DISEASE SURVEILLANCE AND MONITORING USING GIS

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ABSTRACT

Epidemiology is an independent branch of medicine studying aetiology and spreading of infectious diseases in an human community and is aimed at prevention, control, and final eradication of these diseases. The combination of routes by which the pathogenic microorganisms are transmitted from an infected microorganism to a healthy one is called the mechanism of infection transmission. An infection process is the interaction of a pathogenic microorganism with a macro organism under certain environmental and social conditions. Four mechanisms of infection transmission are distinguished: (1) faecal-oral route; (2) air-borne; (3) transmissive; (4) contact and the main factors involved in transmission of infection are: air, water, foods, soil, and arthropods. Human activities are the most potent factors driving disease emergence; Main factors are: Social, economic, political, climatic, technologic, environmental factors, shape, disease patterns and influence emergence.

Geographical Information System (GIS) provides excellent means for visualizing and analyzing epidemiological data, revealing trends, dependencies and inter-relationships. GIS serves as a common platform for convergence of multi-disease surveillance activities. Public health resources, specific diseases and other health events can be mapped in relation to their surrounding environment and existing health and social infrastructures. Such information when mapped together creates a powerful tool for monitoring and management of epidemics.

The paper deals with the application of GIS in identifying the prone area of epidemics. The paper discusses the different GIS operations, mainly overlay analysis, buffer analysis, network analysis, statistical analysis, query, time series analysis, temporal cluster analysis, spatial-temporal analytic techniques to identify the catchment areas, vulnerable groups, health centers, movement of carriers etc. A case study is taken at campus of Birla Institute and Technology and Science, Pilani and analysis is confirmed by the cases reported at medical center at campus.

INTRODUCTION

There are various categories under which the infectious diseases fall. These include vector borne diseases, airborne diseases, waterborne diseases, food borne diseases, and plant and fish diseases. These categories are influenced by various factors. Three obligatory factors are necessary for the onset and continuous course of an epidemic process: source of pathogenic microorganism, the mechanism of their transmission, and microorganisms susceptible to infection. Basic concepts in disease emergence are: Emergence of infectious diseases is complex; Infectious diseases are dynamic; Most new infections are not caused by genuinely new

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pathogens; Agents involved in new and reemerging infections cross taxonomic lines to include viruses, bacteria, fungi, protozoa, and helminthes.

High-risk areas can be identified using GIS and remote sensing technologies that would otherwise be difficult to detect using traditional methods. Control and education programs can be directed toward these areas with more confidence and effectiveness. The following images shows the analysis part done in arcview GIS. GIS provides excellent means for visualizing and analyzing epidemiological data, revealing trends, dependencies and inter-relationships. GIS serves as a common platform for convergence of multi-disease surveillance activities. Public health resources, specific diseases and other health events can be mapped in relation to their surrounding environment and existing health and social infrastructures. Such information when mapped together creates a powerful tool for monitoring and management of epidemics. GIS helps us out in many ways. These include the following applications.

- Find out geographical distribution and variation of diseases
- Identify gaps in immunizations
- Map populations at risk and stratify risk factors
- Forecast epidemics
- Monitor diseases and interventions over time
- Manage patient care environments, materials, supplies and human resources
- Monitor the utilization of health centers
- Route health workers, equipments and supplies to service locations
- Locate the nearest health facility.

FACTORS INFLUENCING DISEASES

Climate

Infectious diseases that are responsive to climate can be divided into two groups. The first group comprises those diseases for which there are clearly documented links between incidence and climate and weather factors. The second group comprises diseases whose incidence is cyclical, thereby suggesting a link to climate, but for which the potential mechanisms linking climate factors to incidence are either unknown or only tentatively established (Giesecke 1999).

Temperature

Microorganisms carried by vectors, such as mosquitoes, ticks, and other blood-sucking arthropods, are strongly influenced by temperature of the microenvironment within their cold-blooded vector hosts. The survival rates of vectors and the rates of multiplication and transmission of the microorganisms that infect them are temperature dependent. Over the low temperature threshold, the rates of development of the parasite and the vector population increase with temperature, thereby increasing transmission capacity.

Precipitation

Precipitation, especially in the form of rainfall, can affect disease transmission via the effects of normal, as well as severe (i.e., flooding and drought), events on vector populations. Flooding can influence disease transmission in a number of ways, most notably by increasing run-off and disturbing breeding grounds and habitats (Clark, 1993).

Wind and ocean currents

Sea-surface temperature, height, and concentration of nutrients in seawater are associated with waterborne diseases. Ocean currents and tides are connected with various epidemiological patterns (Colwell, 1996).

Human population movement

Human population movement (HPM) is a term that encompasses a variety of ways that people travel from one area to another. Population movement has historically contributed to the spread of many infectious diseases that have left their mark on human growth and progress. Humans travel for a variety of reasons and causes. The understanding of these factors is the first stage in controlling the development and spread of communicable diseases. These various factors include push and pull factors, circulation, temporal dimensions, spatial dimensions and migration. Depending on these factors the infectious diseases are categorized and the transmission settings and the vulnerable groups are tabulated in Table I.

Circulation

Daily: Leaving place of residence for up to 24 hours (e.g. commuting, trading, and cultivation)

Periodic: Period varies from 1 day to 1 year but usually of shorter duration than seen in seasonal circulation (e.g. trading, pilgrimage, mining, and tourism).

Seasonal: Period defined by marked seasonality in the physical or economic environment (e.g. fishing, laboring, and pastoralism).

Long-term: Absence from place of residence for longer than 1 year (e.g. urbanization, colonization, and traders).

Migration: Long-term: Population movement resulting in a permanent change of residence. (e.g.

Infectious disease category	Important examples	Transmission settings	Affected populations
Vaccine-preventable diseases in children	Measles Mumps Rubella Varicella Pertussis Hepatitis B* Hib Polio Tetanus Diphtheria Pneumococcal disease*	Population ECC Schools	Children
Vaccine-preventable diseases in adults	Influenza Pneumococcal disease Tetanus Hepatitis B	Population Workplace	Adults, especially elderly
Respiratory diseases (often linked to socioeconomic deprivation and crowding)	Meningococcal disease Tuberculosis Rheumatic fever Mycoplasma RSV Pneumococcal disease Respiratory infectious diseases generally	Home, especially deprived communities with high level of household crowding Prisons	Socioeconomically deprived

urbanization, refugees, and colonization).

Infectious disease category	Important examples	Transmission settings	Affected populations
Enteric disease with food-borne transmission	Campylobacteriosis* Salmonellosis VTEC* Yersiniosis Listeriosis* Norwalk-like virus Food intoxicants (eg, staphylococcal) Botulism Marine biotoxins	Home Commercial food premises	All, especially children
Enteric disease with water-borne transmission	Cryptosporidiosis* Giardiasis* Campylobacteriosis*	Anywhere with a water supply	All
Diseases from close physical contact	Giardiasis* Rotavirus Helicobacter Hepatitis A* Adenonvirus EBV Skin infections and cellulitis Invasive streptococcal disease Impetigo Head lice Scabies Mycotic diseases (including dermatophytes)	Population ECC and schools	Children
Zoonotic disease linked to direct animal contact	Leptospirosis* Typhus Emerging diseases (eg, lysavirus) VTEC, cryptosporidiosis and other enteric diseases*	Farms Homes with pets	All, especially in rural areas
Occupational infectious disease	Hepatitis B* Leptospirosis* Enteric diseases in some occupational groups*	Workplaces, especially farms, health care, laboratories	All, especially farmers, health workers, laboratory workers
Diseases from contaminated environments	Legionellosis Cryptosporidiosis* Amoebic meningoencephalitis	Recreational water and pools Contact with soil/compost Farms	All
Travel-associated and imported infectious diseases	Dengue fever Malaria Rabies Schistosomiasis Yellow fever Typhoid Cholera Shigellosis Traveller's diarrhoea Leprosy Hepatitis A* Tuberculosis* HIV/AIDS*	Overseas countries, especially developing countries	Travellers Immigrants, especially refugees

Infectious disease category	Important examples	Transmission settings	Affected populations
Vector-borne diseases (especially with introduction potential)	Ross River virus Dengue fever*	Borders and airport	All, if diseases introduced
Congenital and perinatal infections	Hepatitis B* Listeriosis* Congenital rubella syndrome Toxoplasmosis Group B streptococcal disease Cytomegalovirus	Maternal and neonatal care settings	Pregnant women Neonates
Blood-borne diseases and those linked to transplants and sharing injecting equipment	Hepatitis C HIV/AIDS* HTLV 1&2 CJD Newly recognised blood-borne diseases	Population Health care settings Prisons	All, especially hospitalised Injecting drug users
Sexually transmitted infections	Chlamydia Gonorrhoea Syphilis HIV/acquired immune deficiency syndrome* HPV HSV Hepatitis B*	Population	All, especially young adults Men who have sex with men Immigrant populations
Hospital acquired infections	MRSA *Clostridium difficile* Surgical-site infections (SSI) Blood-stream infections (BSI) Device-related infections Opportunistic infections	Health care settings	All, especially elderly
Diseases caused by antibiotic-resistance organisms	Penicillin resistant pneumococci VRE (enterococci) MDR TB PPNG (gonococci) Newly emerging resistance organisms	Human populations Animal populations Health care Veterinary Farming	All, especially hospitalised
Bioterrorism agents	Anthrax Other agents	Population, especially in government facilities	All, especially 'first responders'

* Disease appears in more than one category because it has more than one important mode of transmission or control.

CASE STUDY

This case aims at finding out the population that is vulnerable to vector borne disease in Birla Institute and Technology and Science, Pilani (BITS) campus. The digital map of the campus is taken and the basic operations such as Geo referencing, digitizing, etc. are carried out. The different hostels, institute, staff quarters, wells, market places were digitized as a polygon theme and the road network was also digitized as a separate theme.

The first phase utilizes landscape epidemiology to explore the relationship between landscape elements and the vectors breeding sites. The goal of this phase was to assess the capabilities of GIS and remote sensing to identify high vector breeding sites. The approach utilizes landscape composition methods. Using remotely sensed data to distinguish between different landscapes elements, it was determined that dairies, stagnating water, areas of vegetation had the highest vector abundance. The vectors must find larval habitats, blood meal sources and resting sites within a 1-km radius, in order to successfully reproduce. In the second phase GIS was used to determine the landscape composition of a 1-km buffer around each site. Using stepwise discriminant and regression analyses, it was determined that the whole BITS campus was vulnerable to the vector disease. The only restriction is that the climatic factors influence the breeding of the vectors. The climatic conditions of Pilani don't favour many vectors to survive.

Common methodology to identify vector borne disease

1. The data on different types of vectors causing infectious diseases, their survival conditions and other data's relevant to the vectors are collected.
2. The distribution of the population in a given region is gathered and sorted according to age group.
3. The map of the given region is obtained from the respective source. All the features in the map are digitized into their respective themes.
4. The vector breeding sites in that particular region is identified using suitable techniques.
5. The landscape composition and the population distribution are digitized on the map. The population database is also stored corresponding to the population age wise.
6. Buffers are created for the given population categorizing them into commercial area, institutes, and residential areas. Depending on the flight range of different vectors, suitable buffers are created from the vector breeding sites taking into consideration all the environmental and seasonal factors.
7. All these buffers are analyzed and using suitable operations such as union, intersection, overlay, network the vulnerable areas and the vulnerable group of population are assessed.
8. Depending on the results suitable preventive and control measures are taken.

Common methodology to identify airborne disease

1. The details of microorganisms present in air are obtained from suitable sources.
2. The data regarding the sustainable environmental factors are gathered and analyzed with respect to the given region.
3. The directions, flow rate, humidity conditions of air are obtained from Indian meteorological department.
4. For the given region, a direction profile for the flow of air is created.

5. Humidity and temperature profiles are created from the data obtained.
6. From all the data's, an analysis is performed and the vulnerable areas of airborne disease are identified.
7. Depending on these results suitable preventive and control measures are taken.

Common methodology to identify water borne diseases

1. All water sources are marked on the map of the given region. These are further classified as running water, stagnating water. The stagnating water is further classified as shallow and deep waters. Mostly the stagnating water causes diseases.
2. The stagnating water bodies are identified, since these are the sources.
3. Buffers are created for these water bodies and hence the nearby areas prone to these microorganisms are identified depending on the pipe network and flow condition from these sources.
4. The population distribution vulnerable to these diseases is identified using suitable analysis depending on the data obtained.
5. Depending on these results suitable control and preventive measures are taken.

The Fig. 1 shows the map of BITS campus. It also shows the different hostels, staff quarters, institute, wells, stagnant water bodies, shopping centre, and grounds. Fig. 2 shows the 2d view of the flow pattern of water depending on the elevation of ground at different sites. Fig. 3 shows a particular flow direction of air taken into consideration. The flow of air is considered to be point vectors and the vulnerable areas to that particular flow direction are identified. Fig. 4 shows the overlay of the buffers created for the hostels, staff quarters, institute, market place and the vector breeding sites. Since the flight range of vectors are generally within 1km radius from different vector sites, the whole BITS campus falls vulnerable to vector disease. But certain environmental and seasonal changes prevent the survival of many vectors.

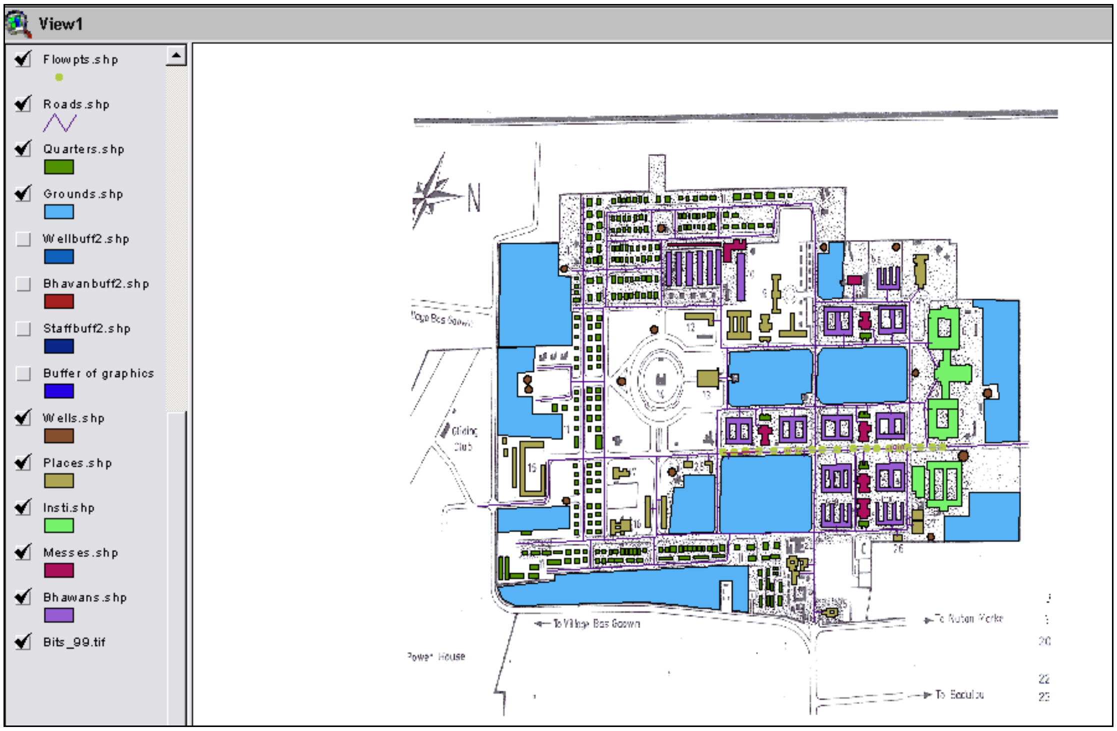
View1
Flowpts.shp
Roads.shp
Quarters.shp
Grounds.shp
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Fig. 1

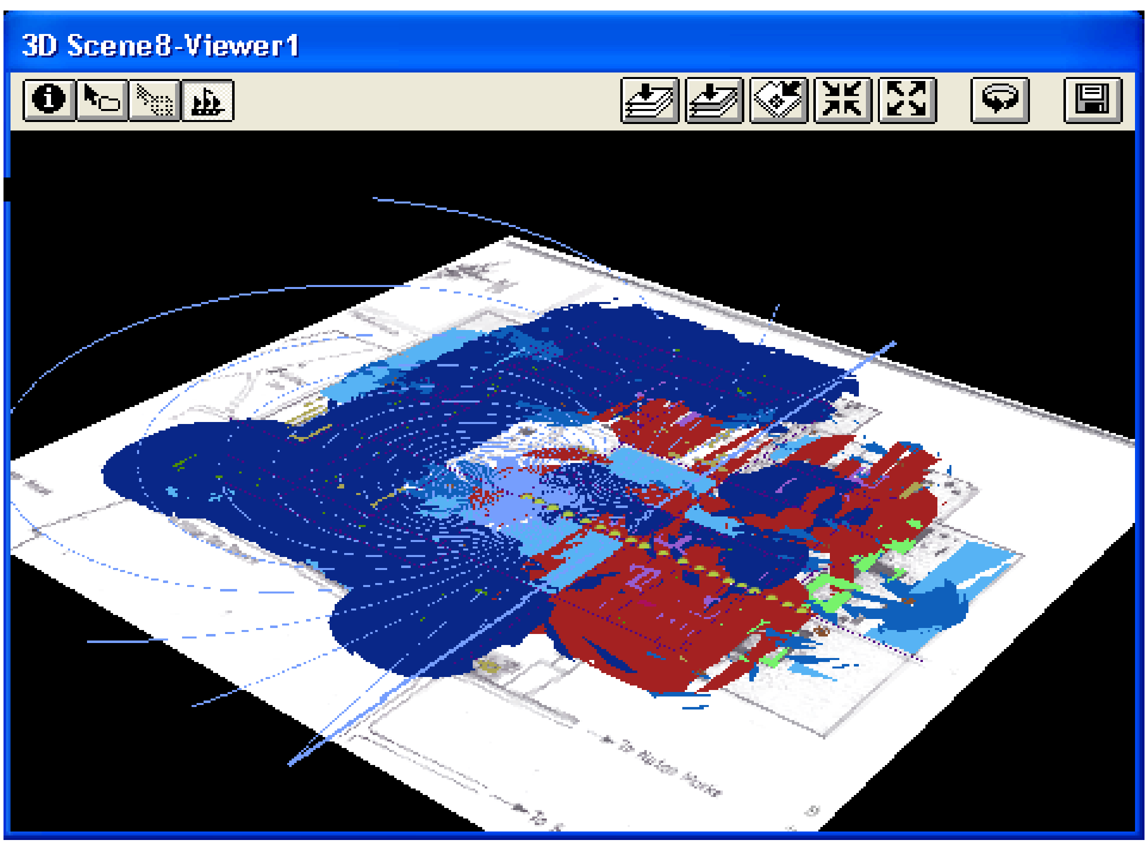
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Fig. 2

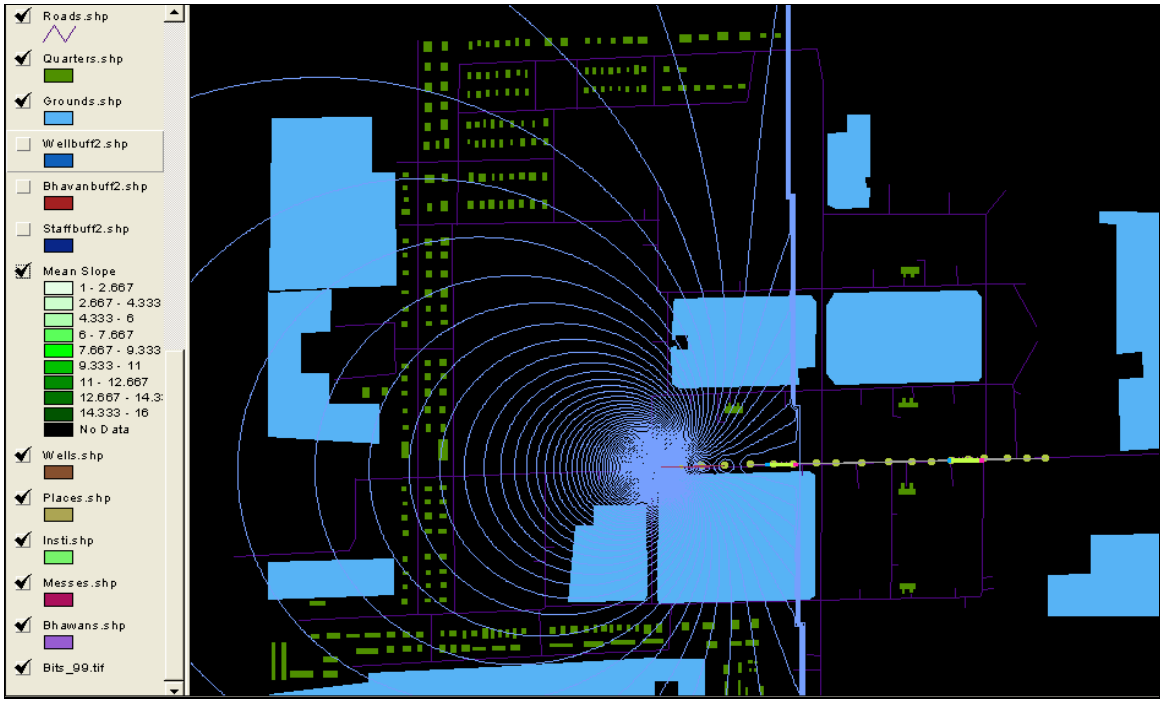

Fig. 3

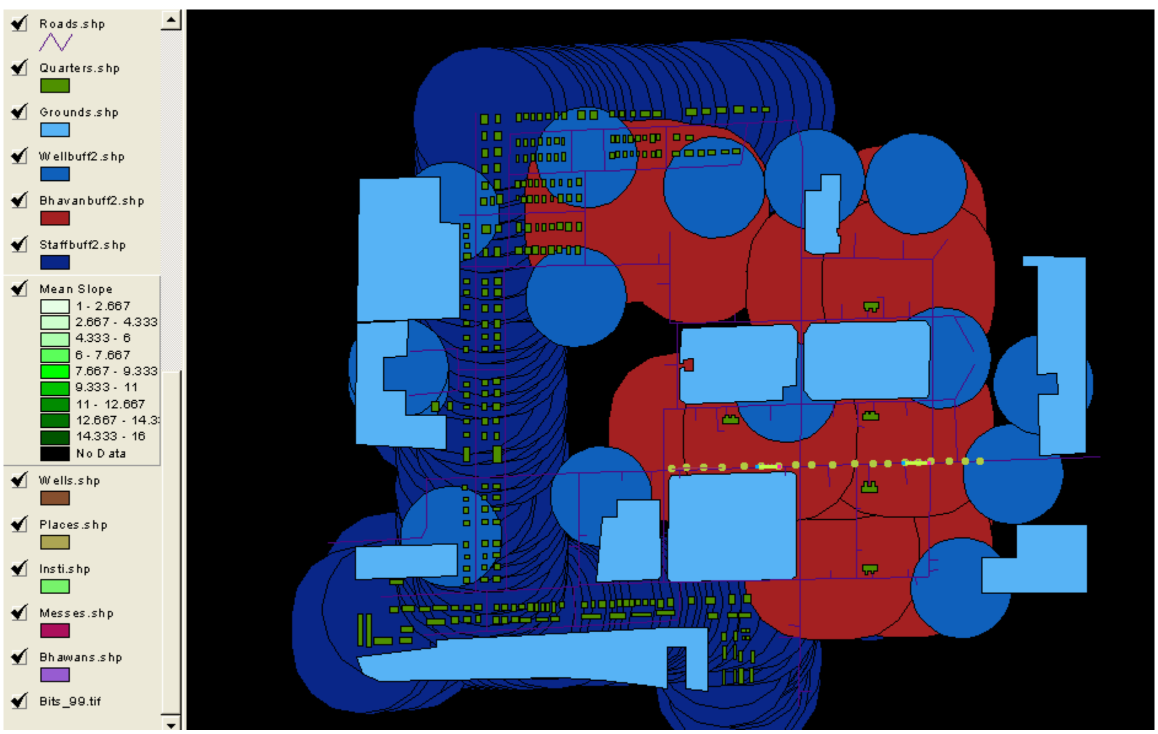

Fig. 4

A GIS contains four types of information and computer files: geographic, map, attribute, and data-point files. In general, modeling involves the integration of GIS with standard statistical and health science methods. Spatial interaction models analyze and predict the movements of people, information, and goods from place to place. By accurately modeling these movements, it is possible to identify areas most at risk for disease transmission and thus target intervention efforts. Spatial diffusion models analyze and predict the spread of phenomena over space and time and have been widely used in understanding spatial diffusion of diseases. By incorporating a temporal dimension, these models can predict how diseases spread, spatially and temporally, from infected to susceptible people in an area. Spatial variation in health related data is well known, and its study is a fundamental aspect of epidemiology. Representation and identification of spatial patterns play an important role in the formulation of public health policies. Some of the graphic and exploratory spatial data analytic techniques are: point patterns, line patterns, area patterns, time series analysis, temporal cluster analysis, and spatio temporal analysis.

CONCLUSION

Factors like movement of population, social conditions, environmental, soil conditions were analyzed and the diseases were classified accordingly. The populations at risk, catchment area, forecasting of outbreaks was found using suitable analysis. In this paper, the diseases were classified as water borne, vector borne, air borne, food borne and an analysis were made in campus. The vulnerable regions prone to these diseases were identified. This analysis was carried out by identifying the vector breeding sites, flow direction of the air, locating the places of stagnant water. By tracking the sources of diseases and the movement of contagions, the populations at risk were identified. Buffers were created for the hostels; staff quarters and the population at risk were identified. The present paper is a step towards to find a common methodology to identify the vulnerable area of infectious disease using GIS. However, in some cases it requires highly accurate data.

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