**Outstanding Questions**

1. Can we learn by synthesizing macroecological and population genetic theory whether observed non-equilibrium states are driven by natural disturbance regimes or by anthropogenic forces?
2. Can we learn the relative roles of evolutionary processes (speciation, extinction) vs. successional processes (driven by, e.g., competition, mutualism, dispersal) as drivers of non-equilibrium macroecology?
3. How can functional genomics be used to better distinguish between purely demographic and niche-based drivers of non-equilibrium? Can understanding the gene content of genomes, gene expression patterns, and occurrence of mutations across taxa in a community help predict potential for non-equilibrium responses to future perturbations?
4. How can relative abundance data derived from ancient DNA and fossil data be leveraged within a joint model that generates predictions of spatiotemporal distributions of genetic polymorphism and species abundances? One such opportunity is the availability of highly resolved estimates of relative abundance distributions of forest tree assemblages that are derived from paleo-pollen data [75] which could allow for joint inference in conjunction with assemblage-level genomic sampling. Likewise, obtaining community-level DNA preserved in lake sediments sampled at different late Pleistocene and Holocene could provide for a whole new lense for testing models that account for historical dynamics at both evolutionary and ecological time scales [76].