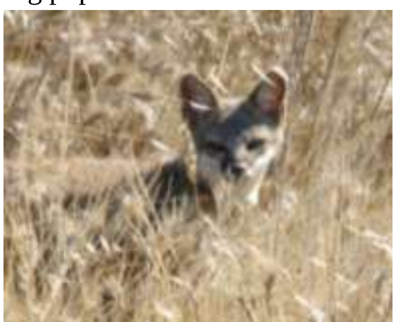
# Spatial Ecology of the Island Fox

08-308

## Background:

Four of the six island fox subspecies have been listed for protection under the Endangered Species Act (ESA) due to rapid population declines caused by invasion of a novel predator or disease. The Department of Defense considers all six subspecies species at risk.. The threat of an epidemic of a virulent disease, such as rabies or canine distemper virus (CDV) remains a concern for unlisted fox populations managed by the U.S. Navy on San Clemente and San Nicolas Islands, and mitigating that threat is a likely prerequisite for delisting populations on other islands. Predicting the course of a potential epidemic will facilitate a rapid and effective response and reduce the need for intensive captive-rearing programs or for further protection under the ESA.



San Clemente Island fox. Photo: Brian Hudgens

## Objective:

Fox densities on San Clemente and San Nicolas Island are unusually high, making this population particularly susceptible to the spread of a novel virulent disease. Furthermore, fox densities vary among habitats within each island in ways that influence home range behaviors, making it difficult to predict the outcome of a disease introduction. Our goals are 1) to determine how density-mediated changes in fox behaviors affect disease spread through changes in the frequency of contact among neighboring foxes, and 2) to use that information to inform a spatially explicit epidemic model which can then be used to evaluate effective monitoring, vaccination, and response strategies to minimize the impact of diseases (rabies and CDV) likely to infect island foxes.

## Summary of Approach:

We used radio telemetry coupled with contact loggers to determine how home-range size, overlap of neighboring home-ranges, and contact rates between neighboring foxes varied in habitats supporting different densities of island foxes on San Clemente Island, California. We measured home-range overlap as the percent of a fox's home-range shared by another fox, averaged over both members of the pair, and contact rates as the number of times/day two foxes were within ~5 meters of each other. We used these data to inform spatially explicit simulation models of rabies and CDV epidemics to determine 1) how the course of an epidemic will change depending on the disease and where the first infection is, 2) the potential for disease monitoring strategies recommended in phases I and II of this project to detect an epidemic before a large fraction of the population has been infected, and 3) the potential of an ongoing vaccination program to impact an epidemic beyond protection of vaccinated individuals.

## Benefit:

High densities of foxes and proximity to the mainland put island foxes at high risk for an epidemic such as the one the led to the listing of the Catalina Island fox under the ESA. The model developed for this project will inform the development of monitoring, vaccination, and epidemic response plans to minimize the impact of an epidemic on island fox populations and thus minimize the risk that island foxes will require captive-rearing programs or for further protection under the ESA.

## Accomplishments:

We recorded home-range data on 40 foxes and contact rates among 70 fox pairs from 4 areas of San Clemente Island ranging from 3-43 foxes/km$^2$. We found that foxes have smaller home-ranges at higher densities but that home-range overlap was not influenced by fox density. Neighboring foxes with greater home-range overlap came into contact with each other more frequently. The relationship between home-range overlap and contact rates did not differ with fox density. We completed simulations for both rabies and CDV. Simulations suggest that diseases beginning where fox densities are highest will have the greatest impact. Monitoring is likely to detect rabies but not CDV in time to prevent a large outbreak. In contrast, current vaccination programs are more likely to reduce the severity of a CDV than a rabies epidemic.

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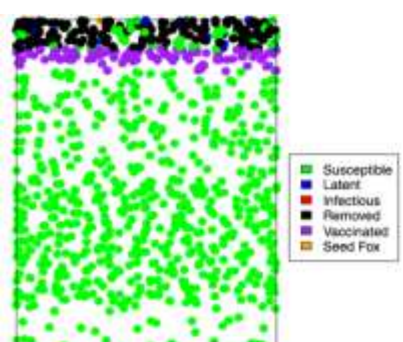


Example simulation showing distribution of susceptible, vaccinated, diseased and dead animals one year after introduction of rabies to the high density region.