

**Introduction:** Anthropogenic mass extinction is happening<sup>1,2</sup>. Even if the human race radically overhauls worldwide environmental policy, recovery will take generations. Debate rages over how much extinction is inevitable<sup>3-5</sup>, but the problem's urgency is clear. I am interested in what we are likely to lose and how conservation efforts can be focused for maximum impact.

Extinction risk is not randomly distributed with respect to taxonomy.<sup>6</sup> As we race to preserve biodiversity, Phylogenetic Diversity (PD) has emerged as a key metric in biodiversity and conservation research. Synthesis of conservation and phylogenetics is still hampered by critical knowledge gaps, including: 1) incomplete or poorly resolved phylogenies, and 2) assessments of extinction risk that neglect ecological context.<sup>7</sup> I propose to correct the former, and address the latter by studying extinction risk through the lens of a complete phylogeny and an explicit accounting of community structure.

At a macroevolutionary scale, community assembly is driven by a continuum of evolutionary processes. At one end, early adaptive radiation (EAR) and diversification shape community structure at a global scale. At the other, repeated patterns of opportunistic colonization and local *in situ* diversification (regional assembly or RA) shape communities at a regional scale.<sup>8</sup> Building on Webb et.al.'s work,<sup>9</sup> explicitly evolutionary methods now quantify phylogenetic community structure and use phylogeny to estimate where community assembly processes fall on the continuum from EAR to RA.<sup>8</sup> At the extremes of this continuum, closely related species' degree of sympatry should have important implications for extinction risk. In particular, my work will ask: **are RA-evolved species more likely to be vulnerable because of the recency of their niche specialization and co-occurrence of closely-related competitors?**

I plan to investigate this question using two deeply divergent groups of diurnal raptors (Accipitriformes and Falconiformes). These typically large apex predators are globally distributed (except in Antarctica). Wide distribution, convergent trait evolution, variance in abundance and natural history, and diversity of local communities make raptors ideal for examining patterns in extinction vulnerability. They will provide two independent estimates of evolution and trait conservation's impact on community assembly at a global scale, and the strongest predictors of extinction risk. My interrelated **Research Questions** are: **1) What is the phylogenetic tempo and pattern of evolution in raptors? 2) Are patterns of community assembly in raptors consistent with patterns of morphological evolution? 3) Is extinction risk concentrated in phylogenetically and/or morphologically similar species?** These guide my **Research Aims**:

**1) Generate a species-level phylogeny of raptors.** There are 333 species of Accipitriformes and Falconiformes. The most complete phylogeny to date is that of Burleigh et.al.<sup>10</sup> My advisor and co-investigators have a recently funded NSF grant to estimate a phylogeny of all birds based on Ultra-Conserved Element sequence data, enabling inference of the most comprehensive phylogenies of these clades to date and providing research opportunities for minority undergraduates. I will use the resulting phylogeny in collaborative K-12 outreach programs at the Gabbert Raptor Center (GRC) and Bell Museum of Natural History (Bell; see Broader Impacts).

**2) Generate a global map of raptor community phylogenetic dispersion.** With a complete phylogeny and detailed spatial data on breeding ranges I will create a global map of raptor community composition in terms of species richness, turnover, and phylogenetic dispersion<sup>9</sup> (a powerful tool for my GRC and Bell K-12 programs). I will estimate regional patterns of community phylogenetic dispersion by comparing local community composition to species pools

selected by a) maximum radius and b) continent. Under a pure EAR scenario, I expect relatively uniform overdispersion of raptor communities at local and global scales. If the RA model has had some impact on raptor evolution, I expect hotspots of underdispersion where local radiations of raptors have diversified into communities at smaller spatial scales.

**3) Reconstruct the evolutionary history of raptor morphology.** From museum specimens, I will measure relevant morphological traits (e.g. body mass, wing, talons) as a proxy for extinction-risk-related natural history traits.<sup>11</sup> Museum trips will involve undergraduates via the University of Minnesota's Undergraduate Research Opportunities Program (UROP). Analysis using phylogenetic principal components analysis (PCA)<sup>12</sup> will establish major axes of differentiation in raptors. Using maximum likelihood methods I will determine the best-fit models of evolution (as implemented in *GEIGER*<sup>13</sup>) and local rate shifts across the tree (as implemented in BAMM). Under a pure EAR scenario, I expect early burst or directional trend models to fit best across the entire radiation, with little evidence for evolutionary bursts in specific subclades. Under an RA scenario, any early burst should be overlain by subsequent radiations correlating with intercontinental dispersal events. Resulting estimates of regional morphological variation patterns will elucidate the relationship between phylogenetic and morphological diversification, and illustrate convergent evolution and adaptive radiation in my GRC and Bell programs.

**4) Compare phylogenetic and morphological dispersion data to IUCN extinction risk classifications.** Finally, I will determine if phylogenetic and morphological patterns correlate with IUCN risk classifications, using standard phylogenetic generalized linear model approaches.<sup>14</sup> If, as I expect, raptor communities exist in a continuum from low to high morphological diversity and from low to high phylogenetic diversity, I hypothesize that to the degree that species are morphologically and phylogenetically underdispersed, extinction risk will be concentrated in certain clades and morphospaces. Phylogenetic or morphologic data may be virtually the only thing we know about certain data deficient species and clustering of risk may provide critical data to advocate for their protection. These results will help me communicate the urgency of conservation to a diversity of audiences from K-12 students to policy makers.

Integrating phylogenetics, community assembly, and morphological diversification will provide a framework for conducting global assessments of extinction risk in a large taxonomic group, including data deficient taxa whose risk is otherwise difficult to assess. This work will have broad applications to elucidate where conservation work could have maximum impact.

**Broader Impacts:** In addition to training undergraduates in specimen-based research, I will leverage my existing relationships with the Bell and GRC to bring my work into marginalized communities, especially lower income Native, rural, and inner-city schools. Capitalizing on GRC's and Bell's existing networks in Native communities and plans to begin offering digital programs, I will conduct virtual lab tours and culturally sensitive interpretive K-12 programs. My enthusiasm for raptors, my existing teaching skills, and my love of children will open a dialog about the value of scientific inquiry, and empower children in underfunded Native, rural, and urban schools with scientific methods, language, and perspectives.

1. Ceballos et.al. *Proc. Natl. Acad. Sci.* (2017). 2. Barnosky et.al. *Nature* (2011). 3. He & Hubbell. *Nature* (2011). 4. Pereira et.al. *Nature* (2012). 5. Urban. *Science* (2015). 6. Bennett et.al. *Phylogeny and Conservation Ch.8* (2005). 7. Forest et.al. *Philos. Trans. R. Soc. B Biol. Sci.* (2015). 8. Cavender-Bares et.al. *Ecol. Lett.* (2009). 9. Webb et.al. *Annu. Rev. Ecol. Syst.* (2002). 10. Burleigh et.al. *Mol. Phylogenet. Evol.* (2015). 11. Gamauf et.al. *Auk* (1998). 12. Revell. *Evolution* (2009). 13. Harmon et.al. *Bioinformatics* (2008). 14. Hadfield. *J. Stat. Softw.* (2010).