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GIS for Disease Surveillance and Monitoring

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Laboratory tools and techniques that enable scientists to peer deep inside pathogenic organisms are the stock-in-trade of infectious disease research. By revealing a pathogen's innermost molecular secrets, these methods have been instrumental in developing new drugs and vaccines against parasitic, bacterial, and viral diseases. There are various categories under which the infectious diseases fall.

- Air borne diseases
- Water borne diseases
- Vector borne diseases
- Food borne 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 pathogens; Agents involved in new and reemerging infections cross taxonomic lines to include viruses, bacteria, fungi, protozoa, and helminthes [1-4].

High-risk areas can be identified using GIS and remote sensing technologies that would otherwise be difficult to detect using traditional methods. 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.

- Risk Analysis
- Integrated environmental information systems
- Surveillance and Monitor diseases
- Geographical distribution and variation of diseases
- Identify gaps in immunization
- Map populations at risk and stratify risk factors
- Forecast epidemics

- Vaccination programmes
- Manage health care materials, supplies and human resources
- Route specialists to the affected farms
- Locate the nearest health laboratory
- Control and educational programs.

Tracking Lyme disease ticks

An NIAID/NASA study was done to determine Lyme disease risk on private properties in Westchester County, N.Y., illustrates one way that RS/GIS can be employed against emerging diseases. Lyme disease has been endemic in Westchester County since 1982, and more than 2,000 cases of the disease are reported there each year. Researchers hypothesize that Lyme disease hotspots such as this are caused by specific vegetation and landscape patterns that can be described and predicted by RS/GIS. To test their hypothesis, Dr. Fish and his colleagues obtained enhanced satellite images of the county that allowed them to make property-by-property comparisons of the vegetation.

On the ground, researchers measured tick populations on 337 different residential properties in the county. Combining this information with the satellite data, they found the greatest number of ticks on properties that had a high proportion of broad-leafed canopy trees and the smallest number on properties with mostly open lawn. Using these data, the researchers developed a model of Lyme disease risk for each residence in the county. A survey to determine the history of deer tick bites among a random sample of 1,000 county residences showed that the model was more than 70 percent accurate at predicting Lyme disease risk.

The model demonstrates how remote sensing and GIS technologies can be used to rapidly assess vector-borne disease risk over a large geographic area. "In this case, the information provided by these methods can be used for precise targeting of Lyme disease prevention efforts, such as education, vector control, and, ultimately, vaccination".

Cholera on the high seas

In a study of recent cholera outbreaks in India and Bangladesh researchers looked retrospectively at satellite-derived measurements of ocean temperature, height, turbidity, and phytoplankton concentration. Scientists have shown that ocean organisms known as zooplankton harbor cholera bacteria. Blooms, or dense concentrations, of these minute animals follow blooms of tiny plants called phytoplankton. By determining the oceanic conditions that favor the development of phytoplankton and zooplankton blooms, the researchers hope to develop a model that will provide an early warning system for potential cholera outbreaks.

Preliminary analyses show that the number of cholera cases in recent years has correlated directly with both ocean height and temperature. As these measures rose, cholera cases increased. Other possible factors affecting cholera emergence are still being examined.

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.

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.

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.

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.

Common methodology to identify vector borne disease

- The data on different types of vectors causing infectious diseases, their survival conditions are collected
- The distribution of the population in a given region is gathered and sorted according to age group
- The map of the given region is obtained from the respective source. All the features in the map are digitized into their respective themes
- The vector breeding sites in that particular region is identified using suitable techniques
- The landscape composition and the population distribution are digitized on the map. The population database is also stored corresponding to the population age wise
- Buffers are created for the given population categorizing them into commercial area, institutes, and residential areas
- Depending on the results suitable preventive and control measures are taken.

Common methodology to identify airborne disease

- The details of microorganisms present in air are obtained from suitable sources
- The data regarding the sustainable environmental factors are gathered and analyzed with respect to the given region
- The directions, flow rate, humidity conditions of air are obtained from Indian meteorological department
- For the given region, a direction profile for the flow of air is created
- Humidity and temperature profiles are created from the data
 obtained
- From all the data's, an analysis is performed and the vulnerable areas of airborne disease are identified
- Depending on these results suitable preventive and control measures are taken.

Common methodology to identify water borne diseases

- 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
- 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
- The population distribution vulnerable to these diseases is identified using suitable analysis depending on the data obtained
- Depending on these results suitable control and preventive measures are taken.

Important diseases in fisheries and aquaculture

Affected Transmission Disease **Important Examples** Settings Species Viral WSSV Water Shrimps Yellow head virus Seed/Shrimps MBV Crabs Taura Syndrome virus Prawns Human Lymphocystis Disease Water Finfish Herpes virus salmonis Seed Channel Catfish Virus Human Epithelioma papillosum (Fish Pox) Infectious Hematopoietic Necrosis (IHN) Viral Hemorrhagic septicemia Spring Viremia of Carp (SVC) and Swim Bladder Infection virus (SBI) Infectious Pancreatic Necrosis (IPN) Bacterial Vibrios Water Shrimps/ Edwarsiella Feed Finfish Aeromonas Human Pseudomonas Fungus Branchiomycosis (Gill Water Shrimps/ Finfish rot) Feed Human Ichthyosporidiosis Saprolegniasis

Table 1

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