



**CALIFORNIA STATE SCIENCE FAIR
2010 PROJECT SUMMARY**

Name(s) Meredith P. Lehmann	Project Number S1607
Project Title Transportation Networks and the Propagation of Novel H1N1 Swine Flu-like Epidemics	
<p style="text-align: center;">Abstract</p> <p>Objectives/Goals The recent SARS and novel H1N1 pandemics have rekindled interest in the spread of epidemics. Recently, Colizza et al. simulated epidemics on a 3100 airport network across 220 countries. Their analysis shows that epidemics propagate primarily through large hub airports as preferred epidemic pathways. This study uses different US air travel data and, for the first time, long distance auto travel data to examine three main hypotheses suggested by their work: (H1) County travel flows per capita should be increasing in population size and highly connected counties should experience higher average county to county traffic flows; (H2) County infected evolution should differ markedly from that of a Susceptible-Infected-Removed model without travel; and (H3) Air traffic should be the main force driving epidemics.</p> <p>Methods/Materials The model is a network comprised of all 3076 counties in the continental US. Each county is a separate node in which epidemics propagate according to an SIR model subject to daily air and auto travel inflows and outflows. Roughly 1 billion long distance auto and 262 million air round trips from county-to-county comprise the travel model. Epidemic parameter values and initial conditions are based on swine flu data from spring 2009. This large scale simulation model is used to simulate US epidemics under different transportation network configurations.</p> <p>Results These simulated epidemics behave nothing like the Colizza et al. simulations. Long distance auto travel is the main driver of epidemics contra H3. In contrast to H2, travel essentially disperses infecteds across the country and county infected evolution behaves like an SIR model without travel once the incidence of infection reaches 1/100,000. Per capita travel is not higher in large counties contra part one of H1 but more connected counties experience disproportionately larger travel flows consistent with the second part. However, such hub counties are not preferred epidemic pathways in the simulations.</p> <p>Conclusions/Discussion More effective travel restriction and quarantine policies and targeted pharmaceutical interventions can be designed when large hub airports are the primary epidemic pathways through which epidemics propagate but there are no preferred epidemic pathways if these simulations are correct. The social importance of the resulting inability to materially alter epidemic outcomes in this fashion cannot be overstated.</p>	
Summary Statement This project shows that long distance auto, not air, travel is the main epidemic propagation mechanism in the US and that no travel mode is a preferred epidemic pathway that can be used to improve prediction and policy interventions.	
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