REFERENCES

- [1] Reid, A. H. & Taubenberger, J. K. The origin of the 1918 pandemic influenza virus: a continuing enigma. *Journal of general virology* **84**, 2285–2292 (2003).
- [2] Dos Santos, G., Neumeier, E. & Bekkat-Berkani, R. Influenza: Can we cope better with the unpredictable? *Human vaccines & immunotherapeutics* **12**, 699–708 (2016).
- [3] Shao, W., Li, X., Goraya, M. U., Wang, S. & Chen, J.-L. Evolution of influenza a virus by mutation and re-assortment. *International journal of molecular sciences* **18**, 1650 (2017).
- [4] Wille, M., Geoghegan, J. L. & Holmes, E. C. How accurately can we assess zoonotic risk? *PLoS biology* **19**, e3001135 (2021).
- [5] CDC. Influenza risk assessment tool (irat) pandemic influenza (flu) cdc. https://www.cdc.gov/flu/pandemic-resources/national-strategy/risk-assessment.htm. (Accessed on 07/02/2021).
- [6] Gamblin, S. J. & Skehel, J. J. Influenza hemagglutinin and neuraminidase membrane glycoproteins. *Journal of Biological Chemistry* **285**, 28403–28409 (2010).
- [7] Posada, D. & Crandall, K. A. Modeltest: testing the model of dna substitution. *Bioinformatics (Oxford, England)* **14**, 817–818 (1998).
- [8] Eng, C. L., Tong, J. C. & Tan, T. W. Predicting host tropism of influenza a virus proteins using random forest. *BMC medical genomics* **7**, 1–11 (2014).
- [9] Grange, Z. L. et al. Ranking the risk of animal-to-human spillover for newly discovered viruses. *Proceedings of the National Academy of Sciences* **118**, e2002324118 (2021).
- [10] Ahlquist, P. Rna-dependent rna polymerases, viruses, and rna silencing. *Science* **296**, 1270–1273 (2002).
- [11] Chen, R. & Holmes, E. C. Avian influenza virus exhibits rapid evolutionary dynamics. *Molecular biology and evolution* **23**, 2336–2341 (2006).
- [12] Woolthuis, R. G., van Dorp, C. H., Keşmir, C., de Boer, R. J. & van Boven, M. Long-term adaptation of the influenza a virus by escaping cytotoxic t-cell recognition. *Scientific reports* **6**, 1–8 (2016).
- [13] Fan, K. *et al.* Role of itk signalling in the interaction between influenza a virus and t-cells. *Journal of general virology* **93**, 987–997 (2012).
- [14] van de Sandt, C. E. *et al.* Differential recognition of influenza a viruses by m158–66 epitope-specific cd8+ t cells is determined by extraepitopic amino acid residues. *Journal of virology* **90**, 1009–1022 (2016).
- [15] Berkhoff, E., Geelhoed-Mieras, M., Fouchier, R., Osterhaus, A. & Rimmelzwaan, G. Assessment of the extent of variation in influenza a virus cytotoxic t-lymphocyte epitopes by using virus-specific cd8+t-cell clones. *Journal of General Virology* **88**, 530–535 (2007).
- [16] Van de Sandt, C. E., Kreijtz, J. H. & Rimmelzwaan, G. F. Evasion of influenza a viruses from innate and adaptive immune responses. *Viruses* **4**, 1438–1476 (2012).
- [17] Chattopadhyay, I., Wu, K., Li, J. & et al. Emergenet: Fast scalable pandemic risk assessment of influenza a strains circulating in non-human hosts (2022). URL https://doi.org/10.21203/rs.3.rs-2336091/v1. 2336091.
- [18] Hothorn, T., Hornik, K. & Zeileis, A. Unbiased recursive partitioning: A conditional inference framework. *JOURNAL OF COMPUTATIONAL AND GRAPHICAL STATISTICS* **15**, 651–674 (2006).
- [19] Cover, T. M. & Thomas, J. A. *Elements of Information Theory (Wiley Series in Telecommunications and Signal Processing)* (Wiley-Interscience, New York, NY, USA, 2006).
- [20] Agor, J. K. & Özaltın, O. Y. Models for predicting the evolution of influenza to inform vaccine strain selection. *Human vaccines & immunotherapeutics* **14**, 678–683 (2018).
- [21] Boni, M. F. Vaccination and antigenic drift in influenza. *Vaccine* **26**, C8–C14 (2008).
- [22] Huddleston, J. *et al.* Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza a/h3n2 evolution. *Elife* **9**, e60067 (2020).
- [23] Zhao, X. *et al.* Expanding the tolerance of segmented Influenza A Virus genome using a balance compensation strategy. *PLoS Pathog* **18**, e1010756 (2022).

- [24] Ganti, K., Han, J., Manicassamy, B. & Lowen, A. C. Rab11a mediates cell-cell spread and reassortment of influenza A virus genomes via tunneling nanotubes. *PLoS Pathog* **17**, e1009321 (2021).
- [25] Han, J. et al. Host factor Rab11a is critical for efficient assembly of influenza A virus genomic segments. PLoS Pathog 17, e1009517 (2021).
- [26] Kandasamy, M., Furlong, K., Perez, J. T., Manicassamy, S. & Manicassamy, B. Suppression of Cytotoxic T Cell Functions and Decreased Levels of Tissue-Resident Memory T Cells during H5N1 Infection. *J Virol* **94** (2020).
- [27] Li, P. et al. Luciferase. Viruses 10 (2018).
- [28] Tundup, S. *et al.* Endothelial cell tropism is a determinant of H5N1 pathogenesis in mammalian species. *PLoS Pathog* **13**, e1006270 (2017).
- [29] Perez, J. T., a Sastre, A. & Manicassamy, B. Insertion of a GFP reporter gene in influenza virus. *Curr Protoc Microbiol* **Chapter 15**, 1–15 (2013).
- [30] Manicassamy, B. *et al.* Analysis of in vivo dynamics of influenza virus infection in mice using a GFP reporter virus. *Proc Natl Acad Sci U S A* **107**, 11531–11536 (2010).
- [31] Manicassamy, B. *et al.* Protection of mice against lethal challenge with 2009 H1N1 influenza A virus by 1918-like and classical swine H1N1 based vaccines. *PLoS Pathog* **6**, e1000745 (2010).
- [32] Medina, R. A. *et al.* Glycosylations in the globular head of the hemagglutinin protein modulate the virulence and antigenic properties of the H1N1 influenza viruses. *Sci Transl Med* **5**, 187ra70 (2013).
- [33] Ganti, K., Han, J., Manicassamy, B. & Lowen, A. C. Rab11a mediates cell-cell spread and reassortment of influenza a virus genomes via tunneling nanotubes. *PLoS Pathogens* 17, e1009321 (2021).
- [34] Wittwer, C. T., Reed, G. H., Gundry, C. N., Vandersteen, J. G. & Pryor, R. J. High-resolution genotyping by amplicon melting analysis using legreen. *Clinical chemistry* **49**, 853–860 (2003).
- [35] Marshall, N., Priyamvada, L., Ende, Z., Steel, J. & Lowen, A. C. Influenza virus reassortment occurs with high frequency in the absence of segment mismatch. *PLoS pathogens* **9**, e1003421 (2013).
- [36] Matrosovich, M. *et al.* Avian influenza a viruses differ from human viruses by recognition of sialyloligosaccharides and gangliosides and by a higher conservation of the ha receptor-binding site. *Virology* **233**, 224–234 (1997).
- [37] Shinya, K. et al. Influenza virus receptors in the human airway. Nature 440, 435–436 (2006).
- [38] Chan, M. C. *et al.* Tropism and innate host responses of the 2009 pandemic h1n1 influenza virus in ex vivo and in vitro cultures of human conjunctiva and respiratory tract. *The American journal of pathology* **176**, 1828–1840 (2010).
- [39] Neumann, G. et al. Generation of influenza a viruses entirely from cloned cdnas. *Proceedings of the National Academy of Sciences* **96**, 9345–9350 (1999).
- [40] Goldberger, A. L. & Peng, C.-K. Genomic classification using an information-based similarity index: application to the sars coronavirus. *Journal of Computational Biology* **12**, 1103–1116 (2005).
- [41] Huelsenbeck, J. P. & Crandall, K. A. Phylogeny estimation and hypothesis testing using maximum likelihood. *Annual Review of Ecology and systematics* **28**, 437–466 (1997).
- [42] Neher, R. A., Russell, C. A. & Shraiman, B. I. Predicting evolution from the shape of genealogical trees. *Elife* **3**, e03568 (2014).
- [43] van der Meer, F. J. U. M., Orsel, K. & Barkema, H. W. The new influenza A H1N1 virus: balancing on the interface of humans and animals. *The Canadian veterinary journal = La revue veterinaire canadienne* **51**, 56–62 (2010).
- [44] Smith, G. J. D. *et al.* Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. *Nature* **459**, 1122–1125 (2009).
- [45] Rulli, M. C., Santini, M., Hayman, D. T. & D'Odorico, P. The nexus between forest fragmentation in africa and ebola virus disease outbreaks. *Scientific reports* 7, 41613 (2017).
- [46] Chua, K. B., Chua, B. H. & Wang, C. W. Anthropogenic deforestation, el niiio and the emergence of nipah virus in malaysia. *Malaysian Journal of Pathology* **24**, 15–21 (2002).

- [47] Childs, J. Zoonotic viruses of wildlife: hither from yon. In *Emergence and Control of Zoonotic Viral Encephalitides*, 1–11 (Springer, 2004).
- [48] Fair, J. & Fair, J. Viral forecasting, pathogen cataloging, and disease ecosystem mapping: Measuring returns on investments. *Current Topics in Microbiology and Immunology* 75–83 (2019).
- [49] for Disease Control, C. & Prevention. Seasonal influenza (2021). URL https://www.cdc.gov/flu/about/index.html.
- [50] of Defense, U. D. Report on effects of a changing climate to the department of defense (2020). URL https://media.defense.gov/2020/Jul/21/2002462222/-1/-1/1/Report_on_Effects_of_a_Changing_Climate_to_the_Department_of_Defense.PDF.
- [51] Wells, K. B. & Lewis, M. J. Influenza: Evolution, detection, and response. *Clinical Microbiology Reviews* **18**, 80–103 (2005).