The last decade has seen incredible advances in technology regarding molecular and computational methods in evolutionary research. We are able to collect more genetic data faster to address questions regarding how organisms evolve and determine biodiversity measures from the microbial to macroorganism level. The next decade will see molecular biologists spending less time with pipettes and more time organizing and coordinating mass amounts of data. I will discuss recent research in which nDNA Expressed Sequence Tag (EST) data was used to test an empirical method to identify hybridization from lineage sorting incorporating molecular data and bioinformatics applications, ultimately recognizing the limitations of both. Developing projects in my lab will also be introduced that will utilize Next Generation Sequencing NGS techniques (ddRAD and Environmental Sequencing) to address evolutionary questions. These projects will require a substantial bioinformatics component utilizing newly developing software to organize and analyze data. The collaboration among scientists with theoretical, lab and bioinformatics expertise has become essential for the next generation of research in evolutionary biology.