Modeling Disease Transmission in Long-Tailed Macaques (Macaca fascicularis) in Bali, Indonesia
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Introduction:
- Emerging infectious diseases are an ever increasing part of our global landscape. Primates have been implicated as both host and reservoir in multiple disease emergences [2, 4, 5].
- As human population increases lead to greater landscape changes, human-wildlife interactions increase. These increased interactions can potentially lead to bi-directional pathogen transmission [3, 4].

- In Bali, Indonesia, a unique system of temples and habitat modification has existed in the landscape for centuries. (Figure 3). These temples act as sanctuaries for the macaques (Macaca fascicularis) that live there, but increases in both overall human density and tourism have substantially increased the amount of human to non-human primate contact occurring at these sites [1, 7, 8].

- Using an agent-based modeling incorporating real GIS data [6], we are addressing disease transmission and spread of immunity in an anthropogenically changing environment. We are answering the following questions:
  1. What are the rate and route of disease spread in macaques across the island?
  2. What are the rate and route of immunity spread in macaques across the island?
  3. Do the answers change with anthropogenic change over time?

Methods:
- This study models infected and non-infected agents (macaques) which are mostly gathered at preferred geographic locations (blue spots in Figure 1). The individual's behavior mainly differs in accordance with their sex and their period of life. Agent Based Modeling is an appropriate technique to answer the questions above.
- The choice of the implementation language and the implementation toolkit was primarily driven by their ability to process and visualize geographic information. The agent-oriented design is implemented with the Java based simulation toolkit Repast [9]. This package provides an interface to OpenMap [10], which allows the use of geospatial information. The macaques' movements are based on their geographic position. Mark Southem developed several GIS files of the island of Bali (Figure 2).
- The island measures around 130 kilometers east-west by 80 kilometers north-south. In order to realistically move the macaques throughout the island, the granularity of space was chosen to be about 40 meters per grid cell. As most macaques live closely-packed at 44 temple sites, each population site is represented by a blue rectangle (blue spots in Figure 1) on the geographic map. Each temple site can be enlarged such that each individual can be seen. The migrating macaques between temple sites are visualized individually by disproportionately large spots on the geographic map (red spots in Figure 1).

Results:
- Provides predictive power to for identifying patterns to be more closely examined through field collection.
- Will support hypothesis of male dispersal being a genetic link between populations island wide and acting as a mechanism in disease transmission. The role of virulence and initial site of infection still needs to be elucidated.
- Demonstrates the importance of integrating landscape data, in GIS format, with biological data in understanding and predicting patterns at the population level.

Discussion:
- Our results will demonstrate that male macaques have historically dispersed across populations, acting as a link for genes and diseases between seemingly isolated macaque populations.
- Additionally, our model will identify potential barriers to gene flow, based on anthropogenic landscape change. Further, the model will identify the critical number of males needed to create genetic homogenization of populations and the critical amount of males needed to create a genetic barrier based on lack of gene flow across the island.
- In light of the increasing anthropogenic changes in Bali, the high density of native human populations, and the ever-increasing tourist populations, if this link between macaque populations does facilitate pathogen transmission, the implications for emerging infectious diseases could have worldwide ramifications in the advent of a bi-directional pathogen transmission event.
- We are evaluating the genetic structure of known pathogens of macaques both to track transmission throughout populations and to better understand the coevolutionary relationship between macaques and their pathogens.

Future Directions:
- In an effort to validate and verify our model and to understand the complete picture of the genetic and social structure of M. fascicularis in Bali, we will examine additional genetic markers (including additional neutral and disease-resistance Y-chromosomal, autosomal, and mitochondrial DNA loci and microsatellite markers).
- We also plan to investigate any east-west, north-south, or other model-predicted population dispersal trends.
- We are evaluating the genetic structure of known pathogens of macaques to track transmission throughout populations and to better understand the coevolutionary relationship between macaques and their pathogens.
- We then plan to overlay the genetic patterns of macaque populations with the genetic patterns of pathogens collected from those same populations in order to determine how macaque population structure can influence the evolution of disease itself.

References:

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