

AVIAN INFLUENZA
Gathering information
and network modelling approaches

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INTRODUCTION

The world is currently seeing the worst avian influenza outbreak ever, which killed¹ about 54,000 poultry birds worldwide only between 2 and 22/june/2023 (WOAH, 2023a). In Brazil, the first case was identified by 15/may/2023 (BRASIL, 2023a) and by 31/may the national authorities has declared an national zoonotic emergency case (BRASIL, 2023b, 2023c). There are reports from other countries stating that this virus reached some mammals species (WOAH, 2023b), including a few cases of human contagion (CDC, 2023), therefore narrowing the gap to another pandemic. In summary, avian influenza is a threat to public health and wildlife.

In this sense, modeling the problem, by leveraging data and working with disease dynamics, may provide insights or tools that aid in the decision making process for mitigating the disease, thus preventing losses and achieving the broad aim of preserving the life of birds. For mitigation of disease spread risk and the evaluation of possible scenarios/plans to contain the spread of disease, three actions may coexist: corrective, predictive and preventive. Examples of these paths were models can aid are: detect sites/hubs of superspread (try to control then/corrective), sites, species and other traits that are most suitable for fast and effective detection of ongoing outbreak thus implementing a reliable active vigilance (detect local outbreak as soon as possible and act on it/predictive), and forecast geographical site risk of disease spread in rear real time (reinforce biosafety measures on terrain/preventive) by revealing chains of transmission/spread.

In simple terms, to construct any model, we need to first understand the avian influenza among birds and, mainly, how the spread occur. Then identify possible chain(s) of spread and gather data about theses chains. Next step is to adopt a suitable model for the disease dynamics and validate its output against past cases to ensure the model is reasonably feasible. Finally, the model can be applied to the current disease state.

OBJECTIVES

To review information about avian influenza, bird ecology and computational network models.

AVIAN INFLUENZA²

Avian Influenza, also known as Bird flu, is a disease caused by a virus that has the same name and is highly variable. There is a High Pathogenic Avian Influenza – HPAI, identified by its hemagglutinin glycoprotein (HA) found on virus' external envelope and also by the severe symptoms and death caused in some species of birds. Under HPAI, the H5N1 subtype that arise on Asia in 1996 has significant range and damage on average on the myriad of

¹including birds that was killed as contingency plans

²The main content reviewed in this section come from CUBAS; SILVA; CATÃO-DIAS (2014).

bird species, including wild birds. However, its pathogenicity varies between virus clade and specie. Waterfowl species are the main types affected by H5N1 with relatively moderate symptoms, therefore being a natural reservoir for the virus, and the spatial distribution of virus being biased close to coast, lakes, rivers and other types of waterbodies. Poultry birds are highly affected by H5N1 symptoms. Ideally, one can construct a table with the following information to aid in modeling parameters: specie, taxonomic group, presence in Brazil, estimated population, n° of cases, n° of deaths and main virus clade detected

There is an historical seasonality in global incidence of Avian influenza in poultry according to WOA (2023b), shown in Figura 1. However, the reason for this seasonality was not shown.

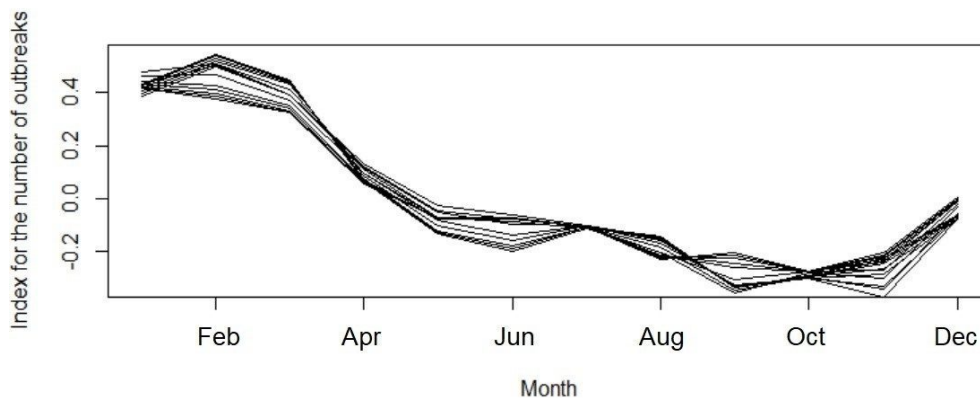


Figura 1: Seasonality in global incidence of Avian influenza in poultry.
Source: WOA (2023b)

Regarding the virus transmission mechanisms from an infected individual, the virus is expelled on breath, secretions (nostril, eyes) and excrements (urine and feces). Secretions and excrements transform objects into fomites once it remains on the bird environment. Fomite is an object that serves as a vehicle to pathogens, like a feather, a piece of wood, dirt, etc. Animal flesh is also a source of biohazard. The virus is mostly viable on water, especially on cold and fresh water. Interesting information for modeling purposes are the viral charge of distinct fomites and the time viability of virus in different environments and surfaces.

BIRD ECOLOGY³

Birds have a huge number of species and their characteristics vary widely. The birds, as living beings, move, eat, excrete, interact with other individuals from the same and other species, etc. Somewhere in the middle, they may contract or spread diseases, therefore the aforementioned actions must be reviewed.

Regarding birds habitats, some species lives exclusively on coast environments, near the sea, while other lives on the continent, the latter being

³The main content reviewed in this section come from PPGEEB (2023).

threatened by deforestation, living mainly in forest fragments. Farms of poultry birds have industrial purposes, like food supply chain, and gather a huge number of confined animals, like chickens, turkeys and other similar species. Virus spread will be discussed further, but the condition of confined dense population of susceptible birds is highly favorable to virus spread and mutation. These species also appear on small farms in lower densities along with other common species among humans like goose and ducks.

Birds have ease to move, since they have wing that allow them to fly. There are short range movements, in the order of 10km, where they make daily activities, like looking for food and water. But some species perform migrations, in the order of 100km or more kilometers, mainly through weather stations and in/out reproductive cycles.

Birds have varying social behavior. Some species are more territorial, repelling intruders of the same or other species. Other species are much more social, living in groups/colonies. Some species lives in groups only in the reproductive season and others for the entire season. All species make direct contact in reproductive or cooperative tasks and indirect contact when sharing perch, food sources and others.

That being said, another table may gather information for modeling purposes: susceptible specie in brazil, Population/Density, Geographical range, migration trajectory and habitat type.

DISEASE SPREAD AND INFECTION

An individual can become infected by direct contact with contaminated secretions, feces, big particles suspended in the air, and flesh. This direct contact may occur by individual of the same species in colonies or different species in cases of shared locations of rest and migrations. Infection also occur by indirect contact through fomites, which have direct influence of human lack of biosafety measures for its dissemination. Markets and commerce, animal byproducts, animal traffic, clothes and transportation vehicles are examples of human interference on ease of fomite displacements. There are also bridge species that can transport the virus directly (becoming infected) and indirectly (behaving like a moving fomite)

The development of general immunity effect by previous exposure to virus is unknown (CUBAS; SILVA; CATÃO-DIAS, 2014) but the wild species are generally more tolerant/resistant to disease, therefore being a natural reservoir for the virus.

The virus is spread all over the world, but its detection depends on the sampling effort and the presence of humans nearby. Biosafety measures on farms and active vigilance on wildlife made by state agents may lower the risk of contamination and contain the spread of the virus.

From the aforementioned topics, more parameters should be gathered for modeling regarding the analyzed regions: concentration of poultry farms, biosafety measures, unsafe practices and other relevant risk factors.

CURRENT OUTBREAK IN BRAZIL

From the first case in 15/03 (BRASIL, 2023a) to 09/07, there were a total of 61 cases, geographically located in the Southeast coast, as shown on Figura 2. Cases are growing in a linear fashion, mainly affecting *Thalasseus acuflavidus* (trinta réis de bando) and *Thalasseus maximus* (trinta réis real) species.

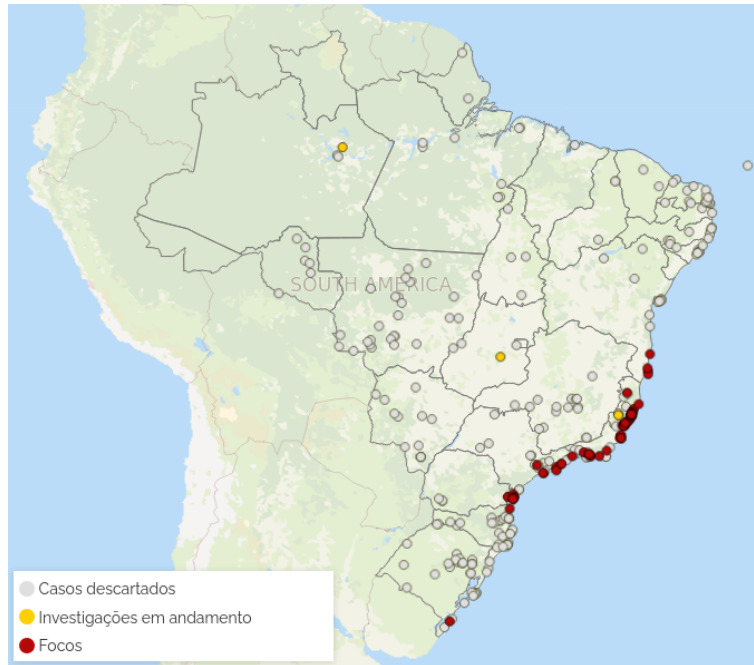


Figura 2: Cases of Avian influenza in Brazil until 09/July. Source: MAPA

In Brazil, only the Animal Defense Laboratory at Campinas-SP can make the task of virus genetic sequencing.

LARIDAE FAMILY, STERNINAE SUBFAMILY

Both of the most affected birds in the current outbreak ongoing on Brazil, namely *Thalasseus acuflavidus* (trinta réis de bando) and *Thalasseus maximus* (trinta réis real) species, as shown on Figura 3, are from the Laridae family.



Figura 3: Photography of a trinta-réis flock. Adapted from: ABREU (2015)

The Laridae family comprises “gaviotas” e “trinta réis”. Some species belonging to this family perform long migration. These birds lives on coasts, near the sea, where are their main source of food: fish. They may live on colonies.

COMPLEX NETWORKS ON AVIAN INFLUENZA

After a non-exhaustive search of articles using the string “avian influenza” network in Google Scholar base, a few works employing tools of network analysis and simulation were found.

SCALE-FREE DISTRIBUTION OF AVIAN INFLUENZA OUTBREAKS (2007)

SMALL; WALKER; TSE (2007) gathered about 3000 cases of avian influenza on Vietnam spanning about 5 years. These data were taken from World Organization for Animal Health alerts and World Health Organization case reports. Nodes were set at locations of outbreaks and links were formed based on time interval and a constant propagation velocity, i.e. there is a link for consecutive outbreaks. This network modeling strategy tries to reconstruct probable infection pathways from observed data. As shown on Figura 4, the authors found scale free distribution of infection sites and clusters of unconnected network elements.

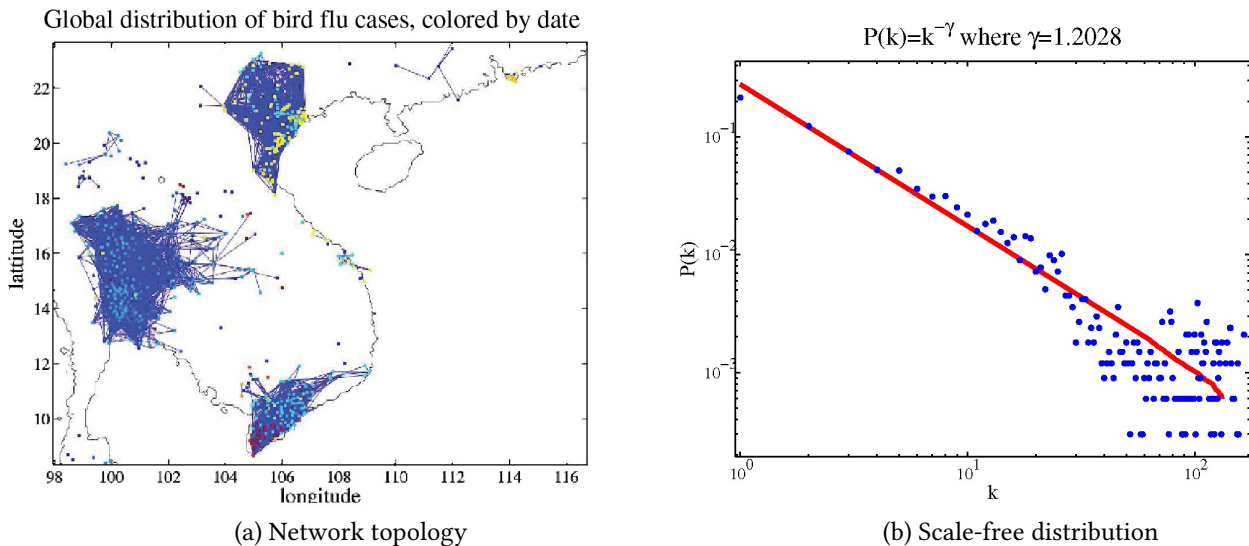


Figura 4: Network of avian influenza in Vietnam. Topology shown on (a) and scale free distribution on (b). Source: @small2007scale

AVIAN INFLUENZA H5N1 VIRAL AND BIRD MIGRATION NETWORKS IN ASIA (2015)

TIAN *et al.* (2015) combined H5N1 outbreak records, whole-genome sequences of viral samples, and satellite tracking data for four species of migratory birds in Asia in order to model the viral migration network, as shown on Figura 5. Data were obtained from the Food and Agriculture Organization of the United Nations and the World Organization for Animal Health. Authors found that viral migration and bird migration routes are closely related in time and that little viral exchange between different flyways occur.

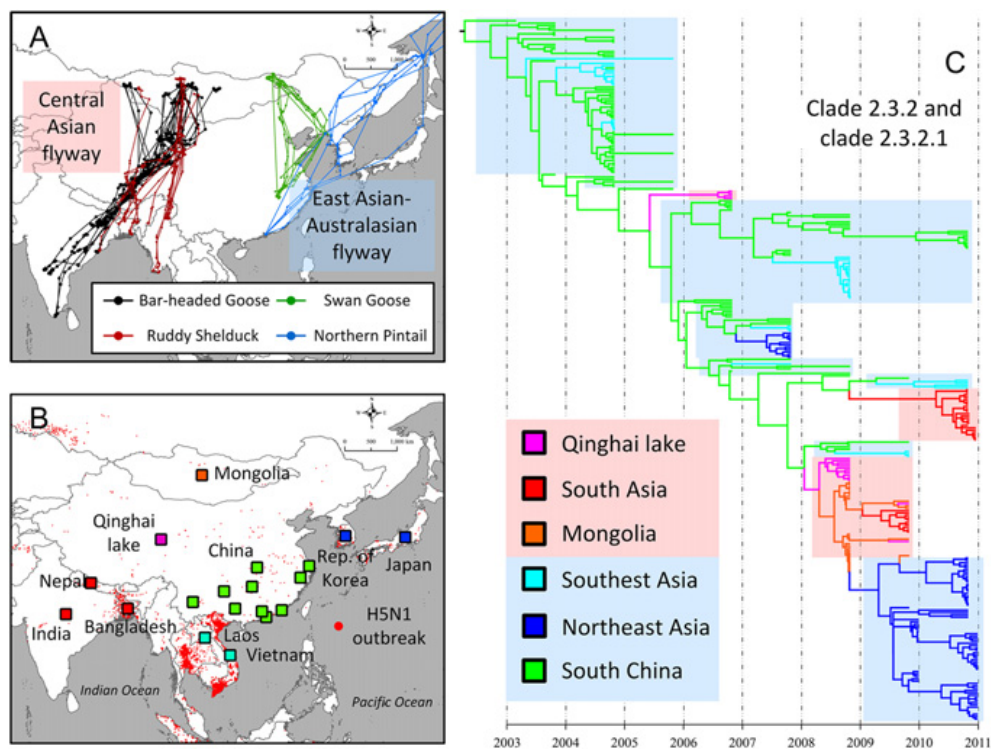


Figura 5: Asia migration network of migratory birds. Tracked moves on (a), sites of viral samples on (b) and virus phylogenetic tree on (c). Source: TIAN *et al.* (2015)

PREDICTION OF THE SPREAD OF HIGHLY PATHOGENIC AVIAN INFLUENZA USING A MULTIFACTOR NETWORK (2014)

LEE *et al.* (2014) gather data from South Korean 2008 outbreak of avian influenza in a region having multiple poultry farms. Data were composed of visits from feed and medicine services providers in addition to wind and geographical data of farms. Also, infected/noninfected farms were known. They were trying to analyze the indirect spread of virus from business persons/vehicles and direct airborne spread. For feed and med, two social-business undirected and unweighted networks were built from each visit made by the same company between to farms, i.e. if a service provider go from farm A to farm B, then a link was formed between A and B. Wind

and geo data were inputs of a CFD model whose results defined the links between farms in another network. A total of 3 networks were modeled. A first investigation was done by analyzing centrality measures of the farms in these nets and they found correlation between the most central nodes and infection. A second investigation was done for tracing the spread path along the network and the effect of quarantine high centrality nodes to reduce the number of infected farms.

DISEASE SPREADING IN POPULATIONS OF MOVING AGENTS (2008)

BUSCARINO *et al.* (2008) builds a model in which a number of nodes walks randomly, eventually taking long distance jumps, and has some probability to infect the neighbor inside an arbitrary action radius.

PREVENTABLE H5N1 AVIAN INFLUENZA EPIDEMICS IN THE BRITISH POULTRY INDUSTRY NETWORK EXHIBIT CHARACTERISTIC SCALES (2010)

JONKERS; SHARKEY; CHRISTLEY (2010) showed evidence of discrete scale invariance in poultry industry network, which depart some of the network epidemic properties from pure scale free behavior.

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