want our distance to be sensitive to changes that are not biologically relevant. The intuition is that not all sequence variations brought about by substitutions are equally important or likely. Even with no selection pressure, we might still see random variations at an index if such variations do not affect the replicative fitness. Under that scenario, the corresponding Φ_i will predict a flat distribution no matter what the input sequence is, thus contributing nothing to the overall distance. And even if two strains x, y have the same entry at some index i, the remaining residues might induce different distributions Φ_i based on the remote dependencies, i.e., the entries in x_{-i}, y_{-i} . Also, it matters if the sequences come from two different background populations P,Q,~i.e., if the induced Qnets Φ^P,Φ^Q are different. Thus, if we construct Qnets for H1N1 Influenza A separately for the collection years 2008 and 2009, then the same exact sequence collected in the respective years might have a non-zero distance between them, reflecting the fact that the background population the sequences arose from are different, inducing possibly different expected mutational tendencies (See SI-Table 1).

Next, we induce q-distance between a sequence and a population and between two populations.

Definition 1 (Pseudo-metric between populations). Using the notion of Hausdorff metric between sets:

$$\forall x \in P, y \in Q,$$

$$\theta(x, Q) = \min_{y \in Q} \theta(x, y)$$
(1)

$$\theta(x,Q) = \min_{y \in Q} \theta(x,y)$$

$$\theta(P,Q) = \max \left\{ \max_{x \in P} \theta(x,Q), \max_{y \in Q} \theta(y,P) \right\}$$
(2)

In-silico Corroboration of Qnet Constraints

We carry out in-silico experiments to corroborate that the constraints represented within an inferred Qnet are indeed reflective of the biology in play. We compare the results of simulated mutational perturbations to sequences from our databases (for which we have already constructed Qnets), and then use NCBI BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to identify if our perturbed sequences match with existing sequences in the databases (See SI-Fig. 1). We find that in contrast to random variations, which rapidly diverge the trajectories, the Qnet constraints tend to produce smaller variance in the trajectories, maintain a high degree of match as we extend our trajectories, and produces matches closer in time to the collection time of the initial sequence suggesting that the Qnet does indeed capture realistic constraints.

Significance Test for Population Membership

For our modeling to be reliable, we need a quantitative test of how well the Qnet represents the data. Here, we formulate an explicit membership test to ascertain if individual samples may indeed be generated by the Qnet with sufficiently high probability.

^{*}To whom correspondence should be addressed: e-mail: ishanu@uchicago.edu.

Definition 2 (Membership probability of a sequence). Given a population P inducing the Qnet Φ^P and a sequence x, we can compute the membership probability of x:

$$\omega_x^P \triangleq Pr(x \in P) = \prod_{j=1}^N \left(\Phi_j^P(x_{-j})|_{x_j} \right) \tag{3}$$

 x_j is the j^{th} entry in x, and is thus an element in the set Σ_j . Since we are mostly concerned with the case where Σ_j is a finite set, $\Phi_j^P(x_{-j})|_{x_j}$ is the entry in the probability mass function corresponding to the element of Σ_j which appears at the j^{th} index in sequence x.

We can carry out this calculation for a sequence x known to be in the population P as well, which allows us to define the membership degree ω_x^P .

Definition 3 (Membership degree). Let X be a random field representing a population P, i.e., X = x is a randomly drawn sequence from P. Then the membership degree ω^P is a function of the random variable X:

$$\omega^{P}(X) \triangleq \prod_{j=1}^{N} \left(\Phi_{j}^{P}(X_{-j})|_{X_{j}} \right) \tag{4}$$

Note that ω^P takes values in the unit interval [0,1], and the probability x is a member of the population P is $\omega^P(X=x)$, denoted briefly as ω^P_x or ω_x if P is clear from context.

Since $\omega^P(X)$ is a random variable, we can now compute sets of sequences that better represent the population P, and ones that are on the fringe. We can also evaluate using a pre-specified significance-level if a particular sequence is not from the population P, thus identifying if we need to recompute the predictors Φ , or split the base population. We can set up a hypothesis testing scenario to determine if sequences are indeed from a test population, as follows:

Given a population P, inducing a Qnet Φ^P , and a sequence x, we assume the null hypothesis is $x \notin P$. We reject the null hypothesis at a pre-specified significance α , if

$$Pr(\omega^{P}(X) \ge \omega^{P}(X=x)) \le \alpha$$
 (5)

The fraction of newly observed sequences that do not reject the null hypothesis can then be used as an estimate of the species-specific divergence in population characteristics.

Proof of Probability Bounds

Theorem 1 (Probability bound). Given a sequence x of length N that transitions to a strain $y \in Q$, we have the following bounds at significance level α .

$$\omega_y^Q e^{\frac{\sqrt{8}N^2}{1-\alpha}\theta(x,y)} \ge Pr(x \to y) \ge \omega_y^Q e^{-\frac{\sqrt{8}N^2}{1-\alpha}\theta(x,y)}$$
(6)

where ω_y^Q is the membership probability of strain y in the target population Q (See Def. 2), and $\theta(x,y)$ is the q-distance between x,y (See Def. ?? in Qnet Framework).

Proof. Using Sanov's theorem¹ on large deviations, we conclude that the probability of spontaneous jump from strain $x \in P$ to strain $y \in Q$, with the possibility $P \neq Q$, is given by:

$$Pr(x \to y) = \prod_{i=1}^{N} \left(\Phi_i^P(x_{-i})|_{y_i} \right) \tag{7}$$

Writing the factors on the right hand side as:

$$\Phi_i^P(x_{-i})|_{y_i} = \Phi_i^Q(y_{-i})|_{y_i} \left(\frac{\Phi_i^P(x_{-i})|_{y_i}}{\Phi_i^Q(y_{-i})|_{y_i}} \right)$$
(8)

we note that
$$\Phi_i^P(x_{-i})$$
, $\Phi_i^Q(y_{-i})$ are distributions on the same index i , and hence:
$$|\Phi_i^P(x_{-i})_{y_i} - \Phi_i^Q(y_{-i})_{y_i}| \le \sum_{y_i \in \Sigma_i} |\Phi_i^P(x_{-i})_{y_i} - \Phi_i^Q(y_{-i})_{y_i}|$$
(9)

Using a standard refinement of Pinsker's inequality², and the relationship of Jensen-Shannon divergence with total variation, we get:

$$\theta_{i} \ge \frac{1}{8} |\Phi_{i}^{P}(x_{-i})_{y_{i}} - \Phi_{i}^{Q}(y_{-i})_{y_{i}}|^{2} \Rightarrow \left| 1 - \frac{\Phi_{i}^{Q}(y_{-i})_{y_{i}}}{\Phi_{i}^{P}(x_{-i})_{y_{i}}} \right| \le \frac{1}{a_{0}} \sqrt{8\theta_{i}}$$

$$\tag{10}$$

where a_0 is the smallest non-zero probability value of generating the entry at any index. We will see that this

parameter is related to statistical significance of our bounds. First, we can formulate a lower bound as follows:

$$\log\left(\prod_{i=1}^{N} \frac{\Phi_{i}^{P}(x_{-i})|_{y_{i}}}{\Phi_{i}^{Q}(y_{-i})|_{y_{i}}}\right) = \sum_{i} \log\left(\frac{\Phi_{i}^{P}(x_{-i})|_{y_{i}}}{\Phi_{i}^{Q}(y_{-i})|_{y_{i}}}\right) \ge \sum_{i} \left(1 - \frac{\Phi_{i}^{Q}(y_{-i})_{y_{i}}}{\Phi_{i}^{P}(x_{-i})_{y_{i}}}\right) \ge \frac{\sqrt{8}}{a_{0}} \sum_{i} \theta_{i}^{1/2} = -\frac{\sqrt{8}N}{a_{0}}\theta$$
(11)

Similarly, the upper bound may be derived as

$$\log \left(\prod_{i=1}^{N} \frac{\Phi_{i}^{P}(x_{-i})|_{y_{i}}}{\Phi_{i}^{Q}(y_{-i})|_{y_{i}}} \right) = \sum_{i} \log \left(\frac{\Phi_{i}^{P}(x_{-i})|_{y_{i}}}{\Phi_{i}^{Q}(y_{-i})|_{y_{i}}} \right) \leq \sum_{i} \left(\frac{\Phi_{i}^{Q}(y_{-i})_{y_{i}}}{\Phi_{i}^{P}(x_{-i})_{y_{i}}} - 1 \right) \leq \frac{\sqrt{8}N}{a_{0}} \theta$$
(12)

Combining Eqs. 11 and 12, we conclude

$$\omega_{y}^{Q} e^{\frac{\sqrt{8}N}{a_{0}}\theta} \ge Pr(x \to y) \ge \omega_{y}^{Q} e^{-\frac{\sqrt{8}N}{a_{0}}\theta}$$
(13)

Now, interpreting a_0 as the probability of generating an unlikely event below our desired threshold (*i.e.* a "failure"), we note that the probability of generating at least one such event is given by $1 - (1 - a_0)^N$. Hence if α is the pre-specified significance level, we have for N >> 1:

$$a_0 \approx (1 - \alpha)/N \tag{14}$$

Hence, we conclude, that at significance level $\geq \alpha$, we have the bounds:

$$\omega_y^Q e^{\frac{\sqrt{8}N^2}{1-\alpha}\theta} \ge Pr(x \to y) \ge \omega_y^Q e^{-\frac{\sqrt{8}N^2}{1-\alpha}\theta}$$
(15)

Remark 1. This bound can be rewritten in terms of the log-likelihood of the spontaneous jump and constants independent of the initial sequence x as:

$$\left|\log Pr(x \to y) - C_0\right| \le C_1 \theta \tag{16}$$

where the constants are given by:

$$C_0 = \log \omega_y^Q \tag{17}$$

$$C_1 = \frac{\sqrt{8}N^2}{1-\alpha} \tag{18}$$

Multivariate Regression to Identify Factors in Strain Prediction

We investigate the key factors that contribute to our successful prediction of the dominant strain in the next season. We carry out a multivariate regression with data diversity, the complexity of inferred Qnet and the edit distance of the WHO recommendation from the dominant strain as independent variables. Here we define data diversity as the number of clusters we have in the input set of sequences, such that any two sequences five or less mutations apart are in the same cluster. Qnet complexity is measured by the number of decision nodes in the component decision trees of the recursive forest.

We select several plausible structures of the regression equation, and in each case conclude that data diversity has the most important and statistically significant contribution (See SI-Tab. 20).

REFERENCES

- [1] Cover TM, Thomas JA. Elements of Information Theory (Wiley Series in Telecommunications and Signal Processing). New York, NY, USA: Wiley-Interscience; 2006.
- [2] Fedotov AA, Harremoës P, Topsoe F. Refinements of Pinsker's inequality. IEEE Transactions on Information Theory. 2003;49(6):1491–1498.

SUPPLEMENTARY FIGURES & TABLES

SI Tab. 1

EXAMPLES: QNET INDUCED DISTANCE VARYING FOR FIXED SEQUENCE PAIR WHEN BACKGROUND POPULATION CHANGES (ROWS 1 -5), SEQUENCES WITH SMALL EDIT DISTANCE AND LARGE Q-DISTANCE, AND THE CONVERSE (ROWS 6-9)

	Edit dist.	Sequence A	Sequence B	Q-dist.	Year A*	Year B*
1	18	A/Singapore/23J/2007	A/Tennessee/UR06-0294/2007	0.0111	2007	2007
2	18	A/Singapore/23J/2007	A/Tennessee/UR06-0294/2007	0.0094	2008	2008
3	18	A/Singapore/23J/2007	A/Tennessee/UR06-0294/2007	0.0027	2009	2009
4	18	A/Singapore/23J/2007	A/Tennessee/UR06-0294/2007	0.0025	2010	2010
5	18	A/Singapore/23J/2007	A/Tennessee/UR06-0294/2007	0.6163	2007	2010
6	11	A/Naypyitaw/M783/2008	A/Singapore/201/2008	0.8852	2008	2008
7	15	A/Cambodia/W0908339/2012	A/Singapore/DMS1233/2012	0.2737	2012	2012
8	126	A/South Dakota/03/2008	A/Singapore/10/2008	0.3034	2008	2008
9	141	A/Jodhpur/3248/2012	A/Cambodia/W0908339/2012	0.2405	2012	2012

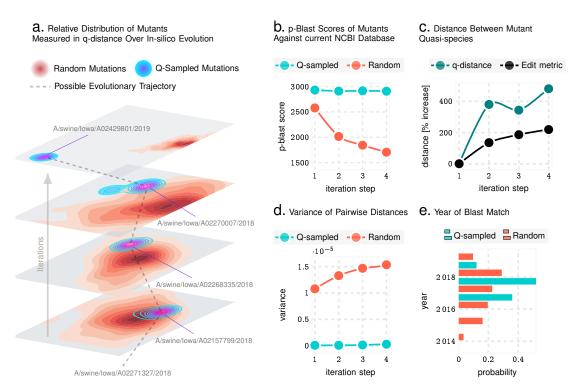
^{*}Year A and year B correspond to the assumed collection years for sequences A and B respectively for the purpose of this example. Sequence A in row 1 is collected in 2007, but is assumed to be from different years in rows 2-4 to demonstrate the change in q-distance from sequence B, arising only from a change in the background population.

SI Tab. 2 CORRELATION BETWEEN Q-DISTANCE AND EDIT DISTANCE BETWEEN SEQUENCE PAIRS

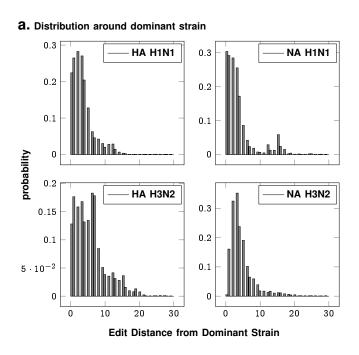
Phenotypes	Correlation
Influenza H1N1 HA	0.76
Influenza H1N1 NA	0.74
Influenza H3N2 HA	0.85
Influenza H3N2 NA	0.79

SI Tab. 3
NUMBER OF SEQUENCES COLLECTED FROM PUBLIC DATABASES

Database	Strain	No. of Sequences
NCBI	Influenza H1N1 HA	17,894
NCBI	Influenza H1N1 NA	16,637
NCBI	Influenza H3N2 HA	18,265
NCBI	Influenza H3N2 NA	14,699
GISAID	Influenza H1N1 HA	1,528
GISAID	Influenza H1N1 NA	1,490
GISAID	Influenza H3N2 HA	13,975
GISAID	Influenza H3N2 NA	13,811
Total		98,299



SI Fig. 1. Q-distance validation in-silico using Influenza A sequences from NCBI database. Panel a illustrates that the Qnet induced modeling of evolutionary trajectories initiated from known haemagglutinnin (HA) sequences are distinct from random paths in the strain space. In particular, random trajectories have more variance, and more importantly, diverge to different regions of the landscape compared to Qnet predictions. Panels b-e show that unconstrained Q-sampling produces sequences maintain a higher degree of similarity to known sequences, as verified by blasting against known HA sequences, have a smaller rate of growth of variance, and produce matches in closer time frames to the initial sequence. Panel c shows that this is not due to simply restricting the mutational variations, which increases rapidly in both the Qnet and the classical metric.



SI Fig. 2. **No. of mutations from the seasonal dominant strain over the years** The quasispecies that circulates each season for each sub-type is tightly distributed around the dominant strain on average.

SI Tab. 4 H1N1 HA NORTHERN HEMISPHERE

Year	WHO Recommendation	Dominant Strain	Qnet Recommendation	WHO Error	Qnet Error
2001-02	A/New Caledonia/20/99	A/Canterbury/41/2001	A/Dunedin/2/2000	4	6
2002-03	A/New Caledonia/20/99	A/Taiwan/567/2002	A/New York/241/2001	3	1
2003-04	A/New Caledonia/20/99	A/Memphis/5/2003	A/New York/291/2002	5	2
2004-05	A/New Caledonia/20/99	A/Thailand/Siriraj-Rama-TT/2004	A/New York/222/2003	7	4
2005-06	A/New Caledonia/20/99	A/Niedersachsen/217/2005	A/Canterbury/106/2004	8	10
2006-07	A/New Caledonia/20/99	A/India/34980/2006	A/Auckland/619/2005	6	1
2007-08	A/Solomon Islands/3/2006	A/Norway/1701/2007	A/New York/8/2006	8	11
2008-09	A/Brisbane/59/2007	A/Pennsylvania/02/2008	A/Kentucky/UR06-0476/2007	2	2
2009-10	A/Brisbane/59/2007	A/Singapore/ON1060/2009	A/Hong Kong/549/2008	119	119
2010-11	A/California/7/2009	A/England/01220740/2010	A/New York/14/2009	5	1
2011-12	A/California/7/2009	A/Punjab/041/2011	A/Kansas/01/2010	7	2
2012-13	A/California/7/2009	A/British Columbia/001/2012	A/Moscow/WRAIR4308T/2011	11	4
2013-14	A/California/7/2009	A/Moscow/CRIE-32/2013	A/Helsinki/1199/2012	10	2
2014-15	A/California/7/2009	A/Thailand/CU-C5169/2014	A/Maryland/02/2013	12	0
2015-16	A/California/7/2009	A/Georgia/15/2015	A/Utah/3691/2014	14	2
2016-17	A/California/7/2009	A/Hawaii/21/2016	A/Adana/08/2015	16	0
2017-18	A/Michigan/45/2015	A/Michigan/291/2017	A/Beijing-Huairou/SWL1335/2016	5	4
2018-19	A/Michigan/45/2015	A/Washington/55/2018	A/India/C1721549/2017	6	1
2019-20	A/Brisbane/02/2018	A/Kentucky/06/2019	A/New Jersey/01/2018	5	1
2020-21	A/Hawaii/70/2019	A/Togo/905/2020	A/Italy/8949/2019	4	8
2021-22	A/Victoria/2570/2019	A/Ireland/20935/2022	A/Togo/45/2021	9	3
2022-23	-1	-1	A/Netherlands/00068/2022	-1	-1

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 5 H1N1 HA SOUTHERN HEMISPHERE

Year	WHO Recommendation	Dominant Strain	Qnet Recommendation		Qnet Error
2001-02	A/New Caledonia/20/99	A/Canterbury/41/2001	A/South Canterbury/50/2000	4	6
2002-03	A/New Caledonia/20/99	A/Taiwan/567/2002	A/Canterbury/41/2001	3	1
2003-04	A/New Caledonia/20/99	A/Memphis/5/2003	A/New York/291/2002	5	2
2004-05	A/New Caledonia/20/99	A/Thailand/Siriraj-Rama-TT/2004	A/Memphis/5/2003	7	4
2005-06	A/New Caledonia/20/99	A/Niedersachsen/217/2005	A/Canterbury/106/2004	8	10
2006-07	A/New Caledonia/20/99	A/India/34980/2006	A/Niedersachsen/217/2005	6	2
2007-08	A/New Caledonia/20/99	A/Norway/1701/2007	A/Thailand/CU68/2006	14	6
2008-09	A/Solomon Islands/3/2006	A/Pennsylvania/02/2008	A/Kentucky/UR06-0476/2007	9	2
2009-10	A/Brisbane/59/2007	A/Singapore/ON1060/2009	A/Belem/241/2008	119	119
2010-11	A/California/7/2009	A/England/01220740/2010	A/Singapore/ON1060/2009	5	1
2011-12	A/California/7/2009	A/Punjab/041/2011	A/England/01220740/2010		2
2012-13	A/California/7/2009	A/British Columbia/001/2012	A/Punjab/041/2011	11	4
2013-14	A/California/7/2009	A/Moscow/CRIE-32/2013	A/India/P122045/2012	10	5
2014-15	A/California/7/2009	A/Thailand/CU-C5169/2014	A/Jiangsuhailing/SWL1382/2013	12	4
2015-16	A/California/7/2009	A/Georgia/15/2015	A/Thailand/CU-C5169/2014	14	2
2016-17	A/California/7/2009	A/Hawaii/21/2016	A/Georgia/15/2015	16	2
2017-18	A/Michigan/45/2015	A/Michigan/291/2017	A/Beijing-Huairou/SWL1335/2016	5	4
2018-19	A/Michigan/45/2015	A/Washington/55/2018	A/Michigan/291/2017	6	1
2019-20	A/Michigan/45/2015	A/Kentucky/06/2019	A/Washington/55/2018	7	1
2020-21	A/Brisbane/02/2018	A/Togo/905/2020	A/Italy/8451/2019	10	8
2021-22	A/Victoria/2570/2019	A/Abidjan/457/2021	A/Togo/0298/2021	9	5
2022-23	-1	-1	A/Cote_D'Ivoire/1270/2021	-1	-1

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 6 H1N1 NA NORTHERN HEMISPHERE

Year	WHO Recommendation	Dominant Strain	Qnet Recommendation	WHO Error	Qnet Error
2001-02	A/New Caledonia/20/99	A/New York/447/2001	A/Memphis/15/2000	4	4
2002-03	A/New Caledonia/20/99	A/Paris/0833/2002	A/New York/341/2001	1	5
2003-04	A/New Caledonia/20/99	A/Memphis/5/2003	A/New York/291/2002	3	5
2004-05	A/New Caledonia/20/99	A/Singapore/14/2004	A/New York/223/2003	2	3
2005-06	A/New Caledonia/20/99	A/Taiwan/5524/2005	A/Florida/3e/2004	3	0
2006-07	A/New Caledonia/20/99	A/Massachusetts/08/2006	A/Sofia/361/2005	4	2
2007-08	A/Solomon Islands/3/2006	A/Tennessee/UR06-0106/2007	A/Sofia/490/2006	9	2
2008-09	A/Brisbane/59/2007	A/Sendai/TU66/2008	A/Maryland/04/2007	0	3
2009-10	A/Brisbane/59/2007	A/Thailand/SR08021/2009	A/Paris/910/2008	87	87
2010-11	A/California/7/2009	A/Finland/2460N/2010	A/Rome/709/2009	2	9
2011-12	A/California/7/2009	A/Tula/CRIE-GSYu/2011	A/Oman/SQUH-40/2010	4	2
2012-13	A/California/7/2009	A/Bangalore/697-32/2012	A/Nizhnii Novgorod/CRIE-ZCA/2011	4	0
2013-14	A/California/7/2009	A/Jiangsugusu/SWL1824/2013	A/LongYan/SWL33/2013	5	3
2014-15	A/California/7/2009	A/LongYan/SWL2457/2014	A/Utah/06/2013	9	3
2015-16	A/California/7/2009	A/Michigan/45/2015	A/Maryland/02/2014	14	4
2016-17	A/California/7/2009	A/Mexico/4436/2016	A/India/Pun151245/2015	14	0
2017-18	A/Michigan/45/2015	A/Illinois/37/2017	A/Utah/02/2016	3	3
2018-19	A/Michigan/45/2015	A/Kenya/47/2018	A/Maine/24/2017	4	0
2019-20	A/Brisbane/02/2018	A/Texas/7939/2019	A/Missouri/03/2018	1	0
2020-21	A/Hawaii/70/2019	A/Togo/897/2020	A/Texas/112/2019	0	5
2021-22	A/Victoria/2570/2019	A/Cote_d'Ivoire/3729/2021	A/Togo/0071/2021	1	5
2022-23	-1	-1	A/Lyon/820/2021	-1	-1

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 7 H1N1 NA SOUTHERN HEMISPHERE

Year	WHO Recommendation Dominant Strain Qnet Recommendation		WHO Error	Qnet Error	
2001-02	A/New Caledonia/20/99	A/New York/447/2001	A/Canterbury/37/2000	4	6
2002-03	A/New Caledonia/20/99	A/Paris/0833/2002	A/New York/447/2001	1	5
2003-04	A/New Caledonia/20/99	A/Memphis/5/2003	A/New York/291/2002	3	5
2004-05	A/New Caledonia/20/99	A/Singapore/14/2004	A/Memphis/5/2003	2	3
2005-06	A/New Caledonia/20/99	A/Taiwan/5524/2005	A/Canterbury/106/2004	3	6
2006-07	A/New Caledonia/20/99	A/Massachusetts/08/2006	A/Sofia/361/2005	4	2
2007-08	A/New Caledonia/20/99	A/Tennessee/UR06-0106/2007	A/Thailand/RMSC-UDN-20/2006	4	8
2008-09	A/Solomon Islands/3/2006	A/Sendai/TU66/2008	A/Tennessee/UR06-0151/2007	15	13
2009-10	A/Brisbane/59/2007	A/Thailand/SR08021/2009	A/Nebraska/07/2008	87	87
2010-11	A/California/7/2009	A/Finland/2460N/2010	A/Rome/709/2009	2	9
2011-12	A/California/7/2009	A/Tula/CRIE-GSYu/2011	A/Finland/2460N/2010	4	2
2012-13	A/California/7/2009	A/Bangalore/697-32/2012	A/Tula/CRIE-GSYu/2011	4	0
2013-14	A/California/7/2009	A/Jiangsugusu/SWL1824/2013	A/Oman/SQUH-63/2012	5	4
2014-15	A/California/7/2009	A/LongYan/SWL2457/2014	A/NanPing/SWL1640/2013	9	6
2015-16	A/California/7/2009	A/Michigan/45/2015	A/LongYan/SWL2457/2014	14	5
2016-17	A/California/7/2009	A/Mexico/4436/2016	A/Michigan/45/2015	14	0
2017-18	A/Michigan/45/2015	A/Illinois/37/2017	A/Mexico/4436/2016	3	3
2018-19	A/Michigan/45/2015	A/Kenya/47/2018	A/Kentucky/26/2017	4	2
2019-20	A/Michigan/45/2015	A/Texas/7939/2019	A/Kenya/47/2018	4	
2020-21	A/Brisbane/02/2018	A/Togo/897/2020	A/Texas/7939/2019	6	5
2021-22	A/Victoria/2570/2019	A/Cote_D'Ivoire/1496/2021	A/NAGASAKI/8/2020	1	6
2022-23	-1	-1	A/Dakar/35/2021	-1	-1

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 8 H3N2 HA NORTHERN HEMISPHERE

Year	WHO Recommendation	Dominant Strain	Dominant Strain Qnet Recommendation		Qnet Error
2005-06	A/California/7/2004	A/Denmark/195/2005	005 A/Tairawhiti/369/2004		2
2006-07	A/Wisconsin/67/2005	A/New York/5/2006	A/South Australia/22/2005	5	4
2007-08	A/Wisconsin/67/2005	A/Tennessee/11/2007	A/Colorado/05/2006	8	5
2008-09	A/Brisbane/10/2007	A/Massachusetts/13/2008	A/Virginia/UR06-0021/2007	3	2
2009-10	A/Brisbane/10/2007	A/Hawaii/14/2009	A/Manhean/03/2008	7	6
2010-11	A/Perth/16/2009	A/Utah/12/2010	A/Philippines/5/2009	8	7
2011-12	A/Perth/16/2009	A/Piaui/14202/2011	A/Singapore/C2010.310/2010	4	4
2012-13	A/Victoria/361/2011	A/Alborz/927/2012 A/Tehran/895/2012		4	3
2013-14	A/Victoria/361/2011	A/Delaware/01/2013 A/Singapore/H2012.934/2012		4	1
2014-15	A/Texas/50/2012	A/Alborz/72205/2014	A/Alborz/72205/2014 A/Nebraska/03/2013		9
2015-16	A/Switzerland/9715293/2013	A/Parma/471/2015	A/Ontario/01/2014	10	0
2016-17	A/Hong Kong/4801/2014	A/Guangdong/12/2016	A/Oregon/02/2015	0	0
2017-18	A/Hong Kong/4801/2014	A/Maryland/25/2017	A/New York/03/2016	3	1
2018-19	A/Singapore/INFIMH-16-0019/2016	A/Vermont/04/2018	A/Ontario/038/2017	8	5
2019-20	A/Kansas/14/2017	A/Kentucky/27/2019	A/California/7330/2018	16	12
2020-21	A/Hong Kong/2671/2019	A/India/Pun-NIV289524/2021_Jan	lan A/California/NHRC- OID_FDX100215/2019		14
2021-22	A/Cambodia/e0826360/2020	A/Human/New_York/PV60641/2022	A/India/Pun-NIV291000/2021_Jan	14	5
2022-23	-1	-1	A/Ireland/14993/2022 -1		-1

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 9 H3N2 HA SOUTHERN HEMISPHERE

Year	WHO Recommendation	Dominant Strain Qnet Recommendation		WHO Error	Qnet Error
2005-06	A/Wellington/1/2004	A/Denmark/195/2005	A/Waikato/21/2004	3	
2006-07	A/California/7/2004	A/New York/5/2006	A/South Australia/22/2005	12	4
2007-08	A/Wisconsin/67/2005	A/Tennessee/11/2007	A/New York/923/2006	8	5
2008-09	A/Brisbane/10/2007	A/Massachusetts/13/2008	A/Tennessee/11/2007	3	2
2009-10	A/Brisbane/10/2007	A/Hawaii/14/2009	A/Manhean/03/2008	7	6
2010-11	A/Perth/16/2009	A/Utah/12/2010	A/Hawaii/14/2009	8	7
2011-12	A/Perth/16/2009	A/Piaui/14202/2011	A/Utah/12/2010	4	4
2012-13	A/Perth/16/2009	A/Alborz/927/2012	A/Piaui/14202/2011	8	4
2013-14	A/Victoria/361/2011	A/Delaware/01/2013	A/Callao/IPE00830/2012	4	7
2014-15	A/Texas/50/2012	A/Alborz/72205/2014	A/Delaware/01/2013	10	7
2015-16	A/Switzerland/9715293/2013	A/Parma/471/2015	A/Alborz/72205/2014	10	0
2016-17	A/Hong Kong/4801/2014	A/Guangdong/12/2016	A/Parma/471/2015	0	0
2017-18	A/Hong Kong/4801/2014	A/Maryland/25/2017	A/Ontario/196/2016	3	4
2018-19	A/Singapore/INFIMH-16-0019/2016	A/Vermont/04/2018	A/Texas/279/2017	8	5
2019-20	A/Switzerland/8060/2017	A/Kentucky/27/2019 A/Santa Catarina/1200/2018		13	12
2020-21	A/South Australia/34/2019	A/India/Pun-NIV289524/2021_Jan	A/Kentucky/27/2019	12	14
2021-22	A/Hong Kong/2671/2019	A/Darwin/9a/2021	A/India/PUN-NIV301718/2021	19	1
2022-23	-1	-1	A/Latvia/04-86261/2022	-1	-1

 $^{^{\}star}$ Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 10 H3N2 NA NORTHERN HEMISPHERE

Year	WHO Recommendation	Dominant Strain Qnet Recommendation		WHO Error	Qnet Error
2003-04	A/Moscow/10/99	A/Denmark/107/2003	A/New York/100/2002	13	3
2004-05	A/Fujian/411/2002	A/Hyogo/36/2004	A/New York/20/2003	3	16
2005-06	A/California/7/2004	A/Denmark/203/2005	A/Hong Kong/HKU20/2004	4	0
2006-07	A/Wisconsin/67/2005	A/Berlin/32/2006	A/Mexico/InDRE2227/2005	1	1
2007-08	A/Wisconsin/67/2005	A/Brazil/80/2007	A/Baden-Wuerttemberg/17/2006	8	7
2008-09	A/Brisbane/10/2007	A/Missouri/05/2008	A/Washington/01/2007	3	2
2009-10	A/Brisbane/10/2007	A/Oklahoma/09/2009	A/Wisconsin/24/2008	3	1
2010-11	A/Perth/16/2009	A/California/17/2010	2010 A/New York/70/2009		3
2011-12	A/Perth/16/2009	A/Texas/14/2011	A/California/14/2010		2
2012-13	A/Victoria/361/2011	A/New York/02/2012	A/Singapore/C2011.493/2011		1
2013-14	A/Victoria/361/2011	A/Michigan/02/2013	A/New York/01/2012		1
2014-15	A/Texas/50/2012	A/Tehran/69634/2014	A/Boston/DOA2-176/2013	3	1
2015-16	A/Switzerland/9715293/2013	A/Parma/471/2015	A/Thailand/CU-B10520/2014	3	0
2016-17	A/Hong Kong/4801/2014	A/North Carolina/62/2016	A/Delaware/02/2015	7	2
2017-18	A/Hong Kong/4801/2014	A/Texas/277/2017	A/New York/03/2016	8	0
2018-19	A/Singapore/INFIMH-16-0019/2016	A/Japan/NHRC_FDX70352/2018	A/Colorado/11/2017	4	3
2019-20	A/Kansas/14/2017	A/Washington/9757/2019	A/Guangxi-Fangcheng/54/2019		11
2020-21	A/Hong Kong/2671/2019	A/Bangladesh/1004005/2020	A/Maryland/02/2019	3	13
2021-22	A/Cambodia/e0826360/2020	A/Stockholm/10/2022	A/Bangladesh/1916/2020	2	2
2022-23	-1	-1	A/lowa/20/2022	-1	-1

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 11 H3N2 NA SOUTHERN HEMISPHERE

Year	WHO Recommendation	Dominant Strain	Oominant Strain Qnet Recommendation		Qnet Error
2003-04	A/Moscow/10/99	A/Denmark/107/2003	A/New York/101/2002	13	3
2004-05	A/Fujian/411/2002	A/Hyogo/36/2004	A/New York/20/2003	3	16
2005-06	A/Wellington/1/2004	A/Denmark/203/2005	A/Wellington/1/2004	2	2
2006-07	A/California/7/2004	A/Berlin/32/2006	A/Mexico/InDRE2227/2005	3	1
2007-08	A/Wisconsin/67/2005	A/Brazil/80/2007	A/Ohio/06/2006	8	10
2008-09	A/Brisbane/10/2007	A/Missouri/05/2008	A/Brazil/80/2007	3	2
2009-10	A/Brisbane/10/2007	A/Oklahoma/09/2009	ahoma/09/2009 A/Wisconsin/24/2008		1
2010-11	A/Perth/16/2009	A/California/17/2010	A/California/17/2010 A/New York/70/2009		3
2011-12	A/Perth/16/2009	A/Texas/14/2011 A/Virginia/05/2010		3	2
2012-13	A/Perth/16/2009	A/New York/02/2012	A/New York/02/2012 A/Texas/14/2011		1
2013-14	A/Victoria/361/2011	A/Michigan/02/2013	A/New York/02/2012	3	3
2014-15	A/Texas/50/2012	A/Tehran/69634/2014	A/Michigan/02/2013	3	1
2015-16	A/Switzerland/9715293/2013	A/Parma/471/2015	A/Tehran/69634/2014	3	2
2016-17	A/Hong Kong/4801/2014	A/North Carolina/62/2016	A/Parma/471/2015	7	2
2017-18	A/Hong Kong/4801/2014	A/Texas/277/2017	A/Guangdong/264/2016	8	0
2018-19	A/Singapore/INFIMH-16-0019/2016	A/Japan/NHRC_FDX70352/2018	A/Texas/277/2017	4	3
2019-20	A/Switzerland/8060/2017	A/Washington/9757/2019	_		10
2020-21	A/South Australia/34/2019	A/Bangladesh/1004005/2020	A/Washington/9757/2019	1	13
2021-22	A/Hong Kong/2671/2019	A/India/PUN-NIV301718/2021	A/India/PUN-NIV301132/2021	6	4
2022-23	-1	-1	A/Michigan/UOM10045036720/2022	-1	-1

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 12 H1N1 NA NORTHERN HEMISPHERE (MULTI-CLUSTER)

Year	WHO Recommendation	WHO Error	Qnet Error 1	Qnet Error 2	Qnet Recommendation 1	Qnet Recommendation 2
2001-02	A/New Caledonia/20/99	4	1	6	A/New South Wales/26/2000	A/Canterbury/37/2000
2002-03	A/New Caledonia/20/99	1	0	5	A/Wellington/1/2001	A/New York/447/2001
2003-04	A/New Caledonia/20/99	3	2	8	A/Paris/0833/2002	A/Taiwan/141/2002
2004-05	A/New Caledonia/20/99	2	3	4	A/Memphis/5/2003	A/Hanoi/1004/2003
2005-06	A/New Caledonia/20/99	3	0	1	A/Denmark/130/2004	A/Paris/650/2004
2006-07	A/New Caledonia/20/99	4	2	8	A/Sofia/361/2005	A/Wellington/11/2005
2007-08	A/Solomon Islands/3/2006	9	4	8	A/Sofia/246/2006	A/New York/8/2006
2008-09	A/Brisbane/59/2007	0	13	19	A/Tennessee/UR06-0151/2007	A/Ohio/UR06-0178/2007
2009-10	A/Brisbane/59/2007	87	88	90	A/Sendai/TU66/2008	A/Japan/618/2008
2010-11	A/California/7/2009	2	1	6	A/South Carolina/WRAIR1645P/2009	A/Wisconsin/629-D00809/2009
2011-12	A/California/7/2009	4	1	3	A/England/21680633/2010	A/Hangzhou/178/2010
2012-13	A/California/7/2009	4	1	22	A/Joshkar-Ola/CRIE-BLP/2011	A/Rio Grande do Sul/578/2011
2013-14	A/California/7/2009	5	4	13	A/Thailand/MR10580/2012	A/Mexico/INMEGEN-INER 15/2012
2014-15	A/California/7/2009	9	3	7	A/Minnesota/02/2013	A/Helsinki/430/2013
2015-16	A/California/7/2009	14	4	7	A/Helsinki/808M/2014	A/Virginia/NHRC430739/2014
2016-17	A/California/7/2009	14	0	3	A/Michigan/45/2015	A/Colorado/30/2015
2017-18	A/Michigan/45/2015	3	3	8	A/Mexico/4436/2016	A/Arizona/03/2016
2018-19	A/Michigan/45/2015	4	0	4	A/California/NHRC_QV11073/2017	A/Minnesota/35/2017
2019-20	A/Brisbane/02/2018	1	0	2	A/Kenya/47/2018	A/Colorado/7682/2018
2020-21	A/Hawaii/70/2019	0	3	8	A/California/NHRC-OID_BOX-ILI- 0012/2019	A/Indiana/30/2019
2021-22	A/Victoria/2570/2019	1	5	51	A/Togo/0071/2021	A/Yunnan-Mengzi/1462/2020
2022-23	-1	-1	-1	-1	A/Netherlands/10646/2022	A/Sydney/234/2022

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 13 H1N1 NA SOUTHERN HEMISPHERE (MULTI-CLUSTER)

Year	WHO Recommendation	WHO Error	Qnet Error 1	Qnet Error 2	Qnet Recommendation 1	Qnet Recommendation 2
2001-02	A/New Caledonia/20/99	4	1	6	A/New South Wales/26/2000	A/Canterbury/37/2000
2002-03	A/New Caledonia/20/99	1	0	5	A/Wellington/1/2001	A/New York/447/2001
2003-04	A/New Caledonia/20/99	3	2	8	A/Paris/0833/2002	A/Taiwan/141/2002
2004-05	A/New Caledonia/20/99	2	3	4	A/Memphis/5/2003	A/Hanoi/1004/2003
2005-06	A/New Caledonia/20/99	3	0	1	A/Denmark/130/2004	A/Paris/650/2004
2006-07	A/New Caledonia/20/99	4	2	8	A/Sofia/361/2005	A/Wellington/11/2005
2007-08	A/New Caledonia/20/99	4	4	8	A/Sofia/246/2006	A/New York/8/2006
2008-09	A/Solomon Islands/3/2006	15	13	19	A/Tennessee/UR06-0151/2007	A/Ohio/UR06-0178/2007
2009-10	A/Brisbane/59/2007	87	88	90	A/Sendai/TU66/2008	A/Japan/618/2008
2010-11	A/California/7/2009	2	1	6	A/South Carolina/WRAIR1645P/2009	A/Wisconsin/629-D00809/2009
2011-12	A/California/7/2009	4	1	3	A/England/21680633/2010	A/Hangzhou/178/2010
2012-13	A/California/7/2009	4	1	22	A/Joshkar-Ola/CRIE-BLP/2011	A/Rio Grande do Sul/578/2011
2013-14	A/California/7/2009	5	4	13	A/Thailand/MR10580/2012	A/Mexico/INMEGEN-INER 15/2012
2014-15	A/California/7/2009	9	3	7	A/Minnesota/02/2013	A/Helsinki/430/2013
2015-16	A/California/7/2009	14	4	7	A/Helsinki/808M/2014	A/Virginia/NHRC430739/2014
2016-17	A/California/7/2009	14	0	3	A/Michigan/45/2015	A/Colorado/30/2015
2017-18	A/Michigan/45/2015	3	3	8	A/Mexico/4436/2016	A/Arizona/03/2016
2018-19	A/Michigan/45/2015	4	0	4	A/California/NHRC_QV11073/2017	A/Minnesota/35/2017
2019-20	A/Michigan/45/2015	4	0	2	A/Kenya/47/2018	A/Colorado/7682/2018
2020-21	A/Brisbane/02/2018	5	2	7	A/California/NHRC-OID_BOX-ILI- 0012/2019	A/Indiana/30/2019
2021-22	A/Victoria/2570/2019	1	7	58	A/Togo/0155/2021	A/Shandong/00204/2021
2022-23	-1	-1	-1	-1	A/Switzerland/86136/2022	A/Wisconsin/04/2021

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 14 H3N2 NA NORTHERN HEMISPHERE (MULTI-CLUSTER)

Year	WHO Recommendation	WHO Error	Qnet Error 1	Qnet Error 2	Qnet Recommendation 1	Qnet Recommendation 2
2003-04	A/Moscow/10/99	13	4	5	A/Auckland/612/2002	A/New York/87/2002
2004-05	A/Fujian/411/2002	3	16	18	A/New York/20/2003	A/New York/12/2003
2005-06	A/California/7/2004	4	1	7	A/New York/358/2004	A/Singapore/36/2004
2006-07	A/Wisconsin/67/2005	1	3	8	A/Macau/557/2005	A/Hong Kong/HKU53/2005
2007-08	A/Wisconsin/67/2005	8	0	10	A/Wisconsin/42/2006	A/Wisconsin/44/2006
2008-09	A/Brisbane/10/2007	3	4	10	A/Missouri/06/2007	A/Japan/72/2007
2009-10	A/Brisbane/10/2007	3	1	7	A/Wisconsin/24/2008	A/Mississippi/UR07-0042/2008
2010-11	A/Perth/16/2009	2	3	8	A/New York/70/2009	A/Japan/883/2009
2011-12	A/Perth/16/2009	3	2	2	A/California/19/2010	A/Virginia/05/2010
2012-13	A/Victoria/361/2011	4	1	12	A/Texas/14/2011	A/Singapore/GP1684/2011
2013-14	A/Victoria/361/2011	3	1	5	A/Idaho/38/2012	A/Pavia/135/2012
2014-15	A/Texas/50/2012	3	1	1	A/Nevada/05/2013	A/Michigan/02/2013
2015-16	A/Switzerland/9715293/2013	3	0	4	A/Nicaragua/6866_14/2014	A/Iran/91244/2014
2016-17	A/Hong Kong/4801/2014	7	1	25	A/New Jersey/13/2015	A/California/NHRC_BRD41056N/2015
2017-18	A/Hong Kong/4801/2014	9	1	4	A/Guangdong/264/2016	A/Victoria/668/2016
2018-19	A/Singapore/INFIMH-16- 0019/2016	3	2	4	A/Netherlands/3530/2017	A/Washington/17/2017
2019-20	A/Kansas/14/2017	3	4	10	A/England/538/2018	A/California/BRD12490N/2018
2020-21	A/Hong Kong/2671/2019	3	1	13	A/England/9738/2019	A/Washington/9757/2019
2021-22	A/Cambodia/e0826360/2020	2	3	7	A/Laos/527/2021	A/Michigan/UOM10045655748/2020
2022-23	-1	-1	-1	-1	A/Maine/02/2022	A/Michigan/UOM10042819294/2021

^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

SI Tab. 15 H3N2 NA SOUTHERN HEMISPHERE (MULTI-CLUSTER)

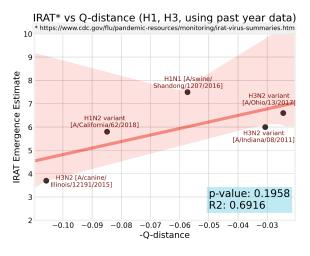
Year	WHO Recommendation	WHO Error	Qnet Error 1	Qnet Error 2	Qnet Recommendation 1	Qnet Recommendation 2
2003-04	A/Moscow/10/99	13	4	5	A/Auckland/612/2002	A/New York/87/2002
2004-05	A/Fujian/411/2002	3	16	18	A/New York/20/2003	A/New York/12/2003
2005-06	A/Wellington/1/2004	2	1	7	A/New York/358/2004	A/Singapore/36/2004
2006-07	A/California/7/2004	3	3	8	A/Macau/557/2005	A/Hong Kong/HKU53/2005
2007-08	A/Wisconsin/67/2005	8	0	10	A/Wisconsin/42/2006	A/Wisconsin/44/2006
2008-09	A/Brisbane/10/2007	3	4	10	A/Missouri/06/2007	A/Japan/72/2007
2009-10	A/Brisbane/10/2007	3	1	7	A/Wisconsin/24/2008	A/Mississippi/UR07-0042/2008
2010-11	A/Perth/16/2009	2	3	8	A/New York/70/2009	A/Japan/883/2009
2011-12	A/Perth/16/2009	3	2	2	A/California/19/2010	A/Virginia/05/2010
2012-13	A/Perth/16/2009	4	1	12	A/Texas/14/2011	A/Singapore/GP1684/2011
2013-14	A/Victoria/361/2011	3	1	5	A/Idaho/38/2012	A/Pavia/135/2012
2014-15	A/Texas/50/2012	3	1	1	A/Nevada/05/2013	A/Michigan/02/2013
2015-16	A/Switzerland/9715293/2013	3	0	4	A/Nicaragua/6866_14/2014	A/Iran/91244/2014
2016-17	A/Hong Kong/4801/2014	7	1	25	A/New Jersey/13/2015	A/California/NHRC_BRD41056N/2015
2017-18	A/Hong Kong/4801/2014	9	1	4	A/Guangdong/264/2016	A/Victoria/668/2016
2018-19	A/Singapore/INFIMH-16- 0019/2016	3	2	4	A/Netherlands/3530/2017	A/Washington/17/2017
2019-20	A/Switzerland/8060/2017	10	4	10	A/England/538/2018	A/California/BRD12490N/2018
2020-21	A/South Australia/34/2019	1	1	13	A/England/9738/2019	A/Washington/9757/2019
2021-22	A/Hong Kong/2671/2019	6	1	49	A/Darwin/11/2021	A/Hawaii/28/2020
2022-23	-1	-1	-1	-1	A/Congo/313/2021	A/Texas/12723/2022

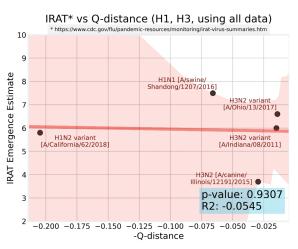
^{*} Dominant strain is calculated as the one closest to the centroid in the strain space that year in the edit distance metric

		SI Tab. 16		
RISKIEST	STRAINS	CURRENTLY CIRCLE	ATING IN	SWINE

H1N1 Strain	HA Risk	NA Risk	Overall Risk	Converted IRAT Score
A/swine/Tennessee/A02524414/2022	0.0201	0.0030	0.0077	6.2
A/swine/Missouri/A02750646/2022	0.0201	0.0070	0.0118	6.2
A/swine/Kansas/A02711847/2022	0.0201	0.0098	0.0141	6.2
A/swine/lowa/A02636572/2022	0.0166	0.0225	0.0193	6.1
A/swine/lowa/A02636308/2021	0.0143	0.0266	0.0195	6.1
A/swine/Illinois/A02750711/2022	0.0166	0.0233	0.0197	6.1
A/swine/lowa/A02636616/2022	0.0166	0.0233	0.0197	6.1
A/swine/Oklahoma/A02246915/2022	0.0166	0.0233	0.0197	6.1
A/swine/Colorado/A02636469/2022	0.0166	0.0233	0.0197	6.1
A/swine/lowa/A02636297/2021	0.0149	0.0267	0.0200	6.1
H3N2 Strain	HA Risk	NA Risk	Overall Risk	Converted IRAT Score
A/swine/Indiana/A02636492/2022	0.0104	0.0113	0.0108	6.2
A/swine/Indiana/A02636512/2022	0.0104	0.0113	0.0108	6.2
A/swine/lowa/A02750695/2022	0.0110	0.0120	0.0115	6.2
A/swine/Oklahoma/A02711859/2022	0.0122	0.0114	0.0118	6.2
A/swine/lowa/A02636351/2022	0.0121	0.0119	0.0120	6.2
A/swine/lowa/A02636476/2022	0.0121	0.0120	0.0121	6.2
A/swine/Texas/A02636569/2022	0.0122	0.0120	0.0121	6.2
A/swine/lowa/A02750726/2022	0.0123	0.0120	0.0121	6.2
A/swine/lowa/A02750740/2022	0.0104	0.0156	0.0127	6.2
A/swine/Indiana/A02636521/2022	0.0104	0.0156	0.0127	6.2

^{*} Converted IRAT Score computed using regression generated from the IRAT vs. Qnet comparison





SI Fig. 3. **IRAT vs. Q-distance relationship for H1- and H3- sub-types, using past year data vs. using all data.** On the result when computing average q-distance between the target strain and the circulating human strains from the past year, and on the right is the result when using all available human strains of that sub-type. Evidently, the former has a much higher correlation, since a strain being "close" to humans at some point does not necessarily mean being close now.

SI Tab. 17
INFLUENZA A STRAINS EVALUATED BY IRAT AND CORRESPONDING QNET COMPUTED RISK SCORES

Influenza Virus	Subype	IRAT Date	IRAT Emer- gence Score	IRAT Impact Score	HA Qnet Sample	NA Qnet Sample	HA Avg. Qdist	NA Avg. Q-dist.	Geom. Mean
A/swine/Shandong/1207/2016	H1N1	Jul 2020	7.5	6.9	1000	1000	0.0941	0.0205	0.0440
A/Ohio/13/2017	H3N2	Jul 2019	6.6	5.8	1000	1000	0.0184	0.0306	0.0238
A/Hong Kong/125/2017	H7N9	May 2017	6.5	7.5	437	437	0.0296	0.0058	0.0131
A/Shanghai/02/2013	H7N9	Apr 2016	6.4	7.2	178	178	0.0055	0.0036	0.0044
A/Anhui-Lujiang/39/2018	H9N2	Jul 2019	6.2	5.9	31	30	0.0290	0.1681	0.0698
A/Indiana/08/2011	H3N2	Dec 2012	6	4.5	1000	1000	0.0523	0.0091	0.0218
A/California/62/2018	H1N2	Jul 2019	5.8	5.7	55	55	0.1089	0.0610	0.0815
A/Bangladesh/0994/2011***	H9N2	Feb 2014	5.6	5.4	-1	-1	0.2078	0.1823	0.1947
A/Sichuan/06681/2021	H5N6	Oct 2021	5.3	6.3	45	45	0.3616	0.0518	0.1369
A/Vietnam/1203/2004	H5N1	Nov 2011	5.2	6.6	258	246	0.1673	0.0111	0.0430
A/Yunnan/14564/2015**	H5N6	Apr 2016	5	6.6	344	331	0.3482	0.2987	0.3225
A/Astrakhan/3212/2020**	H5N8	Mar 2021	4.6	5.2	381	365	0.1603	0.3472	0.2359
A/Netherlands/219/2003	H7N7	Jun 2012	4.6	5.8	46	46	0.2757	0.3521	0.3115
A/American wigeon/South Carolina/AH0195145/2021	H5N1	Mar 2022	4.4	5.1	335	323	0.1722	0.5114	0.2967
A/Jiangxi-Donghu/346/2013***	H10N8	Feb 2014	4.3	6	-1	-1	0.20878	0.2101	0.2094
A/gyrfalcon/Washington/41088/2014**	H5N8	Mar 2015	4.2	4.6	341	328	0.1532	0.3424	0.2290
A/Northern pintail/Washington/40964/2014**	H5N2	Mar 2015	3.8	4.1	341	328	0.1529	0.3799	0.2410
A/canine/Illinois/12191/2015	H3N2	Jun 2016	3.7	3.7	1000	1000	0.0607	0.1509	0.0957
A/American green-winged teal/Washington/1957050/2014	H5N1	Mar 2015	3.6	4.1	326	314	0.1911	0.4482	0.2927
A/turkey/Indiana/1573-2/2016**	H7N8	Jul 2017	3.4	3.9	495	494	0.1130	0.7738	0.2957
A/chicken/Tennessee/17-007431-3/2017	H7N9	Oct 2017	3.1	3.5	496	495	0.1027	0.2569	0.1624
A/chicken/Tennessee/17-007147-2/2017	H7N9	Oct 2017	2.8	3.5	496	495	0.2095	0.2541	0.2307
A/duck/New York/1996 *	H1N1	Nov 2011	2.3	2.4	1000	1000	-1	-1	-1

^{*} HA strain is not available for A/duck/New York/1996, so this strain is omitted.

** Could not construct a Qnet of human sequence data available for that virus sub-type (less than 30 strains), so we constructed a Qnet using all human strains that match the HA sub-type, i.e. H5NX for H5N6.

*** These strains did not have enough human sequence data to generate a Qnet, even when only considering the HA sub-type. Thus, we estimated the risk score using every Qnet from the other IRAT strains, and took the average among NA and HA. Finally, we took the geometric mean of the resulting NA and HA averages.

SI Tab. 18
INFLUENZA A STRAINS EVALUATED BY IRAT AND CORRESPONDING QNET COMPUTED CURRENT RISK SCORES

			T		1				1
Influenza Virus	Subype	IRAT Date	IRAT Emer- gence Score	IRAT Impact Score	HA Qnet Sample	NA Qnet Sample	HA Avg. Qdist	NA Avg. Q-dist.	Geom. Mean
A/swine/Shandong/1207/2016	H1N1	Jul 2020	7.5	6.9	1000	1000	0.0599	0.0417	0.0500
A/Ohio/13/2017	H3N2	Jul 2019	6.6	5.8	1000	1000	0.0091	0.0692	0.0251
A/Hong Kong/125/2017	H7N9	May 2017	6.5	7.5	1000	1000	0.0092	0.0046	0.0065
A/Shanghai/02/2013	H7N9	Apr 2016	6.4	7.2	1000	1000	0.0031	0.0044	0.0037
A/Anhui-Lujiang/39/2018	H9N2	Jul 2019	6.2	5.9	58	58	0.0157	0.0467	0.0271
A/Indiana/08/2011	H3N2	Dec 2012	6	4.5	1000	1000	0.0176	0.0184	0.0180
A/California/62/2018	H1N2	Jul 2019	5.8	5.7	37	37	0.2038	0.0477	0.0986
A/Bangladesh/0994/2011	H9N2	Feb 2014	5.6	5.4	58	58	0.0473	0.4654	0.1484
A/Sichuan/06681/2021	H5N6	Oct 2021	5.3	6.3	46	46	0.3443	0.0600	0.1437
A/Vietnam/1203/2004	H5N1	Nov 2011	5.2	6.6	48	45	0.1323	0.0411	0.0738
A/Yunnan/14564/2015	H5N6	Apr 2016	5	6.6	46	46	0.2187	0.0415	0.0953
A/Astrakhan/3212/2020	H5N8	Mar 2021	4.6	5.2	95	92	0.2366	0.5451	0.3591
A/Netherlands/219/2003	H7N7	Jun 2012	4.6	5.8	1000	1000	0.1658	0.4596	0.2760
A/American wigeon/South Carolina/AH0195145/2021	H5N1	Mar 2022	4.4	5.1	48	45	0.2355	0.3135	0.2717
A/Jiangxi-Donghu/346/2013	H10N8	Feb 2014	4.3	6	-1	-1	-1	-1	-1
A/gyrfalcon/Washington/41088/2014	H5N8	Mar 2015	4.2	4.6	95	92	0.2387	0.5438	0.3603
A/Northern pintail/Washington/40964/2014	H5N2	Mar 2015	3.8	4.1	95	92	0.2327	0.5099	0.3445
A/canine/Illinois/12191/2015	H3N2	Jun 2016	3.7	3.7	1000	1000	0.0179	0.0374	0.0259
A/American green-winged teal/Washington/1957050/2014	H5N1	Mar 2015	3.6	4.1	48	45	0.2352	0.3067	0.2686
A/turkey/Indiana/1573-2/2016	H7N8	Jul 2017	3.4	3.9	1000	1000	0.0438	0.4165	0.1351
A/chicken/Tennessee/17-007431-3/2017	H7N9	Oct 2017	3.1	3.5	1000	1000	0.0335	0.5127	0.1310
A/chicken/Tennessee/17-007147-2/2017	H7N9	Oct 2017	2.8	3.5	1000	1000	0.0839	0.5127	0.2075
A/duck/New York/1996	H1N1	Nov 2011	2.3	2.4	1000	1000	-1	-1	-1

^{*}This table contains Qnet scores for IRAT computed using current sequence data, thereby computing the current risk of these strains. -1 indicates missing data, either from lack of human sequence data available for that virus sub-type (less than 30 strains) or missing IRAT sequence data (in the case of A/duck/New York/1996)

SI Tab. 19
GENERAL LINEAR MODEL FOR EVALUATING EFFECT OF DATA DIVERSITY ON QNET PERFORMANCE

Variable Name	Description
qnet_complexity	Cumulative number of nodes in all predictors in the corresponding Qnet
data_diversity	Number of clusters in set of input sequence where each sequence in a specific cluster is separated by at least 5 mutations from sequences not in the cluster
ldistance_WHO	Deviation of WHO predicted strain from the dominant strain

Dep. Variable: Model: Model Family: Link Function: Method: Date: Time: No. Iterations:	dev GLM Gaussian identity IRLS Thu, 11 Jun 2020 16:45:46 3	No. Observations: Df Residuals: Df Model: Scale: Log-Likelihood: Deviance: Pearson chi2: Covariance Type:	235 230 4 23.214 -700.43 5339.2 5.34e+03 nonrobust
No. Iterations:	3 	Covariance Type:	nonrobust

	coef	std err	Z	P> z	[0.025	0.975]
Intercept qnet_complexity data_diversity qnet_complexity:data_diversity ldistance_WHO	-0.1116	1.090	-0.102	0.918	-2.248	2.025
	0.0005	0.000	1.075	0.282	-0.000	0.001
	0.3197	0.126	2.531	0.011	0.072	0.567
	-6.932e-05	5.01e-05	-1.383	0.167	-0.000	2.89e-05
	-0.0348	0.035	-1.007	0.314	-0.102	0.033

_==============				
Dep. Variable:		dev	No. Observations:	235
Model:		GLM	Df Residuals:	231
Model Family:		Gaussian	Df Model:	3
Link Function:		identity	Scale:	23.306
Method:		IRLS	Log-Likelihood:	-701.41
Date:	Thu,	11 Jun 2020	Deviance:	5383.6
Time:		16:45:47	Pearson chi2:	5.38e+03
No. Iterations:		3	Covariance Type:	nonrobust

	coef	std err	Z	P> z	[0.025	0.975]
Intercept qnet_complexity data_diversity ldistance_WHO	1.0841 -4.12e-05 0.1788 -0.0695	0.665 0.000 0.075 0.024	1.630 -0.156 2.392 -2.930	0.103 0.876 0.017 0.003	-0.219 -0.001 0.032 -0.116	2.387 0.000 0.325 -0.023
		========			=========	

 $$\operatorname{Si}$ Tab. 20 General linear model evaluating QNET emergence risk predictions against IRAT estimates

Dep. Variable: Model: Model Family: Link Function: Method: Date: Time: No. Iterations: Covariance Type:	Tue,	GLM Gaussian identity IRLS 25 Oct 2022 00:58:27 3 nonrobust	Df Resid Df Model Scale: Log-Like Deviance Pearson Pseudo F	l: elihood: e:		22 20 1 0.86853 -28.618 17.371 17.4 0.5919	
		std err		P> z	[0.025	0.975]	
Intercept Geometric_Mean	6.2467	0.356	17.529	0.000	5.548	6.945	
Model: IRAT Emero	ence Score	~ Geometric	Mean + HA	Ava Odist*NA	. Ava Odist	E	
Model: IRAT_Emerg ====================================	IRAT_Eme	rgence_Score GLM Gaussian identity IRLS 25 Oct 2022 00:58:59 3 nonrobust	No. Obse Df Resic Df Model Scale: Log-Like Deviance Pearson Pseudo F	ervations: duals: l: elihood: e: chi2: R-squ. (CS):		22 17 4 0.69369 -24.357 11.793 11.8 0.7797	

SI Tab. 21 ION TO PDM09 AND H3 SCHEMES Νu

Query	H1N1pdm	H3
	-	-
3	-	-
4	-	-
5	-	-
6	-	-
7	-	-
8	-	-
9	-	-
10	-	-
11 12	-	-
13	-	-
14	-	-
15	-	-
16	-	-
17	-	-
	-	1
	-	2
	-	4
-	-	5
	-	6
	-	7
-	<u> </u>	8
-	-	9
-	-	10
18	1	11
19	2	12
20	3	13
21	5	15
23	6	16
24	7	17
25	8	18
26	9	19
27	10	20
28	11	21
29	12	22
30	13	23
31	14	24
33	15 16	25 26
34	17	27
35	18	28
36	19	29
37	20	30
38	21	31
39	22	32
40	23	33
41 42	25	35
43	26	36
44	27	37
45	28	38
46	29	39
47	30	40
48	31	41
49	32	42
50 51	33	43
52	35	45
53	36	46
54	37	47
55	38	48
56	39	49
57	40	50
58	41	51
59	42	52 53
60	43	53
62	45	-
63	46	55
64	47	56
65	48	57
66	49	58
67	50	59
68	51	60
	-	-
-	-	-
-	-	-
-	+ -	-
69	52	61
70	53	62
71	54	63
72	55	64
73	56	65
74	57	66
75	58	67

Query	H1N1pdm	НЗ
77	60	69
78 79	61 62	70
30	63	72
B1	64	73
82	65	74
83	66	75
84	67	76
85 86	68 69	77
87	70	79
88	71	80
89	72	81
90	73	82
91 92	74 75	83
93	76	84
94	77	85
95	78	86
96	79	87
97	80	88
98 aa	81	89
99 100	82 83	90
101	84	92
102	85	L-
103	86	93
104	87	94
105	88	95
106	89	96
107 108	90	97 98
108	91	98
110	93	100
111	94	101
112	95	102
	-	-
	-	-
113	96	103
114 115	97 98	104
116	99	105
117	100	106
118	101	108
119	102	109
120	103	110
121	104	111
122	105	112
123	106	113
124 125	107	114
126	108	116
127	110	117
128	111	118
129	112	119
130	113	120
131	114	121
132	115	122
133	116	123
	-	-
134	117	124
135	118	125
136	119	-
137	120	-
138	121	-
139	122	126
140 141	123	127
	124	128
	-	-
	-	-
	-	-
	-	-
142	125	129
143	126	130
144	127	131
145 146	128 129	132
146	130	-
148	131	134
149	132	135
150	133	136
151	134	137
152	135	138
153	136	139
154	137	140
155	138	141

8 141 144	141	Query 57	H1N1pdm 140	H3 143	Query	H1N1pdm -	H3
9 1 442	142	58	141			-	-
0 143	143	59	142	145	-	-	-
1 144	144	60			238	221	224
2 145 148 240 223 3 3 146 149 241 224 4 4 147 150 242 225 5 5 148 151 244 226 6 6 149 152 244 227 7 7 150 153 245 228 8 8 151 154 246 229 9 9 152 155 247 230 0 153 156 157 249 232 23	146						
3	146	61					_
4 1 477 150 242 225 5 5 148 151 243 226 6 149 152 244 227 7 150 153 245 228 8 151 154 246 229 9 9 152 155 247 230 0 153 156 248 231 1 154 157 249 232 2 25 253 236 231 2 255 233 1 255 233 236 2 252 235 2 251 234 2 252 235 2 253 236 236 237 236 237 236 237 236 237 236 255 233 236 237 236 237 236 237 236 237 236 246 240 66 159 162 255 233 236 255 233 236 246 <td< td=""><td> 147</td><td>62</td><td>_</td><td></td><td></td><td></td><td>_</td></td<>	147	62	_				_
5 148 151 243 226 6 149 152 244 227 7 150 153 245 228 8 151 154 246 229 9 152 155 247 230 0 153 156 248 231 1 154 157 249 232 2 155 158 250 233 - - - 251 234 - - - 252 235 - - - 252 235 - - - 252 235 - - - 252 235 236 - - - 252 235 236 4 157 160 163 259 242 239 5 158 161 257 240 26 289	148	63	146	149	241	224	22
5 148 151 243 226 6 149 152 244 227 7 150 153 245 228 8 151 154 246 229 9 152 155 247 230 0 153 156 248 231 1 154 157 249 232 2 155 158 250 233 - - - 251 234 - - - 252 235 - - - 252 235 - - - 252 235 - - - 252 235 236 - - - 252 235 236 4 157 160 163 259 242 239 5 158 161 257 240 26 289	148	64					_
6 149 152 244 227 7 7 150 153 246 228 3 3 151 154 246 229 9 152 155 158 247 230 0 0 153 156 248 231 1 154 157 249 232 2 2 2 2 2 2 2 2	149	65					
Total Tota	150						_
8 151 154 246 229 9 9 152 155 247 230 0 0 153 156 248 231 1 1 154 157 249 232 2 2 155 158 250 233 251 234 252 253 236 252 235 236 252 235 236 255 238 255 238 4 157 160 256 239 5 5 158 161 257 240 6 6 159 162 258 241 257 240 6 159 162 258 241 160 161 161 161 161 161 161 161 161 161 162 258 244 247 249 162 248 241 161 164 167 263 246 249 242 244 162	151	66					
9 152 155 126 247 230 1 153 156 248 231 1 154 157 249 232 2 155 158 250 233 2	152	67	150	153	245	228	23
9 152 155 126 247 230 1 153 156 248 231 1 154 157 249 232 2 155 158 250 233 2	153	68	151	154	246	229	23
0	153	69	152	155	247	230	23
1 154 157 249 232 232 233 232 251 234 251 234 251 234 251 234 252 255 236 252 255 236 257 252 225 236 255 236 257 240 256 239 4 157 160 256 239 4 157 160 163 256 239 422 240 6 159 162 258 241 7 160 163 260 243 9 162 268 241 1 6 163 166 163 269 242 245 1 166 163 166 262 245 1 164 167 263 246 224 247 3 166 169 265 248 1 164 167 170 266 249 2 247 250 168 171 170 266	154						_
2	155						_
- -		71	154	157	249	232	23
150 150		72	155	158	250	233	23
150 150			-	-	251	234	23
156							_
150	156						_
156	156		-	-			
157	157		-	-	254	237	24
157	157	73	156	159	255	238	24
5 158 161 257 240 6 159 162 258 241 7 160 163 259 242 8 8 161 164 260 243 9 162 165 261 244 260 243 9 162 165 261 244 260 243 9 162 165 261 244 260 243 9 162 165 261 244 260 243 9 162 165 261 244 167 166 168 264 247 3 166 169 162 265 248 4 167 170 266 249	158	74					
Section Sect	159						_
7 160 163 259 242 8 161 164 260 243 9 162 165 261 244 0 163 166 262 245 1 164 167 263 246 2 165 168 264 247 3 166 169 265 248 4 167 170 266 249 - - 267 250 - 5 168 171 268 251 - 6 169 172 269 252 - 7 170 173 270 253 - 8 171 174 272 255 9 252 - 9 172 175 7 275 258 27 255 9 271 254 257 255 9 272 255 <t< td=""><td> 160</td><td>75</td><td></td><td></td><td></td><td></td><td></td></t<>	160	75					
8 161 164 260 243 9 9 162 165 261 244 9 162 165 261 244 1 2 165 166 262 245 1 164 167 263 246 247 3 166 169 265 248 4 167 170 266 249 - 267 250 25 248 4 167 170 266 249 - 267 250 25 27 170 173 270 253 - - 267 250 25 - - 261 249 - - 271 253 - - 271 253 - - 271 253 - - 252 - - 267 250 - 253 - - 261 147 147 174 272 255 - - 261 147	161	76	159	162	258	241	24
8 161 164 260 243 9 9 162 165 261 244 9 162 165 261 244 1 2 165 166 262 245 1 164 167 263 246 247 3 166 169 265 248 4 167 170 266 249 - 267 250 25 248 4 167 170 266 249 - 267 250 25 27 170 173 270 253 - - 267 250 25 - - 261 249 - - 271 253 - - 271 253 - - 271 253 - - 252 - - 267 250 - 253 - - 261 147 147 174 272 255 - - 261 147	161	77	160	163	259	242	24
9	162	78					
0	163		•				_
1 164 167 263 246 247 2 165 168 264 247 3 166 169 265 248 247 3 166 169 265 248 4 167 170 266 249 252 250 252 250 252 250 252 252 270 253 271 266 249 252 271 269 252 271 269 252 271 270 253 272 253 272 253 272 253 273 256 20 272 255 9 172 175 273 256 273 256 273 256 273 256 273 256 273 256 273 256 259 33 176 177 275 258 273 256 259 33 176 177 275 258 251 178 181 177 275 2	164	79					
1 164 167 263 246 247 2 165 168 264 247 3 166 169 265 248 247 3 166 169 265 248 4 167 170 266 249 252 250 250 250 250 252 7 270 253 270 253 270 253 270 253 270 253 270 253 271 253 255 9 172 271 255 273 256 0 273 256 0 273 256 0 173 176 172 275 258 273 256 0 173 176 174 277 275 258 0 173 176 177 275 258 273 256 0 183 180 181 181 181 181 181 181 181 181 181 181 181	164	80	163	166	262	245	24
2 165 168 264 247 3 166 169 265 248 4 167 170 266 249 - - - 267 250 5 168 171 268 251 6 169 172 269 252 7 170 173 270 253 - - - 271 254 8 171 174 272 255 9 172 175 273 256 0 173 176 274 257 258 1 174 177 275 258 27 2 175 178 276 258 3 3 176 179 - - - 4 177 180 - - - 5 178 181 - - -	165	81		167	263	246	24
3 166 169 265 248 4 167 170 266 249 - - - 267 250 5 168 171 268 251 6 169 172 269 252 7 170 173 270 253 - - - 271 254 8 171 174 272 255 9 172 175 273 256 0 173 176 274 257 258 1 174 177 275 258 27 251 27 256 3 176 179 -	166	82					
4 167 170 266 249 5 168 171 268 249 5 168 171 268 251 6 169 172 269 252 7 170 173 270 253 8 171 174 272 255 9 172 175 273 256 0 173 176 274 257 1 174 177 275 258 2 175 178 276 259 3 176 179 - - 4 177 180 - - 5 178 181 - - 6 179 182 - - 7 180 183 - - 8 181 184 - - 9 182 185 - - <td> 167</td> <td>83</td> <td></td> <td></td> <td></td> <td></td> <td></td>	167	83					
Section Sect							_
5 168 171 268 251 6 169 172 269 252 7 170 173 270 253 - - - - 271 254 8 171 174 272 255 9 9 172 175 273 256 9 1 174 177 275 258 251 1 174 177 275 258 259 3 176 179 - <t< td=""><td> 168</td><td>84</td><td></td><td></td><td></td><td></td><td>_</td></t<>	168	84					_
6	169		-	-	267	250	25
6	169	85	168	171	268	251	25
7 170 173 270 253 271 254 271 254 271 254 271 254 271 254 271 254	170	86					
Section Sect							_
8 171 174 272 255 9 172 175 273 256 0 173 176 274 257 258 1 174 177 275 258 258 2175 258 276 259 33 176 179 276 259 33 176 179 277 180 276 259 33 176 179 277 278 258 277 260 38 181 -	171	87	1/0	1/3			
9	172		-	-	271		25
9	172	88	171	174	272	255	25
0 173 176 274 257 1 174 177 275 258 1 175 178 276 258 259 3 176 179 - <t< td=""><td> 173</td><td>89</td><td></td><td></td><td></td><td></td><td></td></t<>	173	89					
1 174 177 275 258 2 175 178 276 259 3 176 179 4 177 180 5 178 181 6 179 182	174	90				l	
2 175 178 276 259 3 176 179 - - 4 177 180 - - 5 178 181 - - 6 179 182 - - 7 180 183 - - 8 181 184 - - 9 182 185 - - 0 183 186 - - 1 184 187 - - 2 185 188 277 260 - 3 186 189 278 262 - 4 187 190 279 262 - 5 188 191 280 263 - 6 189 192 281 265 - 7 190 193 282 265 -	175					l	
3	176	91					
3	176	92	175	178	276	259	26
44 177 180 - - - - 5 178 181 -	177	93			_		-
5 178 181 - - - 6 179 182 -	178				-		
6 179 182 7 180 183 181 184 184 181 184 185 188 186 1 184 187 1 184 187 1 184 187 1 187 188 188 186 189 188 186 189 188 186 189 188 186 189 188 186 189 188 186 189 189 182 185 188 191 180 180 180 180 180 180 180 180 180 18	179	94					
7	180	95	178	181	-	-	-
7	180	96	179	182	-	-	-
8 181 184 - - - 9 182 185 -	181	97			_	-	-
9	182						
0 183 186 - <td> 183</td> <td>98</td> <td></td> <td></td> <td>-</td> <td></td> <td>-</td>	183	98			-		-
1 184 187 - <td> 184</td> <td>99</td> <td></td> <td></td> <td>-</td> <td></td> <td>-</td>	184	99			-		-
2 185 188 277 260 3 186 189 278 261 4 187 190 279 262 5 188 191 280 263 6 189 192 281 264 7 190 193 282 265 8 191 194 283 266 9 192 195 284 267 0 193 196 285 268 1 194 197 286 269 2 195 198 287 270 3 196 199 288 271 - - 289 272 4 197 200 290 273 5 198 201 291 274 6 199 202 292 275 7 200 203 293 276	185 188 277 260 - 186 189 278 261 26 187 190 279 262 26 188 191 280 263 26 189 192 281 264 26 190 193 282 265 26 191 194 283 266 26 191 194 283 266 26 192 195 284 267 26 268 268 268 27 26 193 196 285 268 26 26 194 197 286 269 27 195 198 287 270 27 195 198 287 270 27 27 27 27 27 27 27 27 27 27 27 27 27 27 27 27 27 2	00	183	186	-	-	-
2 185 188 277 260 3 186 189 278 261 4 187 190 279 262 5 188 191 280 263 6 189 192 281 264 7 190 193 282 265 8 191 194 283 266 9 192 195 284 267 0 193 196 285 268 1 194 197 286 269 2 195 198 287 270 3 196 199 288 271 - - 289 272 4 197 200 290 273 5 198 201 291 274 6 199 202 292 275 7 200 203 293 276	185 188 277 260 - 186 189 278 261 26 187 190 279 262 26 188 191 280 263 26 189 192 281 264 26 190 193 282 265 26 191 194 283 266 26 191 194 283 266 26 192 195 284 267 26 268 268 268 27 26 193 196 285 268 26 26 194 197 286 269 27 195 198 287 270 27 195 198 287 270 27 27 27 27 27 27 27 27 27 27 27 27 27 27 27 27 27 2	01	184	187	-	-	-
3 186 189 278 261 4 187 190 279 262 5 188 191 280 263 6 189 192 281 264 7 190 193 282 265 8 191 194 283 266 9 192 195 284 267 0 193 196 285 288 269 1 194 197 286 269 22 2 195 198 287 270 3 3 196 199 288 271 - 289 272 - 4 197 200 290 273 5 198 201 291 274 - 4 197 200 290 275 - 289 272 - 4 197 200 203 293	186 189 278 261 26 187 190 279 262 26 188 191 280 263 26 189 192 281 264 26 190 193 282 265 26 191 194 283 266 26 192 195 284 267 26 193 196 285 268 27 194 197 286 269 27 195 198 287 270 27 196 199 288 271 27 196 199 288 271 27 197 200 290 273 27 197 200 290 273 27 198 201 291 274 27 200 293 293 276 27 200 203 293	02			277	260	
4 187 190 279 262 5 188 191 280 263 3 6 189 192 281 264 263 7 190 193 282 265 3 8 191 194 283 266 3 9 192 195 284 267 3 0 193 196 285 268 3 1 194 197 286 269 28 2 195 198 287 270 3 3 196 199 288 271 270 20 290 273 3 4 197 200 290 273 2 290 273 2 290 273 2 2 292 275 2 20 292 275 2 2 292 275 2 2 200 293	187 190 279 262 26 188 191 280 263 26 189 192 281 264 26 190 193 282 265 26 191 194 283 266 26 192 195 284 267 26 193 196 285 268 269 27 194 197 286 269 27 29 270 27 195 198 287 270 27 29 27 290 273 27 27 290 273 27 297 280						
5 188 191 280 263 6 189 192 281 264 . 7 7 190 193 282 265 . 8 191 194 283 266 .	188	03		189	278	261	26
66 189 192 281 264 7 190 193 282 265 8 8 191 194 283 266 9 9 192 195 284 267 26 0 193 196 285 268 269 22 269 270 33 196 199 286 269 270 33 196 199 288 271 272 272 272 272 4 197 200 290 273 272 272 4 197 200 290 273 272 272 4 197 200 290 273 272 274 6 199 202 292 275 7 200 203 293 276 289 272 274 4 197 200 203 293 276 28 201 294 277 279 200 203 206	189 192 281 264 26 190 193 282 265 26 191 194 283 266 26 192 195 284 267 26 193 196 285 268 27 194 197 286 269 27 195 198 287 270 27 196 199 288 271 27 196 199 288 271 27 197 200 290 273 27 197 200 290 273 27 198 201 291 274 27 199 202 292 275 27 200 293 293 276 27 201 204 294 277 27 202 205 295 278 28 203 203 206	04	187	190	279	262	26
66 189 192 281 264 7 190 193 282 265 8 8 191 194 283 266 9 9 192 195 284 267 26 0 193 196 285 268 269 22 269 270 33 196 199 286 269 270 33 196 199 288 271 272 272 272 272 4 197 200 290 273 272 272 4 197 200 290 273 272 272 4 197 200 290 273 272 274 6 199 202 292 275 7 200 203 293 276 289 272 274 4 197 200 203 293 276 28 201 294 277 279 200 203 206	189 192 281 264 26 190 193 282 265 26 191 194 283 266 26 192 195 284 267 26 193 196 285 268 27 194 197 286 269 27 195 198 287 270 27 196 199 288 271 27 196 199 288 271 27 197 200 290 273 27 197 200 290 273 27 198 201 291 274 27 199 202 292 275 27 200 293 293 276 27 201 204 294 277 27 202 205 295 278 28 203 203 206	05	188	191	280	263	26
7	190						_
8 191 194 283 266 9 192 195 284 267 0 193 196 285 268 1 194 197 286 269 2 195 198 287 270 3 196 199 288 271 - - 289 272 - 4 197 200 290 273 - 5 198 201 291 274 - 6 199 202 292 275 - 7 200 203 293 276 - 8 201 204 294 277 - 9 202 295 295 278 - 9 202 205 295 295 278 - - - - - - - - - - - -	191		1				
9 192 195 284 267 1 1 194 197 286 289 287 270 3 3 196 199 288 271 270 289 272 4 4 197 200 290 273 273 274 6 6 199 202 292 275 276 278 279 279 279 279 279 279 279 279 279 279	192	07					
9 192 195 284 267 1 1 194 197 286 289 287 270 3 3 196 199 288 271 270 289 272 4 4 197 200 290 273 273 274 6 6 199 202 292 275 276 278 279 279 279 279 279 279 279 279 279 279	192	08	191	194	283	266	26
0 193 196 285 268 1 194 197 286 269 2 195 198 287 270 3 196 199 288 271 4 197 200 290 273 5 198 201 291 274 6 199 202 292 225 7 200 203 293 276 8 201 204 294 277 9 202 205 295 278 0 203 206 296 279 1 204 207 297 280 2 205 208 298 281 3 206 209 299 282 4 207 210 300 283 5 208 221 301 284 6 209 212 301	193 196 285 268 27 194 197 286 269 27 195 198 287 270 27 196 199 288 271 27 197 200 290 273 27 197 200 290 273 27 198 201 291 274 27 200 203 293 276 27 201 204 294 277 27 202 205 295 278 28 203 206 296 279 28 204 297 297 28 28 205 208 298 281 28 206 209 299 282 28 206 209 299 282 28 207 210 300 283 28 208 211 -	09		195	284	267	26
1 194 197 286 269 2 195 198 287 270 3 196 199 288 271 - - - 289 272 4 197 200 290 273 5 5 198 201 291 274 6 199 202 292 275 7 200 203 293 276 27 200 203 293 276 294 277 29 202 295 295 278 200 203 206 294 277 29 202 205 295 2295 278 200 203 206 296 279 280 229 229 285 281 3 206 208 228 281 3 206 209 299 282 281 3 206 209 299 282 281 3 206 209 <td> 194</td> <td>10</td> <td></td> <td></td> <td></td> <td></td> <td></td>	194	10					
2 195 198 287 270 3 196 199 288 271 - - - 289 272 4 197 200 290 273 5 198 201 291 274 6 199 202 292 275 7 200 203 293 276 8 201 204 294 277 9 202 205 295 278 0 203 206 296 279 280 1 204 297 280 29 227 278 0 203 206 296 279 280 29 282 281 3 286 279 280 281 281 3 266 299 282 281 3 262 209 289 281 3 262 285 3 286 3	195 198 287 270 27 196 199 288 271 27 - - 289 272 27 197 200 290 273 27 198 201 291 274 27 199 202 292 275 27 200 203 293 276 27 201 204 294 277 27 202 205 295 278 28 203 296 296 279 28 204 207 297 280 28 205 208 298 281 28 206 209 299 282 28 206 209 299 282 28 207 210 300 283 28 208 211 - - - 209 212 301 2						
3 196 199 288 271 - - 289 272 4 197 200 290 292 5 198 201 291 274 6 199 202 292 275 7 200 203 293 226 8 201 204 294 277 9 202 205 295 278 0 0 203 206 296 279 1 1 204 207 297 280 28 281 3 2 205 208 298 281 3 3 206 299 299 282 3 4 207 210 300 283 3 3 26 209 299 282 3 5 208 211 - - - - - - - -	196	11					
		12	195	198	287	270	27
		13	196	199	288	271	27
4 197 200 290 273 5 198 201 291 274 6 199 202 292 225 7 200 203 293 276 8 201 204 294 277 9 202 205 295 278 0 203 206 296 279 1 204 297 297 280 2 205 208 298 281 3 206 209 289 281 3 206 209 289 281 4 207 210 300 283 5 208 211 - - 6 209 212 301 284 7 210 213 302 285 8 211 214 303 286 9 212 215 304	197 200 290 273 271 198 201 291 274 27 199 202 292 275 27 200 203 293 276 27 201 204 294 277 27 202 205 295 278 28 203 206 296 279 28 28 204 207 297 280 28 <		l -	_			
5 198 201 291 274 6 199 202 292 275 7 200 203 293 226 8 201 204 294 277 9 202 205 295 278 0 203 206 296 296 279 1 204 207 297 280 28 281 3 2 205 208 298 281 3 3 206 209 299 282 3 4 207 210 300 283 3 3 26 299 282 3 3 5 208 211 -	198	1.4	107	200			
6 199 202 292 275 7 200 203 293 276 8 201 204 294 227 9 205 295 278 0 205 295 278 0 205 295 278 0 205 295 278 206 296 279 1 204 204 207 297 280 2 205 208 298 281 3 206 209 299 282 3 206 209 299 282 3 206 209 299 282 3 206 209 212 301 284 207 210 300 283 206 209 212 301 284 3 302 285 8 211 214 303 286 3 211 214 303 286 3 211 214 303 286 3 211 214 303 286 3 211 214 303 286 3 211 214 303 286 3 211 214 303 286 3 211 214 303 286 3 211 214 303 286 3 211 214 303 286 3 211 214 217 306 289 3 216 219 308 291 308 291 308 291 308 291 309 292 311 294 310 293 3 216 219 222 311 294 310 293 3 266 219 222 311 294 37 220 223	199	14	t				
7 200 203 293 276 8 201 204 294 277 9 202 205 295 278 0 203 206 296 279 1 204 207 297 280 2 205 208 298 281 3 206 209 299 282 4 207 210 300 283 5 208 211 - - 6 209 212 301 284 7 210 213 302 285 8 211 214 303 286 9 212 215 304 287 0 213 216 305 288 1 214 217 306 289 2 215 218 307 290 3 216 219 308	200 203 293 276 27 201 204 294 277 27 202 205 295 278 28 203 206 296 297 28 28 204 207 297 280 28	15	198	201		274	27
7 200 203 293 276 8 201 204 294 277 9 202 205 295 295 278 0 203 206 296 279 27 1 204 207 297 280 28 2 205 208 298 281 3 3 206 209 299 282 28 4 207 210 300 283 5 5 208 211 - - - 6 209 212 301 284 287 7 210 213 302 285 3 8 211 214 303 286 9 9 212 215 304 287 9 10 213 216 305 288 9 1 214 217 306 2	200 203 293 276 27 201 204 294 277 27 202 205 295 278 28 203 206 296 297 28 28 204 207 297 280 28 281 28 205 208 298 281 28<	16	199	202	292	275	27
8 201 204 294 277 9 9 202 205 295 278 9 0 203 206 296 296 279 1 1 204 207 297 280 2 280 2 280 2 280 2 280 2 282 281 3 206 209 299 282 281 3 284 2 300 283 3 286 2 301 284 3 2 285 3 2 285 3 286 3 2 285 3 3 286 3 2 285 3 3 286 3 3 286 3 3 286 3 3 286 3 3 3 286 3 3 3 286 3 3 3 286 3 3 3 288 3 3 3	201 204 294 277 27 202 205 295 278 28 203 206 296 279 28 204 207 297 280 28 205 208 298 281 28 206 209 299 282 28 207 210 300 283 28 208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 215 218 307 290 29 216 219 308 <	17					_
9 202 205 295 278 1 0 203 206 296 279 1 1 204 207 297 280 2 2 205 208 298 281 3 3 206 209 299 282 4 4 207 210 300 283 5 5 208 211	202 205 295 278 28 203 206 296 279 28 204 207 297 280 28 205 208 298 281 28 206 209 299 282 28 207 210 300 283 28 208 211 - - - - 209 212 301 284 28 28 210 213 302 285 28 28 211 214 303 286 28 28 212 215 304 287 28 28 212 215 304 287 28 29 214 217 306 288 29 215 218 307 290 29 216 219 308 291 29 217 220 309 2						
0 203 206 296 279 1 204 207 297 280 2 205 208 298 281	203 206 296 279 28 204 207 297 280 28 205 208 298 281 28 206 209 299 282 28 207 210 300 283 28 208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 215 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 <	18					
1 204 207 297 280 2 205 208 298 281 3 3 206 209 299 282 4 4 207 210 300 283 5 5 208 211 - - - - 6 209 212 301 284 - </td <td>204 207 297 280 28 205 208 298 281 28 206 209 299 282 28 207 210 300 283 28 208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 212 215 304 287 28 214 217 306 288 29 214 217 306 289 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 218 221 310 293 29 219 222 311 <</td> <td>19</td> <td>202</td> <td>205</td> <td>295</td> <td>278</td> <td>28</td>	204 207 297 280 28 205 208 298 281 28 206 209 299 282 28 207 210 300 283 28 208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 212 215 304 287 28 214 217 306 288 29 214 217 306 289 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 218 221 310 293 29 219 222 311 <	19	202	205	295	278	28
1 204 207 297 280 2 205 208 298 281 3 3 206 209 299 282 4 4 207 210 300 283 5 5 208 211 - - - - 6 209 212 301 284 - </td <td>204 207 297 280 28 205 208 298 281 28 206 209 299 282 28 207 210 300 283 28 208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 212 215 304 287 28 214 217 306 288 29 214 217 306 289 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 218 221 310 293 29 219 222 311 <</td> <td>20</td> <td>203</td> <td>206</td> <td>296</td> <td>279</td> <td>28</td>	204 207 297 280 28 205 208 298 281 28 206 209 299 282 28 207 210 300 283 28 208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 212 215 304 287 28 214 217 306 288 29 214 217 306 289 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 218 221 310 293 29 219 222 311 <	20	203	206	296	279	28
2 205 208 298 281 3 206 209 299 282 4 207 210 300 283 5 208 211 -	205 208 298 281 28 206 209 299 282 28 207 210 300 283 28 208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 29 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 218 221 310 293 29 219 222 311 294 29 220 223 -	21					_
3 206 209 299 282 4 207 210 300 283 . 5 208 211 - - - 6 209 212 301 284 . 282 . <t< td=""><td>206 209 299 282 28 207 210 300 283 28 208 211 - - - - 209 212 301 284 28 28 210 213 302 285 28 28 28 28 28 28 28 28 28 28 28 28 28 28 28 28 29 21 213 216 305 288 29</td><td></td><td></td><td></td><td></td><td></td><td>_</td></t<>	206 209 299 282 28 207 210 300 283 28 208 211 - - - - 209 212 301 284 28 28 210 213 302 285 28 28 28 28 28 28 28 28 28 28 28 28 28 28 28 28 29 21 213 216 305 288 29						_
4 207 210 300 283 5 208 211 - - 6 209 212 301 284 7 210 213 302 285 8 211 214 303 286 9 212 215 304 287 0 213 216 305 288 1 214 217 306 289 2 215 218 307 290 3 216 219 308 291 4 217 220 309 292 5 218 221 310 293 6 219 222 311 294 7 220 223 - -	207 210 300 283 28 208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 215 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - - 312 295 29	22					_
4 207 210 300 283 5 208 211 - - 6 209 212 301 284 7 210 213 302 285 8 211 214 303 286 9 212 215 304 287 0 213 216 305 288 1 214 217 306 289 2 215 218 307 290 3 216 219 308 291 4 217 220 309 292 5 218 221 310 293 6 219 222 311 294 7 220 223 - -	207 210 300 283 28 208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 215 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - - 312 295 29	23	206	209	299	282	28
5 208 211 - - - 6 209 212 301 284 : - <	208 211 - - - 209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 29 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - 312 295 29 29	24			300	283	28
66 209 212 301 284 77 210 213 302 285 88 9 212 215 304 287 90 213 216 305 288 11 214 217 306 289 32 215 215 218 307 290 33 216 219 308 291 309 292 311 294 77 220 223	209 212 301 284 28 210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 216 219 308 291 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - 312 295 29		1				
7 210 213 302 285 3 302 285 3 302 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 286 3 303 289 3 303 289 3 303 289 3 303 289 3 303 289 3 303 289 3 303 3 303 303 303 303 303 303 303 30	210 213 302 285 28 211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 215 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - - - 312 295 29	25				-	-
8 211 214 303 286 9 212 215 304 287 1 213 216 305 288 1 214 217 306 289 2 215 218 307 290 3 216 219 308 291 4 217 220 309 292 5 218 221 310 293 6 219 222 311 294 7 220 223 - -	211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 215 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - - 312 295 29	26					
8 211 214 303 286 9 212 215 304 287 1 213 216 305 288 1 214 217 306 289 2 215 218 307 290 3 216 219 308 291 4 217 220 309 292 5 218 221 310 293 6 219 222 311 294 7 220 223 - -	211 214 303 286 28 212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 215 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - - 312 295 29	27	210	213	302	285	28
9 212 215 304 287 0 213 216 305 288 1 1 214 217 306 289 1 2 215 218 307 290 3 3 216 219 308 291 3 4 217 220 309 292 5 5 218 221 310 293 6 219 222 311 294 7 220 223	212 215 304 287 28 213 216 305 288 29 214 217 306 289 29 215 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - 312 295 29	28	211		303	286	28
0 213 216 305 288 1 1 214 217 306 289 2 2 215 218 307 290 3 3 216 219 308 291 3 4 217 220 309 292 3 5 218 221 310 293 3 6 219 222 311 294 3 7 220 223 - - -	213 216 305 288 29 214 217 306 289 29 215 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - - 312 295 29	29					
1 214 217 306 289 2 215 218 307 290 3 3 216 219 308 291 3 4 217 220 309 292 3 5 218 221 310 293 3 6 219 222 311 294 3 7 220 223 - - -	214 217 306 289 29 215 218 307 290 29: 216 219 308 291 29: 217 220 309 292 29: 218 221 310 293 29: 219 222 311 294 29: 220 223 - - - - - 312 295 29						
2 215 218 307 290 3 216 219 308 291 4 217 220 309 292 5 218 221 310 293 6 219 222 311 294 7 220 223 - -	215 218 307 290 29 216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - 312 295 29	30					
3 216 219 308 291 4 217 220 309 292 5 5 218 221 310 293 6 6 219 222 311 294 7 7 220 223 - - -	216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - - - 312 295 29	31	214	217	306	289	29
3 216 219 308 291 4 217 220 309 292 5 5 218 221 310 293 6 6 219 222 311 294 7 7 220 223 - - -	216 219 308 291 29 217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - - - 312 295 29	32	215	218	307	290	29
4 217 220 309 292 5 218 221 310 293 31 6 219 222 311 294 31 7 220 223 - - -	217 220 309 292 29 218 221 310 293 29 219 222 311 294 29 220 223 - - - - - 312 295 29	33					
5 218 221 310 293 : 6 219 222 311 294 : 7 220 223 - - -	218 221 310 293 29 219 222 311 294 29 220 223 - - - - - - 312 295 29		t				
6 219 222 311 294 : 7 220 223	219 222 311 294 29 220 223 - - - - - 312 295 29	34					
7 220 223	220 223 312 295 29	35					_
7 220 223	220 223 312 295 29	36	219	222	311	294	29
	312 295 29				_	-	-
		3/					

Query	H1N1pdm	H3
-	-	-
-	-	-
238	221	224
239	222	225
240	223	226
241	224	227
242	225	228
243	226	229
244	227	230
245	228	231
246	229	232
247	230	233
248	231	234
249	232	235
250	233	236
251	234	237
252 253	235	238
253	236 237	239 240
255	238	241
256	239	242
257	240	243
258	241	244
259	242	245
260	243	246
261	244	247
262	245	248
263	246	249
264	247	250
265	248	251
266	249	252
267	250	253
268 269	251 252	254 255
270	252	256
271	254	257
272	255	258
273	256	259
274	257	260
275	258	261
276	259	262
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
_	-	-
277	260	-
- 277 278	- 260 261	- 263
		- 263 264
278	261	
278 279 280 281	261 262 263 264	264 265 266
278 279 280 281 282	261 262 263 264 265	264 265 266 267
278 279 280 281 282 283	261 262 263 264 265 266	264 265 266 267 268
278 279 280 281 282 283 284	261 262 263 264 265 266 267	264 265 266 267 268 269
278 279 280 281 282 283 284 285	261 262 263 264 265 266 267 268	264 265 266 267 268 269 270
278 279 280 281 282 283 284 285 286	261 262 263 264 265 266 267 268 269	264 265 266 267 268 269 270 271
278 279 280 281 282 283 284 285 286 287	261 262 263 264 265 266 267 268 269 270	264 265 266 267 268 269 270 271 272
278 279 280 281 282 283 284 285 286 287 288	261 262 263 264 265 266 267 268 269 270 271	264 265 266 267 268 269 270 271 272 273
278 279 280 281 282 283 284 285 286 287 288	261 262 263 264 265 266 267 268 269 270 270 271	264 265 266 267 268 269 270 271 272 273 274
278 279 280 281 282 283 284 285 286 287 288	261 262 263 264 265 266 267 268 269 270 271	264 265 266 267 268 269 270 271 272 273
278 279 280 281 282 283 284 285 286 287 288 289	261 262 263 264 265 266 267 268 269 270 271 272 273	264 265 266 267 268 269 270 271 272 273 274 275
278 279 280 281 282 283 284 285 286 287 288 289 290	261 262 263 264 265 266 267 268 269 270 271 272 273 274	264 265 266 267 268 269 270 271 272 273 274 275 276
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 293	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 276	264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278	264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 292 293 294 295	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279	264 265 266 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280	264 265 266 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281
278 279 280 281 281 282 283 284 285 286 287 288 299 290 291 292 293 294 295 296	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 277 278 279 280 281	264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298	261 262 263 264 265 266 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281	264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284
278 279 280 281 281 282 283 284 285 286 287 288 299 290 291 292 293 294 295 296	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 277 278 279 280 281	264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 282	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298	261 262 263 264 265 266 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281	264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 286
278 279 280 281 282 283 284 285 286 287 288 299 291 291 292 293 294 295 296 297 298 299 300 - 301 301	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 - 284 285	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 - 286 287
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 297 300 301 302	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 286 287 288
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 - 301 302 303	261 262 263 264 265 266 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 - 284 285 286 287	264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 280 281 282 283 284 285 - 286 287 288 289
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 - 301 302 303 304 305 306	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 - 286 287 288 289 290 291
278 279 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 300 301 302 303 304 305 306 307 308	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 - 284 285 286 287 288 289 290 291	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 286 287 289 290 291
278 279 280 281 282 283 284 285 286 287 288 299 291 292 293 294 295 297 298 299 300 - 301 302 303 304 305 306 307	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 - 284 285 286 287 288 289 290 291	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 288 289 290 291
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 - 301 302 303 304 305 306 307 308 309	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 278 279 280 281 282 283	264 265 266 267 268 269 270 271 272 273 274 275 276 277 288 289 280 281 282 283 284 285 - 286 287 288 289 290 291 292 293
278 279 280 281 282 283 284 285 286 287 288 299 291 292 293 294 295 297 298 299 300 - 301 302 303 304 305 306 307	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 - 284 285 286 287 288 289 290 291	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 288 289 290 291
278 279 280 281 282 283 284 285 286 287 288 299 291 292 293 294 295 296 297 298 299 300 - 301 302 303 304 305 306 307 308 309 310 311	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 - 284 285 286 287 288 289 290 291 292 293 294	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 288 289 290 291 292 293 294
278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 - 301 302 303 304 305 307 308 309 310 311	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 278 279 280 281 282 283	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 - 286 287 288 289 290 291 292 293 294 295 297
278 279 280 281 282 283 284 285 286 287 288 299 291 292 293 294 295 296 297 298 299 300 - 301 302 303 304 305 306 307 308 309 310 311	261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 - 284 285 286 287 288 289 290 291 292 293 294	264 265 266 267 268 269 270 271 272 273 274 275 276 277 280 281 282 283 284 285 288 289 290 291 292 293 294