**COURSE RESEARCH PROJECT PREPARATION**

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**EMERGING AREA OF INTEREST**: INFORMATICS IN INFLUENZA VIRUS IMPACT ANALYSIS; ANALYZING THE SPREAD AND IMPACT OF INFLUENZA.

**RESEARCH TITLE**: THE SPREAD AND IMPACT OF INFLUENZA VIRUS IN UNDER-FIVE CHILDREN IN THE UNITED STATES.

**TARGET POPULATION**: UNDER FIVE CHILDREN

**ABSTRACT**

Influenza Virus has been a public health major concern globally. It is exceedingly common in children worldwide and the global incidence of influenza in children is estimated to be 90 million cases per year (Nair et al. 2011), with children in the United States estimated 19/1000 per year (Fowlkes et al. 2014). Worldwide, influenza causes a considerable amount of illness in children because of its high hospitalization rates, severe morbidity, and fatality rates. While children's influenza clinical presentations are like those of adults, certain distinct features of children's influenza presentations should be noted. Furthermore, children contribute significantly to the spread of viruses within communities.

Every year, influenza viruses produce global epidemics of respiratory illnesses that impact every demographic. The severity of the circulating viral strain, the population's preexisting immunity to the epidemic virus, and the degree of virus exposure all influence how severe an influenza epidemic is and how it affects people year to year. Conventional measures of an epidemic's impact on a community comprise infection, hospitalization, and fatality rates related to influenza and influenza-like illnesses during the outbreak. It has been challenging to determine the direct effects of influenza in children since they are prone to contracting numerous other respiratory viruses whose activities coincide with those of the influenza virus. It has been possible to identify the symptoms linked to influenza virus infection and the effects of influenza epidemics in children thanks to new and improved methods of viral diagnostics. Growing evidence supports the idea that early influenza infection can uniquely establish lasting immunologic memory, making an understanding of how viral immunity develops in this population critical to better protect children from infection and to facilitate efforts to develop a more universally protective influenza vaccine.

The impact of the influenza virus poses a socio-economic burden for both children and families. School and work absenteeism for children and parents respectively, and parents may hire caregivers for sick children, which may incur additional costs for the family and place a burden on a country’s healthcare system due to the increased number of outpatients and hospital admissions in cases of severe illness. (Ambrose et al.2014). The burden of severe influenza in infants may be twice that of current global estimates. (Thompson et al. 2019). This is because there is no vaccine available for children less than 6 months of age and the children’s immune system is not fully developed to fight the infection. The way that influenza presents clinically varies depending on the age group of the children. Compared to other respiratory viruses, influenza is generally linked to non-specific fever and lower respiratory tract infections more frequently. Infections with influenza frequently result in secondary bacterial pneumonia, otitis media, febrile seizures, Reye syndrome, myositis, and central nervous system involvement. Children who suffer from underlying or chronic disorders, especially cardiac ailments, are more prone to undergo lung disease exacerbations.

Annual vaccination is the best way to protect children against seasonal influenza virus infection. Recommendations in the United States are for vaccination of all individuals 6 months of age and older with Inactivated Influenza Vaccine (IIV), with administration of Live Attenuated Influenza Vaccine (LAIV) an option, but only in children > 24 months of age owing to a reported increased risk of post- LAIV wheezing in infants. (Belshe et al.2007; Grohskopt et al. 2019). Most countries recommend vaccination for high-risk children only. Influenza vaccination in children remains suboptimal and future research may look at total coverage of influenza vaccine in children as a preventive measure and to combat the virus.

**INTRODUCTION**

In the rapidly changing landscape of public health, the combination of informatics and influenza research has emerged as a powerful force in understanding, monitoring, and combating infectious diseases.

PHI improves disease surveillance and prediction by leveraging technology for data collection, analysis, and dissemination, as well as enabling targeted intervention strategies and global collaboration.

This paper explores the challenges and opportunities inherent in influenza informatics, shedding light on the transformative power of incorporating technology into public health efforts.

**THE IMPACT ON POPULATION/HEALTH INFORMATICS**

* Increased Transmission: Children in this age group are more likely to spread influenza due to their close contact in settings like daycare centers, schools, and playgrounds.
* Hospitalization Rates: Children under 5, especially those under 2 years old, have higher rates of hospitalization due to influenza compared to older children and adults. This places a strain on healthcare resources, including hospital beds, medical staff, and medical supplies, particularly during influenza seasons with high activity.
* Informatics improves the effectiveness of public health responses and understanding of influenza transmission dynamics, leading to better management of outbreaks and reduction in their impact on public health. It also helps in enhanced disease surveillance and detection, predictive modeling, data integration, targeted intervention strategies, global collaboration and data sharing, and decision support systems. Also, informatics is an essential tool for estimating morbidity and mortality.
* Public health informatics (PHI) enhances healthcare by employing technology to collect, analyze, and utilize data to promote public health and prevent disease. Unlike traditional paper-based systems like the Public Health Information Network (PHIN), PHI focuses on population health monitoring utilizing more effective and efficient modern surveillance technology. These systems combine several data sources, such as geographic information systems (GIS), to help detect and handle epidemics, natural disasters, and bioterrorism early on.

**CHALLENGES OF INFORMATICS IN ANALYZING INFLUENZA VIRUS IMPACT**

* Data Quality Issues: The quality of data collected for influenza surveillance in young children may vary, affecting the reliability and validity of analysis results.
* Age-specific Considerations: Analyzing influenza impact in children under 5 requires consideration of age-specific factors such as developmental stage, immune response, and healthcare-seeking behavior.
* Diagnostic Challenges: Diagnosing influenza in young children can be challenging due to nonspecific symptoms, overlapping with other respiratory illnesses, and limited access to healthcare services, especially in rural or underserved areas.
* Inconsistent reporting practices among nations impede effective pandemic assessment and response, making it difficult to compare and aggregate influenza data globally. Low-resource countries face additional challenges due to differences in lab testing capabilities and surveillance infrastructure. Furthermore, variations in how influenza cases are defined and reported impede international data comparisons.
* In the United States, privacy concerns, data reporting delays, and inconsistent collection methods jeopardize real-time data access and quality, preventing accurate analysis. Furthermore, interoperability issues, budget constraints, and a shortage of trained public health informatics personnel exacerbate the situation, emphasizing the importance of improved technological adaptation and surge capacity for data processing during critical periods.

**RELATED STUDIES DONE IN THIS FIELD BY OTHER RESEARCHERS**

1. **INFLUENZA RESEARCH DATABASE (IRD)**

Funded by the US National Institute of Health (NIH) or the National Institute of Allergy and Infectious Diseases (NIAID), this is an online bioinformatics resource that offers resources for searching, analyzing, and displaying influenza viral information. Important attributes consist of:   
  
An automated pipeline for sequencing to detect and correct faults in the sequence.   
Resources for grouping H1 and H5 influenza strains using predetermined systems.   
A method to find phenotypic variants in viral sequences through annotation.   
A tool to help compare different influenza strains by converting HA subtype numbers.   
A new tree viewer and metadata tools that allow users to upload and evaluate their own data with customized annotations and visualizations.

IRD facilitates the comprehensive management and analysis of influenza sequence data, which aids in the advancement of diagnoses, therapies, and influenza research.

The database also offers personal storage and sharing choices, and community assistance to aid in the development of vaccines, diagnostics, and therapies. changes to phenotype-associated sequence markers, mechanisms for evaluating user-provided data and forecasting novel virus variants, improvements to cloud and high-performance computing, and better hemagglutinin (HA) categorization and numbering are just a few of the recent changes. The IRD website offers all resources free of charge.

1. **NETWORK ANALYSIS OF GLOBAL INFLUENZA SPREAD**

Explores dynamics of influenza spread using network analysis and has developed a probabilistic model that addresses biases in regional and seasonal data. The model uses clustering of virus sequences by similarity, region, and season to understand transmission patterns, emphasizing the interconnectedness of regions and suggesting targeted vaccination strategies based on identified source and sink regions in the global flue network.

The paper titled "Network Analysis of Global Influenza Spread" by Joseph Chan, Antony Holmes, and Raul Rabadan, presents a novel probabilistic model to track the spread of influenza using network analysis and data from global influenza sequence databases. The study identifies East-Southeast Asia as a significant origin for new influenza strains, with a notable influence on global spread patterns.

**Key point from the paper:**   
  
By simulating regional and seasonal transmission patterns and utilizing spatiotemporal clustering, the probabilistic model takes into account biases in data collection.   
The model verified that the tropics, especially East-Southeast Asia, play a pivotal role in dispersing novel influenza strains that impact populations worldwide.   
Network analysis approaches offer valuable insights into the ways in which various locations impact the worldwide spread of influenza. These insights can be leveraged to recommend targeted vaccination tactics that effectively hinder transmission.

The analysis also emphasized the shortcomings of the available data, particularly the underrepresentation of sequences from South America and Africa, which highlights the need for more equitable worldwide surveillance. The study makes the case that choosing vaccine strains more carefully and managing public health reactions to epidemics can both be enhanced by an awareness of the worldwide dynamics of influenza transmission.

**OPPORTUNITIES FOR NEW AREAS OF RESEARCH**

* Predictive modeling and machine learning: With more data accessible, there is a chance to create more advanced predictive models that can more precisely forecast the spread and mutation of influenza viruses.This might involve the use of deep learning methods to analyze complex data patterns to predict outbreaks and evaluate the effectiveness of control measures.
* Real-Time Surveillance Systems: Improving real-time surveillance and making dynamic models that can include live data feeds like social media, travel data, and clinical reports can help quickly assess outbreaks and make decisions on public health response.
* Personalized Medicine: As informatics develops to securely handle more personalized data, personalized vaccination plans based on a person's or a region's genetic susceptibility to influenza may become more effective in treating the disease and preventing it.
* Global Data Sharing Platforms: Creating worldwide platforms to facilitate the exchange of influenza data between researchers, medical professionals, and the general public may improve the cooperative efforts required to contain influenza outbreaks. These platforms might also include artificial intelligence tools to help with decision-making and data analysis.
* Integration of Genomic and Epidemiological Data: Combining the virus's genomic information with the epidemiological data pertaining to its transmission presents a substantial opportunity. This could increase awareness of the relationship between the virus's genetic modifications and its virulence and patterns of transmission, which could lead to the development of new vaccinations and treatments.

**OVERALL ASSESSMENT AND CONCLUSION OF THE SELECTED TOPIC**

In conclusion, the use of informatics in influenza virus impact analysis represents a significant step forward in understanding and managing the complexities of influenza outbreaks. Informatics allows for the collection, analysis, and interpretation of massive amounts of data, resulting in more precise predictive modeling, real-time surveillance systems, and the integration of genomic and epidemiological data.

Informatics improves the effectiveness of public health responses by enabling targeted intervention strategies and better decision-making. Despite challenges such as data disparities and technological limitations, informatics' transformative potential in influenza research highlights its critical role in reducing the global burden of influenza on public health.

**CITATIONS**

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