

FRED: A Framework for Reconstructing Epidemiological Dynamics

FRED (Framework for Reconstructing Epidemiological Dynamics) is an open source modeling system developed by the University of Pittsburgh MIDAS National Center of Excellence in collaboration with the Pittsburgh Supercomputing Center and the School of Computer Science at Carnegie Mellon University. It supports research on the dynamics of infectious disease epidemics and the interacting effects of mitigation strategies, viral evolution, and personal health behavior.

FRED was designed as a flexible and modular framework for epidemic modeling, rather than a model of a particular infectious disease. Key features include:

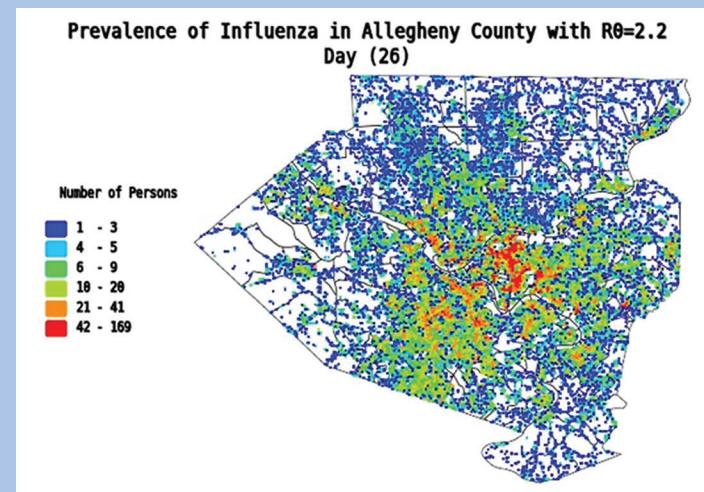
- **Highly modular, object-oriented software design** to support rapid adaptation to a wide variety of infectious disease scenarios.
- **Scalable and efficient simulation of large epidemics.** FRED can run on a variety of computer platforms from laptops to supercomputers, depending on the size of the population being simulated. Simulations of an influenza epidemic like the H1N1 pandemic in a population of 1 million people takes less than 2 minutes on a laptop computer.

- **Realistic synthetic populations** based on the US Census Bureau's Public Use Microdata (PUMs) data and Census aggregated data. The synthetic populations used by FRED were developed by RTI International as part of the MIDAS project and are freely available.
- **Flexible ways to specify agent health behavior and decision rules.** Agents in FRED may exhibit a number of health-related behaviors involving individual health decisions, such as handwashing, staying home when sick, accepting a vaccine or taking an anti-viral drug. The FRED platform is designed to accommodate a range of models of health behavior and supports a variety of strategies to determine an agent's willingness to adopt a behavior.

FRED is intended for use by investigators interested in the effects of mitigation strategies, viral evolution, and personal health behavior on the dynamics of infectious disease epidemics. FRED can be run locally or accessed through a Web interface that permits users to run simulations remotely at the Pittsburgh Supercomputing Center. The system uses census-based synthetic populations that capture the demographic, household, school and workplace distributions of the U.S. population. Multiple circulating and evolving strains can be simulated.

Analysis and visualization of results from FRED can be displayed using GAIA (The Geospatial Area and Information Analyzer). A stand-alone application called FRED Navigator is being developed for end-users for use in high schools and research institutions.

FRED is made available to contribute to the goal of making large-scale agent-based epidemic models more useful to the policy-making community, the research community, and as a teaching tool for students in public health.



More information about FRED, including a link to download, is available at <http://fred.publichealth.pitt.edu>.

For more information about MIDAS

MIDAS Web site: <http://www.midasmodels.org>

National Institute of General Medical Sciences (NIGMS):
<http://www.nigms.nih.gov/Research/FeaturedPrograms/MIDAS/>

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About MIDAS

Funded by the National Institute of General Medical Sciences, NIH, MIDAS is a collaborative network of research scientists who use computational, statistical and mathematical models to understand infectious disease dynamics and thereby assist the nation to prepare for, detect and respond to infectious disease threats.

<http://www.midasmodels.org>