# Assessing potential viral spill-over events

Introduction

Whilst the Covid-19 pandemic has led to a surge of interest and analysis of potential viral spillover events into humans less attention has been paid to disease ecology and spillover events within animals. However, spillover events into other closely related animal species can be ecologically catastrophic and may lead to extinction events, particularly in already threatened species:

* Saiga antelope have suffered multiple mass mortality events. While some of these are attributed to pathogenic changes in normally benign bacteria, others have been attributed to spillover events of ovine rinderpest/peste des petits (*Morbillivirus caprinae*).
* African wild dogs suffer from considerable mortality through exposure to viruses, such as canine parvovirus and canine distemper virus (*Morbillivirus canis*), carried by domestic dogs.
* The Bornean bearded pig has recently seen extremely high mortality from spillover of African Swine Fever (*Asfivirus*).

These events are obviously of huge conservation concern, as well as providing new routes for potential zoonotic outbreaks. The likelihood of a spillover event varies due to several factors such as the population density of the two species, their life-histories and interactions (e.g. predator-prey relationships) and the closeness of the phylogenetic relationship between the two species (viruses are more likely to ‘jump’ between closely related species). Not all of this data is readily available, so this assessment asks you to make use of what data is available to make as strong an analysis as possible of spillover events. The most critical shortfall is likely the lack of spatial distributions of population densities for overlapping species. This would allow us to more precisely identify where larger numbers of individuals from two species are likely to come into contact, but is not possible with simple maps of area of occurrence that just provide binary presence-absence data. One alternative might be to use species distribution models for species and use relative probability of occurrence as a surrogate for population density, but that is quite an assumption!

Objectives

In this assessment, we ask you to explore possible routes to zoonotic transmission to humans and other mammals from the morbilliviruses (distempers, measles). These viruses are widespread geographically, often cause diseases with extremely high mortality rates and are quite capable of infecting new species given the opportunity. The assessment includes the following objectives.

1. Develop a phylogenetic tree of morbillivirus.

You will be given a partially completed dataset of morbillivirus polymerase sequences. Using your knowledge gained from the lectures and practicals, you should identify, download, and align additional sequences from the bioinformatics databases and then construct a phylogeny of the virus sequences. You do not need to identify every known morbillivirus so you could choose just a few that are specific to a certain geographic location or host species/genus/family.

You will be expected to:

* Provide a clear explanation of the methods used to construct the phylogeny and your selection of additional sequences.
* Provide a well-annotated phylogeny of the resulting set of viruses.
* Provide an appendix containing your alignment of the sequence data. You can either provide the complete alignment or a representative section.

1. Identify focal mammalian host species with which to explore spatial patterns of possible overspill events and select related species at risk of such events.

You should select at least one host species associated with a focal virus in your phylogeny and then identify an appropriate group of related species that are likely spillover targets for that virus. Appropriate species of concern are likely to: overlap spatially with the focal host; be closely related to the focal host; be of conservation concern (IUCN categories: VU, EN, CR or DD); or any combination of those categories. You should aim for around 6-10 species of concern.

You will be expected to:

* Provide a clear explanation of your selection of focal host species and virus, and then your selection of related mammalian species of concern.
* Provide a well-annotated map or maps showing of spatial distribution of those species.

1. Assess the degree of spatial overlap between your focal species and selected species of concern for overspill events. Your approach to this could just look at the proportion of range overlap between each species of concern and the focal host species.

You will be expected to:

* Tabulate the overlap between the focal host and species of concern.
* Discuss the risk and severity of possible spillover events to the species of concern given the spatial overlap, ecology of the species, and potential mortality/morbidity of the virus .

1. Explore the overlap of your focal species and species of concern with areas of high human population density. For each mammal species, identify the range and median human population density within the species’ range and then identify potential hotspots of spillover within the range that fall in the top 5% of the human population density.

You will be expected to:

* Tabulate the human population density data within each mammal’s range.
* Generate a map showing potential hotspots of spillover events into humans.
* Discuss how spillover into other mammal species may alter the geographic range and likelihood of eventual spillover into humans.

1. Monitoring and mitigation.

Given your findings above, you will be expected to:

* Propose a monitoring and mitigation plan, with specific spatial and species level actions in order to minimize the risk of spillover events

Learning objectives

* To be able to extract and align nucleotide sequences from bioinformatic databases
* To construct phylogenies of the aligned sequences and understand the implications of the relationships shown
* To learn how to construct species distribution maps of animal species
* To integrate information bioinformatic, phylogenetic, ecological and other sources and resources

Report format and length

Your assessment should be submitted as a 5 page maximum length report, using standard 12 point font sizes and line spacing. This limit includes all text, figures, tables and legends. The only exception is the sequence alignment, which can be included as appendix.

Resources

* You will be provided with an (incomplete set) of morbillivirus RNA polymerase (L protein) DNA sequences along with a suitable outgroup.
* We will also provide a central download of mammal shapefiles and recent population density. These data can be freely downloaded from the following locations but require registration and approval. The provided data should only be used for the purposes of this assessment. The sources of the data sets are shown below:

<https://www.iucnredlist.org/resources/spatial-data-download>

<https://earthdata.nasa.gov/data/catalog/sedac-ciesin-sedac-gpwv4-popdens-r11-4.11>

* You can use the OneZoom phylogeny browser to explore a recent phylogeny of mammals, to help in your selection of species of concern: <https://vertlife.org/data/mammals/>