**Chapter 3: Using phylogeography to investigate the influence of human activity on CDV transmission**

1. Paragraph on human activity and disease transmission
2. Paragraph on phylogeograhy
3. Paragraph on distemper
4. Hypotheses etc

Urbanization is occurring at an ever-increasing rate worldwide and indeed plays a large part in altering the composition of wildlife communities with some species suffering and some thriving under the altered conditions. Not only does this altered landscape influence the macroscopic species themselves, but this consequently has a huge role to play in the pathogen landscape at this wildlife-domestic-human interface (Bradley and Altizer 2007, Gottdenker et al. 2014). **Make some comments about landuse and pathogen dynamics.**

# Land use-induced spillover: a call to action to safeguard environmental, animal, and human health

(Plowright et al. 2021)

# Emerging challenges of infectious diseases as a feature of land systems

(Vanwambeke et al. 2019)

# Land-use change and rodent-borne diseases: hazards on the shared socioeconomic pathways

(Garcia-Pena et al. 2021)

Phylogeography allows the matching of evolutionary patterns in pathogens with space time and environemntla factors. **Talk about phylogeography in general and use some references**

Phylgeographic studies in multihost viruses of mesocarvores have largely focused on rabies REFS. With those studies in the united states focusing particularly on the spread of south central skunk rabies.REFS With CDV the phylogeographic studies have often focused on large scale global spread of the vvirus over its known history PANZERA REF. There have been some efforts in specific CDV outbreaks in other parts of the world to use phylogeographic methods to plot the spread of the outbreak BIANCO. However to date there have been no such studies in the united states.

Canine distemper virus (CDV) is a significant cause of illness and death in wild carnivore species. This is a major conservation concern, and the virus has been implicated in severe population declines in multiple species, including the near extinction of the black-footed ferret in the US (Williams et al. 1988). It is also an important disease in domestic dogs, with the virus being able to pass back from wildlife to dogs (Kapil and Yeary 2011). It has also been proposed as a danger to human health, as the risk of CDV infection in humans increases with reduction in population-level measles immunity (Martinez-Gutierrez and Ruiz-Saenz 2016). Canine distemper virus differs from closely related viruses in its ability to infect a wide variety of carnivore hosts. However, the dynamics of CDV infection within multi-host systems, such as carnivore communities, is poorly understood. The role that particular species plays in the maintenance and spread of the disease in this system is not understood and consequently the targeting of mitigation measures is not well informed. The southeastern US is one such multi-host system, containing a wide variety of potential host species. Raccoons are frequently the most reported wild carnivore species in distemper outbreaks and have been suggested as the possible reservoir host (Roscoe 1993). Preliminary work from necropsy data of wild carnivores diagnosed with CDV has demonstrated that CDV is widely spread in the SE USA with at least 9 carnivore species experiencing mortality as a result of infection. In the most commonly infected species, raccoons and gray foxes, there appeared to be a trend of cases clustering in suburban areas with fewer cases occurring in highly urbanized and in rural areas(Taylor et al. 2021). However, the preliminary work is based on diagnoses of CDV, with no information on the virus itself. Genomic sequence data of the virus isolated from wildlife cases will provide vital information needed to elucidate the transmission dynamics in this multihost system across land-use gradietns. In order to effectively predict the outcome of outbreaks of CDV in wild carnivores and develop effective counter measures, it is vital to understand the dynamics of the disease in this kind of system.

Here, we investigat how human activity and land use influence the dynamics and persistence of CDV within the southeastern mesocarnivores system. First, we investigate dynamics of spatial spread across ladnuse gradient. We then, identify land use types corresponding to the source of outbreak. We hypothesize that CDV will spread from suburban areas, with rapid expansion through suburbia, followed by slowing of transmission in urban and rural areas.

* How does?
* The hypothesis of this study is
* Aim1 :
* Aime 2:
* Rural-urban gradient spatio-temporal spread
  + How do the dynamics change across rural-urban gradient with change in host density? (Bianco et al., 2020)
  + Role of anthropophilic species
* Land use effects on host population size and connectedness of population
  + Map spread over time and space
* **Phylogeography:** Matching evolutionary patterns with space, time, and environmental factors
* What are the dynamics of transmission across space?
* When did an outbreak most likely originate?
* Are there specific regions that are at a greater risk?

Preliminary data

* Significant clustering of cases in raccoon and gray fox within GA
* Cases were more likely to occur in areas of medium to high human population density.
* This pattern was most prominent for raccoons

Research Q

* How does human activity and land use influence the dynamics and persistence of CDV within the southeastern mesocarnivore system?

**Chapter 4: Using phylogeography to investigate the influence of human activity on CDV transmission**

**Research Question**

How does human activity and land use influence the dynamics and persistence of CDV within the southeastern mesocarnivore system?

**Rationale**

Give a chapter 4 we're going to look at the special temporal dynamics in more detail and pull our land use in here. So from preliminary data rural urban gradient important and spatial temporal spread the relevance of this being and disease control do we have epidemics and suburbia with spread out? And how does the dynamics change across a rural urban gradient with a change in host density Bianco 2020. On going back to our conceptual model is there a selection for either generality or reduce transmission. So the questions to answer with laundry's are one map spread over time and space to model diffusion rates across different landscapes three where does it break occur and spread and for where does the persist.

·Rural-urban gradient spatio-temporal spread

·How do the dynamics change across rural-urban gradient with change in host density? (Bianco et al., 2020)

·Role of anthropophilic species

·Land use effects on host population size and connectedness of population

oMap spread over time and space

´**Phylogeography:** Matching evolutionary patterns with space, time, and environmental factors

´What are the dynamics of transmission across space?

´

´When did an outbreak most likely originate?

´

´Are there specific regions that are at a greater risk?

ØSignificant clustering of cases in raccoon and gray fox within GA

ØCases were more likely to occur in areas of medium to high human population density.

ØThis pattern was most prominent for raccoons

# The Phylogeography and Spatiotemporal Spread of South-Central Skunk Rabies Virus

# (Kuzmina et al. 2013)

# On the Use of Phylogeographic Inference to Infer the Dispersal History of Rabies Virus: A Review Study

(Nahata et al. 2021)

**Using phylogeographic approaches to analyse the dispersal history, velocity and direction of viral lineages - Application to rabies virus spread in Iran**

(Dellicour et al. 2019)

# Using Viral Gene Sequences to Compare and Explain the Heterogeneous Spatial Dynamics of Virus Epidemics

(Dellicour et al. 2017)

# Sampling bias and model choice in continuous phylogeography: Getting lost on a random walk

(Kalkauskas et al. 2021)

# Predicting spatial spread of rabies in skunk populations using surveillance data reported by the public

(Pepin et al. 2017)

# On the importance of negative controls in viral landscape phylogeography

(Dellicour et al. 2018)

**Hypothesis**

The hypothesis of this study is that CDV will spread from suburban areas, with rapid expansion through suburbia, followed by slowing of transmission in urban and rural areas.

The objective of this study is to model the spatio-temporal dynamics of an outbreak of canine distemper in wild mesocarnivores in the outheastern united states across human landuse types.

Aim1 : investigate dynamics of spatial spread across ladnuse gradient

Aime 2: identify land use types corresponding to the source of outbreak

**Methods**

Graphical user interface, text

Description automatically generated

**´Expected results**

´Expect to find a predominance of cases within suburban areas

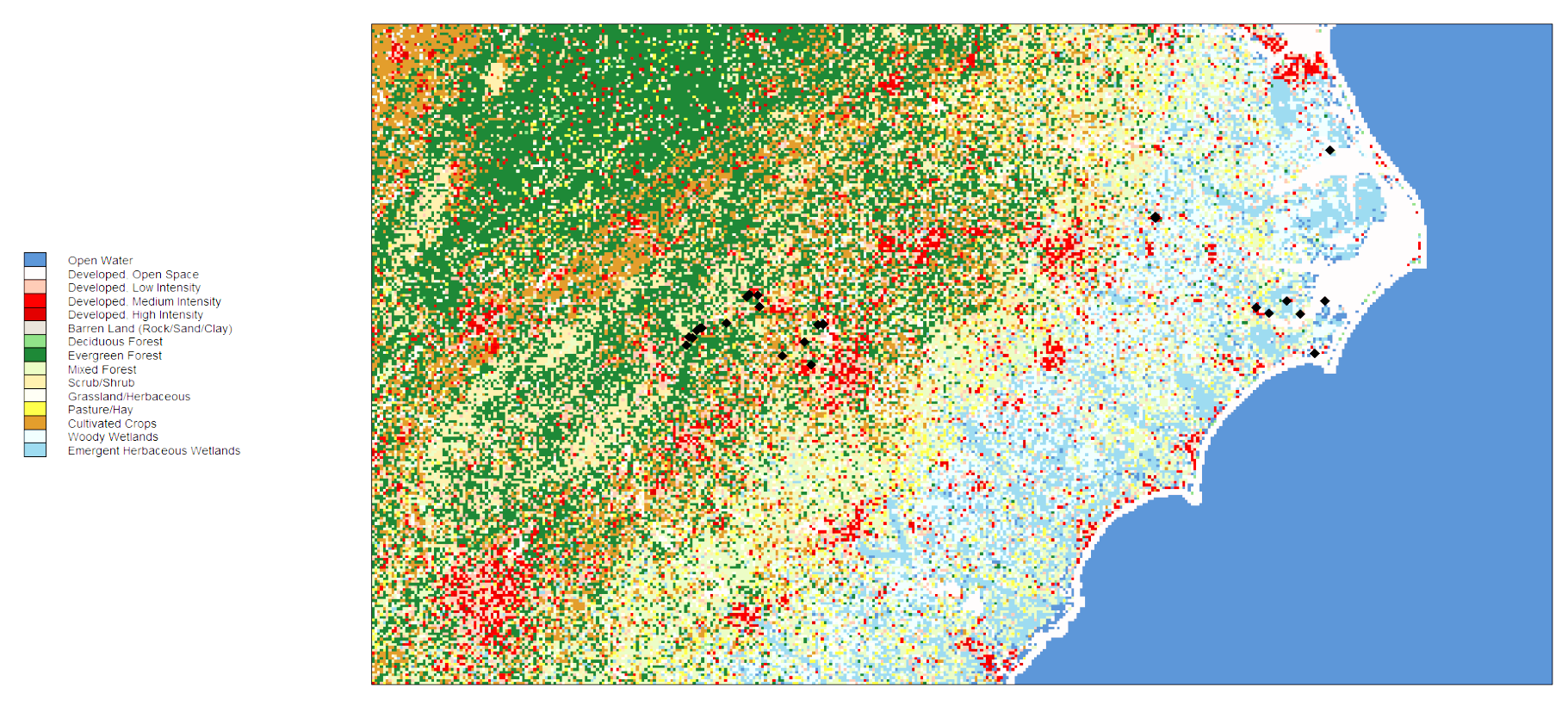
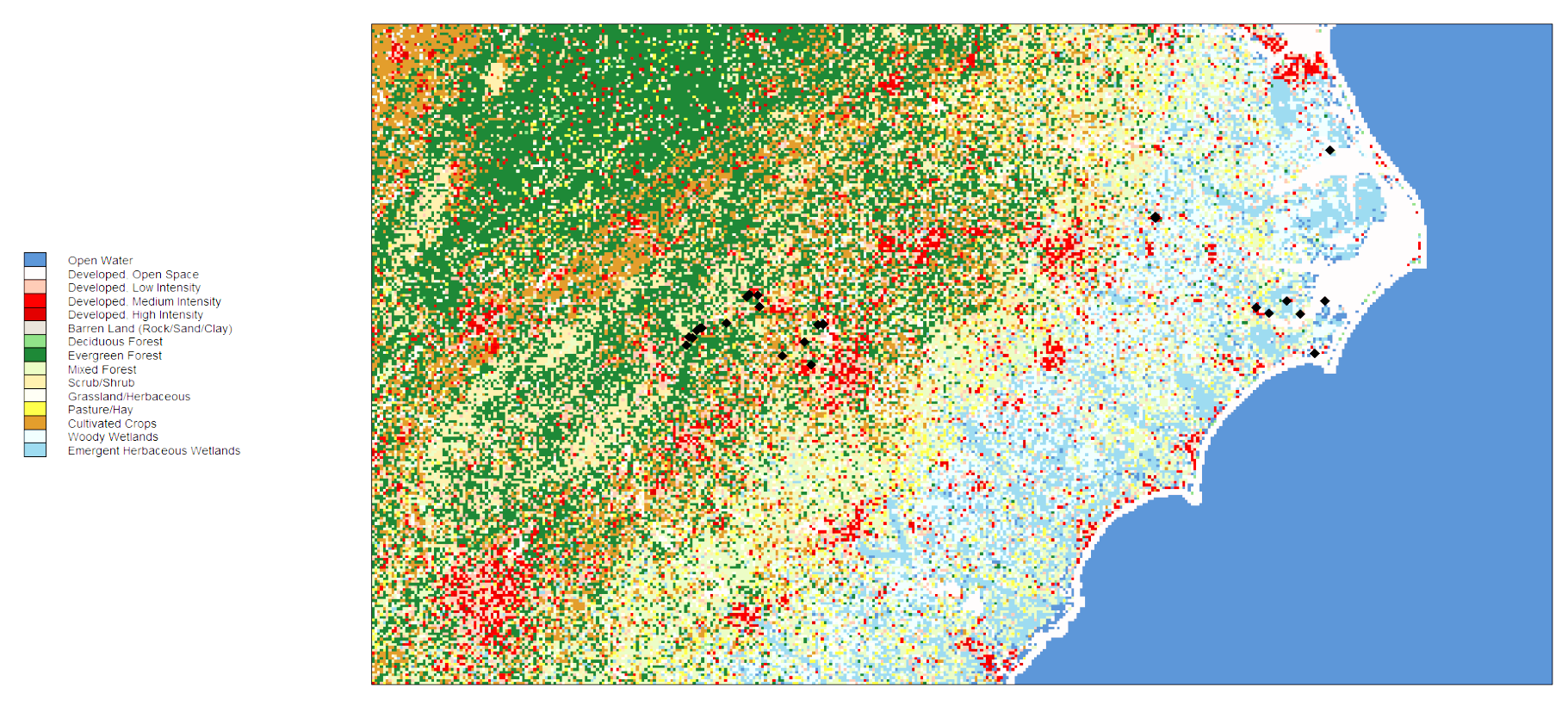
´Spread of cases out into more rural and very urban areas

**´Preliminary results**

Table

Description automatically generated  
the initial breakdown of the data geographically shows a large outbreak in northcaralina (Fig X) wit 28 cases occurring there, the next largest being in missourri with 16. As a preliminary study, I will focus on North Carolina before expanding out into the rest of the data. Raster data for landcover from 2019 fro North Carolina was pulled from the National Land Cover Database (NCLD). The cases in Northcarolina are layered over this land cover layer and shown in figure X. On initial study there are two fairly distinct outbreaks. There is one coastal outbreak and one inland outbreak. The coastal outbreak occurs in the “Emergent Herbaceous Wetlands” and “Woody Wetlands”, these are areas that are favoured natural envrironments for raccoons and sustain large populations (ref). The second larger outbreak occurs in and adjacent to our developed regions. This follows closely with our initial hypothesis that surban and urban will be the source of outbreaks with rapid spread through these regions. Further statisitical and modeling work on this data and on the rest of the data will hopefully shed more light on this initial observation.   
  
  
  
  
  
  
  
  
  
  
Chart, histogram

Description automatically generated



**limitations**

The limiatiions agaijn mostly apply to the type of sampling. The samples are collected passively through submissions by Georgia DNR and the equivalent departments in other states. This is dependent on a number of factors; a dead or ill animal being reported to the authorities or seen by them and a willingness to submit for necropsy. There are likely to be large numbers of subclinical cases which are missed. This leads to a number of potential areas of sampling bias, with more populated areas and areas with state/national parks likely to have more cases submitted. Additionally, areas with rabies concerns are likely to submit more cases as the two diseases present very similarly.

Additionally the raster data from NLCD is from 2019 which is before any of our samples were taken, however the landcover is unliklely to have changed much in this timeframe, particular with the economic impact of the COVID-19 pandemic, the the effects of this time lag are likely to be minimal.

**State**

**State**

***´Timeline***

***+funding***

***coursework***

Refs

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