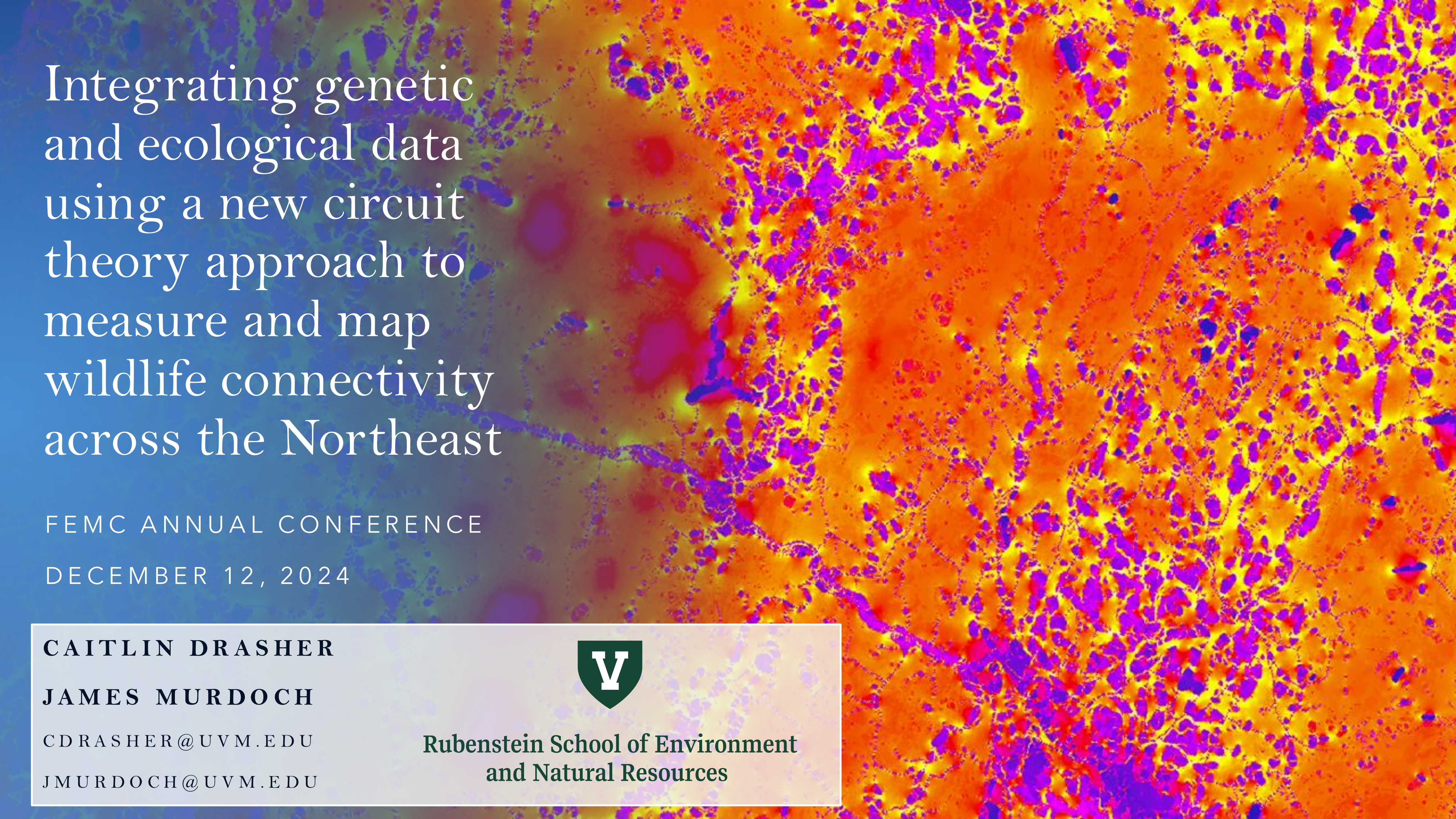

Integrating genetic and ecological data using a new circuit theory approach to measure and map wildlife connectivity across the Northeast

FEMC ANNUAL CONFERENCE

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Acknowledgments

FUNDING: Northeastern States Research Cooperative

PARTNERS:

US Forest Service, Green Mountain and Finger Lakes: Suzanne Gifford

VT Fish and Wildlife Department: Kim Royar

New Hampshire Fish and Game: Patrick Tate

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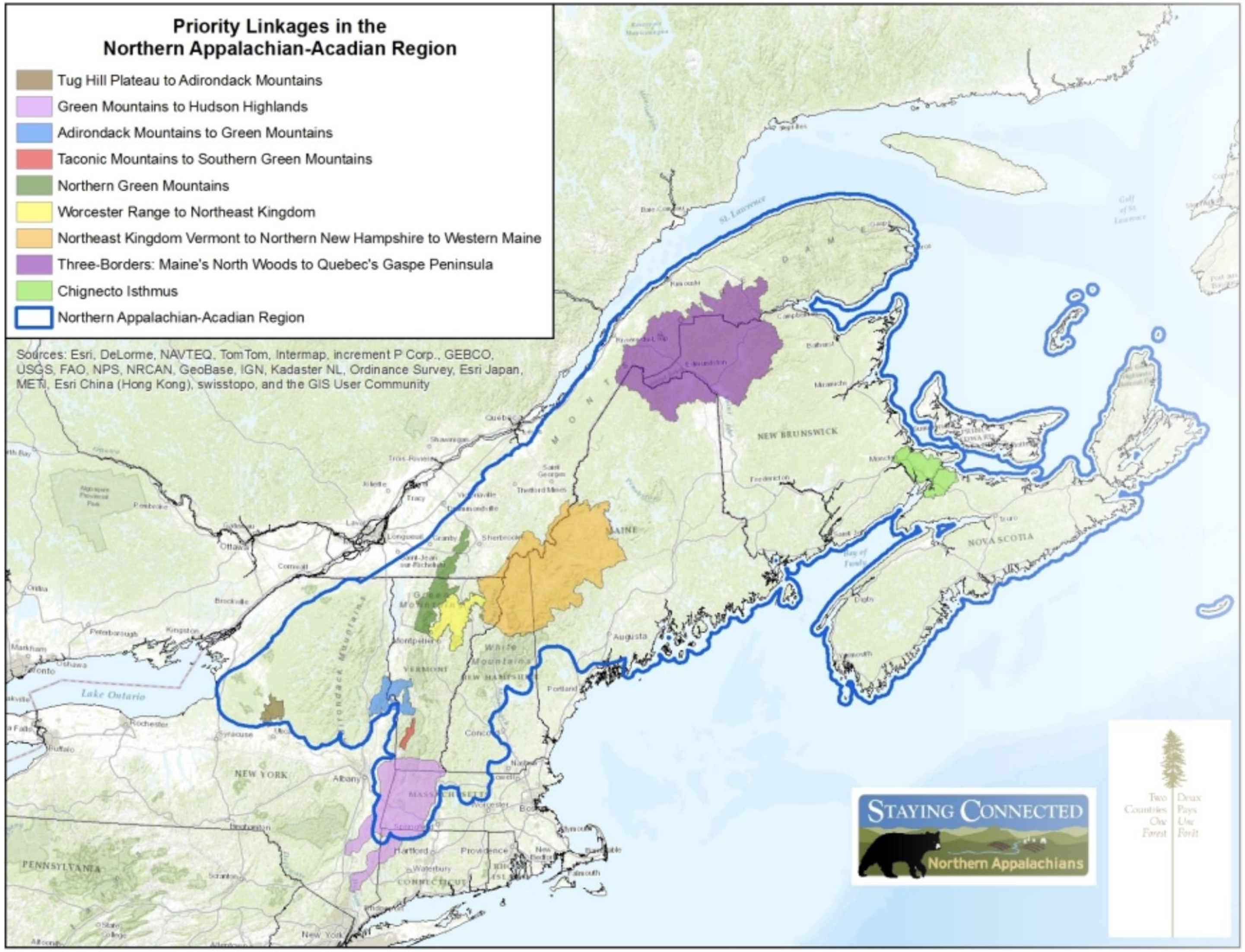


Critical wildlife linkage areas identified by the Staying Connected Initiative.

Regional Context

Northern Appalachian/ Acadian Region

- 330,000 km^2
- Important forest blocks, coastline, mountain ranges
- Wildlife corridors

Regional Context

Regional conservation challenges:

- Persistent problems of habitat fragmentation, alteration, and loss.
- Substantial impact on wildlife populations, restricting movement and gene flow across the landscape.
- There is a need for more information on landscape genetic patterns of historic species movements and gene flow that will help land and wildlife managers support and maintain connectivity.

Genetic connectivity

- Benefits to species: reduce inbreeding depression, genetic drift; adaptation to stochasticity
- Different landscape variables will *facilitate* or *impede* gene flow
- Species movements associated with gene flow may tell a different story than day-to-day movements


Connectivity requirements vary by species

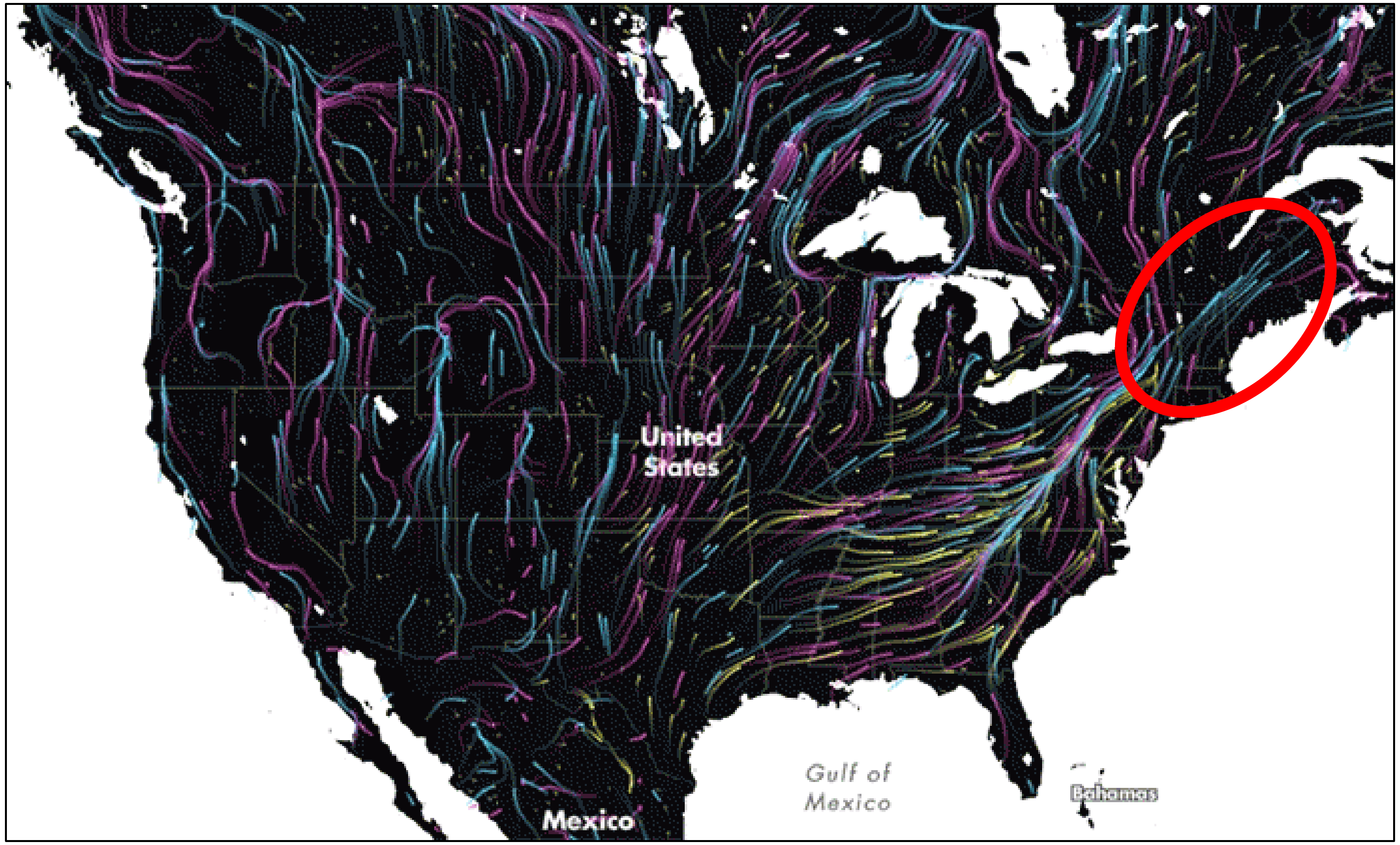

Images: VT Fish & Wildlife

Connectivity Models

- Models of species movements created using electrical circuit theory
- Wildlife movement = electricity
- Landscape = circuit

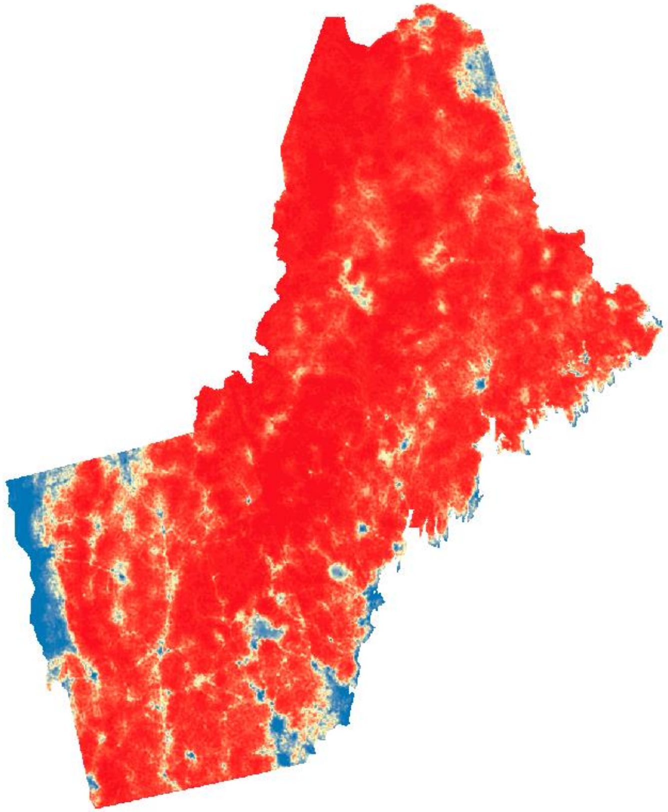
Omniscape.jl

(Landau et al. 2021, McRae et al. 2016)

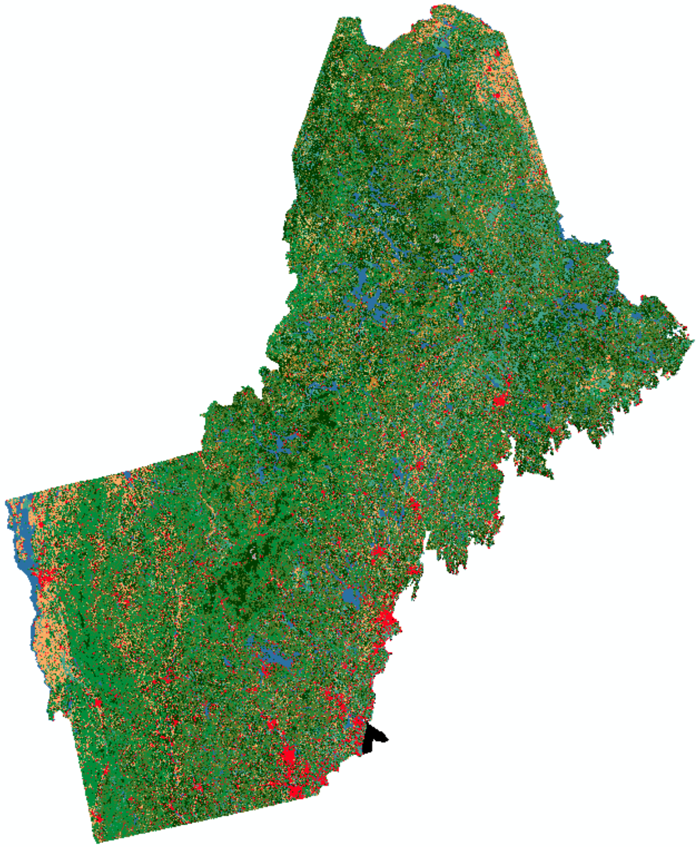


Circuit models used to map predicted movement paths of 2,954 species under climate change projections, (Lawler et al. 2013, McGuire et al. 2016). "Migrations in Motion" map created by Dan Majika, TNC.

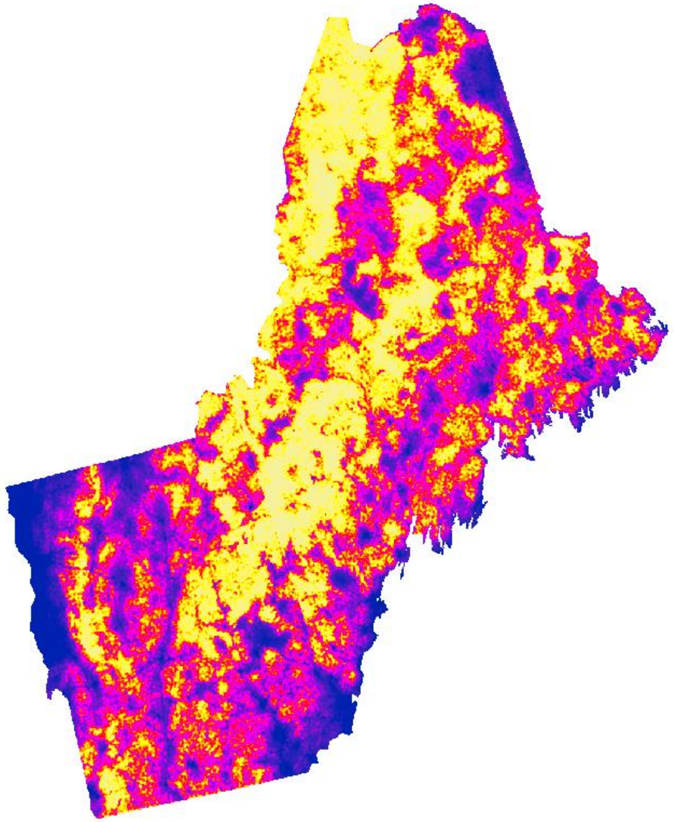
Methods



Source Strength
Species occurrence data
(Pearman-Gillman et al. 2020)



Resistance
Genetically-optimized resistance
surface (genetic data & NALCMS
landcover)



Omniscape gene flow models
Species-specific maps of gene
flow across northeastern US
(900m resolution)

Methods

Genetic sample collection:

- Extensive effort to collect tissue or hair samples from all focal species.
- Samples were primarily collected from hunters and trappers who harvested animals during regulated seasons.
- Additional samples collected from roadkill animals; many collected by USDA Wildlife Services in each state.
- Samples placed into cryovials, organized by species, and sent to UC Davis for DNA extraction and analysis.

Methods

Genetic analyses:

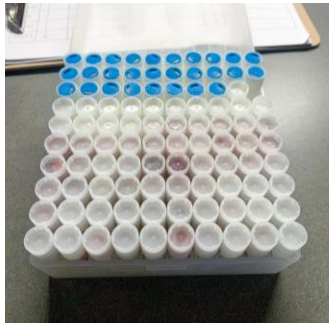
- The Mammalian Ecology and Conservation Unit at UC Davis performed DNA extraction on the samples.
- Bobcat, coyote, fisher, raccoon, red fox, and skunk samples: SNP markers sequenced using Genotype-by-Sequencing (GBS) methods.
- Bear and deer samples had microsatellite loci sequenced for analysis.
- Existing sample data for moose (Rosenblatt et al. 2022) and marten (Aylward et al. 2020) were used for these species.
- Data were filtered to remove null alleles using PLINK.

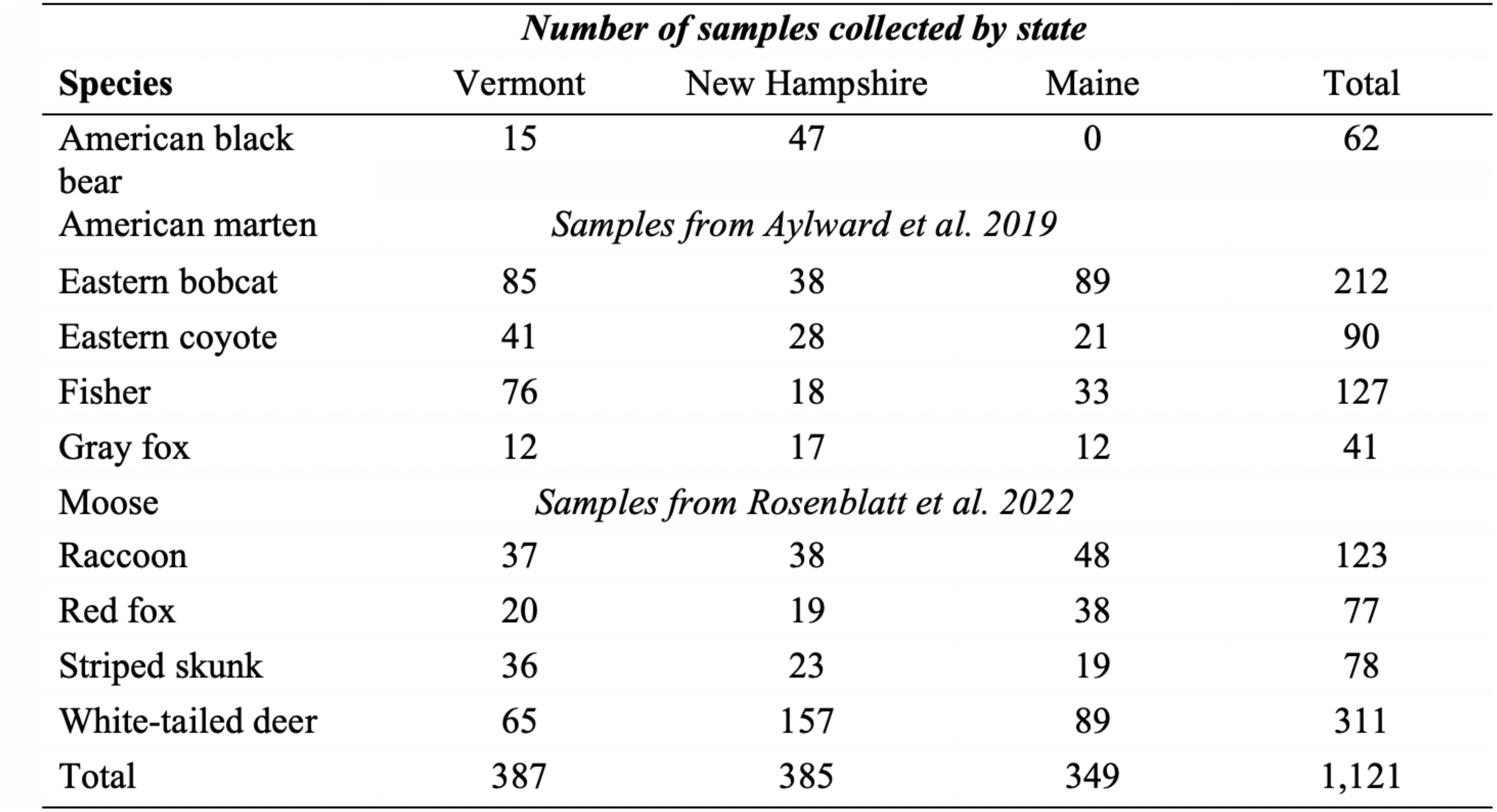
ResistanceGA analyses:

- ResistanceGA package (Peterman 2018) used to optimize categorical landcover surface (NALCMS) of 8 variables, individually for each species.

Graduate student Caitlin Drasher with 700 wildlife samples sent to the Mammalian Ecology and Conservation Unit at UC Davis for DNA extraction and sequencing.

Results

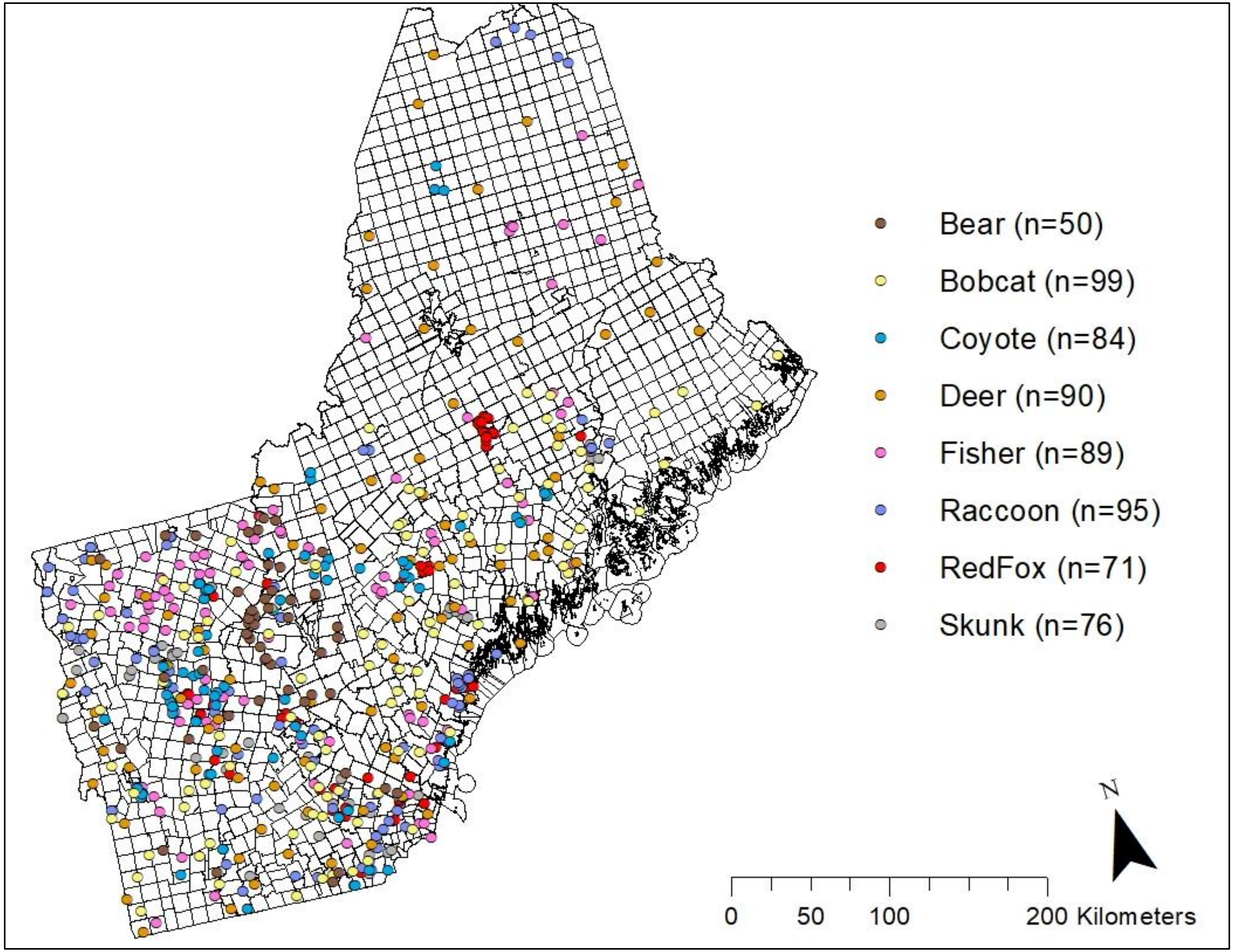




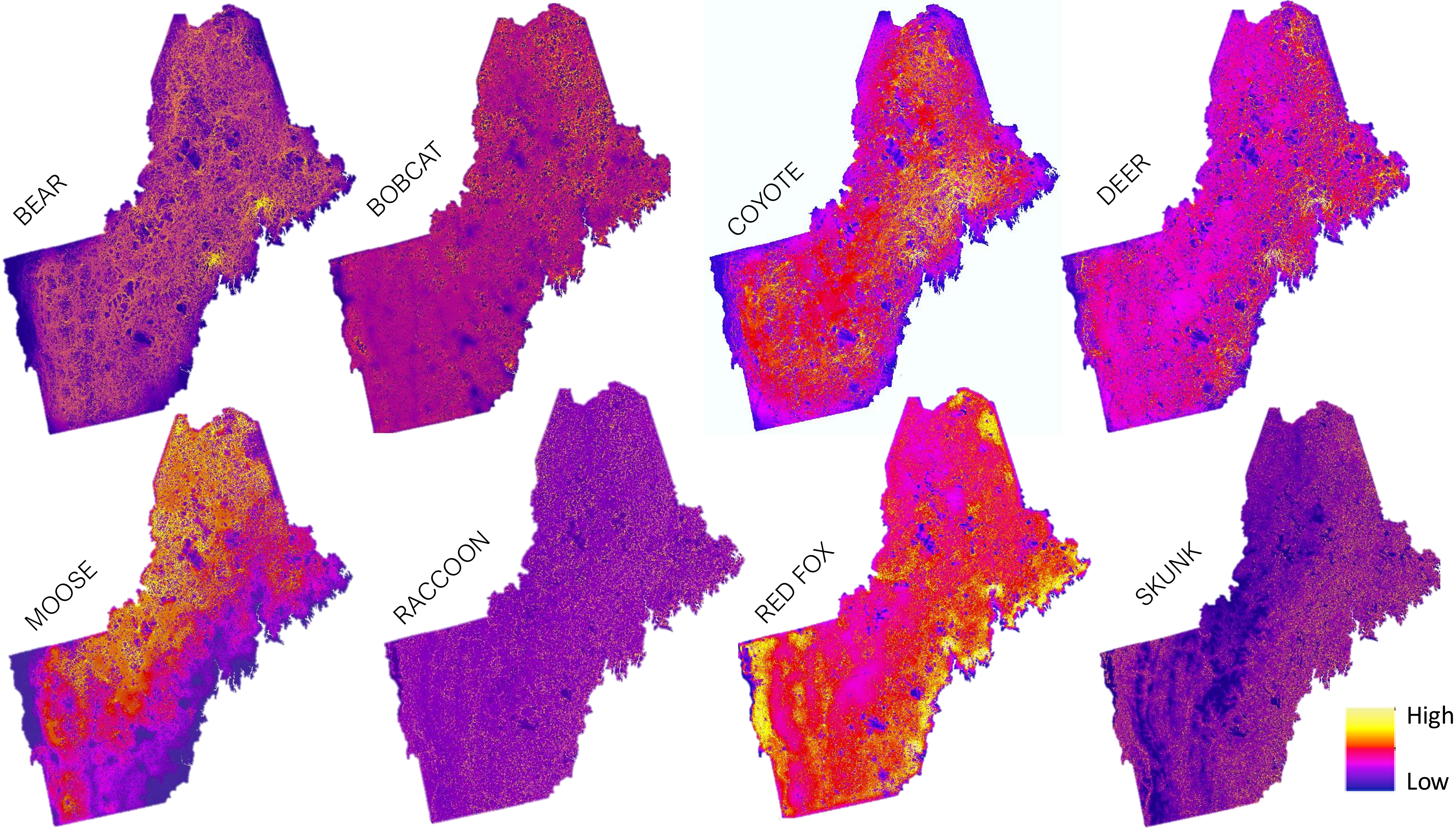
Number of samples collected by state

Species	Vermont	New Hampshire	Maine	Total
American black bear	15	47	0	62
American marten	*Samples from Aylward et al. 2019*			
Eastern bobcat	85	38	89	212
Eastern coyote	41	28	21	90
Fisher	76	18	33	127
Gray fox	12	17	12	41
Moose	*Samples from Rosenblatt et al. 2022*			
Raccoon	37	38	48	123
Red fox	20	19	38	77
Striped skunk	36	23	19	78
White-tailed deer	65	157	89	311
Total	387	385	349	1,121

Results



Total number of samples analyzed for landscape genetic analyses, after filtering problematic loci and individuals. Samples that maximized geographic distribution were selected for analysis.

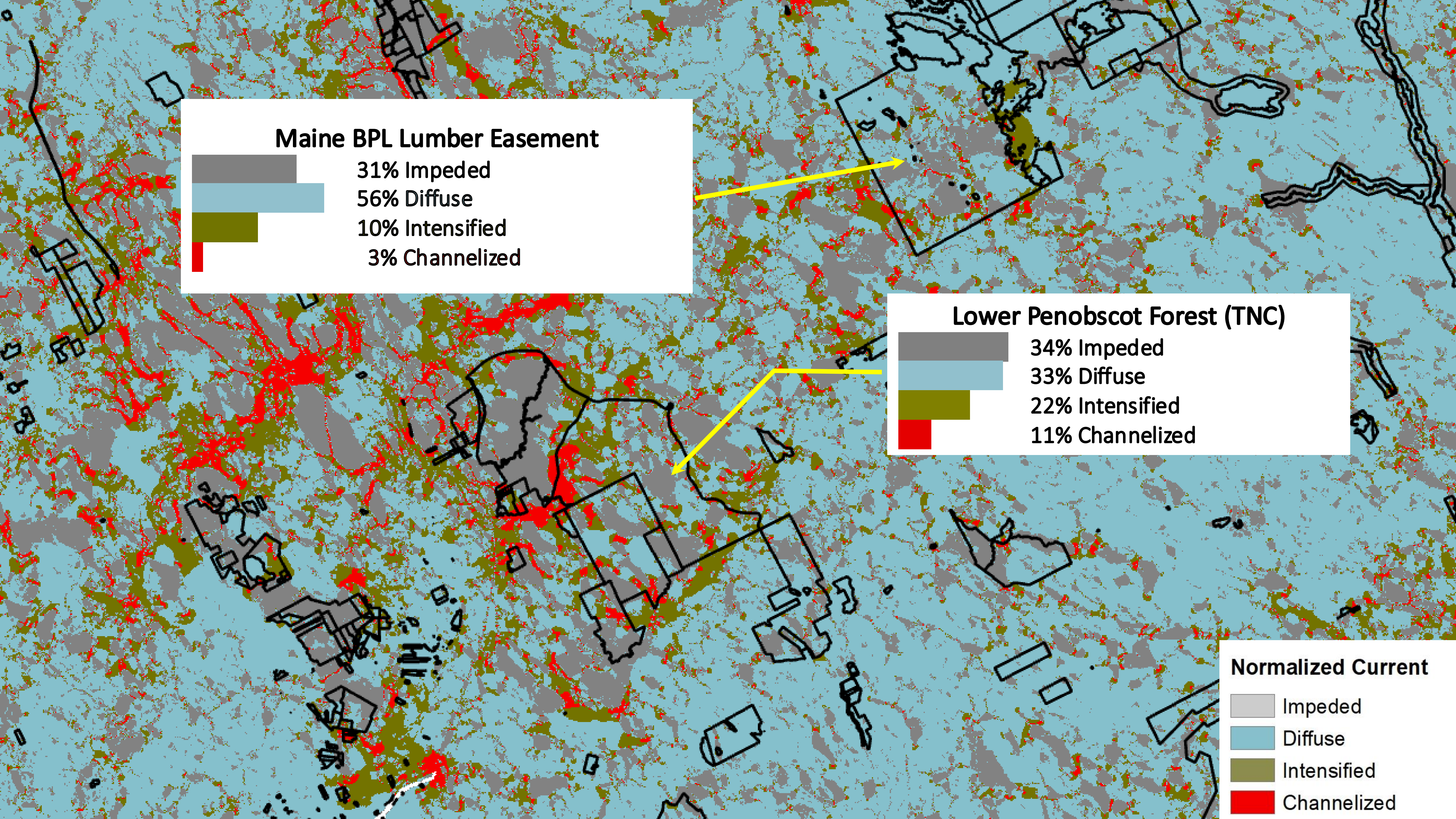

BEAR
BOBCAT
COYOTE
DEER
MOOSE
RACCOON
RED FOX
SKUNK
High
Low

Results

Classifications of current density: compare current to a 'null' model of flow potential (in 'perfect' landscape)

- **Channelized:** much greater current than expected
- **Intensified:** greater current than expected
- **Diffuse:** as much current as expected
- **Impeded:** less current than expected

$$\text{Normalized Current Density} = \frac{\text{Model Electrical Current Density}}{\text{Null Model Electrical Current Density}}$$



Maine BPL Lumber Easement

- 31% Impeded
- 56% Diffuse
- 10% Intensified
- 3% Channelized

Lower Penobscot Forest (TNC)

- 34% Impeded
- 33% Diffuse
- 22% Intensified
- 11% Channelized

Implications and Applications in the Northern Forest Region

- Genetically-optimized resistance surfaces describe the importance of different landcover variables for genetic connectivity in the northeastern US. Can be applied to various modeling applications (i.e., future scenarios of climate change) or to better understand what landcover types facilitate gene flow.
- Regional species-specific maps of gene flow can inform the management of species and habitats across the region to promote genetically connected and resilient populations.
- These models can help us quantify genetic connectivity for different species in areas of interest.

Continued work

- Update landscape genetic models to include additional covariates such as elevation/terrain ruggedness.
- Continue to use model results to inform USFS management objectives in the Green Mountain National Forest and within state-managed lands.
- Connectivity models will also be available publicly and to state & federal agency partners to inform species management objectives.

Thank you!

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