



A Novel Sequence-Based Antigenic Distance Measure for H1N1, with Application to Vaccine Effectiveness and the Selection of Vaccine Strains

[Keyao Pan](#), [Krystina C. Subieta](#), [Michael W. Deem](#)

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H1N1 influenza causes substantial seasonal illness and was the subtype of the 2009 influenza pandemic. Precise measures of antigenic distance between the vaccine and circulating virus strains help researchers design influenza vaccines with high vaccine effectiveness. We here introduce a sequence-based method to predict vaccine effectiveness in humans. Historical epidemiological data show that this sequence-based method is as predictive of vaccine effectiveness as hemagglutination inhibition (HI) assay data from ferret animal model studies. Interestingly, the expected vaccine effectiveness is greater against H1N1 than H3N2, suggesting a stronger immune response against H1N1 than H3N2. The evolution rate of hemagglutinin in H1N1 is also shown to be greater than that in H3N2, presumably due to greater immune selection pressure.

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