

Development of population genomic tools for Wyoming pronghorn



Melanie LaCava^{1,2}, Erick B. Gagne²,
Sierra M. Love Stowell², Holly B. Ernest^{1,2}

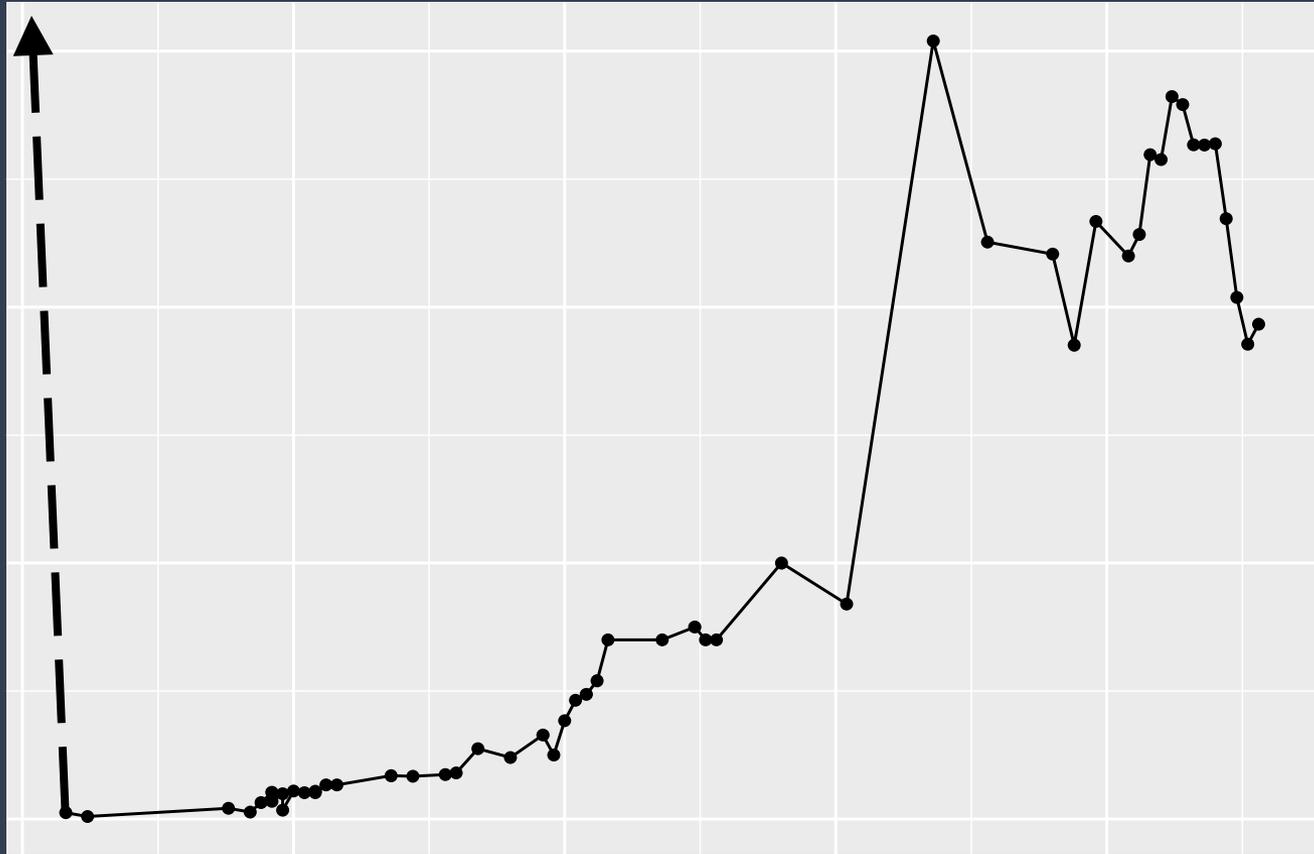
¹Program in Ecology, University of Wyoming, Laramie, WY.

²Department of Veterinary Sciences, University of Wyoming, Laramie, WY.



**WILDLIFE GENOMICS
& DISEASE ECOLOGY**

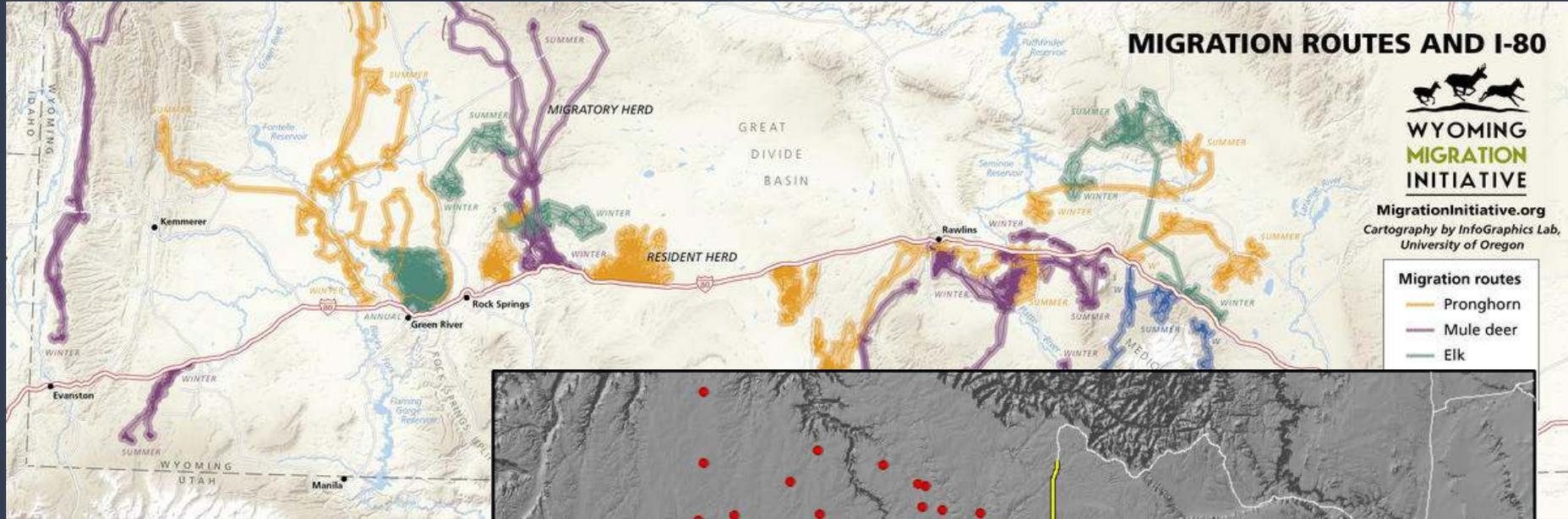
Historic population fluctuations



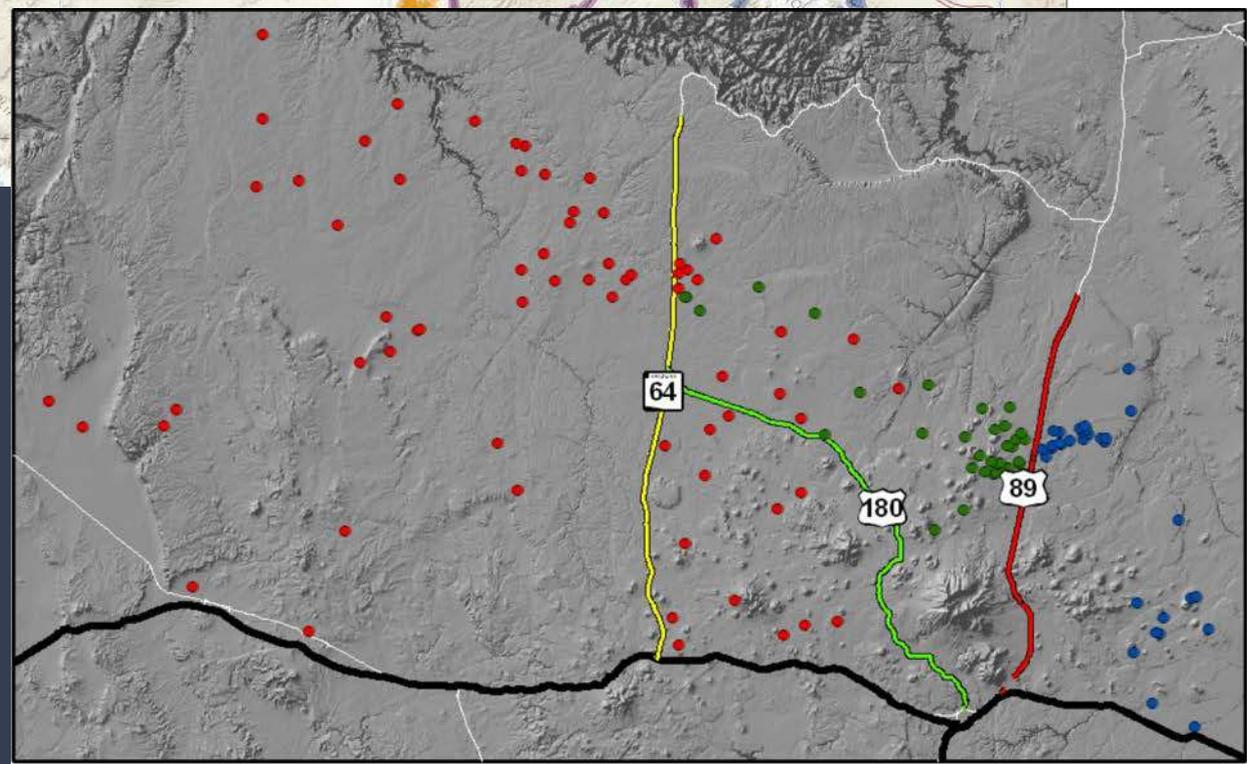
Contemporary threats to pronghorn



Known impacts of roads



Northern Arizona
pronghorn



How do historic populations declines and current anthropogenic stressors affect Wyoming pronghorn at a statewide scale?

1. Develop statewide genomic data for WY pronghorn
2. Produce baseline genetic indices
 - Genetic diversity, inbreeding coefficients
3. Assess broad-scale patterns of genomic differentiation
 - Identify landscape barriers to gene flow
 - Delineate genetic population units



Why do we care about genetic connectivity?

- Maintain genetic diversity
 - Adapt to new conditions / threats
- Reduce indications of CWD resistance in
(Devivo 2015)

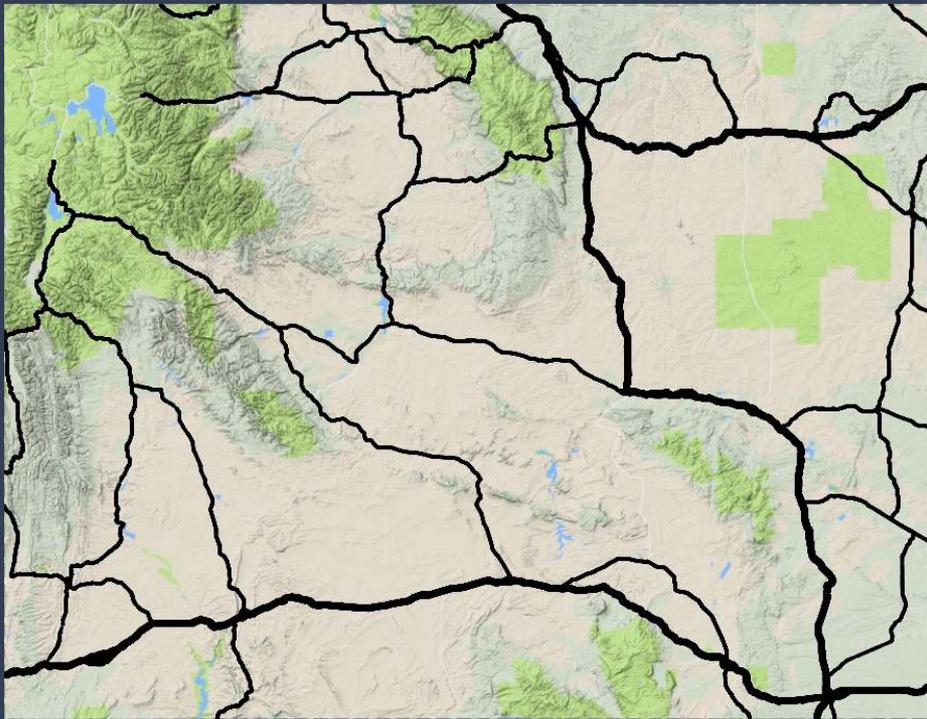
Stillborn offspring in European adder
(Madsen et al. 1996)

Problem: Population isolation → inbreeding → stillborn offspring → population decline

Solution: Introduce outside snakes → decline in stillborn offspring → population recovery

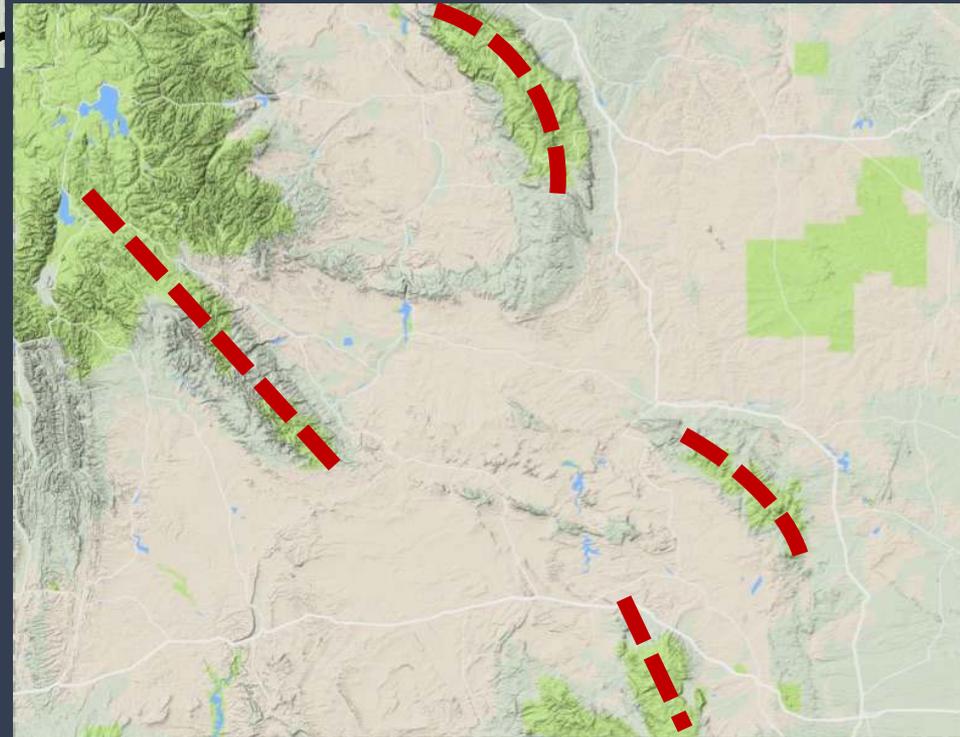


Human-constructed barriers

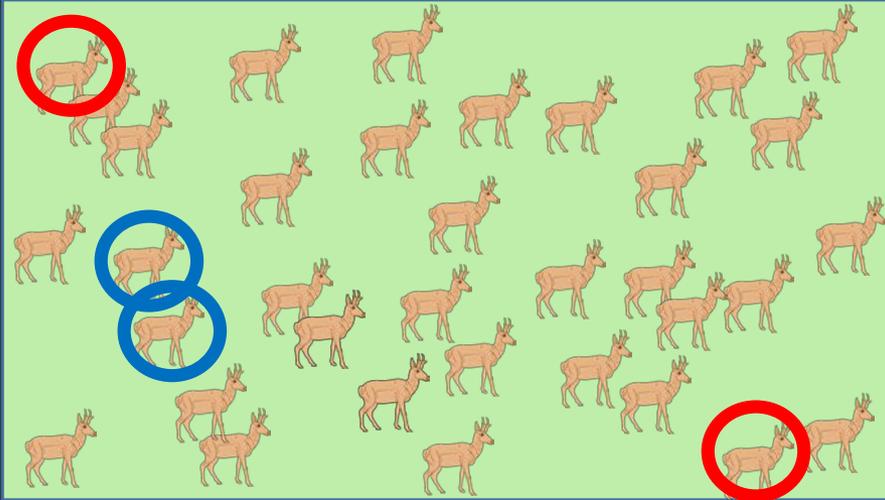


Adapted from WyDOT Highways OpenData 2015

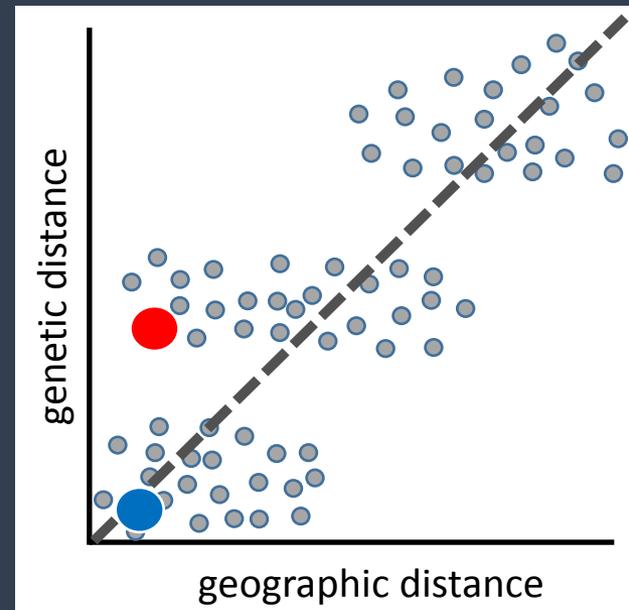
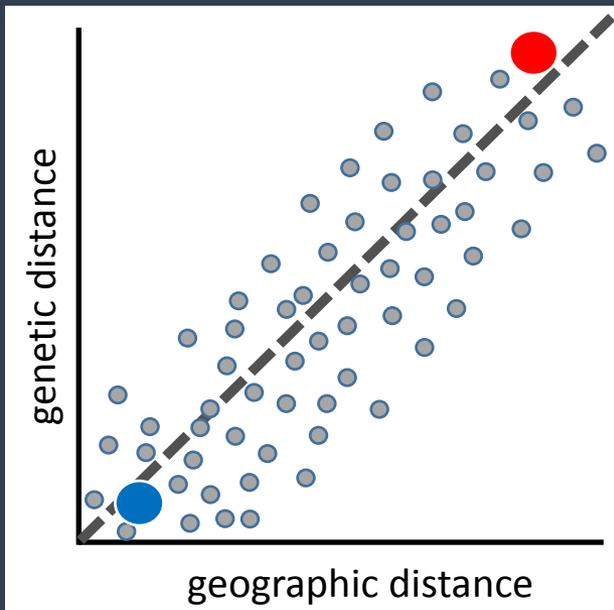
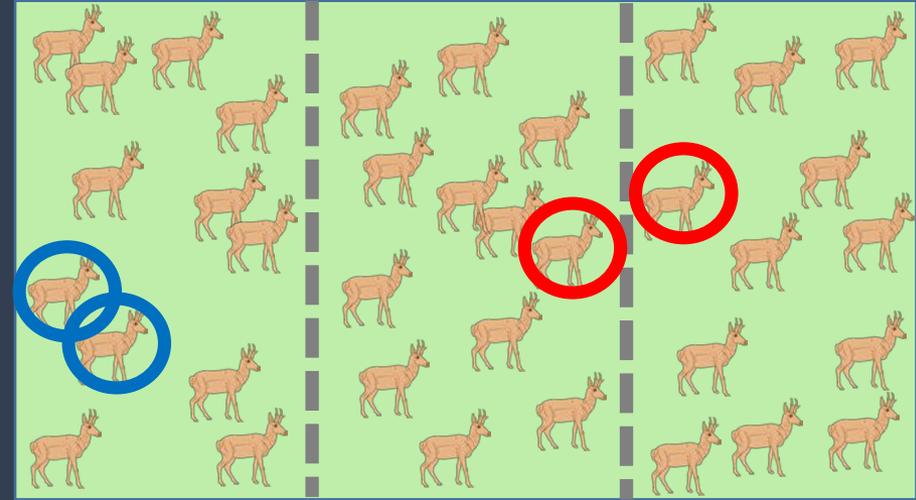
Natural barriers



Continuous population with isolation by distance



Three populations separated by barriers



Sample sources:

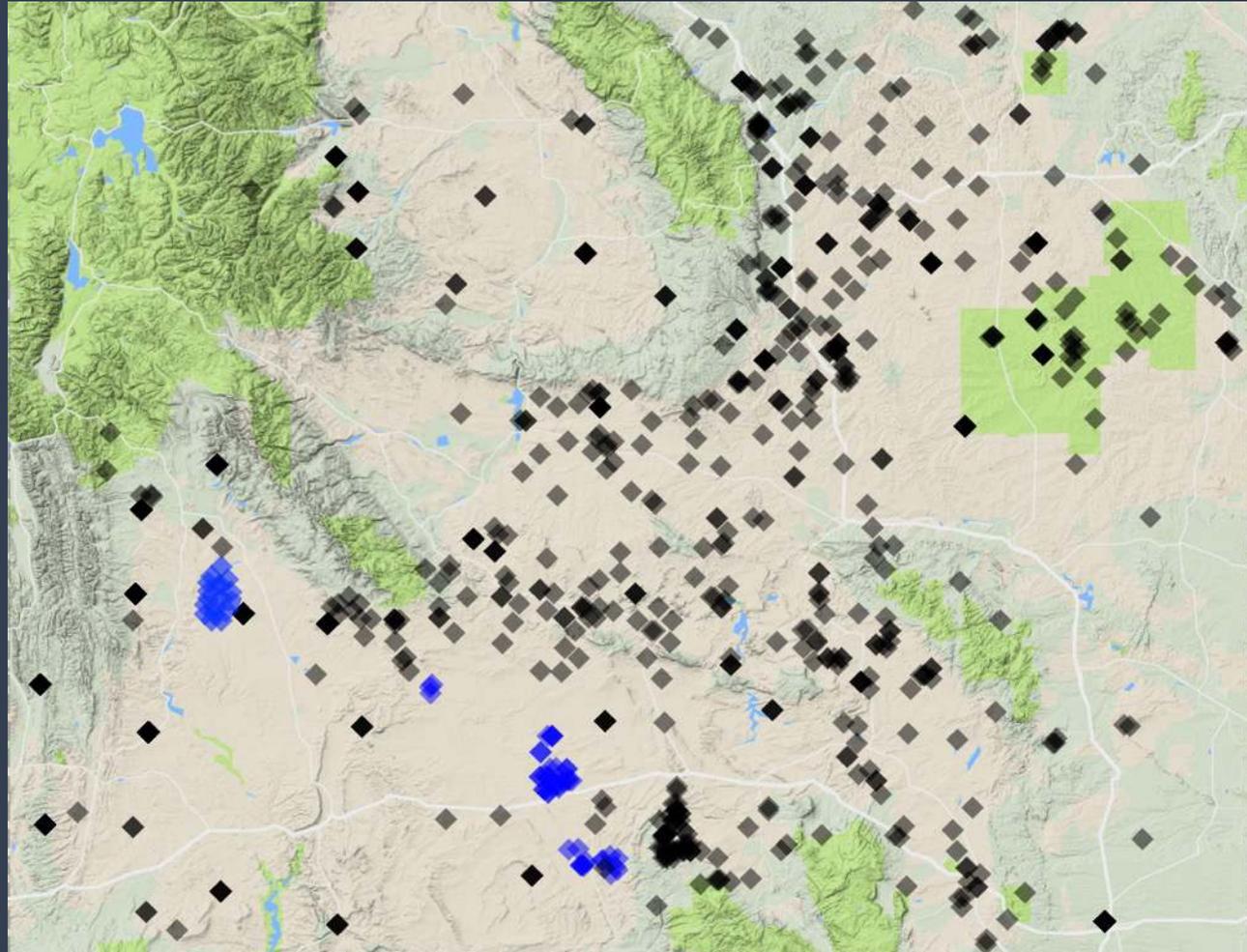
- WGFD check stations & WGFD forensics lab
- WSVL necropsies
- West, Inc. & UW captures

304 ♀

589 ♂

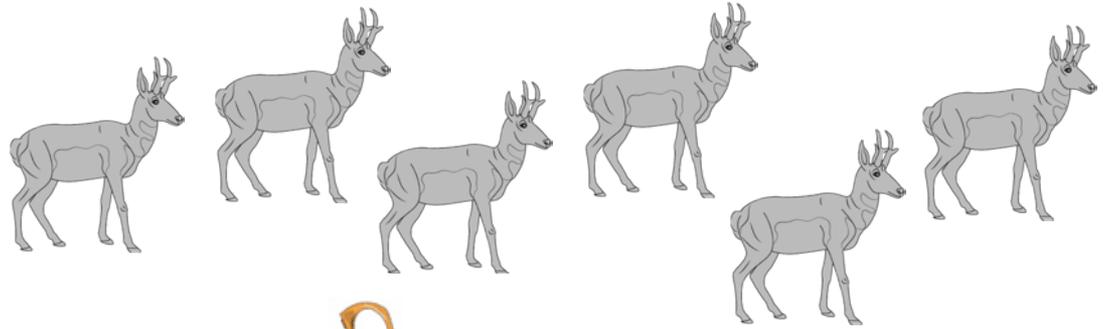


Adele Reinking

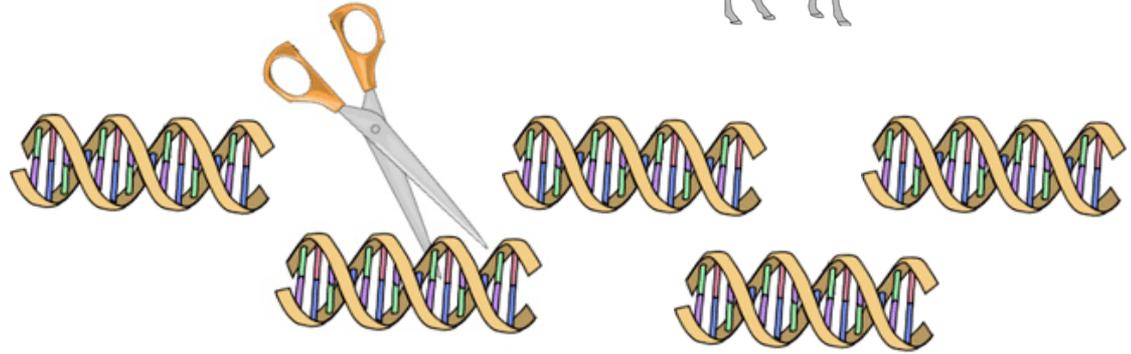


Double digest restriction site-associated DNA (ddRAD) sequencing

Extract DNA from samples



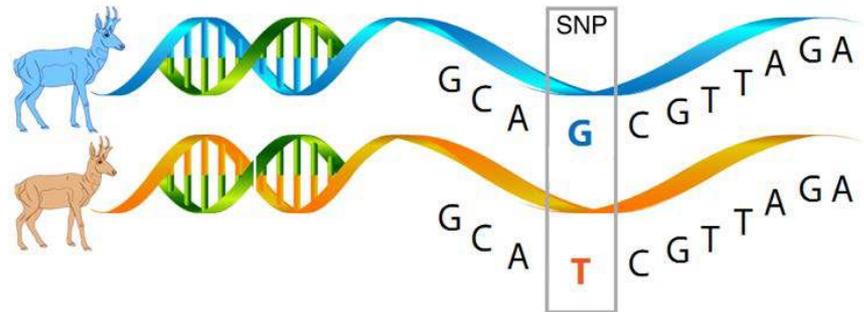
Cut DNA from entire genome into short fragments



Sequence DNA fragments

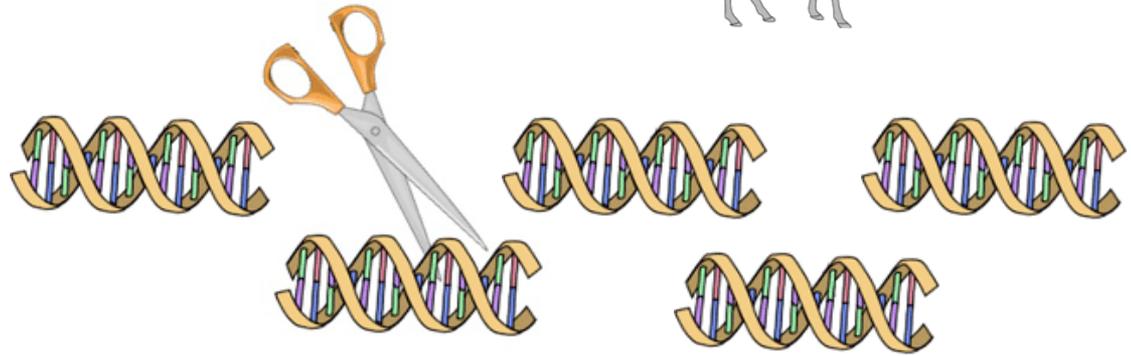
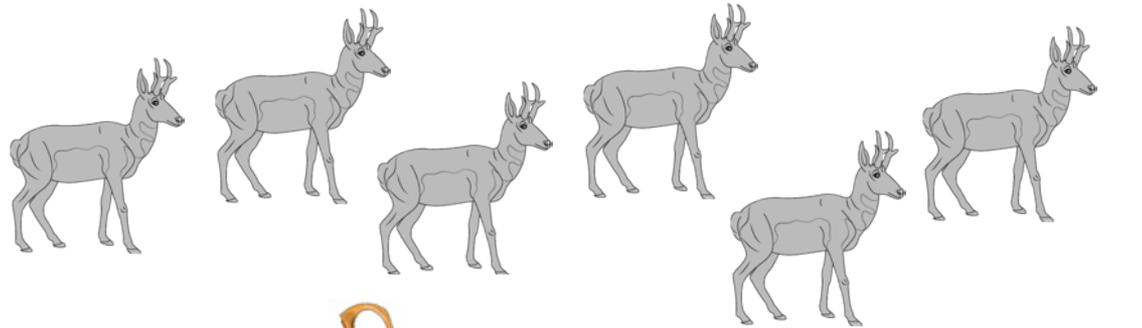
GCAGCGTT GATTCGAG TAACGTCA
CATGGCAA TTCAGCCT TTGAGGCT TTGAGGCT

Align fragments & compare across individuals



Pronghorn pilot study

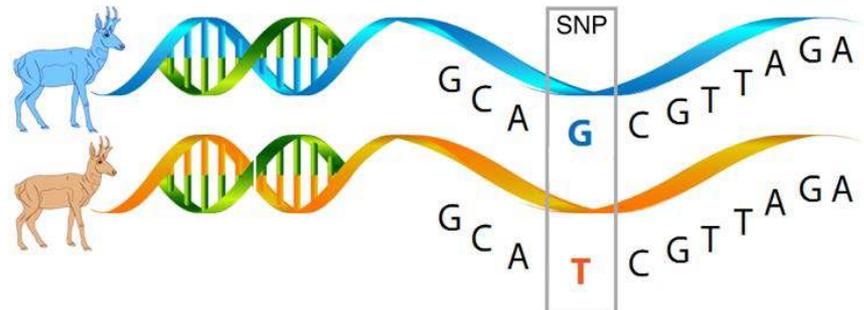
48 samples



85 million DNA sequences

GCAGCGTT GATTCGAG TAACGTCA
CATGGCAA TTCAGCCT TTGAGGCT TTGAGGCT

Over 40,000 loci identified



Next steps...

1. Develop statewide genomic data for WY pronghorn
 - Sequence 500 pronghorn
2. Produce baseline genetic indices
3. Assess broad-scale patterns of genomic differentiation



Acknowledgements



Ernest lab members:

Holly Ernest
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Brady Godwin
Sierra Love Stowell
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Wyoming Game and Fish Department:

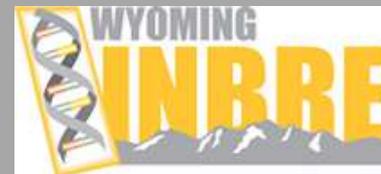
Forensics lab (DeeDee Hawk, Carl Smith)
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Pronghorn Working Group
Scott Smith
Wildlife biologists

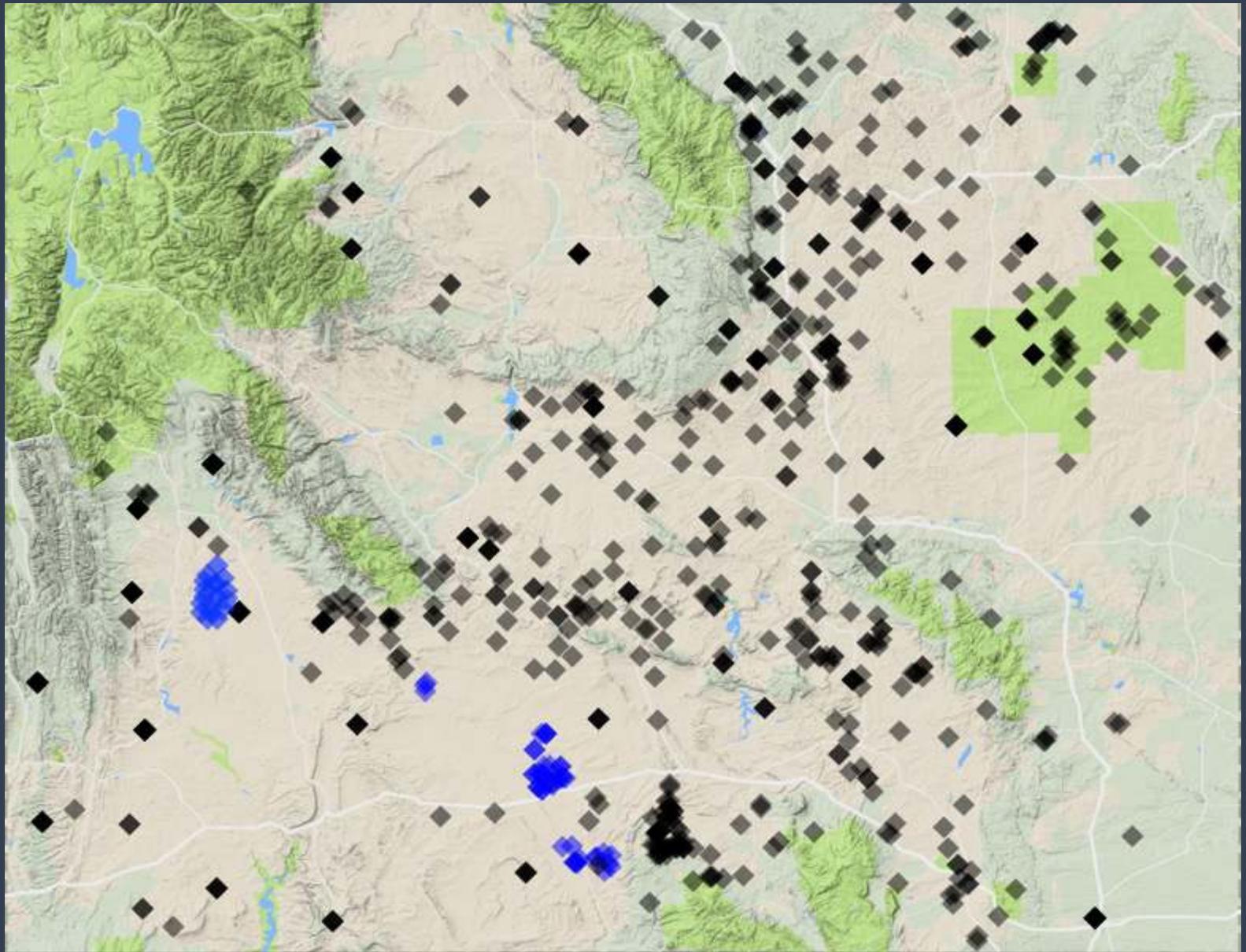


Others:

Hall Sawyer Jeff Beck
Adele Reinking Kevin Monteith
Richard Guenzel

Funders:





Questions?

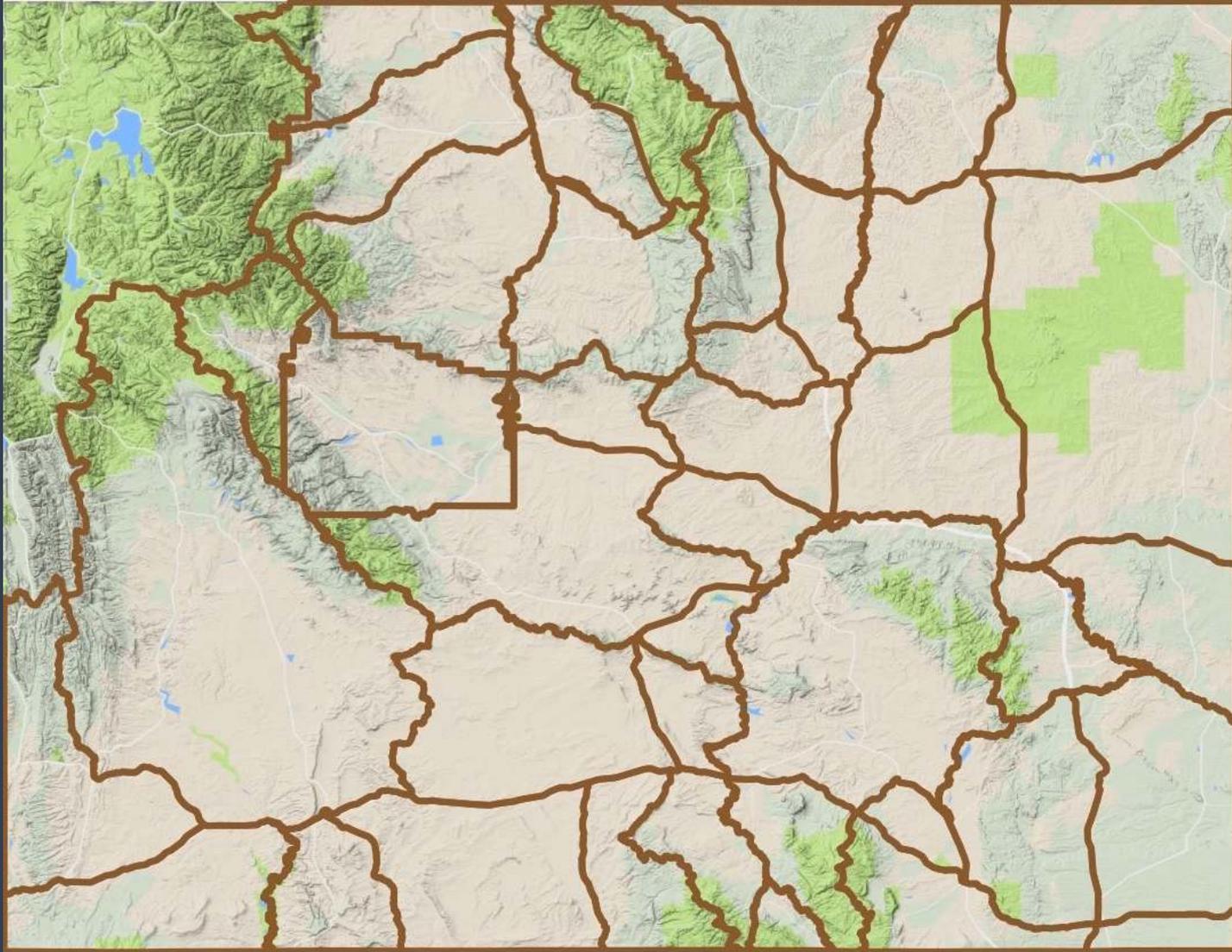


Why ddRAD?

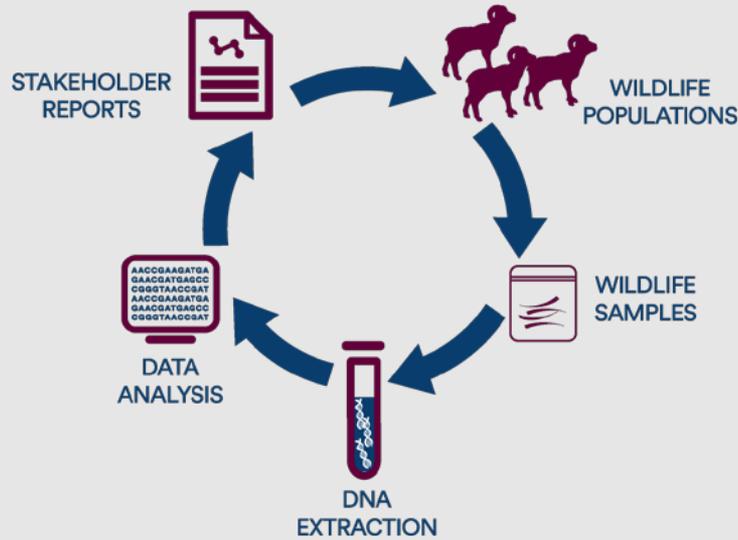
- More data → more statistical power
- Doesn't require reference genome
- Neutral & potentially adaptive markers



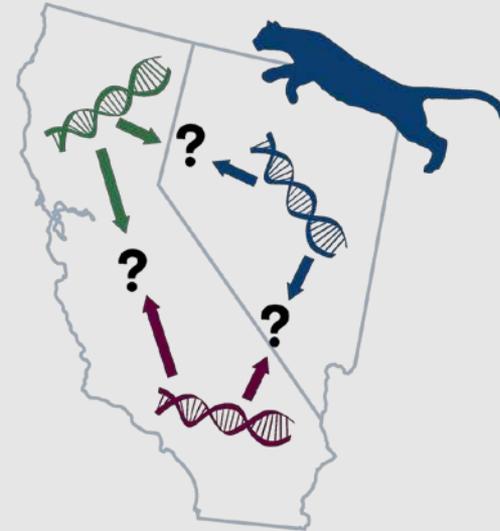
WGFD herd units



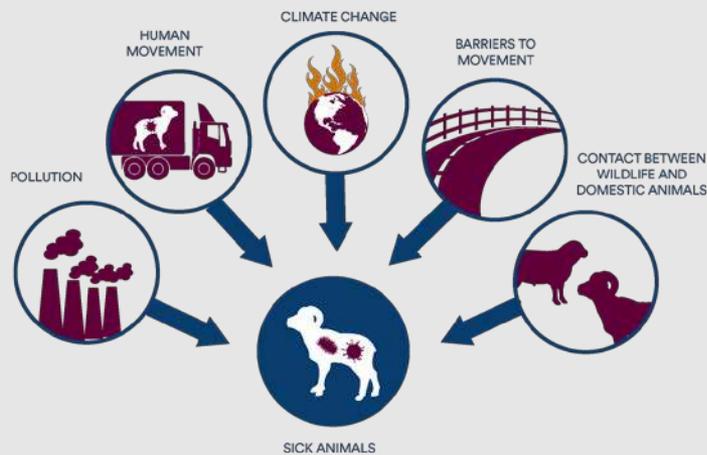
WILDLIFE GENOMICS



LANDSCAPE GENETICS



WILDLIFE DISEASE ECOLOGY



MIGRATION GENOMICS

