Efforts to prioritize conservation areas have typically used species richness to identify hotspots of biodiversity. Although this is a very valuable and necessary step in conservation, species richness only represents a small part of biodiversity. It has long been recognized that the use of species richness alone may fail to capture essential evolutionary processes that underlie and maintain diversity. In the face of climate change, the biodiversity hotspots of today are unlikely to be the hotspots of tomorrow, and it will be difficult or impossible to predict every effect of climate change on natural populations. To avoid extinction, populations may either move to more favorable habitat, or adapt to the new conditions. Unfortunately, with increasing habitat fragmentation, dispersal to new areas is severely limited. It is therefore important to identify areas for protection that not only harbor high species richness, but that also maximize the potential for species to adapt to the changing habitat conditions. Previous studies have shown that adaptive responses can be quick, but heavily rely on the genetic variation available in a population, termed standing genetic variation. In particular the standing genetic variation that is related to environmental conditions, and may therefore be the result of natural selection, is crucial to maximize a species adaptive potential. The significance of the conservation of genetic variation is reflected in policy documents identifying focal areas of conservation needs. For instance, the Convention on Biological Diversity and Europe’s Natura 2000 network specifically include genetic diversity as an essential part of natural ecosystems to be conserved. However, the use of genetic variation in conservation planning has long been stalled by limitations in molecular genetic analyses and the lack of sophisticated modeling approaches to map these measures of biodiversity. Yet, such an integrative approach is now made possible by recent advances in molecular genetics and modeling approaches, and the availability of climate and remote sensing variables that characterize the environment at high resolutions.

With collaborators I have developed a conceptual framework of how intraspecific genetic variation can be integrated with traditionally used measures of biodiversity to improve reserve design and give species the best possible chance for long-term persistence (Fig. 1). We tested this framework in Ecuador and found that the integration of genetic variation is necessary and possible. In the current ‘ProtectingBioFaCCts’ project I sought to further test the general utility of this framework with respect to different areas in the world, harboring a variety of different landscapes and habitats, diverse levels of human disturbance and at small to large scales. I focused on Eastern Europe and Central Africa, where -with collaborators across Europe, Africa, and the US- I collected genetic and morphological data of 11-13 species each, ranging from plants to invertebrates and vertebrates. I used newly developed spatial modeling techniques to map intraspecific variation and identify areas where this variation can be protected most efficiently and effectively.

Two main questions needed to be addressed. First, do current reserves (based on species richness or political motives) represent intraspecific variation sufficiently well? It is unlikely that the spatial configuration of evolutionary processes that have resulted in speciation remains the same today, and species richness is thus improbable to capture relevant intraspecific variation. Second, to what extent do species from taxonomically different groups show the largest amount of variation in the same areas? Because it is not feasible to gather data for all species present in a region under consideration for conservation, reserve design must rely on a limited subset of species that should ideally be representative of the entire community. To address these questions, I focused on the following objectives:

I. Measure morphological characteristics and genetically type 10-15 common species each in Romania and Bulgaria, and West-Central Africa (Cameroon, Equatorial Guinea, Gabon).
II. Map the spatial patterns of intraspecific variation in these regions.
III. Prioritize areas for conservation using intraspecific variation versus species richness.
IV. Measure the effectiveness of intraspecific variation in one species as a surrogate for the broader ecological community.
V. Compare the overlap in reserves based on either intraspecific variation or species richness.
VI. Compare the utility of coding versus non-coding genetic markers.

To do so, thousands of individual plants and animals have been sampled and genetically typed. Results suggest that the framework is useful for conservation planning in a variety of landscape types and at medium scales and resolutions. At these scales and resolutions, important areas for conservation broadly coincide among species. The use of species richness alone did not sufficiently represent intraspecific genetic variation, stressing the importance of explicitly taking into account genetic data into conservation prioritization. Areas important to protect were identified, highlighting that within Romania and Bulgaria, the southern slopes of the Carpathian Mountains are insufficiently protected by existing and planned Natura 2000 sites. To further improve the applicability of the framework, future studies should pay particular attention to sampling design, focusing on initial broad scale, low-density sampling, followed by high-density sampling in identified areas of interest. The data collected for this project also provide the opportunity to answer fundamental questions about the ecology and evolution of species in these areas. Isolation by distance was found to only play a minor role in population divergence, suggesting that natural selection, leading to isolation by environment may be a more common key factor in diversification than previously thought. This signal of selection was even picked up using neutrally evolving microsatellite markers.

To emphasize the need to include intraspecific variation in conservation planning, I have presented this work at scientific conferences and have engaged in discussions with conservation planners and stakeholders. In a large collaborative effort, the African part of this project was further extended, and the Central African Biodiversity Alliance was established (www.caballiance.org). I have also developed two courses in Conservation Biology and Landscape Genetics that aim to teach students the concepts of conservation, how to critically analyze various levels of threats, and the multidimensional challenges and approaches required for mitigating those threats. I will further develop my research in a permanent position, with the mission to tackle conservation-related issues from both fundamental as well as applied research perspectives.

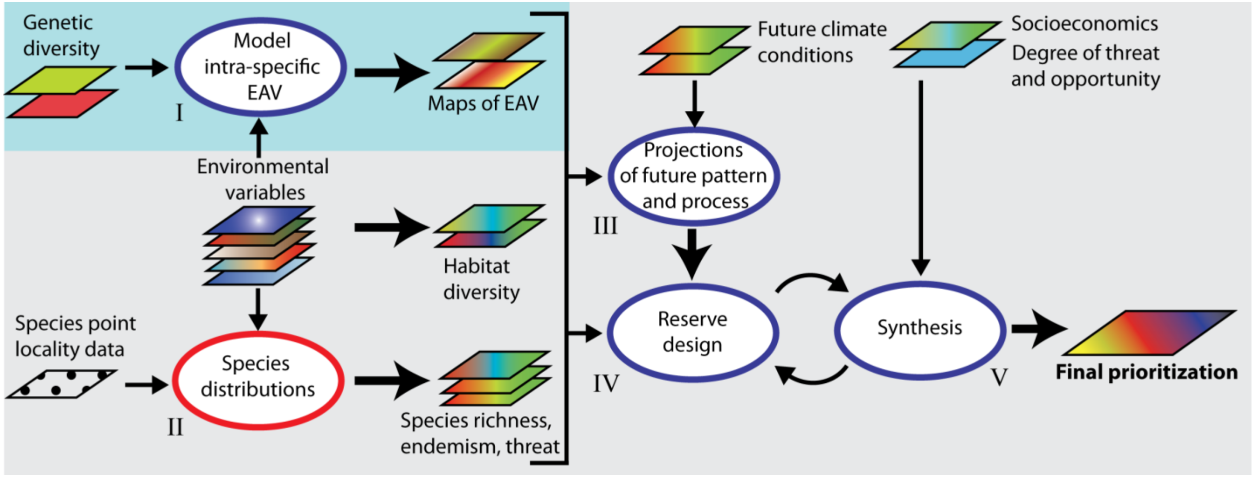

**Fig. 1.** Flowchart of species distribution and spatially explicit modeling approaches to map current and potential future biodiversity across a landscape. The results, when combined with degrees of threat and socioeconomic impacts, can be used to prioritize areas of importance for conserving evolutionary processes under climate change. Steps include: modeling of intraspecific variation that is associated to environmental variables (environmentally associated variation; EAV) (I) and species distributions (II); projections of maps resulting from I and II onto future climate change scenarios (III); reserve design based on biological data (IV); integration of a set of solutions from IV with socioeconomical data and the degree of threat and opportunity, resulting in the final prioritization (V).