Here are some suggested final project ideas:

* A deep dive on a specific technical challenge of de novo genome sequencing and assembly, eg repeats or heterozygosity
* Assembly and annotation of an original or publicly available de novo genome
* Examine the evolution of genome structure (eg synteny, size, intron distribution, etc) with phylogenetic methods
* Explore the fit of models of evolution to genomic or functional genomic data
* Test phylogenetic hypotheses with genomic data
* Analyze one or more categories of functional genomic data in a phylogenetic context to test hypotheses about the evolution of genome function
* Use comparative functional genomic and/or genomic data to identify genes that may relate to specific phenotypes
* Compare within population genome variation to variation at broader phylogenetic scales

Mix phylogeo of ebola, bats and movement or connectivity models.