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PS02.03 (576)

Improved contact tracing using network analysis and spatial-temporal proximity

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Purpose: Contact tracing is a crucial tool in infection prevention and control (IPC), which aims to identify outbreaks and prevent onward transmission. What constitutes a contact is typically based on strict binary criteria (i.e., being at a location at the same time). Missing data, indirect contacts and background sources can however substantially alter contact-tracing investigations. Here, we present StEP, a Spatial-temporal Epidemiological Proximity model that accounts for imperfect data by introducing a network-based notion of contact based on spatial-temporal proximity derived from background flows of patient movement.

Methods & Materials: We showcase StEP by analysing outbreaks of multidrug-resistant bacteria and COVID-19 within a large hospital Trust in London (UK).StEP utilises spatial-temporal patient trajectories and the background hospital movement flows to recover enhanced contact networks. Firstly, we study a well-characterised outbreak of carbapenemase-producing Enterobacteriaceae (CPE) involving 116 hospitalised patients where genetic sequencing is used to learn model parameters. Secondly, our trained model is deployed in an unsupervised manner on three unseen outbreaks involving 867 patients of related CPE-types. Thirdly, we test application to an altogether novel pathogen by analysing a hospital outbreak of COVID-19 among 90 hospital patients, and demonstrate the power of StEP when characterising newly emerging diseases, even when there is a lack of sequencing data.

Results: In addition to recovering core contact structures, StEP identifies missing contacts that link seemingly unconnected infection clusters, revealing a larger extent of transmission than conventional methods. Via genomic analyses we confirm that the additional contacts detected through StEP lead to improved alignment to the plasmid phylogeny (the major outbreak driving force). Hence the StEP contact network is most aligned to the transmission structure.

Conclusion: By considering spatial-temporal information in a continuous manner, StEP tackles several challenges associated with traditional contact-tracing. StEP allows both direct and indirect contacts as possible routes of disease transmission and is tuneable to a pathogen's epidemiological characteristics. Such flexible use of heterogeneous data in uncertain situations can significantly enhance IPC.

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Intra-genotypic Recombination and Polymorphisms of Hepatitis B Virus Genome Circulating in Bangladesh

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Purpose: Severe liver diseases including cirrhosis are now frequently detected among the Hepatitis B virus (HBV) infected patients. Rapid genetic evolution of HBV with insertions, deletions or frameshift events promotes infection severity. Herein, the purpose of this study is to determine the alterations of the genomic pattern of HBV causing liver cirrhosis.

Methods & Materials: From 92 HBV-positive plasma samples, whole-genome of three samples, specifically one sample each for cirrhotic, chronic liver disease (CLD) and usual chronic (no detectable liver disease) patients confirmed by ultrasonography and fibroscan were sequenced and analyzed for potential mutations. Recombination analysis of the sequenced strain was performed using NCBI Genotyping tool and RDP4 software package.

Results: The whole-genomes of HBV from CLD, cirrhotic and normal chronic patients share a common potential substitution at 210 amino acid (AA) position in the surface (S) protein. Whole-genome of cirrhotic patient comprises mutations T118V, A128V, S207N, I208T and S210R in the S protein and N53D, Y54H, H126R, S219A in the polymerase (P) protein. However, mutations S53L, I126T, S210N and H9Y, N13H, I91L, I269L, V278I were observed in other two patients in the S and P proteins respectively. On the other hand, a vaccine escape mutation, A128V and a frame shift deletion of three amino acids in the S protein were observed in the strain isolated from the cirrhotic patient, which may have implications to cause liver cirrhosis. Moreover, recombination analysis of the sequences denotes that the HBV genome of cirrhotic patients composed of a recombination of three genotypes D, C and E. Of which, genotype E was not documented before in Bangladesh. This unusual tri-genotypic recombinant event is the first report in the world and might promote the severity of the liver abnormalities. Moreover, there is a stop codon at 28 position in the HBV Core protein in the recombinant strain.

Conclusion: The reports of this study emphasize that the genomic alterations of the HBV strains could be highly responsible for evolution of the strain that might boost the severity of the hepatitis B infection. Such evolved and recombinant HBV strains may cause dangerous public health problems in future.

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Topic 03: Climate Change and Ecological Factors in Disease Emergence

OP03.01 (382)

Structural-Equation-Modelling (SEM) to analyze climatic factor's role on COVID-19 spreading

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Purpose: Climate seems to influence the COVID-19 spreading, but the results of the published studies are conflicting. Aim of this study was to perform a world-wide investigation to analyze the role of all the main climatic factors (CF), trying to identify the causes that led to the discrepancy of the results.

Methods & Materials: 134,871 data (from 209 countries) were used for the analysis. These were extrapolated from an initial dataset of 1.200.000 data. To avoid biases present in most of the previously studies, a set of specific requirements was adopted: long observation period (16 weeks),

• the use of a relative time scale to synchronize the beginning of the outbreak among the countries,