**INTRODUCTION**

Bovine tuberculosis (BTB), caused by pathogen *Mycobacterium bovis*, is an infectious disease of importance to domestic livestock, wildlife, and humans. Endemic to bovins, BTB is known to spill over into wildlife populations where they cohabit. First identified in greater kudu and common duiker in 1956, BTB spilled over from infected cattle to African buffalo in South Africa’s Kruger National Park in the 1990s. It has since been diagnosed in a multitude of species ranging from felids (lions, leopards, cheetahs) to canids (African wild dogs) to primates (baboons) to ungulates (gazelles, impala etc.). many of these species are already rare or in decline. The occurrence of BTB in wildlife constitutes an infectious feedback loop, potentiating re-exposure and infection for livestock, thus thwarting eradication efforts. The ability of M. bovis to cause spill-over events and reside in various reservoir species makes it challenging to eradicate and presents a significant risk to wildlife health.

A noteworthy zoonosis for humans, BTB is closely related to M. tuberculosis, the causative agent of human tuberculosis (TB), and the leading infectious cause of death worldwide. Because developing nations often lack the resources for proper speciation, the true proportion of BTB cases is unknown, and the true prevalence is suspected to be severely under-reported. However, due to reasons of increasing multi-drug resistance, it is of vital importance to make this distinction. On the South African landscape level, where wildlife is present to maintain the patient, where livestock range in close proximity to wildlife, and where livestock and people coexist, BTB remains a significant threat to public health, encapsulating how animal, human, and environmental factors collectively drive disease emergence and patterns.

**RESULTS & DISCUSSION**

For the human analysis, the average BTB risk was determined per local municipality. The absolute minimum and maximum scores possible were 0.5 and 8.9, respectively. Average scores per local municipality ranged from 0.62 to 6.82, with the minimum and maximum scores being 0.5 and 7.7, respectively. The highest average risk of BTB was 6.82, in the Middelvlei Local Municipality, within the Sedibeng District Municipality, and the Gauteng Province. For the wildlife analysis, some high-risk areas overlapped with cheetah ranges, while African lions and African wild dogs seem to range in lower-risk areas. Leopard ranges expand across the extent of South Africa, so they may also be considered a potentially-at-risk population.

The value of such a vulnerability project is multifold. Public health agencies can use this geospatial analysis to establish targeted surveillance and prevention programs, engage in public outreach, and disseminate food safety, hygiene, and biosecurity information in highly at-risk areas. This project can also inform conservation efforts, identifying key regions and populations at risk. BTB is also notably a global disease, with varying risk factors. This methodology can be repeated in other regions and modified for different factors. For example, BTB is also a problem in invasive brush-tailed possums in New Zealand, badgers in the UK, and white-tailed deer in Michigan.

There are some limitations to this geospatial analysis. Many livestock production risk factors are challenging to represent geographically, such as age, breed, and various management practices. Other excluded datasets include wildlife population density, other immunosuppressive diseases, food safety (e.g., milk pasteurization vs. souring), and hygiene factors. In addition, wildlife migration routes and livestock movement across the landscape are critical factors influencing BTB ecology, and due to difficulty in presenting such information, were not considered in this analysis. Furthermore, higher spatial resolution may be more informative in the implementation of targeted surveillance programs. Finally, my chosen factors approximate human population density, but perhaps a more nuanced analysis incorporating environmental and human-independent factors may be more suitable.

**METHODS**

A weighted risk analysis was performed for both human and wildlife populations. A variety of tools was used for each analysis (i.e. Euclidean Distance and Kernel Density), and each factor was converted to a raster and reclassified. Zonal Stats applied to the human analysis to determine average risk per local municipality. From the wildlife analysis, the hot zones of risk were manually compared to the ranges of vulnerable species to determine which species might be most susceptible based on geospatial factors. For humans, weight was assigned as follows: 30% HIV prevalence = 30% bovine density = 30% abattoir density = 20% dairy production. For wildlife, weight was assigned as follows: 35% bovine density = 30% distance from African buffalo range = 20% distance from wild dogs = 10% distance from cheetahs = 5% distance from independent kudu and warthog ranges.

**SPATIAL ANALYSIS FACTORS**

- **HIV Prevalence**
  - Immunocompromised can have susceptible opportunities to pathogens (see ATB risk). HIV is one of the most common co- infections with TB globally, and increases risk of developing BTB from an age-peak prevalence of HIV by district municipality was reclassified.

- **Dairy Production**
  - The highest prevalence of BTB areas where intensive dairy production occurs. The consumption of raw, unpasteurized milk is one of the most important modes of transmission. This spatial factor was reclassified and incorporated into both analyses.

- **Bovine Density**
  - The density of cattle within each municipality.

- **Abattoir Density**
  - The number of abattoirs within the municipality.

- **Reservoir Ranges**
  - The ranges of BTB reservoir species include various species ranges, then reclassified.

- **Municipalities of Highest Risk**
  - The local municipalities with the highest risk of BTB spread.