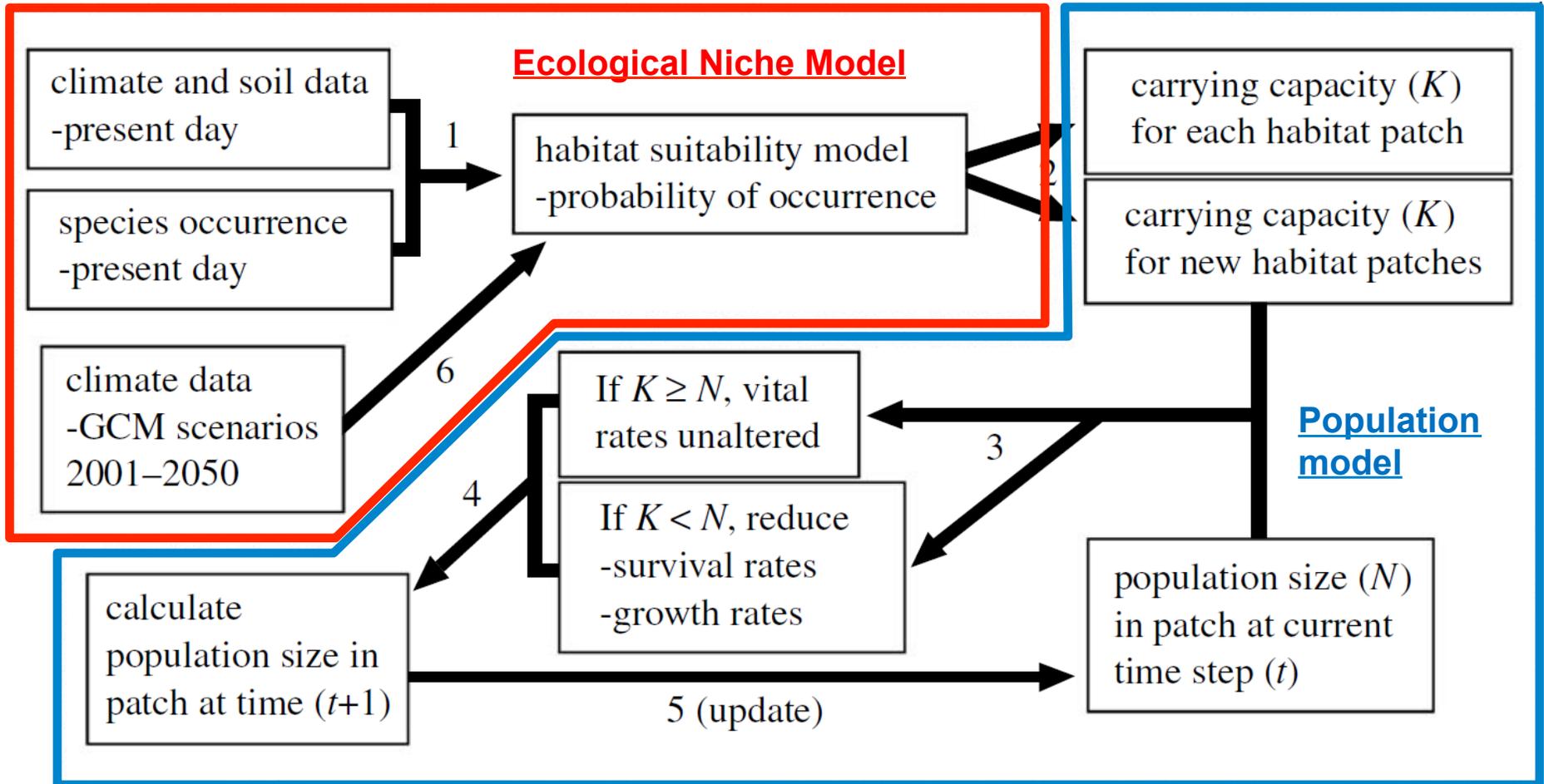


# Integrating Remotely Sensed Data and Ecological Models to Assess Species' Extinction Risks under Climate Change

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# Linking Ecological Niche Models and Demographic Models



Keith *et al.* 2008 *Biology Letters*

Brook *et al.* 2009 *Biology Letters*

Fordham *et al.* 2012 *Global Change Biology*

## Species occurrence data

- 40 endemic amphibian and reptile species, endemic to U.S.
- Variety of life histories
- Data from NatureServe

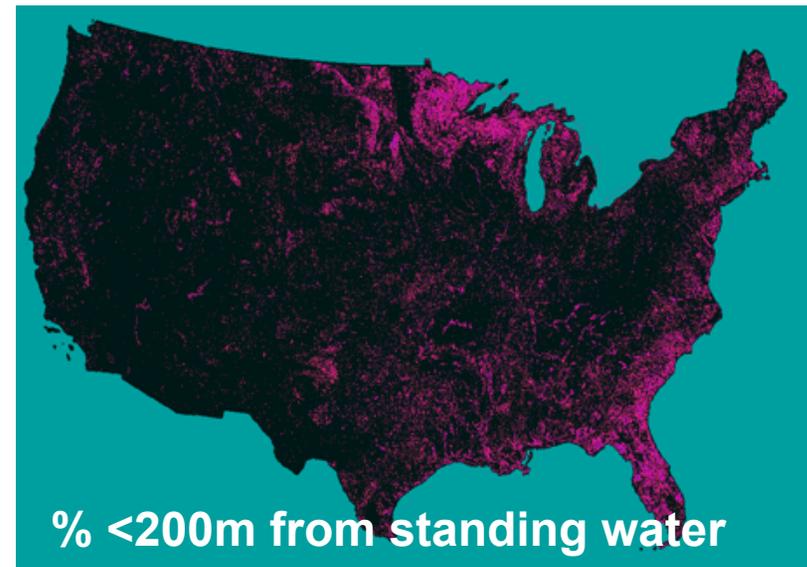


## Climate data and future scenarios

- Baseline are monthly 800m, 1971-2000 normals, PRISM
- Use MAGICC/SCENGEN to emulate multiple GCMs for two emissions scenarios (IPCC 5<sup>th</sup> AR) and annual time slices to 2100
- Generated 7 bioclimate variables relevant to physiology and life history of the species

## “Static” predictor variables, multiple RS sources

- Land cover: National Land Cover Database.
- Land surface form: National Elevation Dataset
- Proximity to water: National Hydrography Dataset



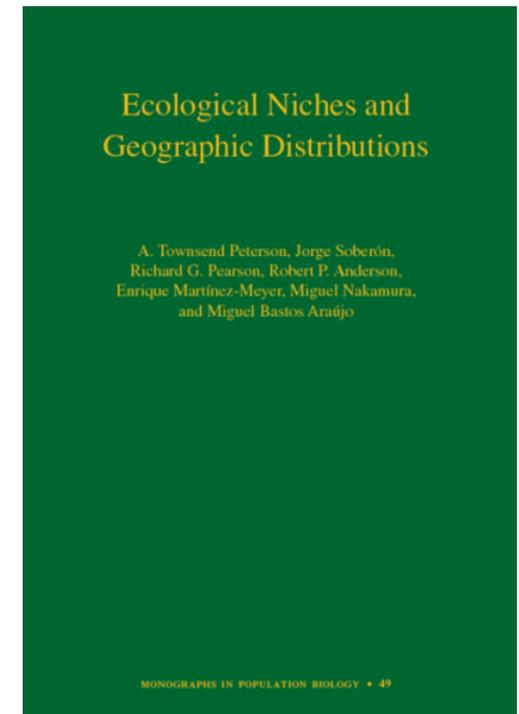
Following: Stanton *et al.* 2012 *Methods in Ecology and Evolution*

## Habitat suitability models (ecological niche models)

- Maxent, parameterized for each species, inc. variable selection
- Final models are an average across 50 replicates, each with different random selection of points from EOs.

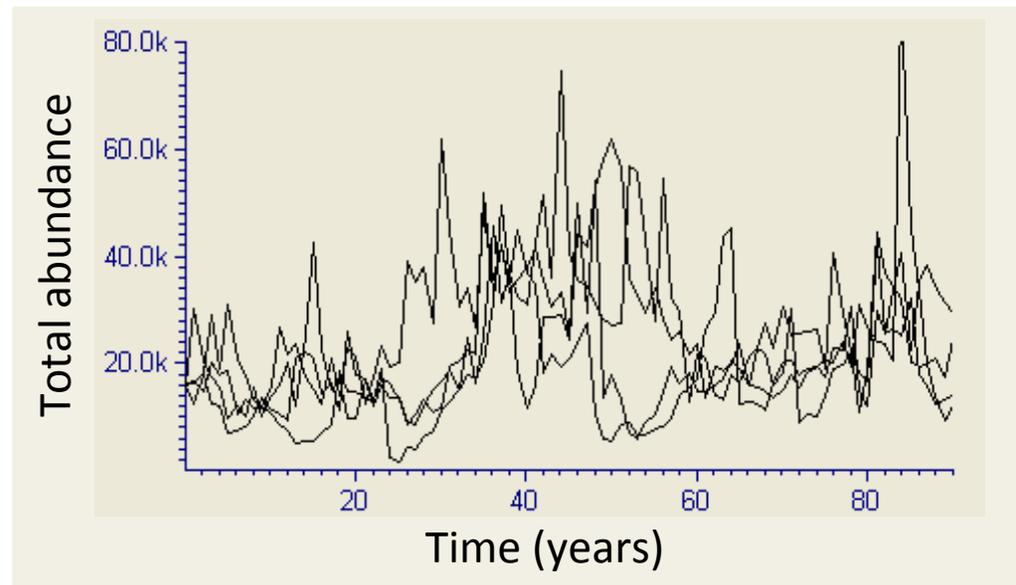
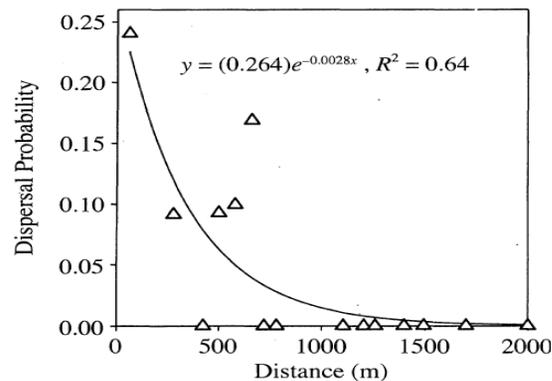
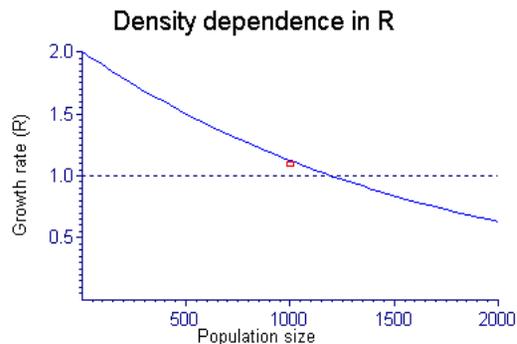
Peterson, A.T., Soberón, J., Pearson, R.G., Anderson, R.P., Martínez-Meyer, E., Nakamura, M. and M.B. Araújo. 2011

Monographs in Population Biology,  
Princeton University Press.



## Demographic models

- Species grouped into 6 life history types, e.g., turtle, snake, lizard
- Generic models for each type, parameters including density-dependent growth rate, mean/max dispersal distance, fecundity



## Simulations: Sensitivity Analysis

- Nested computations:

Life history types (6 generic life history types)

Species (40 species, with species-specific spatial structures, each av. from 50 replicates)

Scenarios (3 scenarios of future climate change, including no change)

Demographic Models (~50 parameterizations selected from the parameter space)

Replications (1,000 iterations to model stochasticity and estimate risks)

Time steps (110 time steps from 1990 to 2100)

**Total of ~1.3 Billion time steps!**

## Endpoints

E.g.,

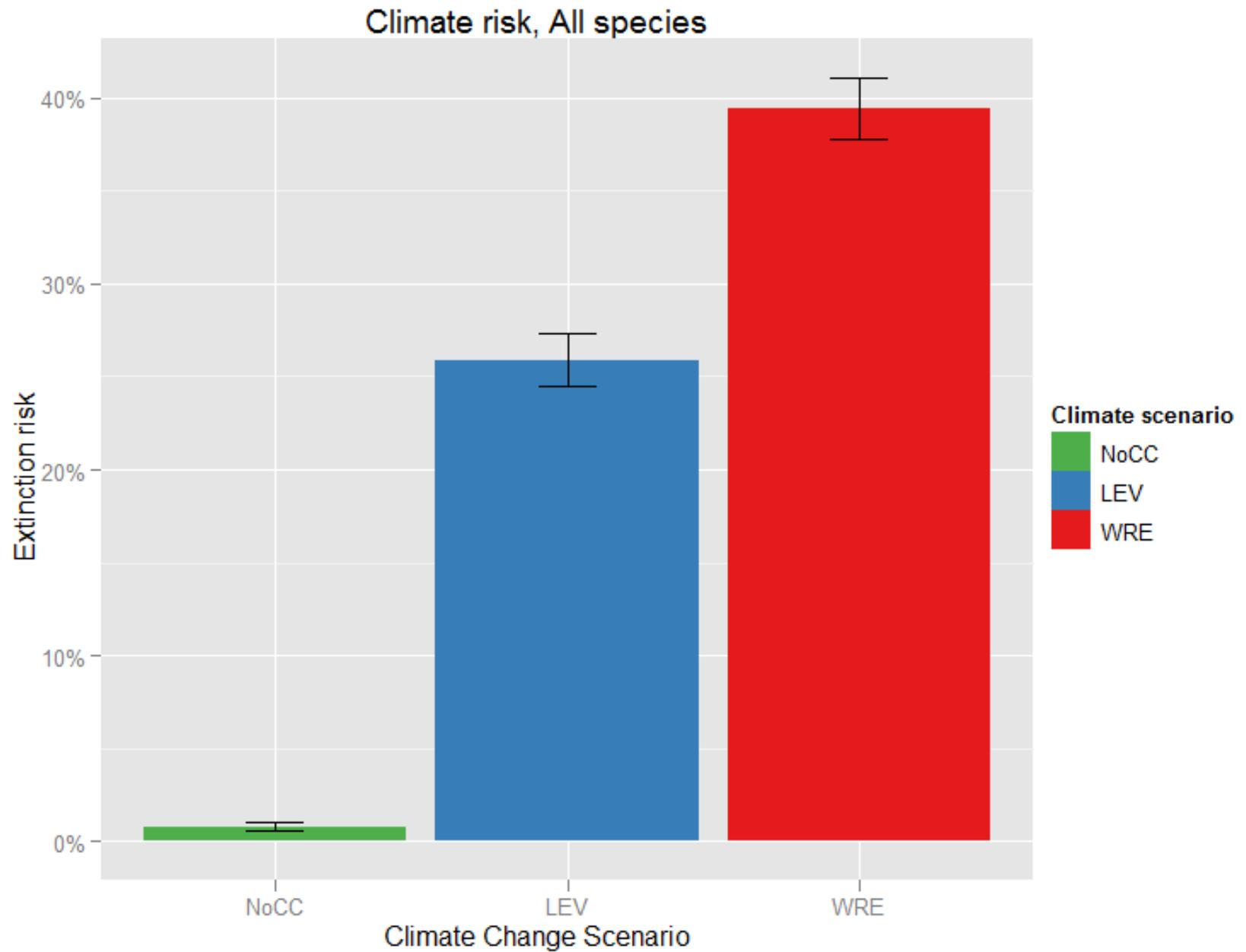
- Expected minimum abundance
- Risk of Extinction
- Risk of 50% decline
- Time to decline to threshold # individuals
- Percent change in total metapop size

## Explanatory variables

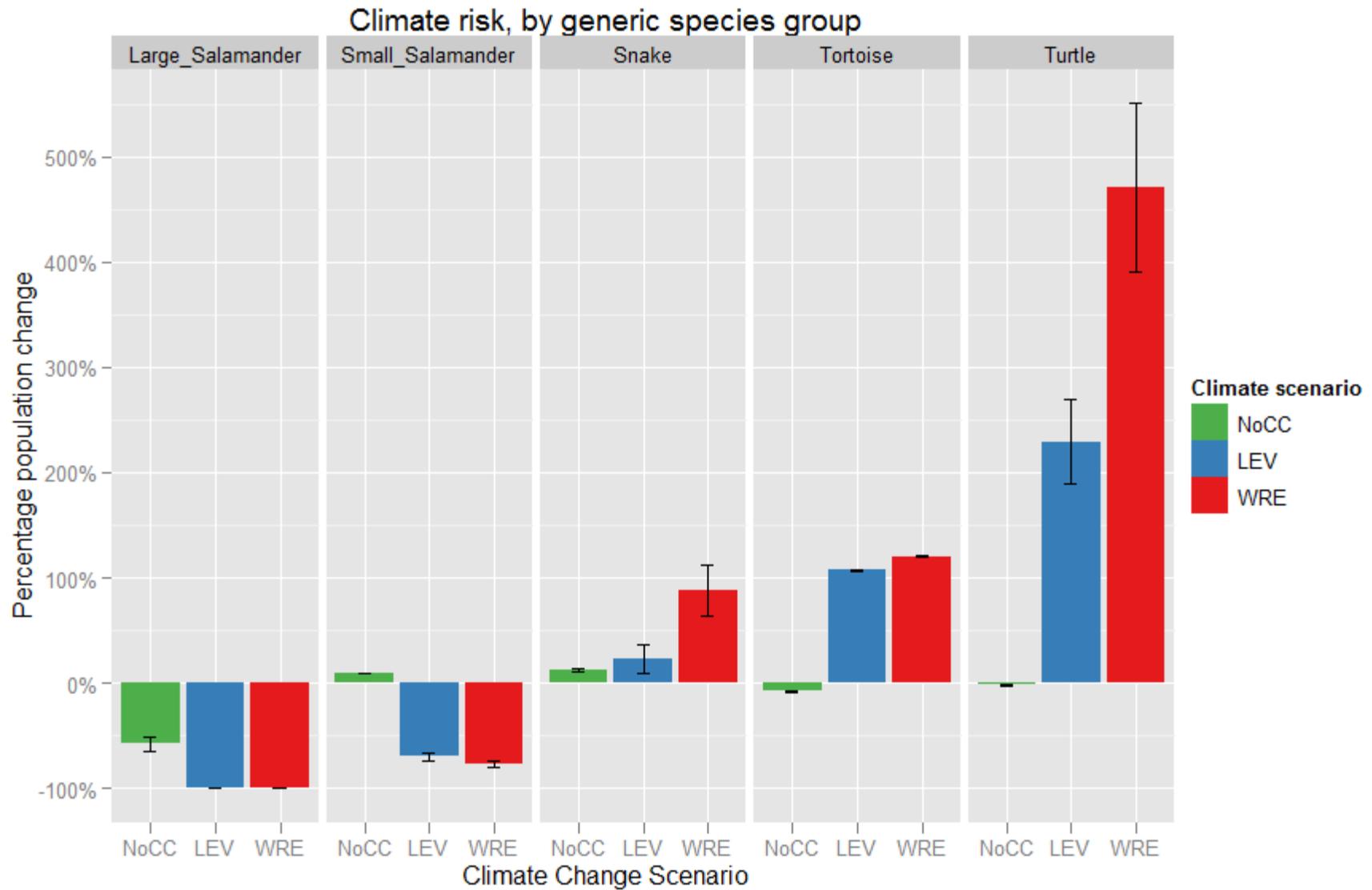
E.g.,

- Demographic (generation time)
- Variability (CV of survival rates)
- Spatial isolation (dist. between pops)
- Area and shape (mean patch area)

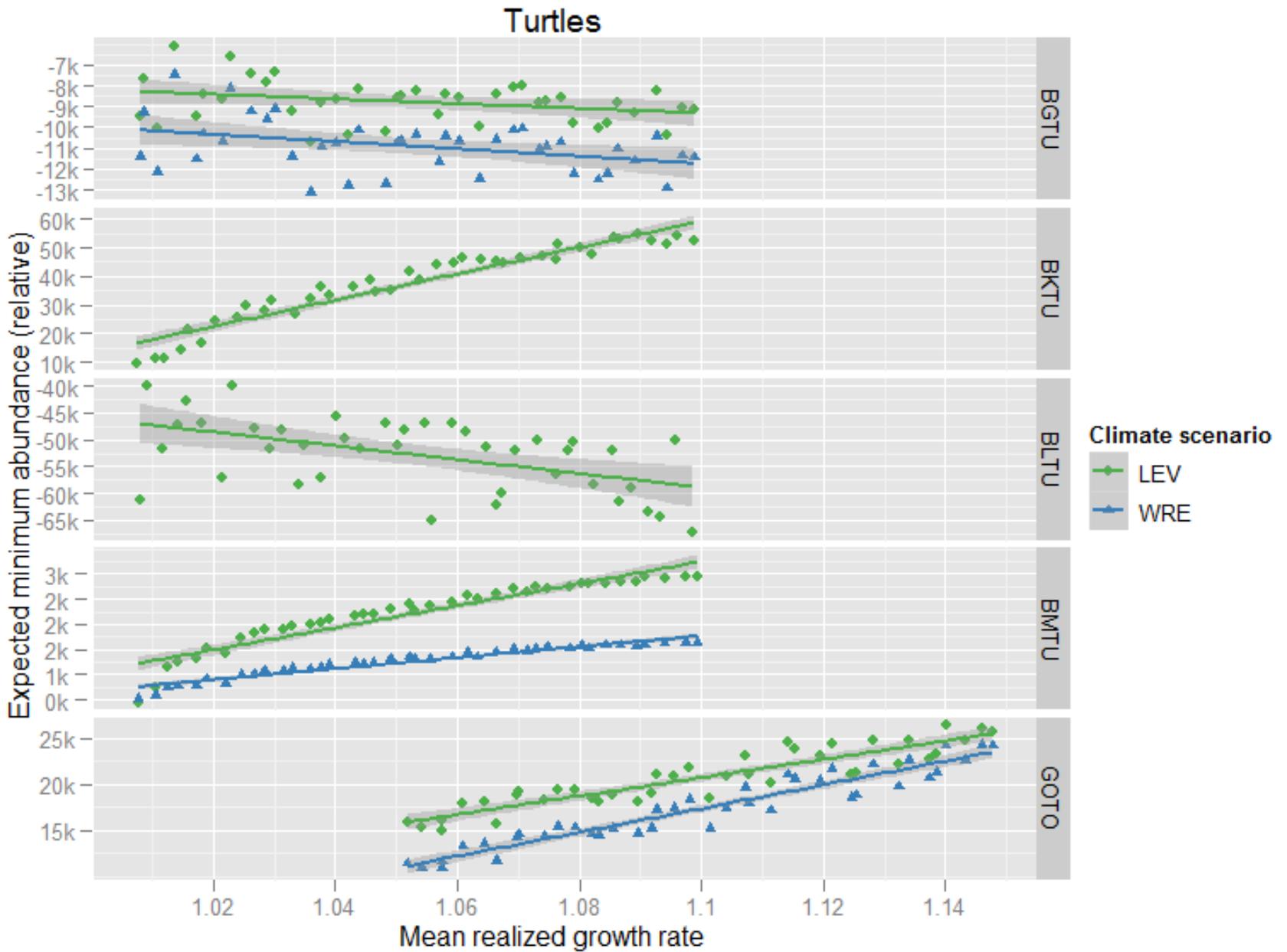
# Preliminary Results



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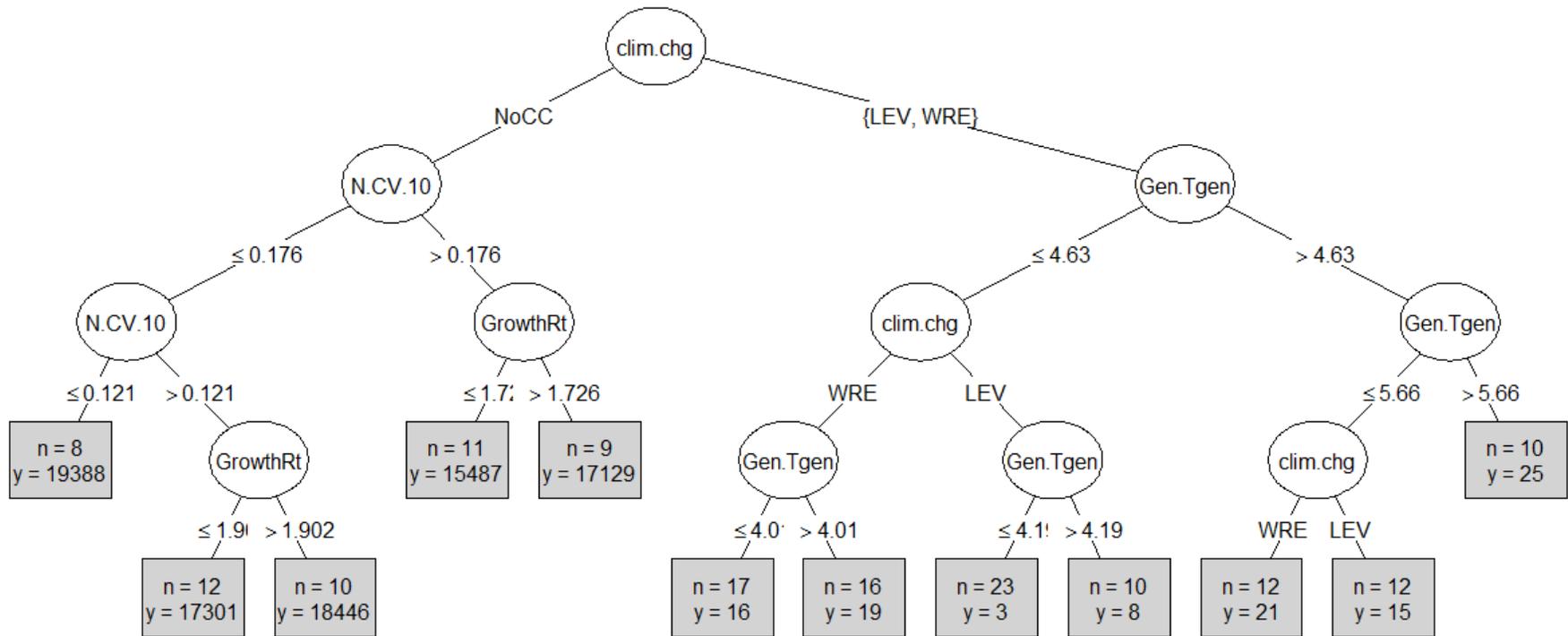


# Preliminary Results



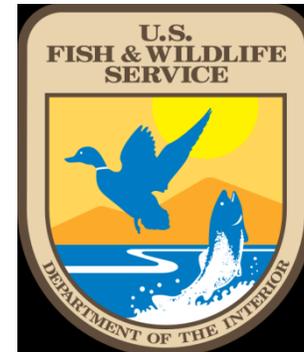
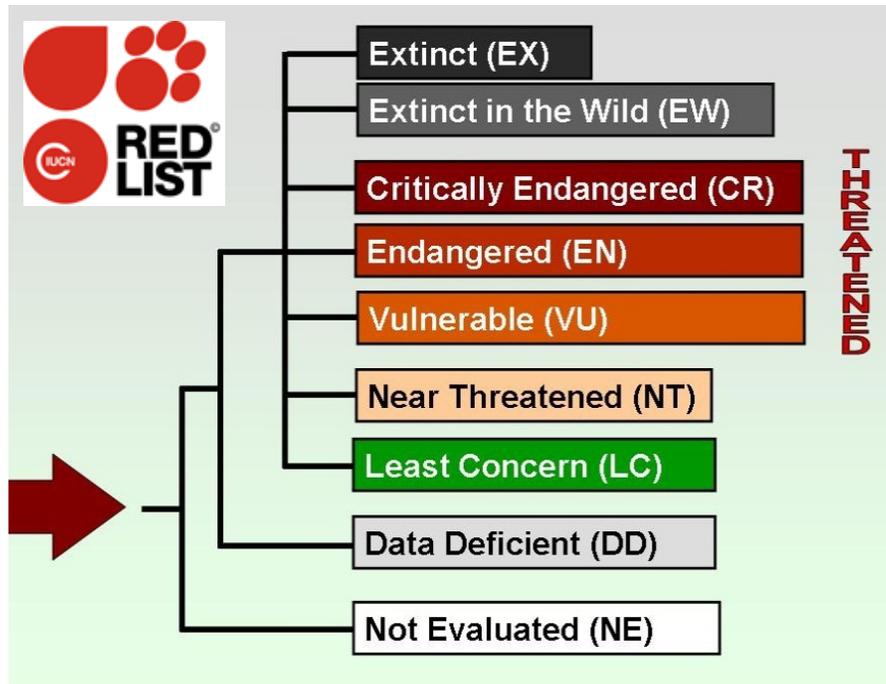
# Preliminary Results: Boosted Regression Trees

Expected minimum abundance, FPSN



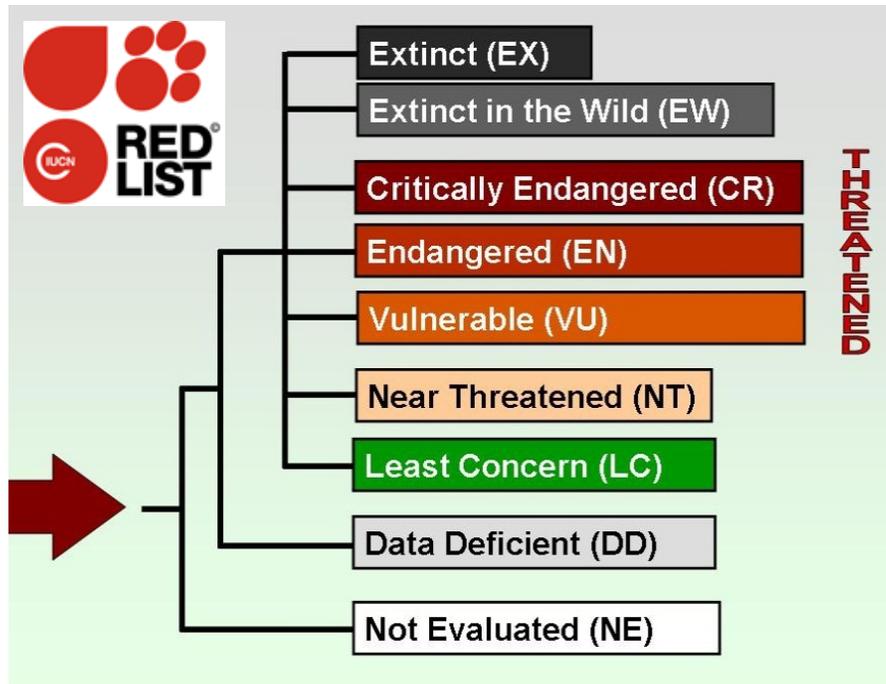
## Ultimate Goal:

- Contribute to the development of guidelines for incorporating climate change in assessments of conservation status



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### *Hypothetical example:*

- 1) Dispersal distance is less than X, AND expected increase in isolation due to shifting climate space
- OR 2)** Habitat loss due to climate change is expected to be more than Y % in the next 50 years
- AND** at least 2 of the following 3 are true:
- (i) population is currently declining;
  - (ii) current distribution is severely fragmented;
  - (iii) taxon is a habitat specialist, **or** has a current Area of Occupancy of less than Z km<sup>2</sup>.

## Acknowledgements

We thank Barry Brook, David Keith, Steven Phillips, Bruce Young, Jason McNees, and NatureServe state member programs for providing data

Funded by

