

Inferring the transmission dynamics of Avian Influenza from news and environmental data

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Avian Influenza (AI) is a highly contagious animal disease, which infects many wild and domestic bird species. Transmission between birds can be direct due to close contact between birds, or indirect through contaminated materials such as feed and water. Particularly, migratory wild birds play a key role in this transmission and make the viruses spread over long distances. Although AI is a well-studied disease in the literature and there exist several surveillance platforms for monitoring the evolution of AI outbreaks, in practice we hardly know about the real transmission routes of the AI viruses, i.e. the provenance information when a new outbreak appears in some location. This makes the early detection of AI outbreaks very challenging.

In this work, we tackle the problem of how the AI disease spreads in the absence of real disease transmission routes. Towards this end, we first reconstruct these transmission routes based on how AI outbreaks evolve in the news articles collected by surveillance platforms, accompanied by environmental data related to the outbreak locations, through an attributed location-aware dynamic network (See Figure 1). Then, we study the underlying network dynamics to unveil the AI transmission patterns. In our network construction, the nodes correspond to outbreak locations extracted in news data and provided by surveillance platforms [1, 3], and the edges between them represent the disease transmission routes that are more likely to occur. Our hypothesis is that the probability of disease transmission between locations is mainly related to two aspects: 1) temporal differences between outbreaks, and 2) distance between outbreak locations.

We analyze the resulting dynamic network with two groups of spatio-temporal measures. The first group characterizes a single node through macroscopic measures (e.g. adapted dynamic Pagerank), which allow identifying key locations in disease transmissions, whereas the second group summarizes the whole network structure (e.g. time-space spreading index based on hotspot analysis [2]). We show the interest of our approach by applying it to the AI outbreak datasets collected by PADI-Web [3] and ProMED [1], two well-known surveillance platforms in Epidemic Intelligence, for the period of 2019-2021. Our preliminary results confirm the existence of super-spreaders, i.e. the locations being particularly effective in transmitting AI disease, in our datasets.

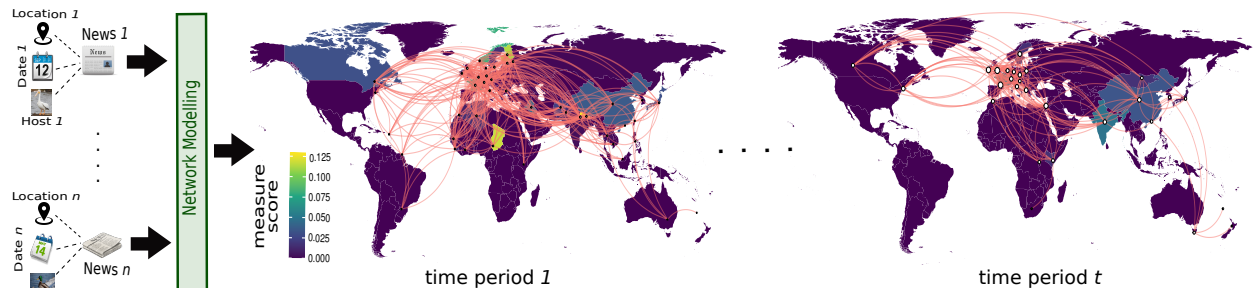


Figure 1: Network modelling for inferring the transmission dynamics of Avian Influenza from news and environmental data.

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References

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