

# A system to forecast the demographic and genetic viability of salmonid fish across broad regions under changing climates

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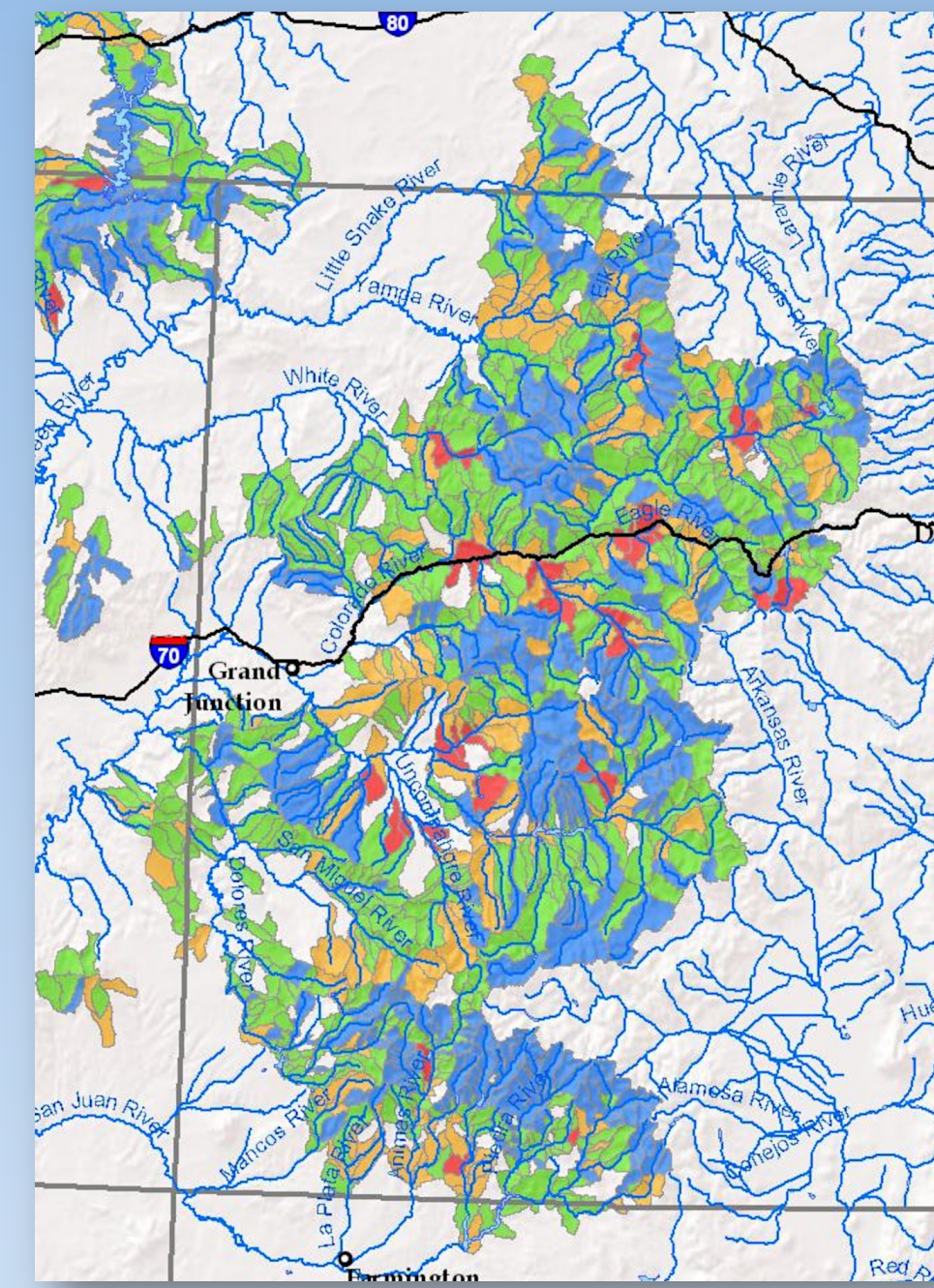
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## The Need: Data-Driven Conservation Planning

Government agencies and NGOs that manage land and wildlife regularly engage in conservation planning exercises to prioritize where to spend limited resources on preservation and restoration activities. These efforts generally rely on indirect indicators of conservation status of populations, usually derived from prior studies but rarely validated with empirical observations

The most fundamental information needed for conservation planning is whether a population will persist, and how this persistence may be affected by management. Population viability analysis (PVA) is the gold standard for producing this information, but traditionally has been limited to sites with long-term observation records. Our approach extends the use of PVA over broad regions.

End users of this system include the U.S. Fish and Wildlife Service, the US Forest Service, the Bureau of Land Management, various state agencies, and conservation NGOs such as Trout Unlimited.



Example of conservation planning: Trout Unlimited's "Conservation Success Index" for Colorado cutthroat trout. Colors indicate different levels of habitat suitability.

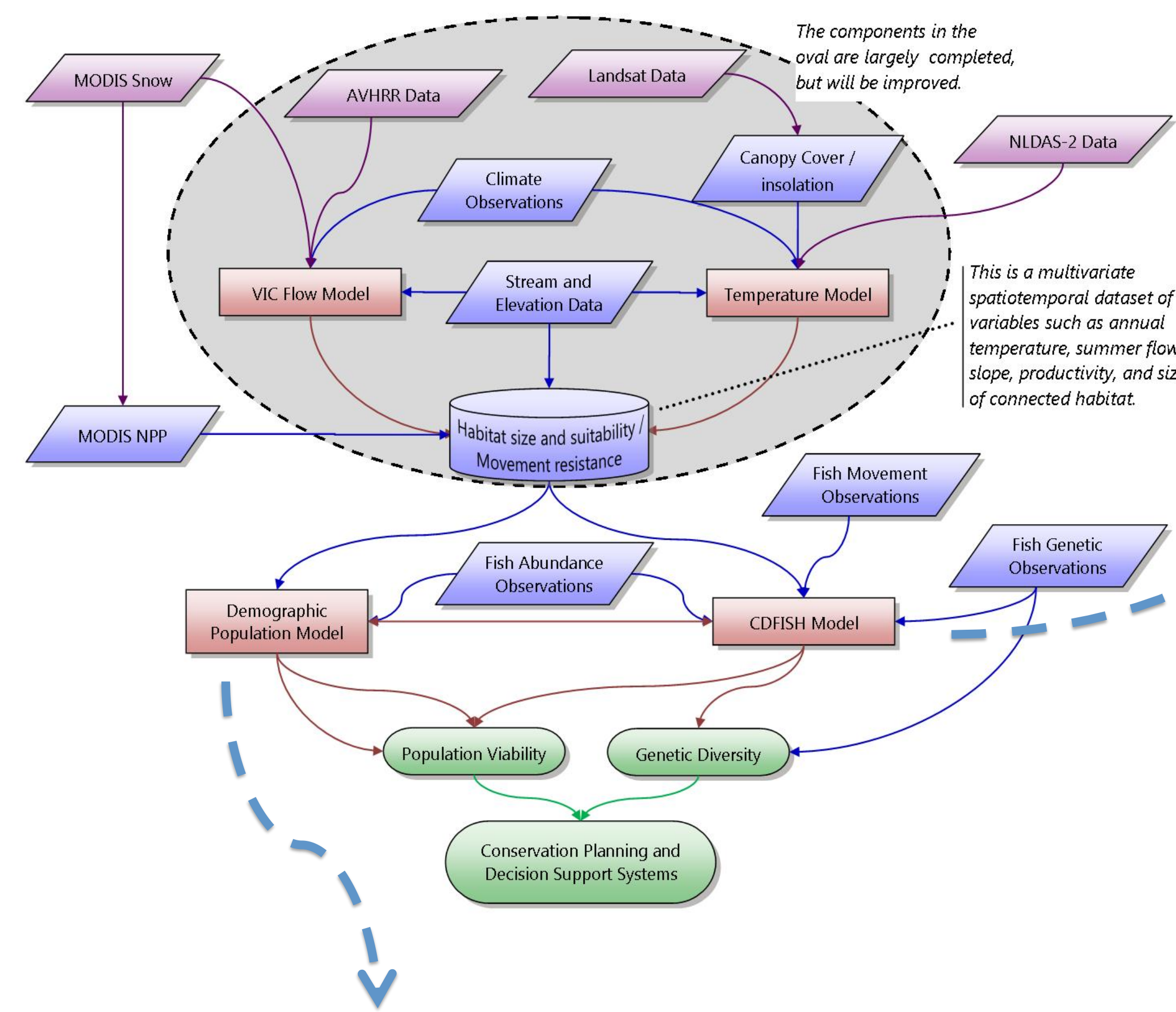
## Pilot Study: Lahontan Cutthroat Trout

The Lahontan cutthroat trout (LCT) is a federally protected subspecies of cutthroat trout that inhabits streams, rivers and lakes in Nevada. Despite its unique adaptations to its harsh desert environment, non-native fishes, stream fragmentation and habitat degradation have led to the decline of many populations. Only 8.6% of the historical stream habitat is currently occupied, and remaining populations are threatened by stream drying and fires (pictures, below), which could increase in frequency with a changing climate.



## Overview

This is an integrated methodology for predicting demographic and genetic population viability across broad scales under current and future climate conditions. The method is both data intensive and spatially extensive, marrying the previously separate methods of population modeling and species distribution modeling. Two complementary models are used: (1) a statistical demographic population model used for isolated and weakly connected populations, and (2) CDFISH, an individually-based model that follows the demographics and genetics of connected populations (metapopulations) through time. Remotely sensed imagery from NASA and other sources are used to extrapolate relationships observed in sampled areas to unstudied locations. This provides an empirically-driven foundation for conservation planning that has been heretofore unavailable.



## Statistical Demographic Population Viability Model

We have developed a new form of population viability analysis that uses covariates derived from satellite imagery and other sources to predict carrying capacity, growth rate, and temporal dynamics. The model is implemented in a Bayesian framework, which permits the use of different types of datasets and allows for readily interpolation and extrapolation to locations with limited or no data. It also provides realistic estimates of uncertainties.

$$N_{pt} = N_{pt-1} * \exp \left( r_p \left( 1 - \frac{N_{pt-1}}{K_p} \right) + E_{pt} \right)$$

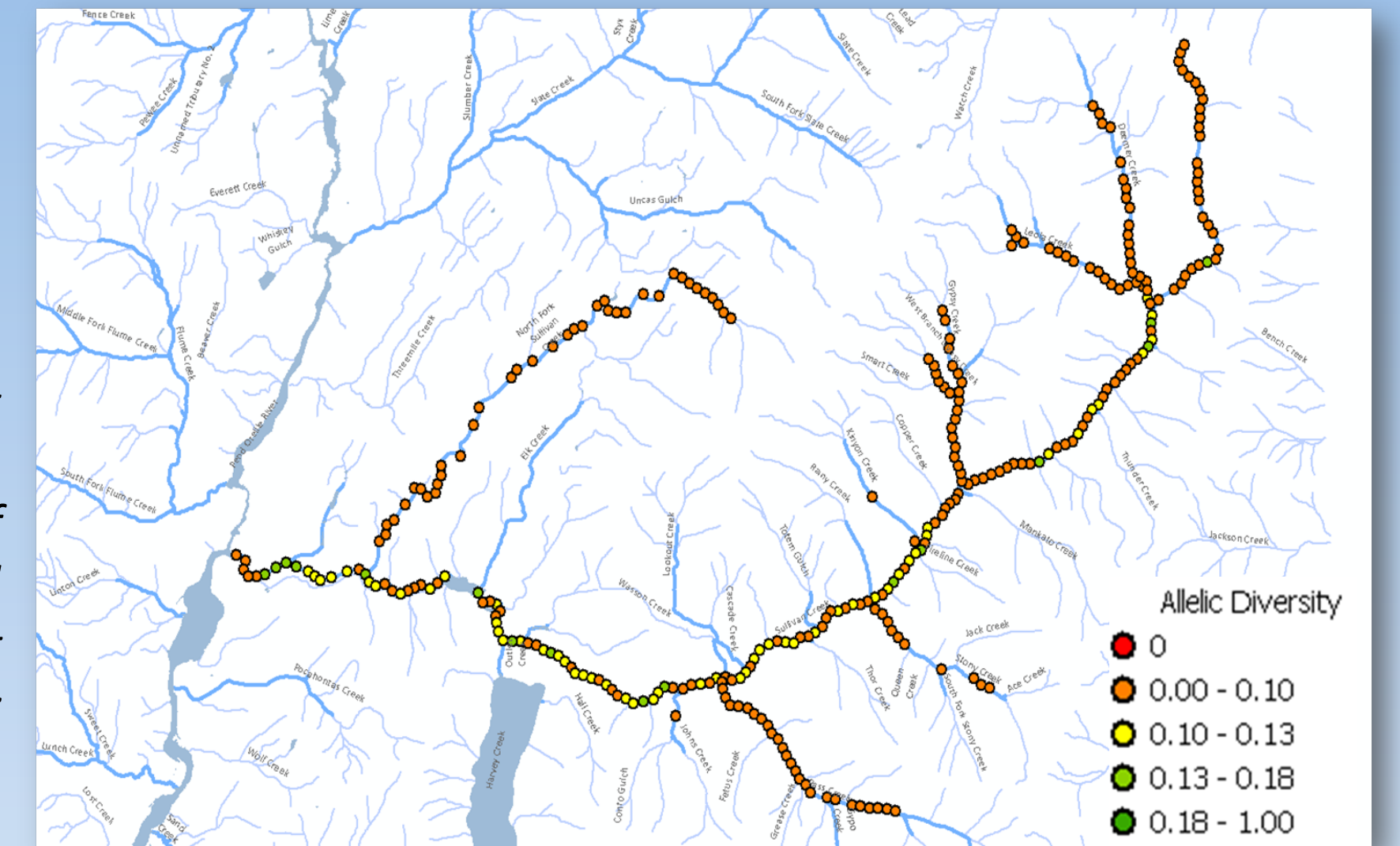
$$K_p = \alpha A_p Q_p + \varepsilon_{1p}(0, \sigma^2)$$

$$r_p = \beta_0 + \beta_1 Q_p + \varepsilon_{2p}(0, \sigma^2)$$

$$E_{pt} = \gamma_0 + \gamma_1 X_{pt} + \dots + \varepsilon_{3pt}(0, \sigma^2)$$

## CDFISH

CDFISH is a landscape genetics program to simulate gene flow in complex riverscapes under a wide range of environmental scenarios for aquatic organisms. The spatially-explicit program implements individual-based population modeling with Mendelian inheritance and a k-allele mutation model on a stream network with an underlying resistance surface (e.g. partial barriers). The program simulates stochastic changes in subpopulations (demography with age structure) and genotype frequencies through time as functions of individual-based movement, reproduction, mortality, and dispersal through migration and straying on a continuous riverscape. Estimates of carrying capacity and other key demographic inputs are derived from the statistical PVA model.

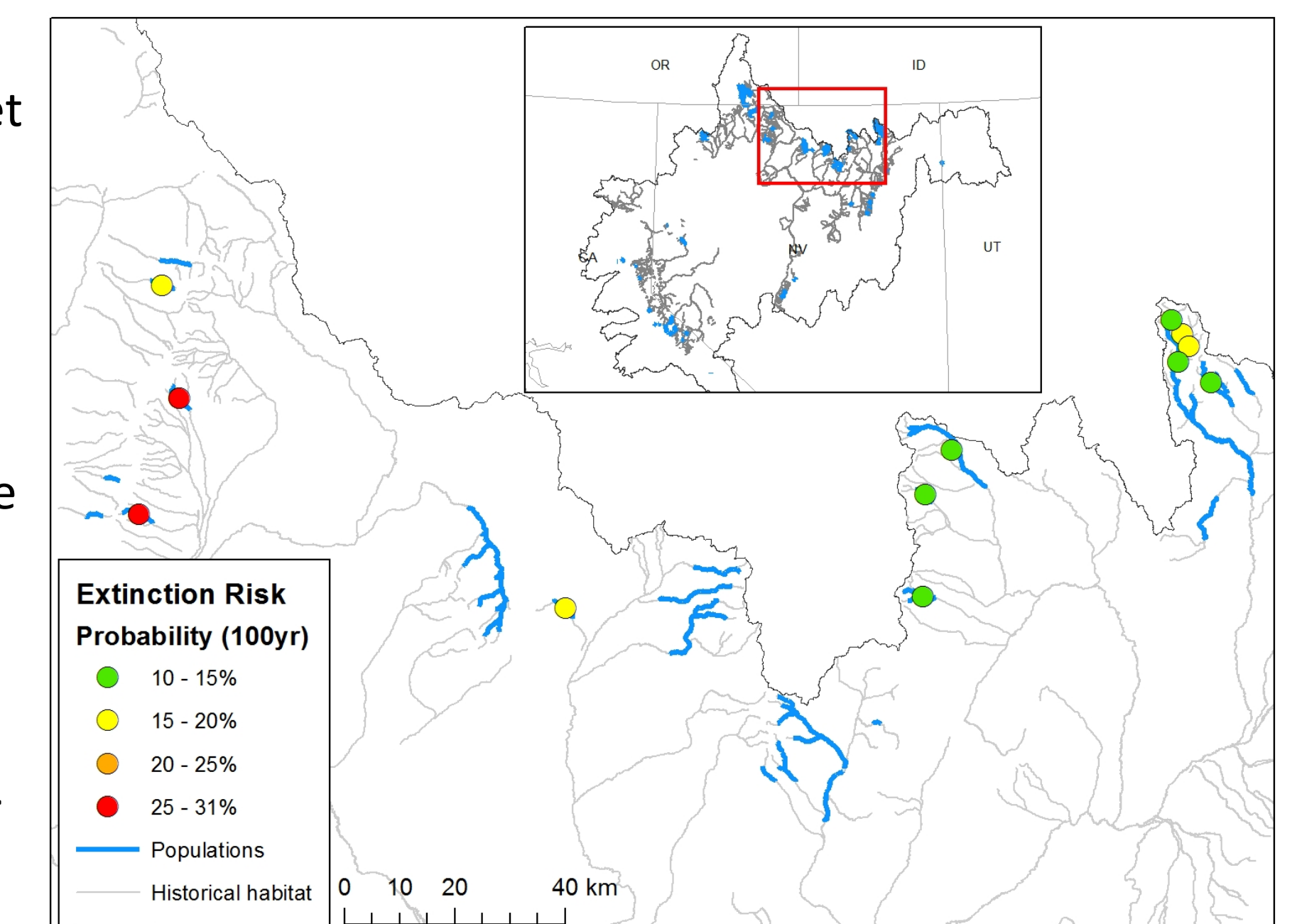


Example output from CDFISH: allelic diversity of semi-isolated cutthroat trout population after 50-year simulation

## Pilot Study Preliminary Results

As a test of the basic methods, we conducted a preliminary analysis of viability of 12 populations of Lahontan cutthroat trout for which repeat samples were available. 100-year extinction probabilities ranged from 10% to 31%. We found (unsurprisingly) that carrying capacity was a function of total stream length, and that annual abundance was negatively correlated with temperature.

We are currently expanding the Lahontan fish dataset and constructing a new stream temperature model using spatial statistical methods and NASA imagery. At the same time we are working with partners to assemble data for additional species across a much larger spatial domain.



## Acknowledgments

Primary funding for this project is provided by NASA grant NNX14AC91G. We thank Nevada Department of Wildlife for sharing some of the data used in the pilot analysis.