



**Population abundance and genetic structure of black bears in coastal South Carolina**



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**Overview of Seminar**

- Background
- Justification
- Objectives
- Study Area
- Methods

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**Background**

- American black bear (*Ursus americanus*)
  - Two disjunct populations
    - Appalachian Mountains
    - Coastal Region
- Fragmentation and habitat loss
  - Roads, canals, railways, cities
  - Pocosin and Carolina Bay

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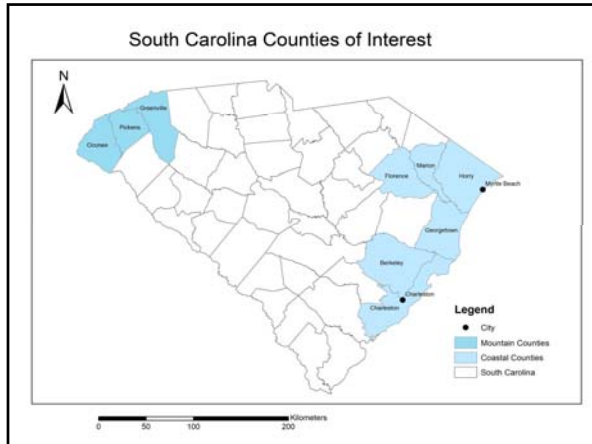
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### Background

- Coastal population limited to Georgetown, Horry, and Marion counties
- Possible range expansion
- Possible population increase

An inset map showing a detailed view of the coastal region of South Carolina. The counties of Marion, Horry, and Georgetown are highlighted in red. Other nearby counties shown include Florence, Williamsburg, Berkeley, and Charleston. Major cities like Myrtle Beach and Charleston are also marked.

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### Justification

- Harter (2001): movements and population characteristics
- Conflicting information
- Comprehensive management plan
  - Population abundance
  - Genetic structure

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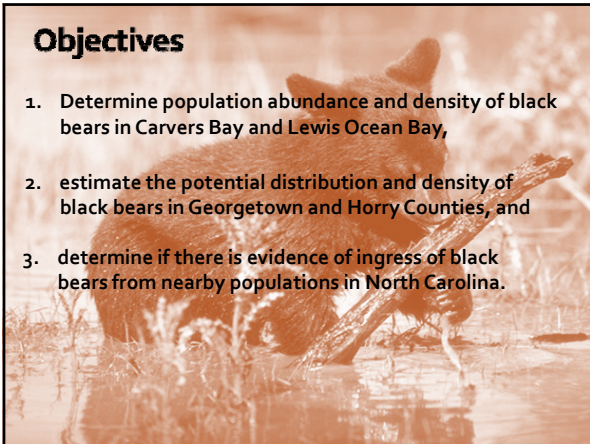
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## Objectives

1. Determine population abundance and density of black bears in Carvers Bay and Lewis Ocean Bay,
2. estimate the potential distribution and density of black bears in Georgetown and Horry Counties, and
3. determine if there is evidence of ingress of black bears from nearby populations in North Carolina.



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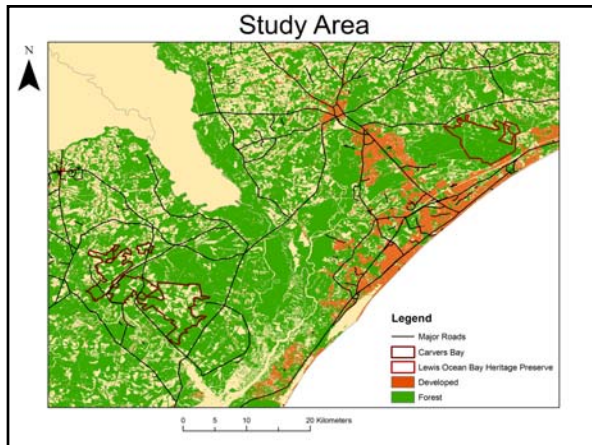
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## Study Area



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## Study Site

- Carvers Bay  
~ 50 km<sup>2</sup>  
Pine plantation  
Hunting clubs



- Lewis Ocean Bay Heritage Preserve  
~ 25 km<sup>2</sup>  
Pocosin and Carolina bay



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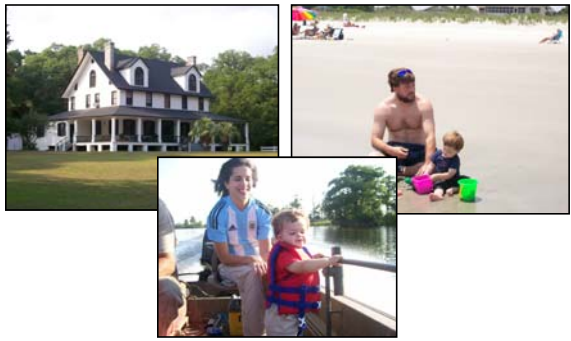
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### Study Site



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### Methods

- DNA 'captures'
- Genetic tagging
- Mark-recapture



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### Sampling Site

- $\geq 4$  sites per home range (Otis et al. 1978)
- Female home range (5 km<sup>2</sup>; Kindall 2004)
- Random placement
  - Minimum >900 m apart
  - Accessibility (<250 m)

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### Field Techniques

- Hair sampling
- 2 wires

- Don't give advisor this look !

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### Field Techniques

- Hair collection
- Re-bait





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### Genetic Analysis

- DNA extraction
- Microsatellites markers
  - Group of molecular markers found in nuclear DNA
  - Heterozygous or homozygous
  - Number of markers
  - Wildlife Genetics International

Gene loci: P, A, B (Dominant allele) and p, a, b (Recessive allele)

Genotype: PP (Homozygous for the dominant allele), aa (Homozygous for the recessive allele), Bb (Heterozygous)

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### Population Abundance and Density

- Closed capture-recapture population model (Otis et al. 1978)
  - Assumptions
  - Capture probability bias


Week 1



Week 2



Week 3



<b>Bear 1</b>	1	1	1
<b>Bear 2</b>	1	0	0

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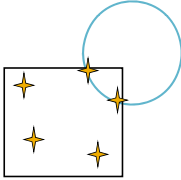
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### Population Abundance and Density

- Program MARK
  - A priori model set; time, heterogeneity, behavior
  - Akaike's Information Criterion ( $AIC_c$ )
- Closure violation
  - $Density = N/Area$
- Program Density
  - Fits spatial detection functions
  - Estimates  $Density$ ,  $N$ , and  $\sigma$



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### Extrapolating Population Estimates

- Possible lack of re-colonization in some areas
- Occupancy model
  - Transects
  - Presence-absence
  - Habitat covariates

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### Habitat Corridors

Linkages that provide connectivity among and between populations while providing the resource requirements needed to sustain permanent use (Kindall and van Manen 2007)

- Based on habitat analysis
- Least-cost-path analysis
- Habitat connectivity

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### Genetic Structure

- Analysis of molecular variance (AMOVA)
  - Distances among all pairs of genotypic alleles
  - Multiple levels of population hierarchy
  - Program Arlequin
- Genetic assignment test
  - Probability of belonging to a sampled population
  - 1<sup>st</sup> generation migrants
  - Program GeneClass 2

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### Genetic Structure

- Gene flow
  - Average number of unique alleles exchanged between populations per generation
  - Program BayesAss

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## Acknowledgments

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Kayla Munnerlyn, Wyatt Morris

MeadWestvaco Timber Co.



Anonymous Donors

Bear Lab

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## Questions



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