LIST OF ABBREVIATIONS, ACRONYMS, AND SYMBOLS

BioNORAD	Proposed early warning system for pandemic risk (this proposal)
AA residue	Amino Acid residue
AI	Artificial Intelligence
CDC	Centre for Disease Control
CIT	Conditional Inference Trees
DMS	Deep mutational scanning
GISAID	Global Initiative on Sharing All Influenza Data
HA	Hemaglutinnin
IAV	Influenza A virus
IRAT	Influenza Risk Assessment Tool
JS Divergence	Jensen-Shannon Divergence
ML	Machine Learning
NA NA	Neuraminidase
NCBI	National Center for Biotechnology Information
NORAD	North American Air Defense
RBD	Receptor Binding Site
SME	Subject Matter Expert
UChicago	University of Chicago
UIowa	University of Cincago University of Iowa
UQ	Uncertainty Quantification
WHO	World Health Organization
E-distance	Emergenet similarity between sequences
E-distance	ML algorithm that uses sequence data to classify
FluLeap	influenza viruses as either avian or human
PRMRP	Peer Reviewed Medical Research Program
BSL2	Bio-safety Level 2
BSL3	Bio-safety Level 2 Bio-safety Level 3
$\theta(x,y)$	E-distance between strains x, y
$\theta^{[t]}(x,y)$	E-distance between strains x , y calculated at time t
(x, y)	recent human strains H_t at time t of similar
H _t	subtypes if available. If the specific sub-type is rare,
	we progressively widen the definition to all strains with similar target gene.
$ ho_{\mathbf{t}}(\mathbf{x})$	time-varying E-risk score for emergence risk of
	strain x
$Pr(x \to y)$	Probability of strain x spontaneously mutating to produce strain y in the wild
$\chi_a^{ m t}$	animal strain observed at time t
$egin{array}{c} x_a^{t} \ x_h^{t} \end{array}$	human strain observed at time t
H1N1, H3N2, H5N1, H5N2, H9N2, H5N8, H7N8, H5N6, H10N8	Influenza A strains
113110, 11/110, 113110, 1110110	