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Tools for Modeling Disease Dynamics

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- MATLAB
 - ✓ Disease Modeling in MATLAB

Disease Modeling

- Disease models can project how infectious diseases progress to show the likely outcome of an epidemic and help inform public health interventions.
- Models use some basic assumptions and mathematics to find parameters for various infectious diseases and use those parameters to calculate the effects of possible interventions, like mass vaccination programmes.

Tools for Modeling Disease Dynamics

- FRED (A Framework for Reconstructing Epidemiological Dynamics)
- ArcGIS (Aeronautical Reconnaissance Coverage Geographic Information System)
- MATLAB (Matrix Laboratory)

About FRED

- FRED (A Framework for Reconstructing Epidemiological Dynamics) is a modeling system that 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, modular, open source framework for epidemic modeling, rather than a model of a particular infectious disease.

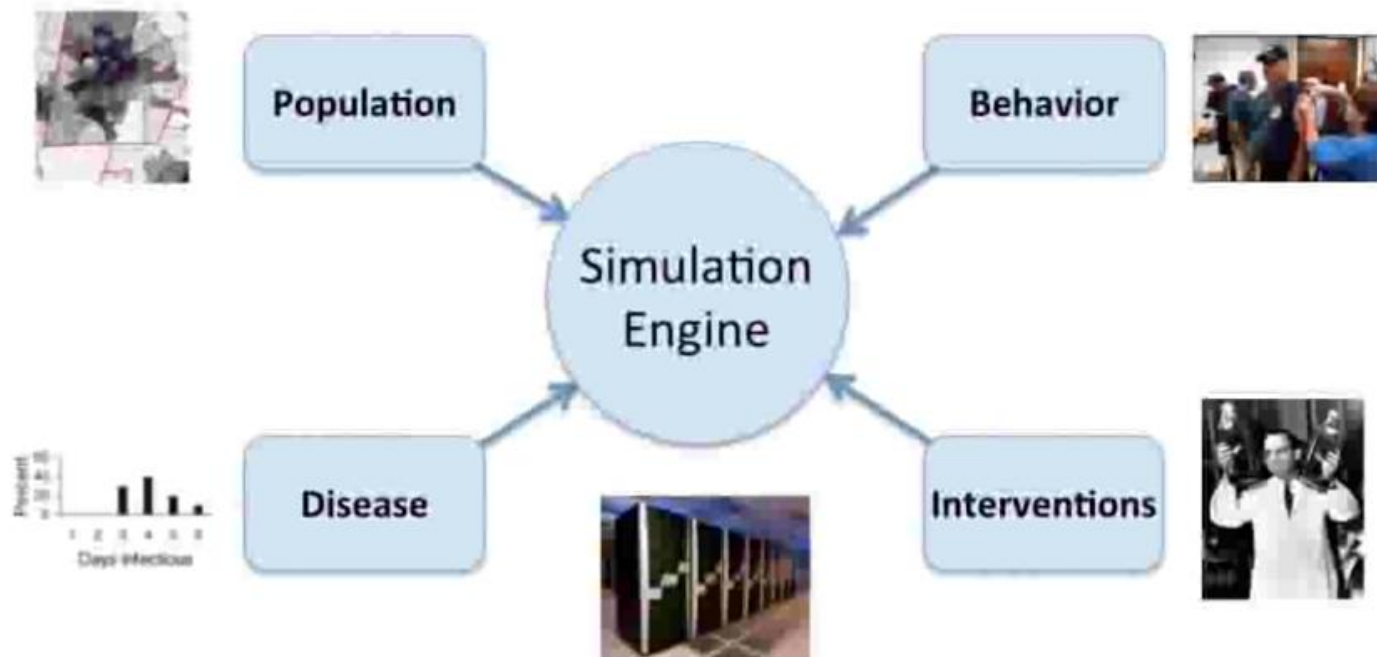
Key features of FRED

- Highly modular, object-oriented software design
- Realistic synthetic populations
- Scalable and efficient simulation of large epidemics
- Flexible ways to specify agent health behavior and decision rules

Synthetic Population

- FRED explicitly represents every individual in a specific geographic region. Each agent has a set of socio-demographic characteristics and daily behaviors that include age, sex, employment status, occupation, and household location and membership in a set of social contact networks.

FRED: Framework for Reconstructing Epidemic Dynamics

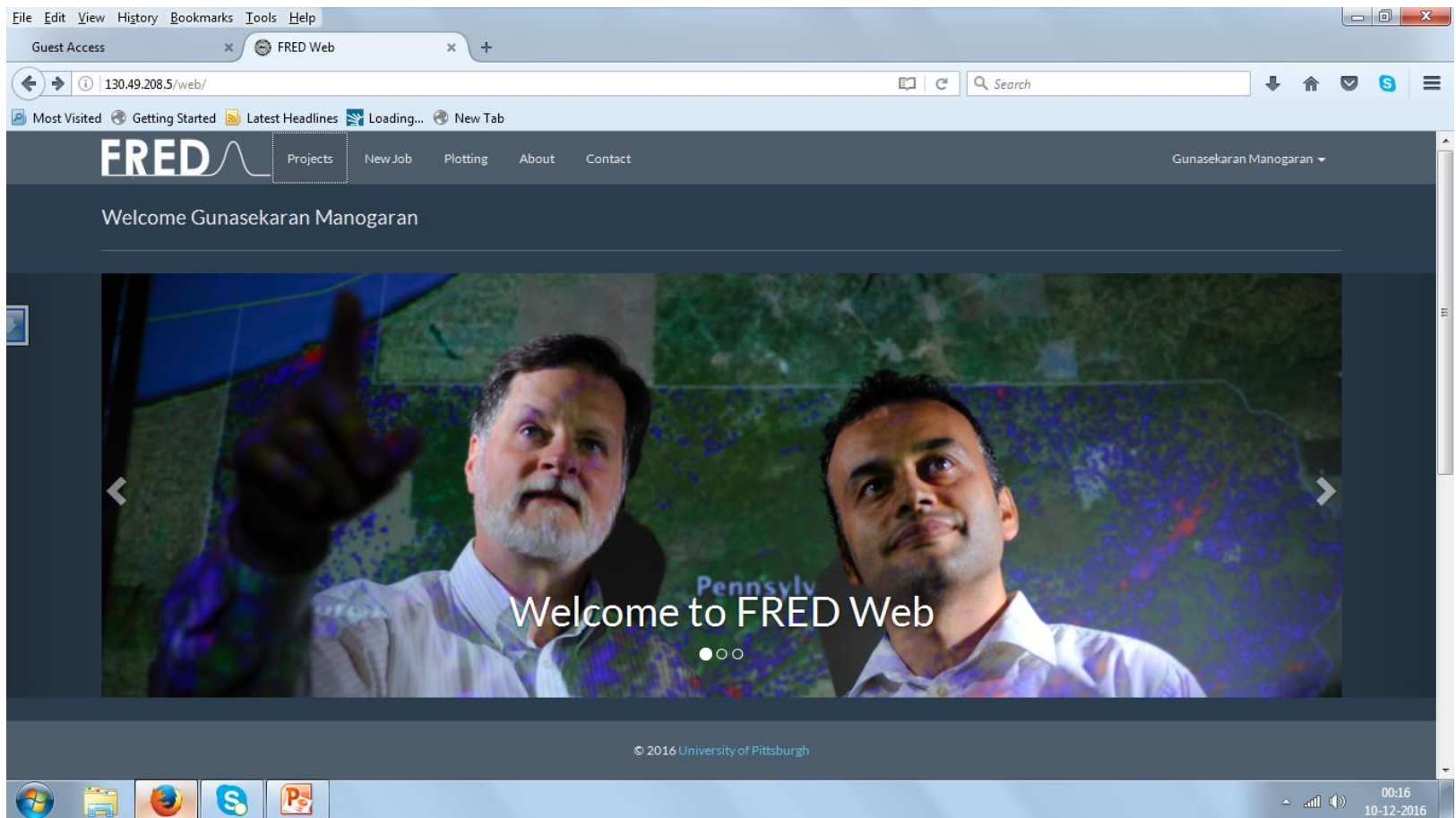


- Agent-based epidemic modeling system using census-based population models
- User settable parameters specify infectiousness of epidemic, control measures and human behaviors
- Simulation available for every county in the U.S.

Prevalence of Influenza in Allegheny County with $R_0=2.2$
Day (76)



FRED



FRED

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130.49.208.5/web/about

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FRED

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Generators/Help/Support

About FRED

FRED (A Framework for Reconstructing Epidemiological Dynamics) is a modeling system that 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, modular, open source framework for epidemic modeling, rather than a model of a particular infectious disease. Key features of FRED include:

- **Highly modular, object-oriented software design** to support rapid adaptation to a wide variety of infectious disease scenarios.
- **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.
- **Scalable and efficient simulation of large epidemics.** FRED can run on a variety of computer platforms from laptop 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.
- **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 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.

Synthetic Population

FRED explicitly represents every individual in a specific geographic region. Each agent has a set of socio-demographic characteristics and daily behaviors that include age, sex, employment status, occupation, and household location and membership in a set of social contact networks. Each household, school, and workplace is mapped to a specific geographic location, reflecting the actual spatial distribution of the area and the distance travelled by individuals to work or to school. For regions within the United States, FRED uses the 2005-2009 U.S. Synthetic Population Database (Version 2) from RTI International: (https://www.epimodels.org/midasdocs/SynthPop/2005-2009_synthpop_ver2_quickstart_20120801.pdf).

The RTI Synthetic Population uses an iterative fitting method to generate an agent population from the US Census Bureau's Public Use Microdata Files (PUMs) and aggregated data from the 2005-2009 American Community Survey (ACS 5-year sample). The synthetic population database contains geographically located synthetic households and household residents for the United States, as well as group quarters locations and residents, schools and assignments of students to schools, workplaces and assignments of workers to workplaces. Each household, group quarters, school and workplace is mapped to a specific geographic location, reflecting the actual spatial distribution of the area and the distance travelled by individuals to work or to school. Each agent has associated demographic information (e.g., age, sex), locations for social activities (household, and possibly school or workplace).

A FRED synthetic population is currently available for every county in the United States and for selected international populations. FRED can simulate any combination of counties in a single run, for example, an epidemic within a state or a Metropolitan Statistical Area (MSA).

Why FRED?

FRED was named in tribute to Fred McFeely Rogers (1928-2003), a famous Pittsburgher best known for his television program *Mister Rogers' Neighborhood* (1968-2001). Mr. Rogers' theme song included the phrases:

It's a beautiful day in the neighborhood ... won't you be my neighbor?

— Fred Rogers

His emphasis of the importance of neighborhoods seems like an appropriate reflection of the importance of social networks in the FRED simulation system.

How to cite FRED

If you use FRED in your research, please use the following citation: Grenfell JJ, Brown ST, Rosenfeld R, Desjardins J, Stone NT, Cooley PC, Wheaton WD, Fyfe A, Galloway DD, Stram A, Gershik M, Abraham T, Burke DC. FRED (A Framework for Reconstructing Epidemiological Dynamics): An open-source software system for modeling infectious diseases and control strategies using census-based populations. *BMC Public Health*. 2013 Oct;13(1): 940. doi: 10.1186/1471-2458-13-940. PubMed PMID: 24064000

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00:21
10-12-2016

FRED

The screenshot shows a web browser window with the FRED Web application. The browser's address bar shows the URL `130.49.208.5/web/projects`. The FRED Web interface has a dark blue header with the FRED logo and navigation links: Projects, New Job, Plotting, About, and Contact. The user's name, Gunasekaran Manogaran, is displayed in the top right corner. The main content area is titled "Projects" and contains two columns. The left column, titled "Description", explains that the page provides a list of current Projects and that a Project is a set of related FRED jobs. The right column, titled "My Projects", contains a table with two columns: "Name" and "Created At". The table has one row with the value "Tutorial" under "Name" and "2016-12-06 09:54:32" under "Created At". Below the table is a "Create New Project" section with a text input field labeled "Name" and a "Submit" button. The footer of the page shows the copyright notice "© 2016 University of Pittsburgh". The Windows taskbar at the bottom displays the time as 00:15 on 10-12-2016.

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Guest Access x FRED Web x +

130.49.208.5/web/projects Search

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FRED Projects New Job Plotting About Contact Gunasekaran Manogaran

Projects

Description

This page provides a list of your current Projects. Projects provide a way to organize your work with FRED. A Project is a set of related FRED jobs, such as all the jobs associated with a given research study.

The **My Projects** list shows the status of your current Projects. Click on a Project to see the list of FRED jobs associated with that Project.

My Projects

Name	Created At
Tutorial	2016-12-06 09:54:32

Create New Project

Submit

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00:15 10-12-2016

FRED

The screenshot shows a web browser window with the FRED application. The browser's address bar shows the URL `130.49.208.5/web/projects/14`. The application's navigation bar includes links for **Projects**, **New Job**, **Plotting**, **About**, and **Contact**. The user's name, **Gunasekaran Manogaran**, is displayed in the top right corner.

The main content area is titled **Project: *Tutorial***. It features a **Description** section on the left and a **FRED Jobs** table on the right.

Description

This page provides a list of your FRED Jobs associated with this project and the job's status. When the status of a job changes, this page automatically refresh and display the updates.

Once the status of a Job is "completed", click on a Job Name to see the job details.

Click the "New Job" tab at the top of the page to create a new job.

FRED Jobs

Name	Status	Build
Baseline	completed	2.13
Base2	completed	2.13
Base3	completed	2.13
Adilabad	completed	2.13
Warangal	completed	2.13

FRED

The screenshot displays the FRED Web application in a web browser. The browser's address bar shows the URL `130.49.208.5/web/fredJobs/create`. The application's header includes the FRED logo, navigation links (Projects, New Job, Plotting, About, Contact), and a user profile dropdown for Gunasekaran Manogaran. The main content area is divided into two tabs: 'General' and 'Infectious Disease'. The 'General' tab is active, showing a description of the form and a series of input fields. The 'Infectious Disease' tab is also visible. The 'General' tab description states: 'This page provides the form used to create a new FRED Job. Currently, influenza is the only available Job Type. Enter the required information using the forms within the "General" and "Infectious Disease" tabs. Once you have completed the forms within each tab, click "Finish".'

The 'General' tab contains the following fields:

- Assign new Job to Existing Project:** A dropdown menu.
- Job Name:** A text input field.
- Build:** A dropdown menu with the value '2.13' selected.
- Number of Runs:** A series of 10 radio buttons, with the 5th button selected.
- Country:** A dropdown menu.
- Start/End Dates:** Two date input fields with the values '01/02/2010' and '06/30/2010' respectively, separated by a 'to' label.

A 'Finish' button is located at the bottom of the form. The footer of the application indicates '© 2016 University of Pittsburgh'.

FRED

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Guest Access x FRED Web x +

130.49.208.5/web/fredJobs/create_plot

Search

↓

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FRED

ProjectsNew JobPlottingAboutContact

Gunasekaran Manogaran ▾

Create Plot

Description

This page provides the form used to create a new FRED Plot.

You can plot the results from any of your "Completed" jobs. Please select the appropriate job(s) and any additional plotting parameters.

Once you have completed the forms within each tab, click "Finish".

Jobs

Baseline
Base2
Base3
Adilabad
Warangal

Output Variables

Attack Rate
Incidence
Symptomatic Incidence
Exposed
Infectious
Prevalence
Recovered
Susceptible

Show All Runs ☐

Bar Chart ☒

Error Bars ☐

Normalize ☐

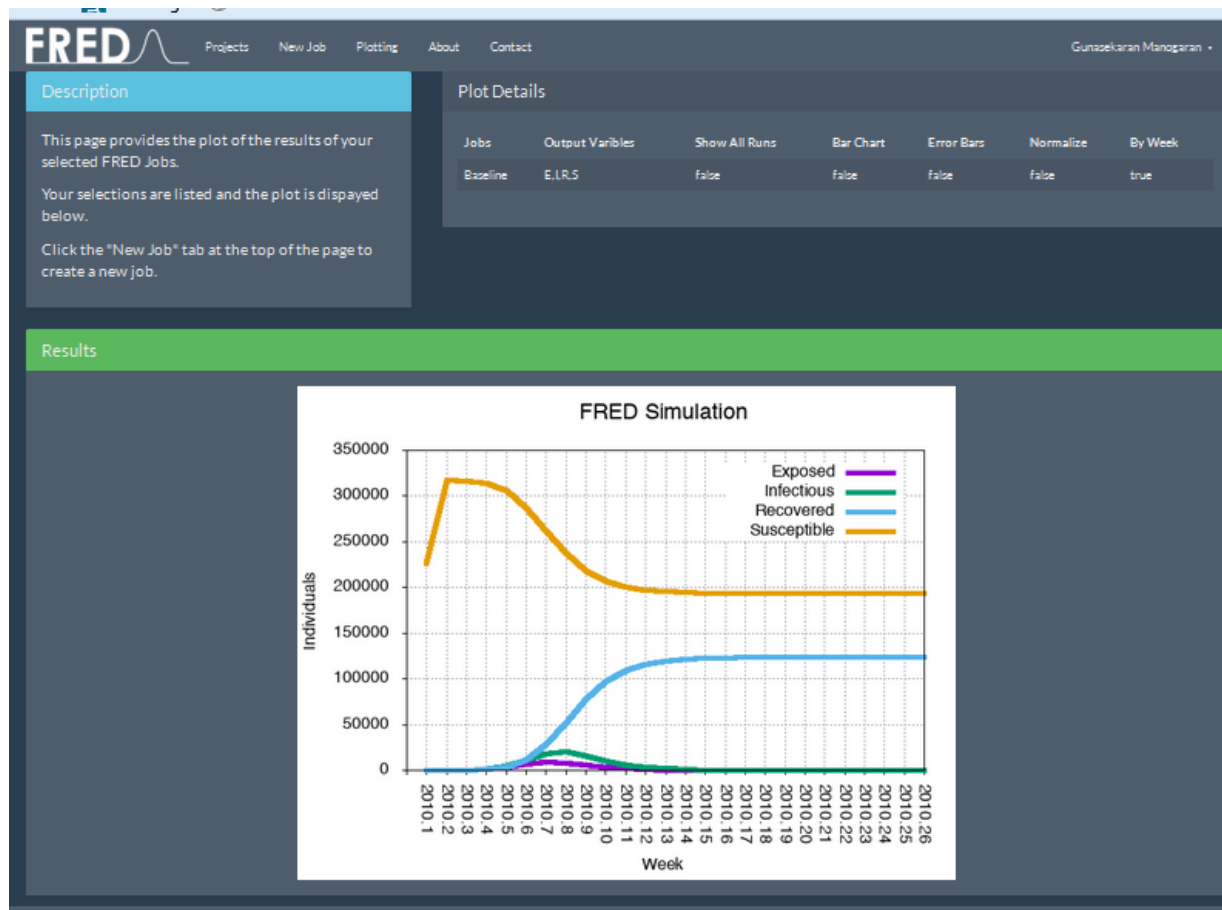
By Week ☒

Plot Results

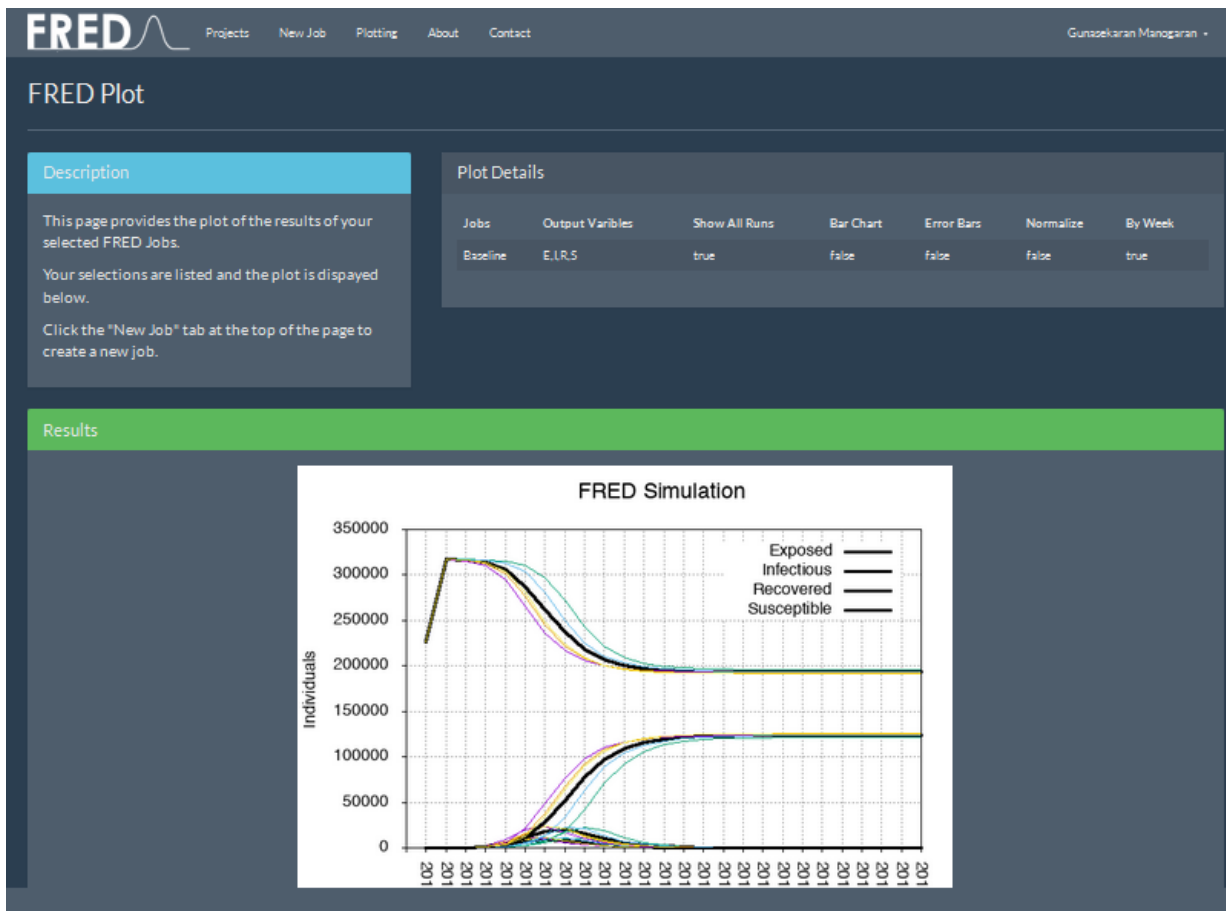
FRED SIMULATION



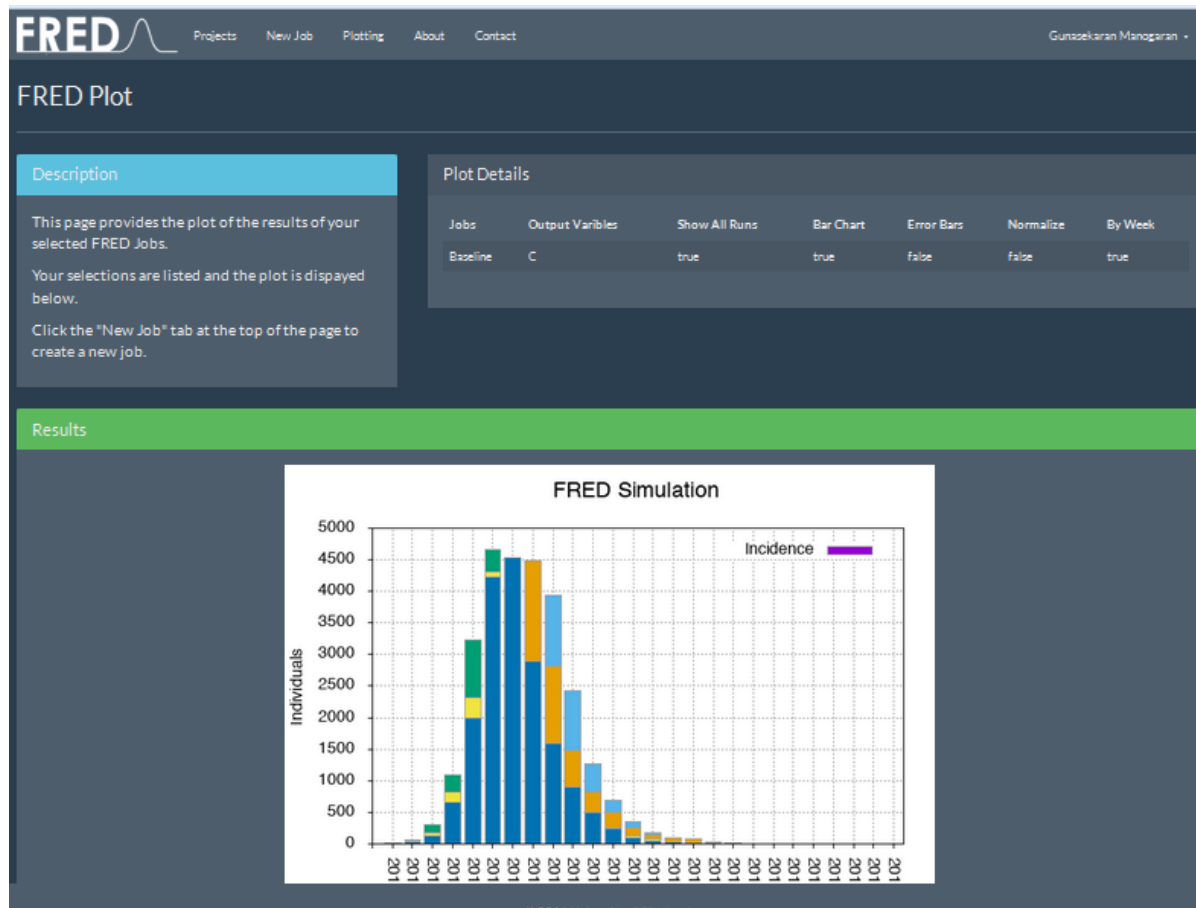
FRED SIMULATION



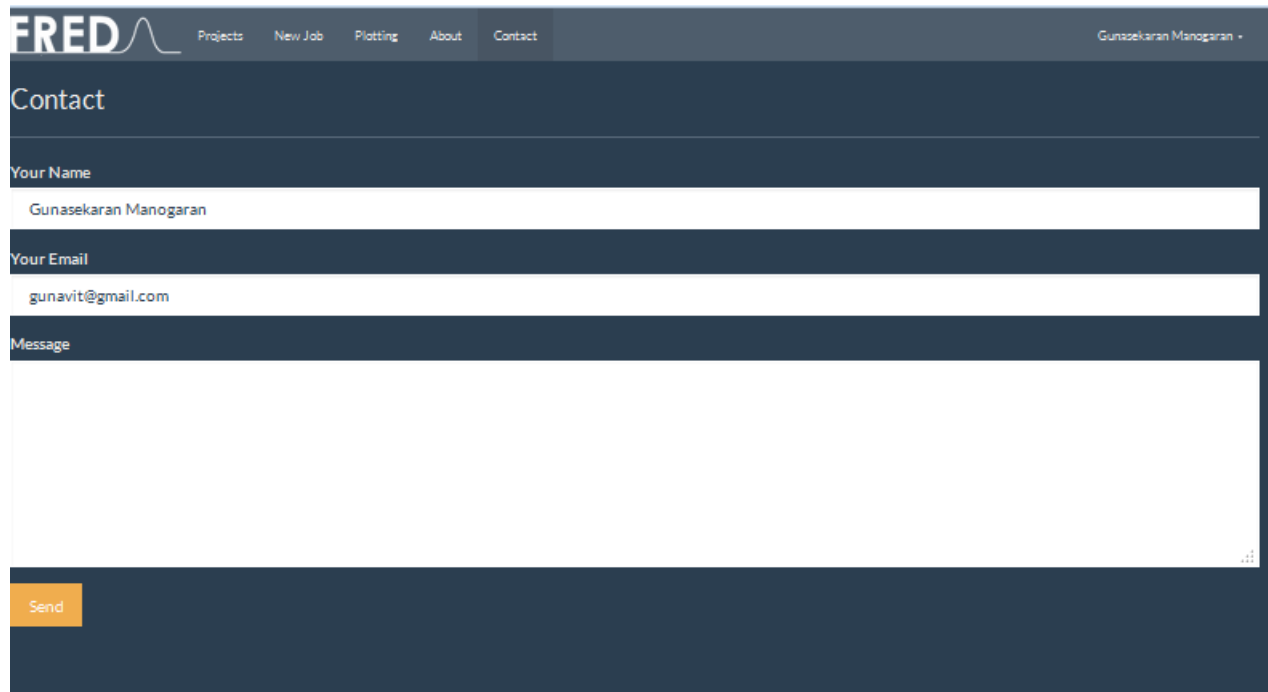
FRED SIMULATION



FRED SIMULATION



FRED SIMULATION



The screenshot shows the contact page of the FRED simulation software. The header features the FRED logo and a navigation menu with links to Projects, New Job, Plotting, About, and Contact. The user's name, Gunasekaran Manogaran, is displayed in the top right corner. The main content area is titled 'Contact' and contains three input fields: 'Your Name' (filled with Gunasekaran Manogaran), 'Your Email' (filled with gunavit@gmail.com), and 'Message' (empty). A 'Send' button is located at the bottom left of the form.

FRED [Projects](#) [New Job](#) [Plotting](#) [About](#) [Contact](#) Gunasekaran Manogaran

Contact

Your Name

Gunasekaran Manogaran

Your Email

gunavit@gmail.com

Message

Send



Contact

Your Name

Gunasekaran Manogaran

Your Email

gunavit@gmail.com

Message

Send

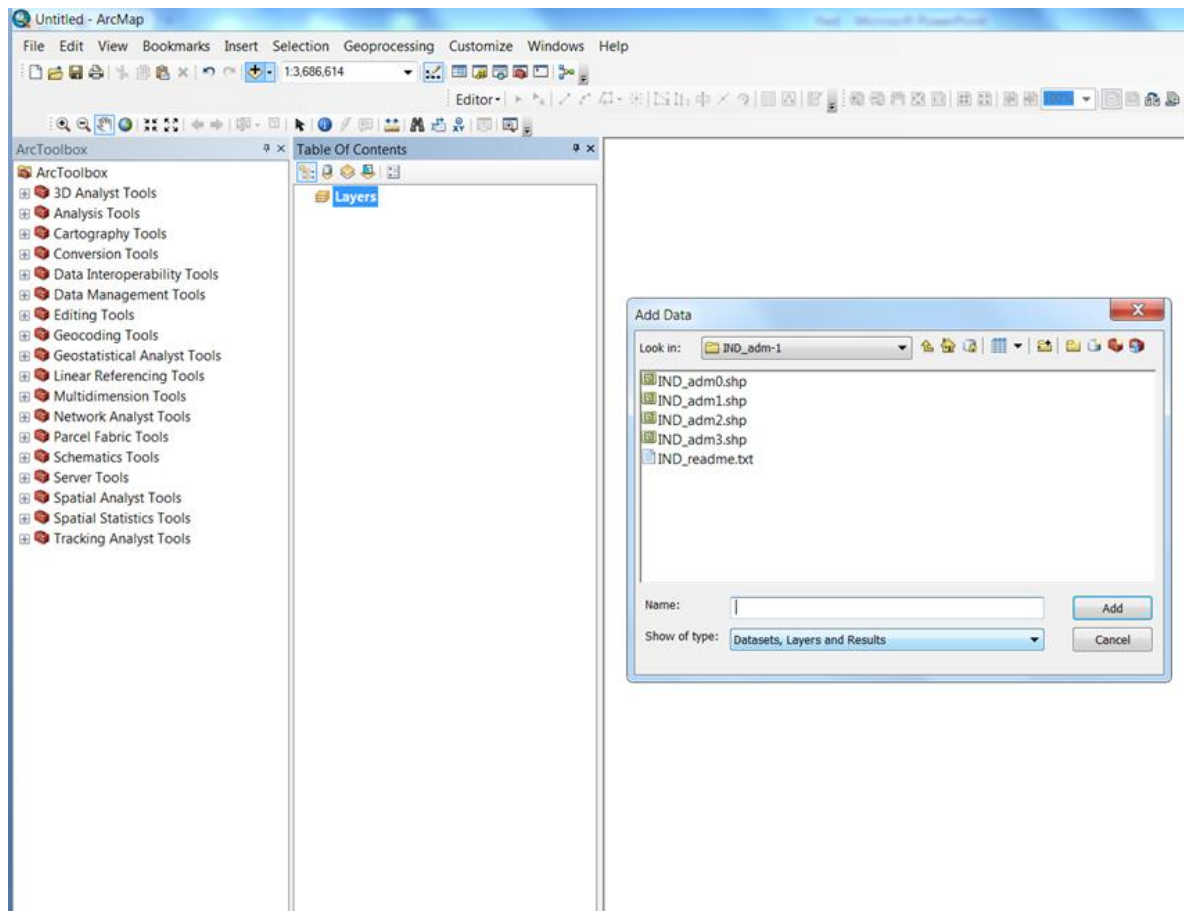
Spatial Epidemic Modeling in ArcGIS

A series of horizontal lines in teal and light blue colors, with varying lengths and offsets, creating a modern, layered effect across the width of the slide.

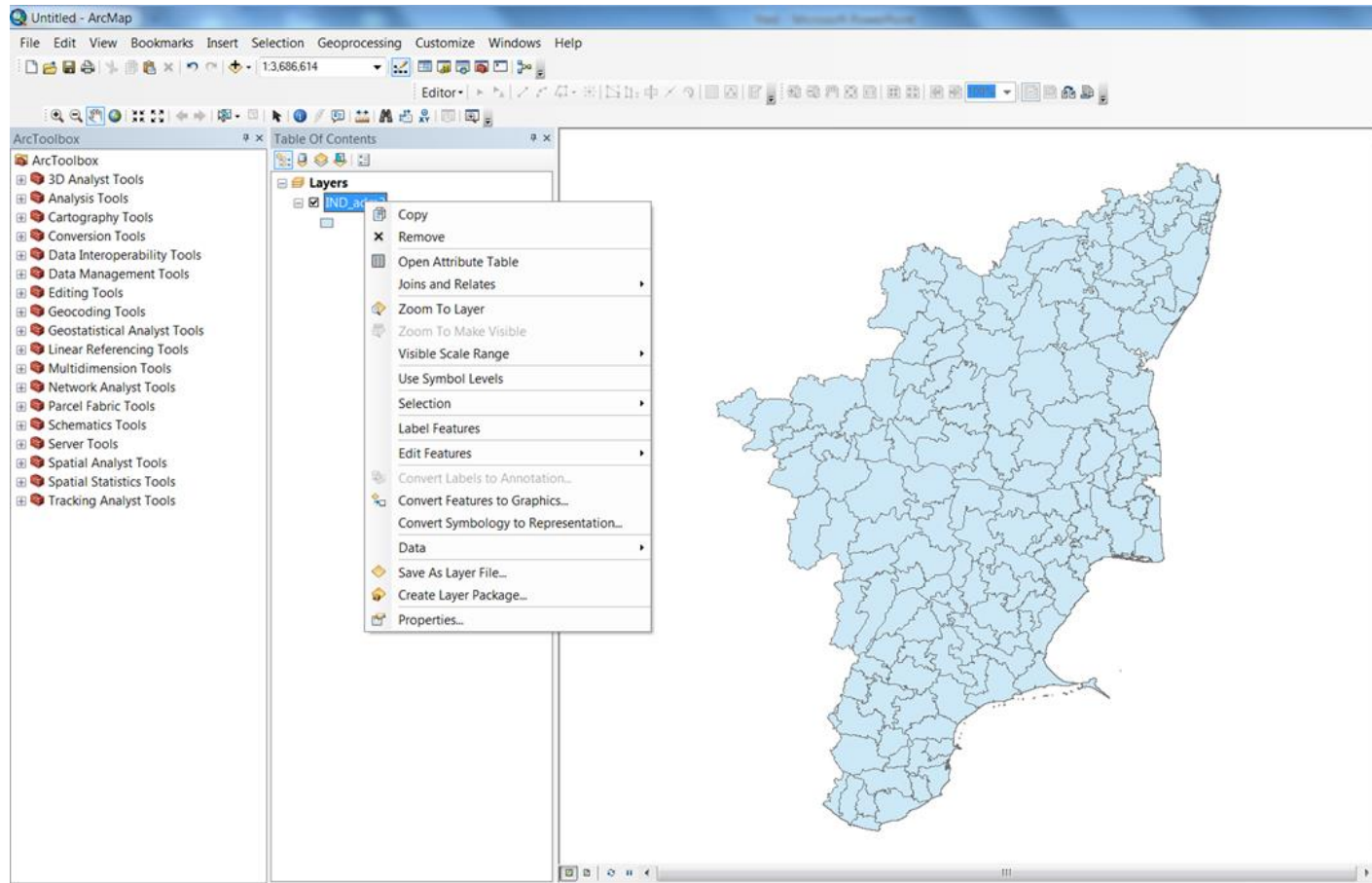
Spatial Modeling of Diseases in ArcGIS Software

ArcGIS for Desktop allows you to analyze your data and author geographic knowledge to examine relationships, test predictions, and ultimately make better decisions.

ArcGIS Simulation



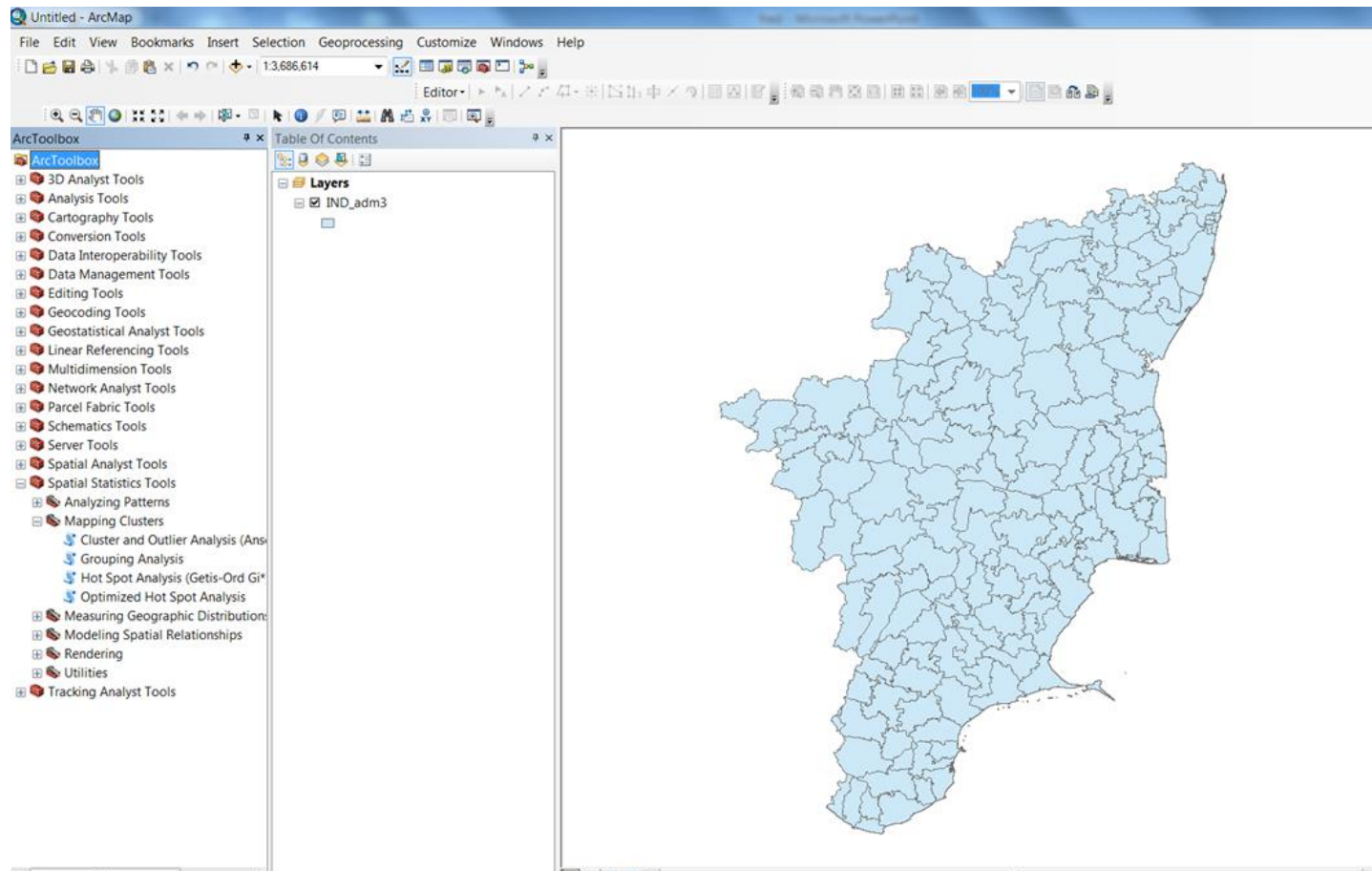
ArcGIS Simulation



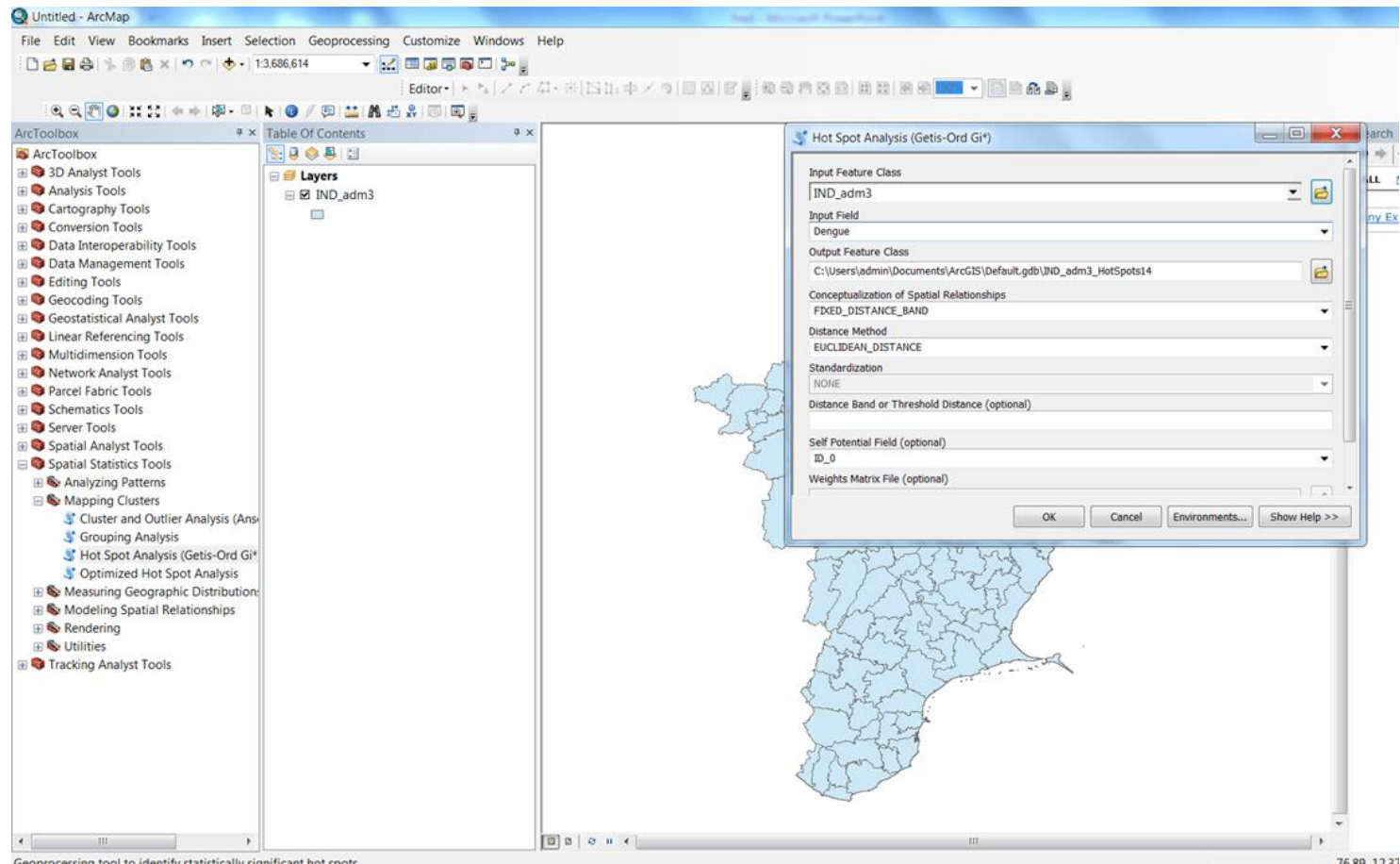
ArcGIS Simulation

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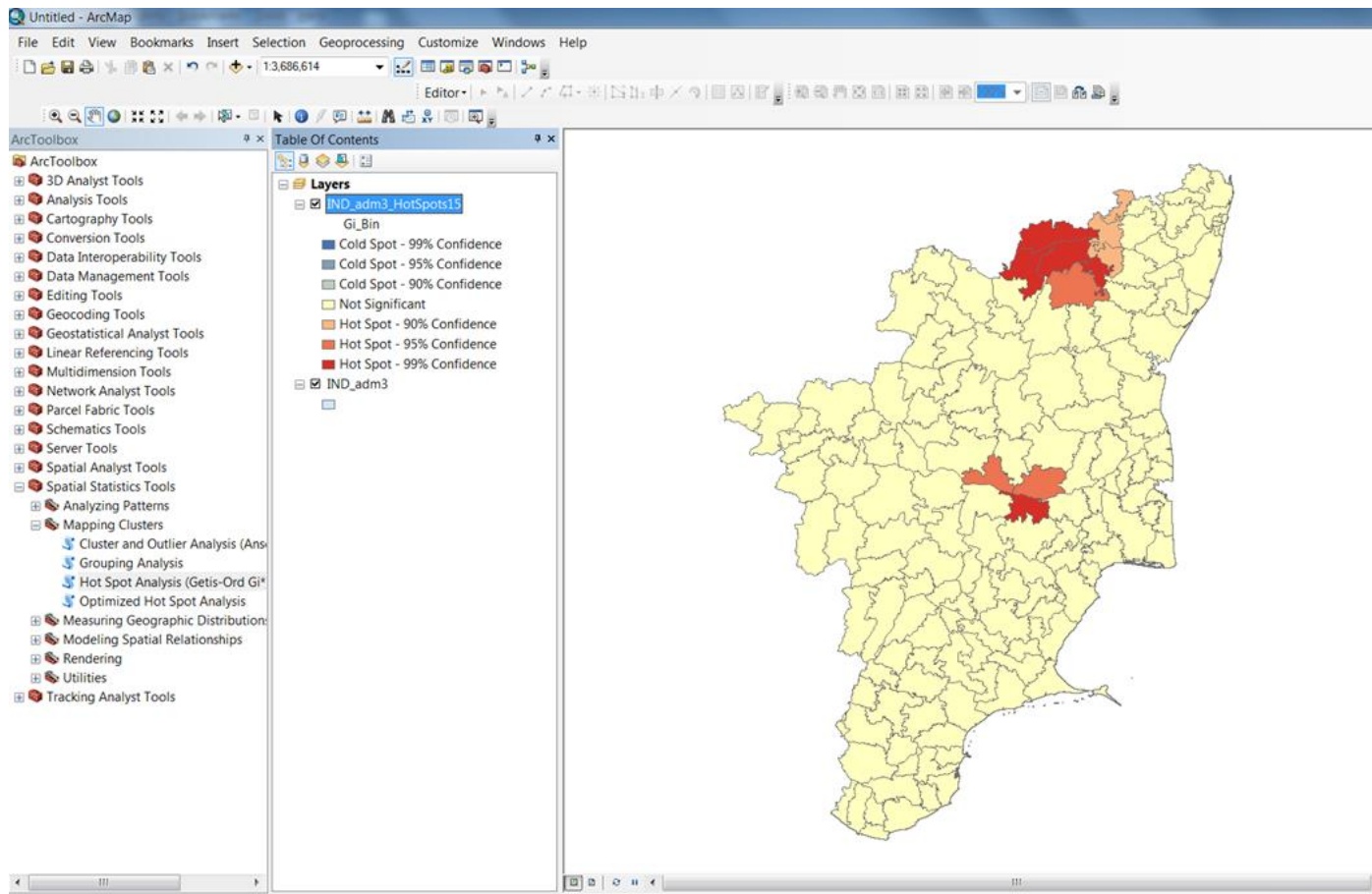
ArcGIS Simulation



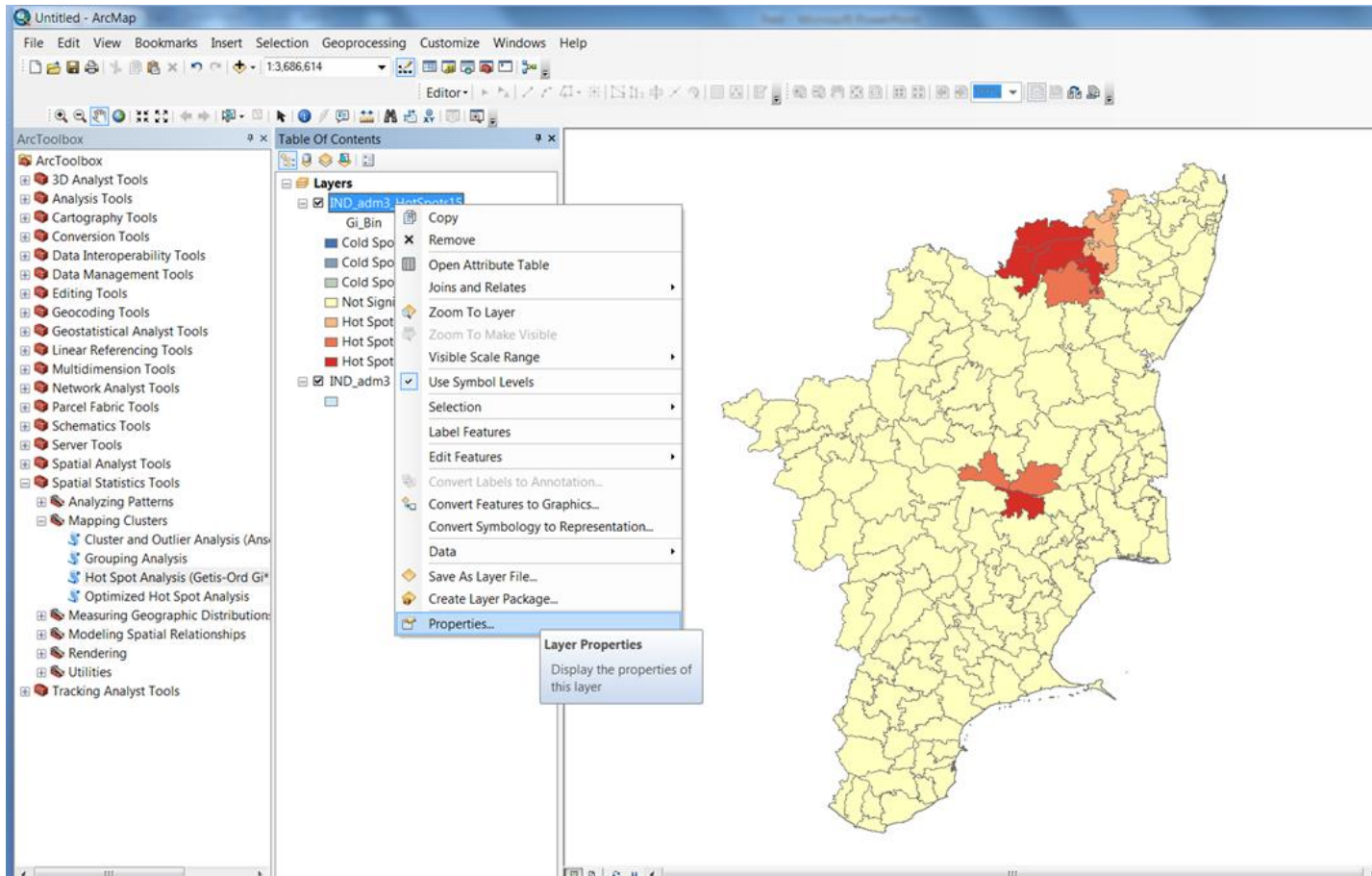
ArcGIS Simulation



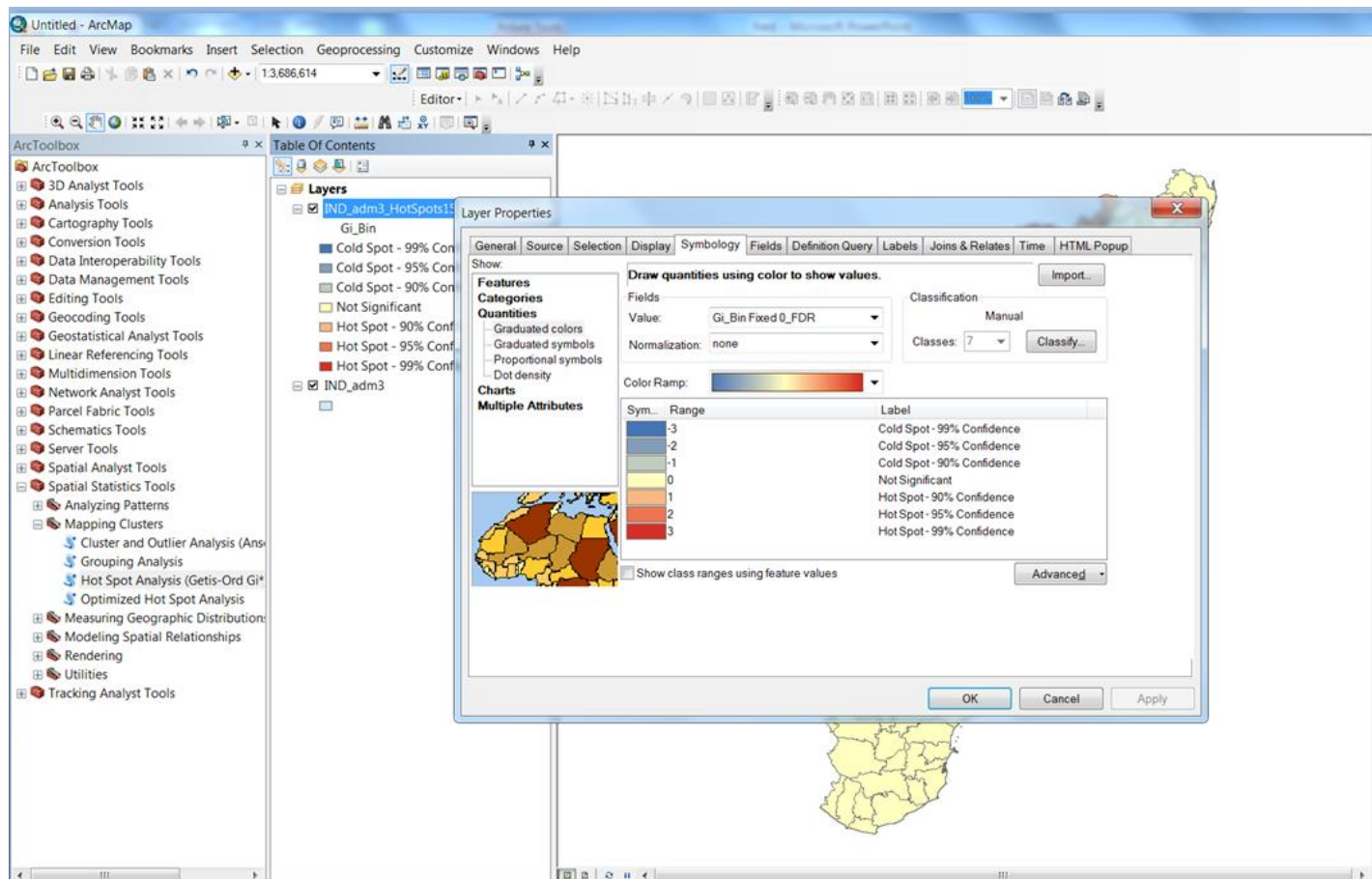
ArcGIS Simulation



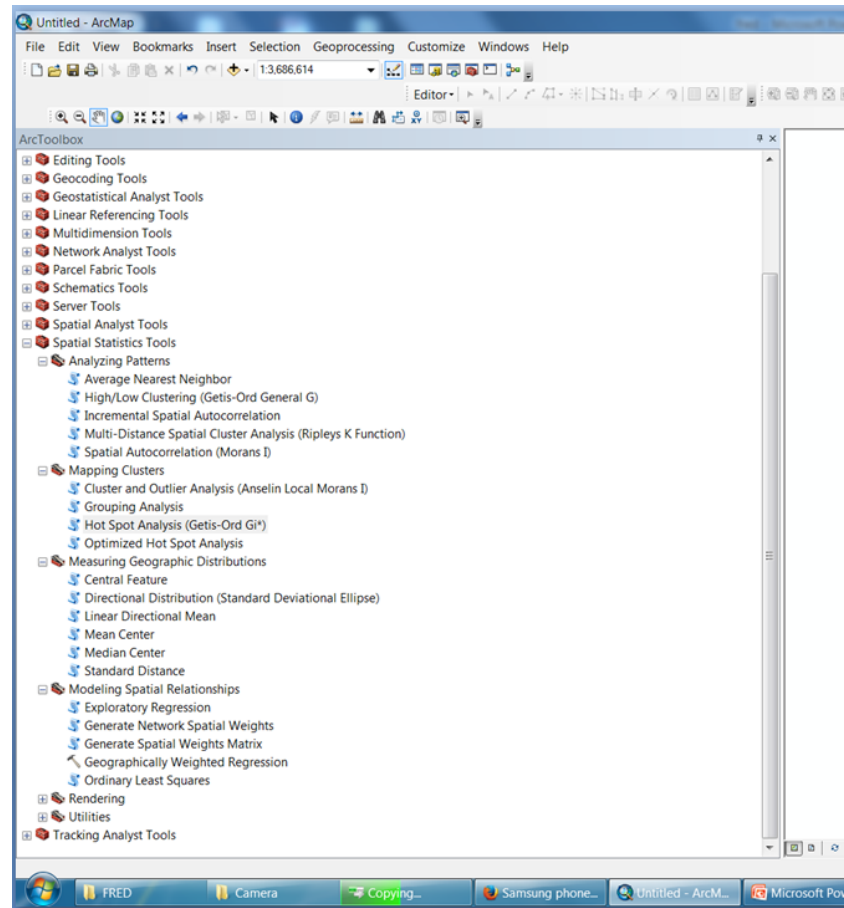
ArcGIS Simulation



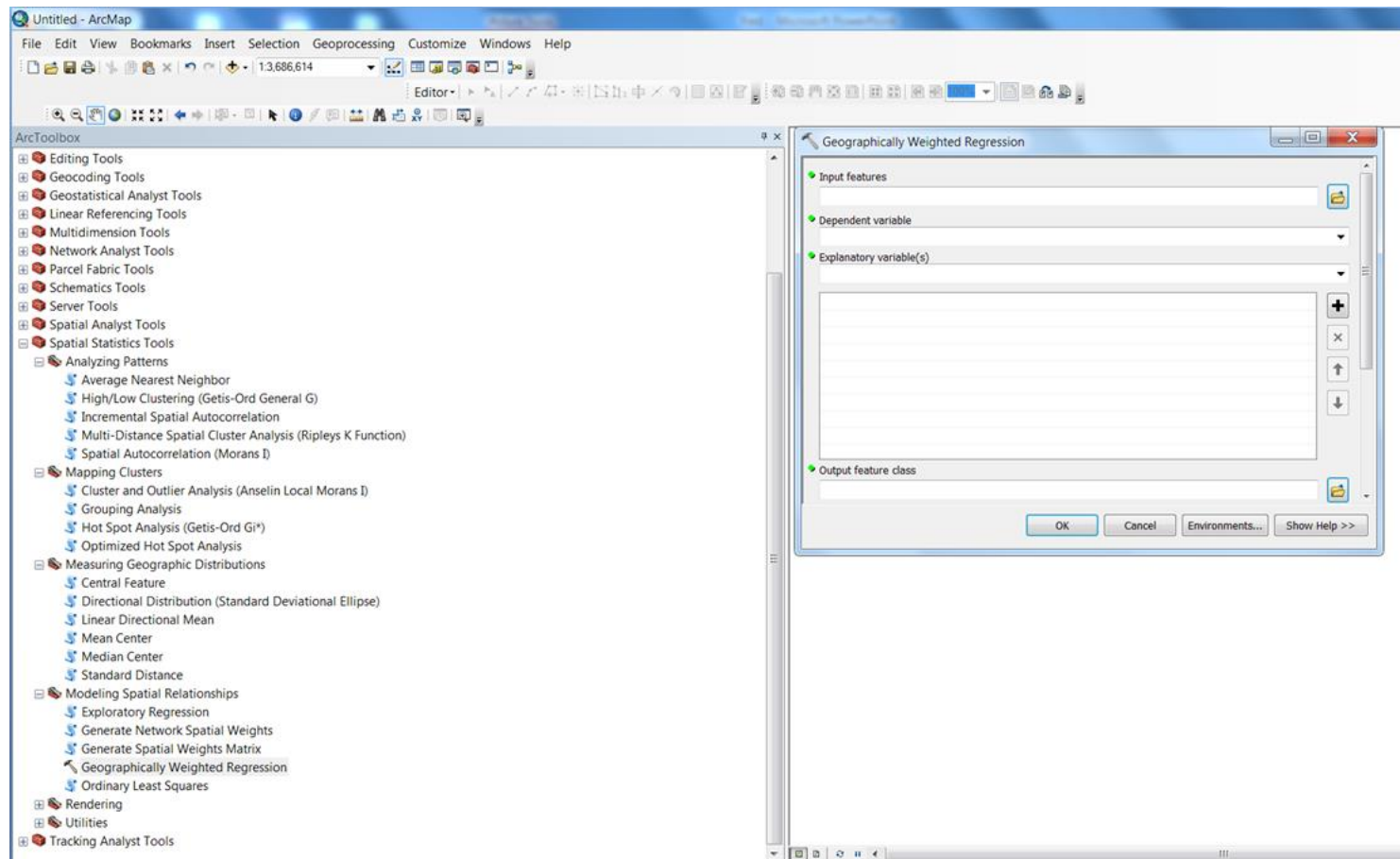
ArcGIS Simulation



ArcGIS Simulation



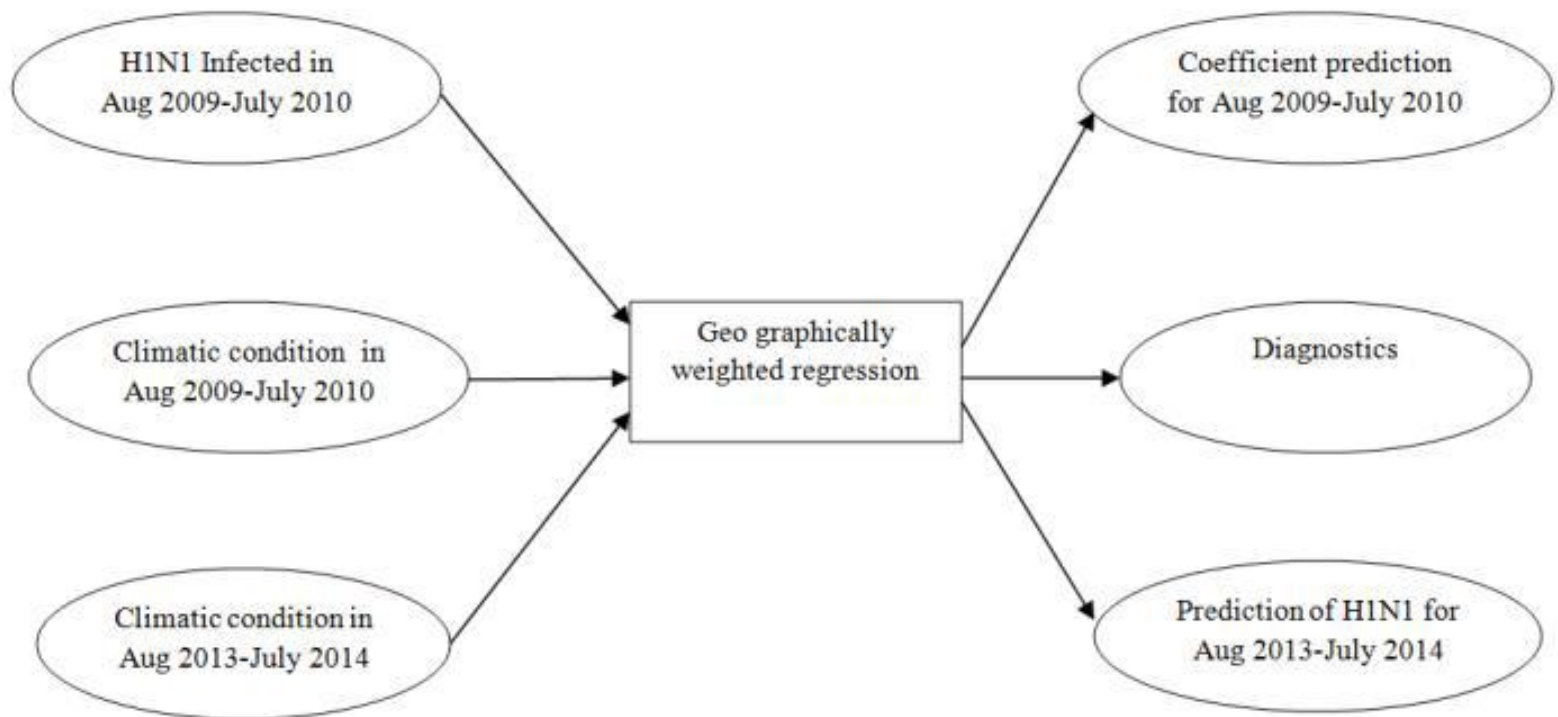
ArcGIS Simulation



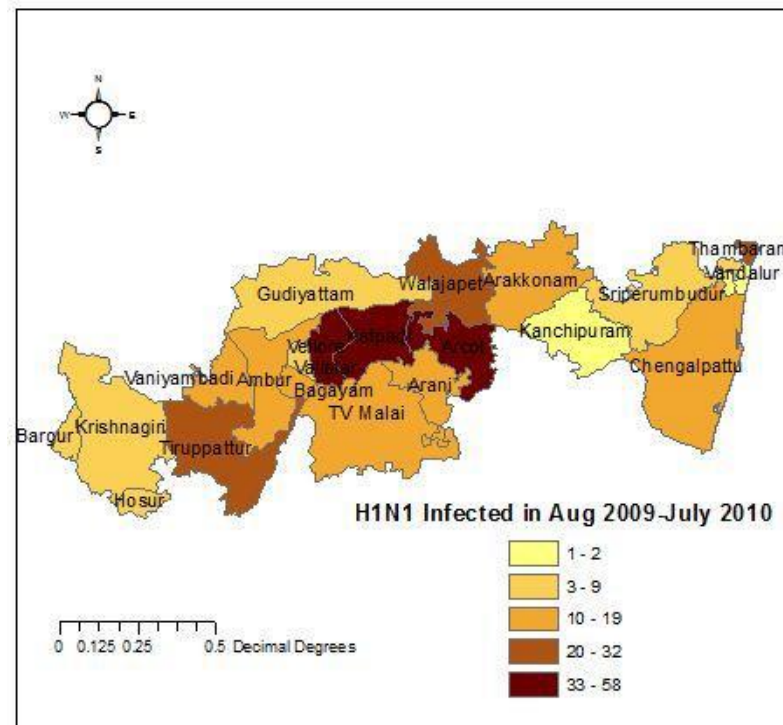
Case Study

The study objective is to develop a spatial data model to predict the epidemiological impact of influenza in Vellore, India.

Geographically Weighted Regression Model of H1N1 Influenza Epidemic



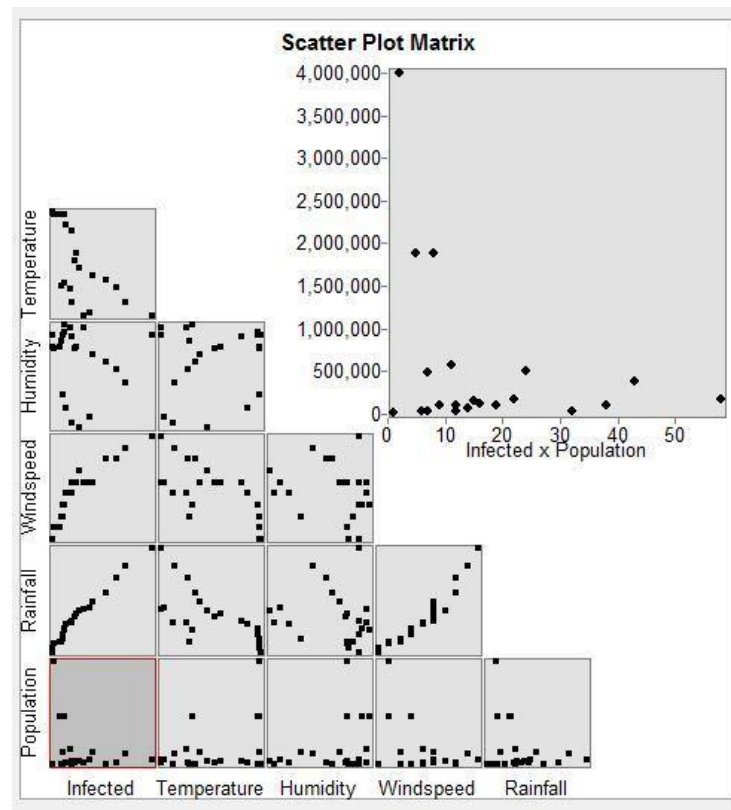
H1N1 influenza prevalence during August 2009-July 2010

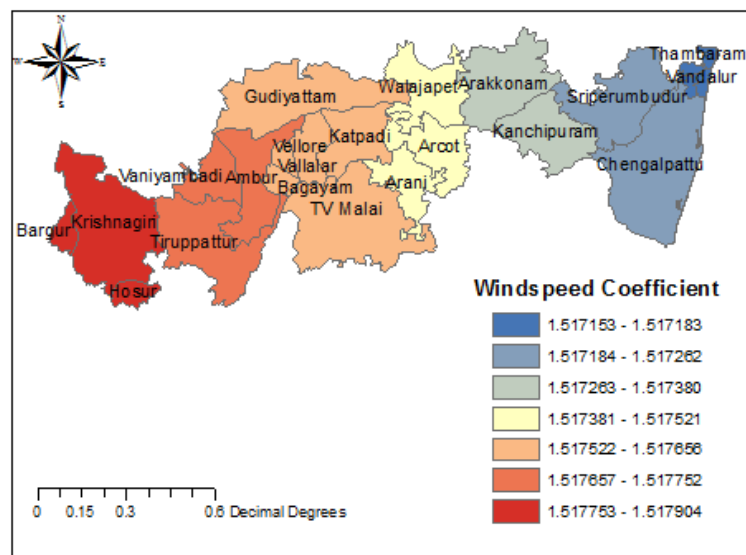
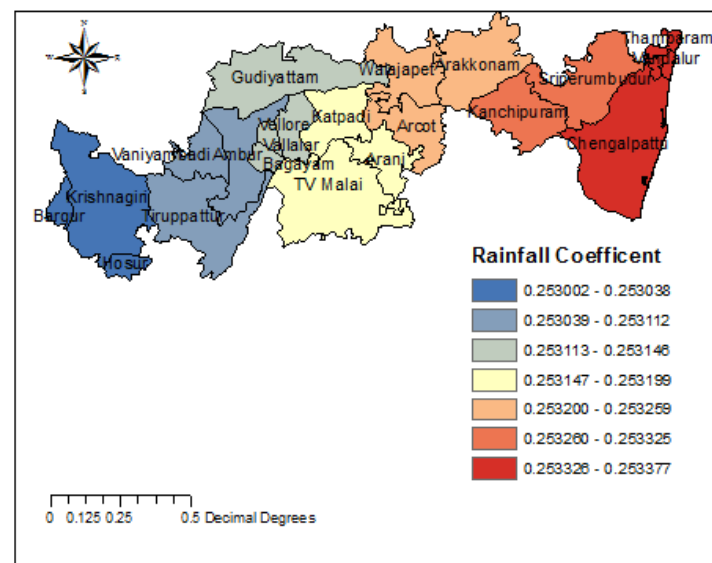
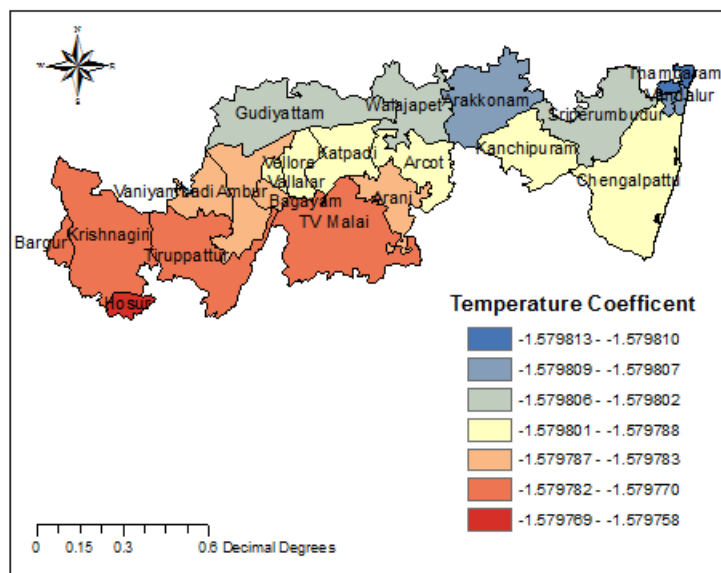


Climate conditions in Vellore.

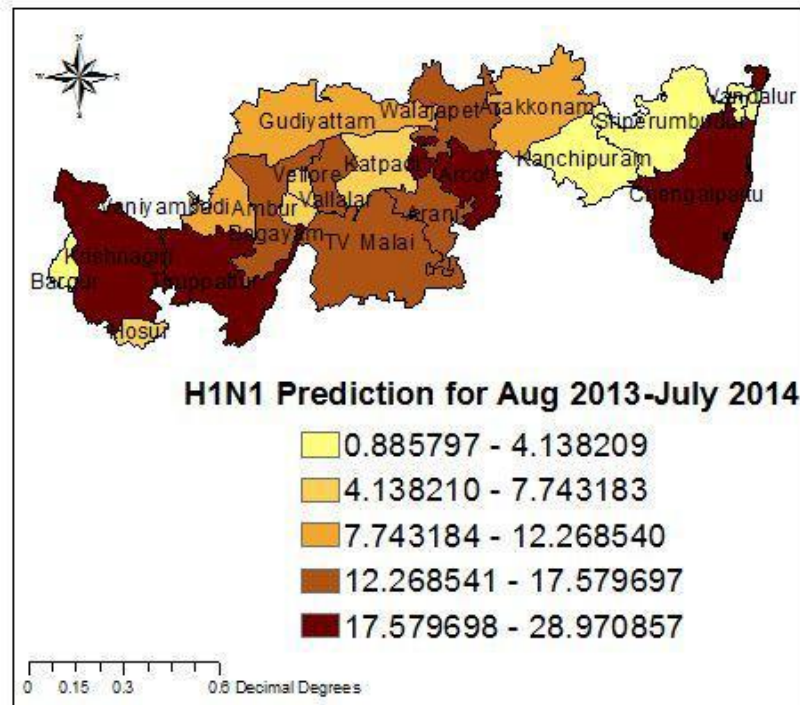
FID	NAME_3	Infected	Temperature	Humidity	Windspeed	Rainfall	Population
0	Kelambakkam	6	24.56	64.21	6	63	23453
1	Thambaram	22	20.76	54.23	9	85	174787
2	Koyambedu	1	35.56	64.98	4	56	12323
3	Vandalur	1	35.24	63.45	4	59	13311
4	Krishnagiri	8	25.02	66.34	7	71	1879809
5	Chengalpattu	11	24.12	65.96	8	75	571254
6	Kanchipuram	2	35.23	63.23	5	62	3998252
7	Sriperumbudur	7	35.23	57.04	6	65	486063
8	Arani	14	28.43	63.12	9	79	63671
9	TV Malai	15	29.45	63.34	9	81	144278
10	Arakkonam	12	32.65	64.85	9	76	101626
11	Arcot	38	24.3	60.4	11	105	95955
12	Gudiyattam	9	33.56	55.34	8	74	91558
13	Tiruppattur	24	26.2	62.34	9	89	500455
14	Ambur	16	27.3	52.76	10	83	114608
15	Katpadi	43	22.3	58.57	12	112	387922
16	Walajapet	32	25.4	61.34	11	95	32397
17	Vaniyambadi	19	20.23	65.87	9	84	95061
18	Bagayam	12	22.12	53.32	8	75	23145
19	Vellore	58	20.3	65.01	13	124	177230
20	Vallalar	7	35.1	64.98	7	68	25092
21	Hosur	8	35.023	65.34	7	72	1879809
22	Bargur	5	35.22	63.3	5	63	1879809

Correlation analysis using scatter plots





Prediction of H1N1 influenza

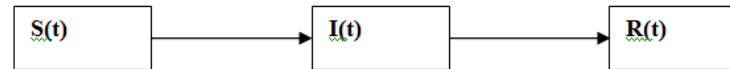


Epidemic Modeling in MATLAB

A decorative graphic consisting of several horizontal lines of varying lengths and colors (teal, light blue, and white) extending from the left edge of the slide towards the right, positioned below the title.

SIR Epidemic Model in MATLAB

SIR Model



Model Equation

$$\frac{di}{dt} = \lambda si - \mu i, \quad I(0) = i_0$$

$$\frac{ds}{dt} = -\lambda si, \quad S(0) = s_0$$

$$\frac{dr}{dt} = \mu i, \quad r_0 = 0$$

$$S(t) + I(t) + R(t) = N$$

Where,

$s \rightarrow$ susceptible

$i \rightarrow$ infected

$r \rightarrow$ recovered

$\lambda \rightarrow$ Contact rate

$\mu \rightarrow$ Recovered rate

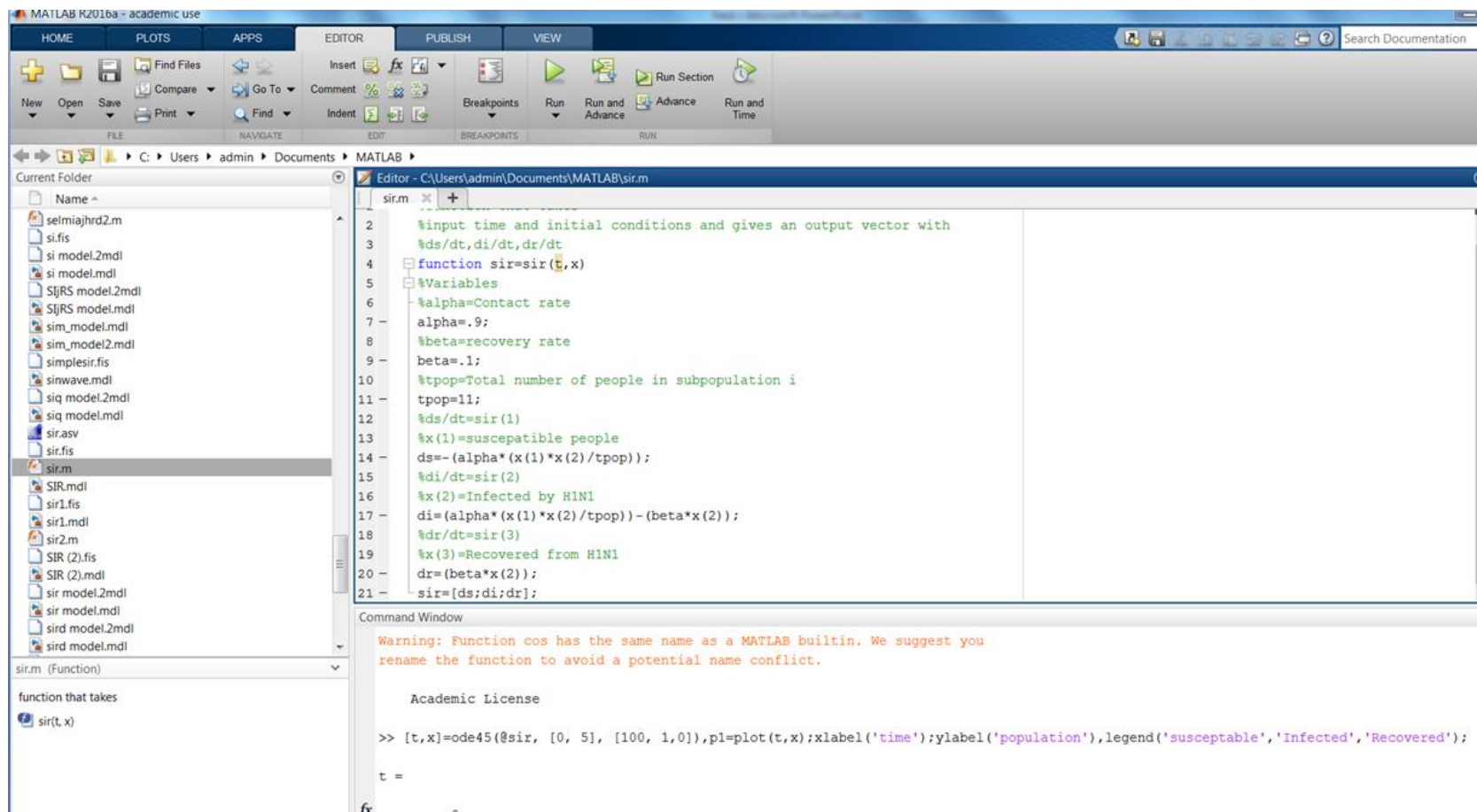
MATLAB Code for SIR Epidemic Model

```
%function that takes
%input time and initial conditions and gives an output vector with
%ds/dt,di/dt,dr/dt
function sir=sir(t,x)
%Variables
%alpha=the global transmission rate
alpha=.3;
%beta=contact rate per day by people in subpopulation i
beta=.9;
%gamma=Infectious mortality of subpopulation i, from infected class
%gamma=.01;
%tow=Rate of progression from exposed to infected ( ? 1 is latent period )
tow=1;
%row=Recovery rate
row=.5;
%tpop=Total number of people in subpopulation i
tpop=10;
%ds/dt=sir(1)
```

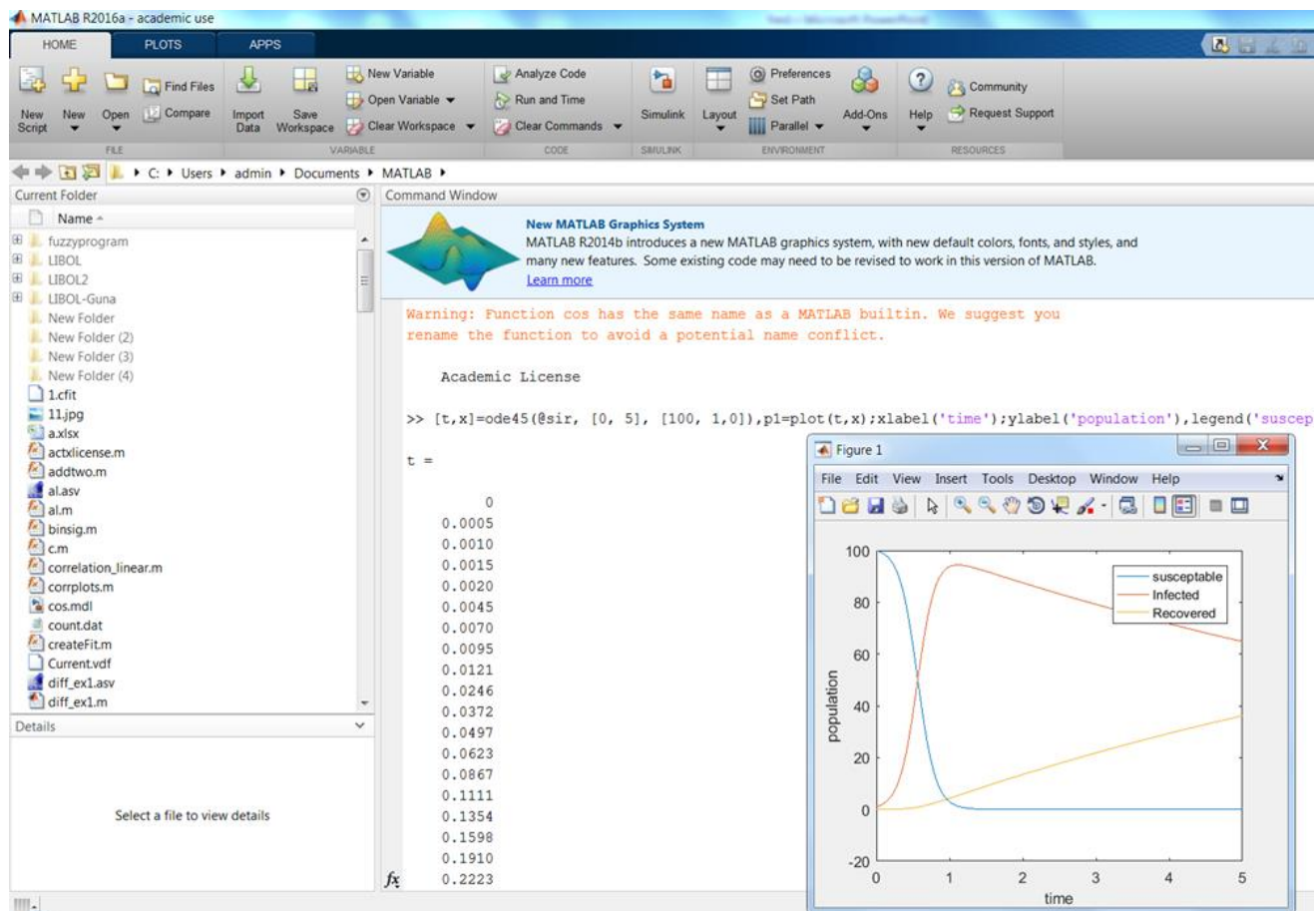
```
%x(1)=susceptible people
ds=-(beta*alpha*(((x(2)+x(3))*x(1))/tpop));
%de/dt=sir(2)
%x(2)=exposed by H1N1
%di=(beta*alpha*(((x(2)+x(3))*x(1))/tpop))-(tow*x(2));
%di/dt=sir(3)
%x(3)=Infected by H1N1
di=(alpha*(((x(2)+x(3))*x(1))/tpop))-(tow*x(2));
%dr/dt=sir(4)
%x(4)=Recovered from H1N1
dr=(row*x(2));
%dr/dt=sir(5)
%x(4)=Death people

sir=[ds;di;dr];
```

MATLAB Simulation



MATLAB Simulation





Thank You!