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# Visualizing Flu Pandemics for Model Validation

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## ABSTRACT

This poster describes the design methodology and results for a pandemic visualization tool that was developed for validating a pandemic model. This work is the result of a collaboration between domain scientists, visualization scientists and a fine artist. While the primary goal of this work is to understand and communicate how an epidemic spreads across a country, we developed new visualization methods for population center glyphs and travel networks. The visualization tool was developed using Processing and uses geographical spatiotemporal views to explore the model dataset. The tool is interactive and easy to use. Close attention was given to visualization design aesthetics to create visualizations that can be easily understood by the general public.

**Index Terms:** J.5 [Computer Applications]: Arts and Humanities—Fine arts; J.3 [Computer Applications]: Life and Medical Sciences—Biology and genetics

## 1 INTRODUCTION

In March/April 2009, a new swine-origin strain of the influenza A/H1N1 virus (pH1N1) was detected in human populations in California and Mexico. At the time of the outbreak, no quantitative models guiding the geo-temporal distribution of the U.S. antiviral stockpile in relation to pandemic spread or severity existed. As a response to this, a new algorithm was developed to efficiently search large strategy spaces and analyze the optimal use of the stockpile against pandemic influenza prior to widespread and effective vaccination. [1]. The data computed using this optimization model is the basis for our work.

Prior to this collaboration, the researchers used basic static plotting tools to graph the simulation data in two dimensions. Our primary goal of visualizing this data was to show and effectively communicate as much of the information contained in the simulation output as possible and to interactively and dynamically display and present this information in an easily understandable and explainable way. Because this topic was of significant importance to the general public, the visualization tool had to provide the capability for researchers to explore and present the data and the visualizations created by the tool need to be equally as effective for decision makers and politicians as it is for the researchers themselves. This led to the development of new visualization methods for displaying network based pandemic data. Specifically, our novel contributions to

the state of the art are: a new three dimensional network visualization tool that allows for multivariate visualization on time-varying network variables, new glyph based visualization techniques for effective multi-variate visualization of pandemic model variables that is suitable for both a two and three dimensional view, and successful integration of a fine artist's perspective for visualizations to communicate more effectively to a lay audience.

### 1.1 Data

The data was produced by the network based simulation model and includes network information of the average daily number of travelers between cities, which allows for computation of number of infected travelers and epidemic information containing a time-based list of the following statistics [1]:

- Number of susceptible individuals
- Number of latent individuals
- Number of asymptomatic individuals
- Number of infectious individuals showing symptoms
- Number of recovered individuals
- Affected individuals representing the cumulative number of individuals that had the disease at some point
- Antivirals or number of distributed antiviral courses
- Vaccine or number of distributed vaccines doses

## 2 VISUALIZATION DESIGN METHODOLOGY

Our pandemic visualization tool incorporates common methods of displaying geo-referenced data on a map. The work was initially implemented in C++, and thereafter implemented using Processing [2] because of its portability, interactivity and ease of modification by the domain scientists, visualization researchers and artist collaborating on the project. Our primary goal was to provide visualizations that can visually validate the model, while also serving as an effective means of communication to the general public.

### 2.1 Initial Work

In 2009, initial visualization efforts focused on providing a map-based visualization with a pie chart glyph at each node (or city) to represent the susceptible, infected and recovered population. It also used directed edges to represent how the pandemic was spreading with travel patterns, and a rectangular glyph to show the amount of antivirals per city. These visualizations provided a quick solution to the domain scientists to begin using for visual validation of their pandemic model. Figure 1 shows a global view of the initial work created in 2009 during the pandemic spread.

### 2.2 Glyph and Edges Implementation

The initial map-based visualization was effective at representing the cities by using a pie-chart style glyph at the cities. Therefore, for this work we adopted a similar approach, but added a third dimension to the glyph at the population centers. The volume of the

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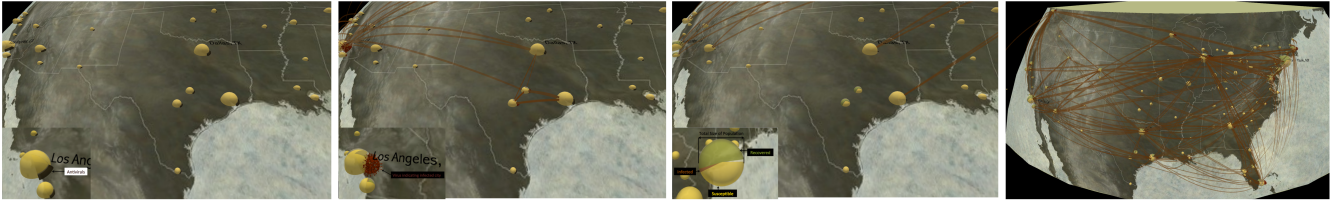


Figure 2: Temporal evolution of simulation over Texas and overall view of map. Legend also describes the representation of node glyphs (susceptible, infected, recovered) and virus sculpture.

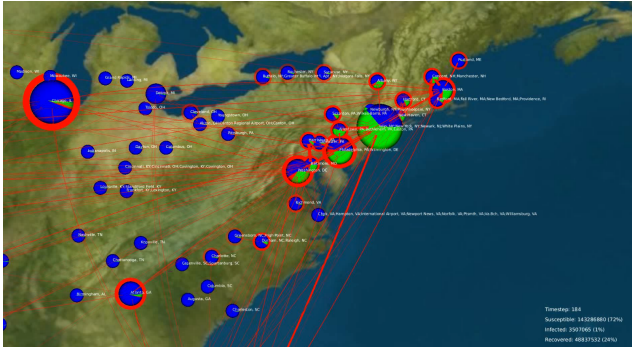


Figure 1: Initial H1N1 Visualization Completed in 2009 for Exploration and Presentation.

glyph represent the city’s total population, while the slices within the glyph represent the percentage of susceptible, infected and recovered population. This glyph representation provides insight to the scientists in understanding what is happening at the population centers in a given time step. We use the method in [4] to scale the radius of the total population sphere. Additionally, each ellipsoid slice and the population sphere have different opacities to enable the viewer to see the changes in the affected population.

To represent the antivirals, we extended the concept of using a rectangular glyph to represent the number of antivirals in a city. Because we wanted to relate the number of antivirals with the size of the population, we added another ellipsoid slice with a 20 percent increase in radius and full opacity. This glyph accurately matches both the circumference extents and height to the number of antivirals per city with respect to the population.

In addition to the population data, the dataset included the average daily number of travelers between each pair of cities. We chose to visualize the average daily number of infected travelers using a three dimensional edge represented by ribbons. Additionally, we mapped the maximum and minimum values of the infected measurement to a logarithmic scale, since the values were clustered in the lower end of the scale, and then used this to map the numbers to opacity. Lower opacity indicates less number of infected travelers and higher opacity depicts a higher number of infected travelers. This allows us to map both height and opacity to indicate levels of infection amongst the travelers.

### 2.3 Color Theory and Aesthetics

A substantial aspect of the success of this visualization effort relies on visual aesthetics. The collaboration team included a fine artist to aid in the design of a color palette and to provide guidance with the artistic aspect of the visualization. The artist worked with Kuler [3] to create our final color palette. The colors chosen are identified by the general public as either warning (yellow-

susceptible), safe/clear (green-recovered) and stop/high-level warning (red/orange-infected). Additionally, the colors selected are a set of analogous colors.

Additionally, the artist also manipulated the map to provide a more harmonious color scheme. Furthermore, the artist created a representation of the H1N1 virus using clay. The sculpture was scanned and the geometry was imported into the visualization tool. When the infected population reaches one percent, the virus appears, indicating the city has been infected. Finally, in this visualization, we only use the names of a few representative cities to orient the observer. Figure 2 gives a visual representation of the glyphs, virus and the color palette chosen.

### 3 RESULTS

We have developed a new set of visualization techniques to design a visualization tool and schema for the validation of a pandemic simulation. The specific simulation run that we evaluated used San Antonio, TX, Los Angeles, CA, and New York City, NY as the starting locations for the epidemic.

Figure 2 shows a clear representation of the number of antivirals per city. As the visualization progresses, we can clearly see the instant when each city is given their antivirals. From the visualization, it is apparent that Chicago, IL, had the highest number of antivirals per capita. We can observe the disease travel patterns as the simulation progresses, with the cities with smaller populations being infected and recovering last. The combination of visualization components, including the ability to browse temporally throughout the dataset, aid in seeing how quickly population centers recover and the timing and magnitude of the epidemic in all the cities involved.

In the future, we will expand the tool to examine the effectiveness of illustrating pandemics in three dimensions and further investigate methods that are effective in both two and three dimensions. Additionally, we will continue to explore the integration of a fine artist’s perspective in the scientific visualization process, particularly for data that is to be communicated to a diverse audience

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