Modeling Disease Transmission in Long-tailed Macaques on Bali

Kelly Lane
Gerhard Niederwieser
Ryan Kennedy

University of Notre Dame
Macaque Background

- Coexisted in temples across the island for at least 2000 years.
- Populations are female philopatric; males migrate from natal populations at age 7.
- Changing land use patterns have resulted in increased macaque-human interactions.
Disease

- Primates are known hosts and reservoirs in several disease emergences
- Increase in human-nonhuman primate interactions leads to potential increase in disease spread
- Long term human-macaque interface could become potential site of global disease emergence
Research Questions

Given the known landscape of Bali and focusing on one disease transmission strategy:

- What are the rate and route of disease spread in macaques across the island?

- What are the rate and route of the spread of immune responses in macaques across the island?

- Do the answers change with anthropogenic change over time?
Model Conceptualization

Starting point:
- Environment: GIS data (ESRI shape files) of Bali (created by Mark Southern); geographic shapes of different types of environment
- Agents: Macaques, with known behavior and certain habitat probabilities for each type of environment

Space / Time granularity:
- Island: 130 km east-west and 80 km north-south
- Space granularity: 50 x 50 m per grid cell → 3000 x 2000 grid
- Time granularity: Monkey travels about 10 km/day → time step: ~ 1 hour
Model Conceptualization II

- **Simplifications:**
  - Population size can be considered steady-state
  - Visualize only moving macaques on geographic map;
  - Visualize specific temple site on request;
  - Necessary because of resolution and performance

- **Internal variables:**
  - Gender, infectivity, virulence, latency, acquired immunity,
  - natural resistance, clearance time

- **Software:**
  - Java, Repast, OpenMap, ArcMap, image converting tools
Model Design

Model core:
- Macaque objects
- Temple objects

Movement decisions

2D raster files
- PGM files
  - Rivers
  - Lakes
  - Roads
  - Cities
  - Fields
  - Forests
  - Coast

Visualization

Geographic vector files
- SHP files
  - Rivers
  - Lakes
  - Roads
  - Cities
  - Fields
  - Forests
  - Coast

Calibration
Macaques have probabilities whether to move

Movement is based on a defined number of surrounding cells and the macaque’s defined direction.
Temple Sites

- Male macaques roam about the island
- Female macaques are restrained to the temple sites
- Males can enter and leave temple sites, but will not reenter a temple they have left
Disease Spread

- **Virulence and infectivity** most directly influence disease spread
- **Virulence** is the range of transmission
- **Infectivity** is the likelihood of the disease being transmitted
Visualization

- Blue squares are temple sites
- Circles are macaques; color indicates healthiness
- Inset is a closeup of a temple site
Visualization II

View of all layers:
- Macaques
- Temple Sites
- Island
- Forests
- Rivers
- Lakes
- Rice Fields
- Cities
Model Improvements

- Reduce startup time:
  - Time to load one raster image takes time
- Reduce runtime overhead:
  - One macaque’s movement needs parts of every raster file

→ Reduce all raster layers to one layer
Demonstration
Results

- We demonstrate the importance of integrating GIS landscape data with biological data to help understand and predict patterns at the population level.
- Our model provides predictive power to identify patterns that can be more closely examined in the field.
- This model will likely support the hypothesis that male dispersal acts as a genetic link between populations island-wide and will act as a mechanism in disease transmission.
- Model results will have potential long term conservation implications for macaque survival.
Future Work

- Verification and validation will be completed through field collection and laboratory analysis of macaque and pathogen genetics.
- Examining genetic markers, including neutral and disease-resistance loci of Y-chromosomal, nuclear, and mitochondrial DNA and microsatellite markers.
- Investigate any east-to-west, north-to-south, or other model-predicted population dispersal trends.
- Better understand the coevolutionary relationship between macaques and their pathogens.
- Overlay the genetic patterns of macaque populations with the genetic patterns of pathogens collected from those same populations to determine how macaque population structure can influence the evolution of disease itself.
Questions or Comments?