Health Bulletin #1

iDAlert
Infectious Disease decision-support tools and Alert systems

A close-up on a multi-model framework for providing epidemiological outlooks

Climate change can have a profound impact on human health, with many infectious diseases being sensitive to changes in temperature, precipitation, and the impacts of extreme weather events. However, predicting these risks is challenging due to the complex interactions between climate, socio-economic factors, demographics and animal hosts.

EpiOutlook aims to bridge this gap by providing a robust early warning system (EWS) that enhances preparedness and response capabilities.

The platform makes use of robust sub-seasonal to seasonal (S2S) climate forecasts, along with data on sea-surface conditions, land use, travel information, population vulnerability and animal/wildlife hosts to estimate future risks of climate-sensitive infectious disease transmission. These forecasts extend from a few weeks to several months in advance, helping to identify high-risk regions and potential seasonality.

EpiOutlook will help a wide range of users, including public health authorities, humanitarian agencies, medical and veterinary practitioners, the travel and tourism sector, and the general public, in making informed health decisions and allocate resources effectively, thereby reducing the impact of climate-related epidemiological risks.

A multi-model framework

EpiOutlook is built around a multi-model framework that integrates and processes data from diverse range of sources, which are influential to a set of climate-sensitive epidemiological risk indicators:

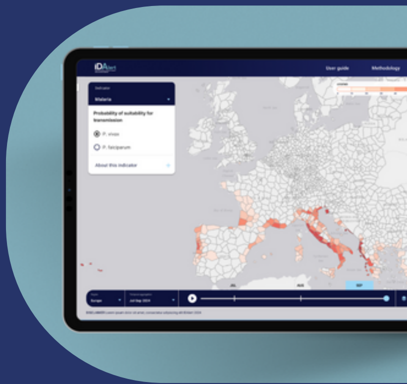
- **Tick-borne diseases**
- **Leishmaniasis**
- **Malaria**
- **Dengue**
- **Chikungunya**
- **Zika**
- **West Nile virus**
- **Vibrio**
- **Drought**

These indicators are derived using a combination of methodologies:

Threshold-based models

Machine learning algorithms

Mechanistic transmission models



The EpiOutlook Platform

The emergence and shifting patterns of some climate-sensitive infectious diseases in Europe, represent a significant public health concern, with the potential for high human and economic tolls.

To address this growing challenge, the EpiOutlook platform is being developed as part of the IDAlert project, serving as a climate-sensitive forecasting tool for epidemiological risks.

By integrating climate predictions and real-time data on other risk factors, EpiOutlook will provide decision-makers with comprehensive and actionable insights into public health risks.

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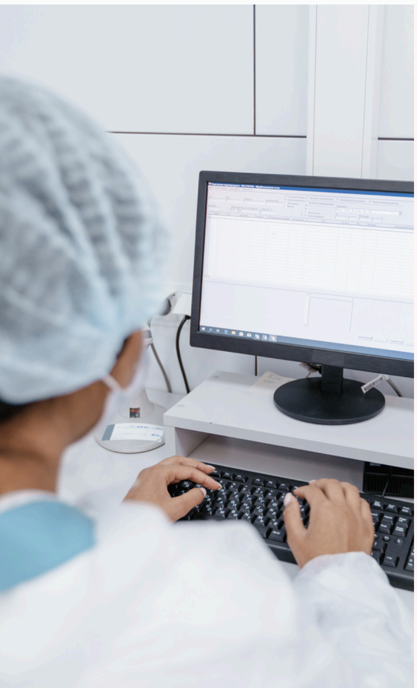
Threshold-based models

This approach estimates the risk of disease transmission via a set of environmental thresholds, predefined by the scientific literature.

The EpiOutlook platform uses threshold-based models to assess suitable climatic conditions for the activity of the *Ixodes* and *Hyalomma* ticks, which transmit diseases such as **Lyme disease**, **tick-borne encephalitis**, and **Crimean-Congo haemorrhagic fever**.

Ticks are ectoparasites that thrive in a specific set of conditions conducive to their feeding behavior and survival, with optimal ranges for air temperature and humidity.

These models provide clear, easy-to-understand indicators, which can be easily integrated with seasonal climate forecasts.



Supervised machine learning approaches

Machine learning algorithms are a flexible method for identifying complex, non-linear associations and providing powerful predictions, without the assumptions that some statistical and mathematical methods require.

A machine learning model is used to study **Leishmaniasis**, an infectious disease influenced by environmental factors like temperature, humidity, and land use. The algorithm analyzes the data to learn the relationships between the environmental factors and the disease outcome.

The model can then predict disease risk using the sub-seasonal to seasonal climate forecasts to provide a metric of future epidemiological risk.

Machine learning approaches can be used to assess seasonal variability, predict regions at higher risk, and issue early warnings for potential outbreaks.

Mechanistic transmission models

These models aim to understand and simulate the underlying cause-and-effect relationships within a system. Rather than merely identifying patterns, they investigate the biological, environmental, and social processes that give rise to them.

This approach is applied to *Aedes* mosquitoes (e.g., *Aedes aegypti and Aedes albopictus*), which can transmit **dengue**, **Zika**, and **chikungunya**.

The model simulates the mosquito life cycle, taking into consideration environmental factors and human population.

The approach helps estimate the mosquito's ability to transmit the virus, enabling predictions of disease transmission risk over time and across regions.

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