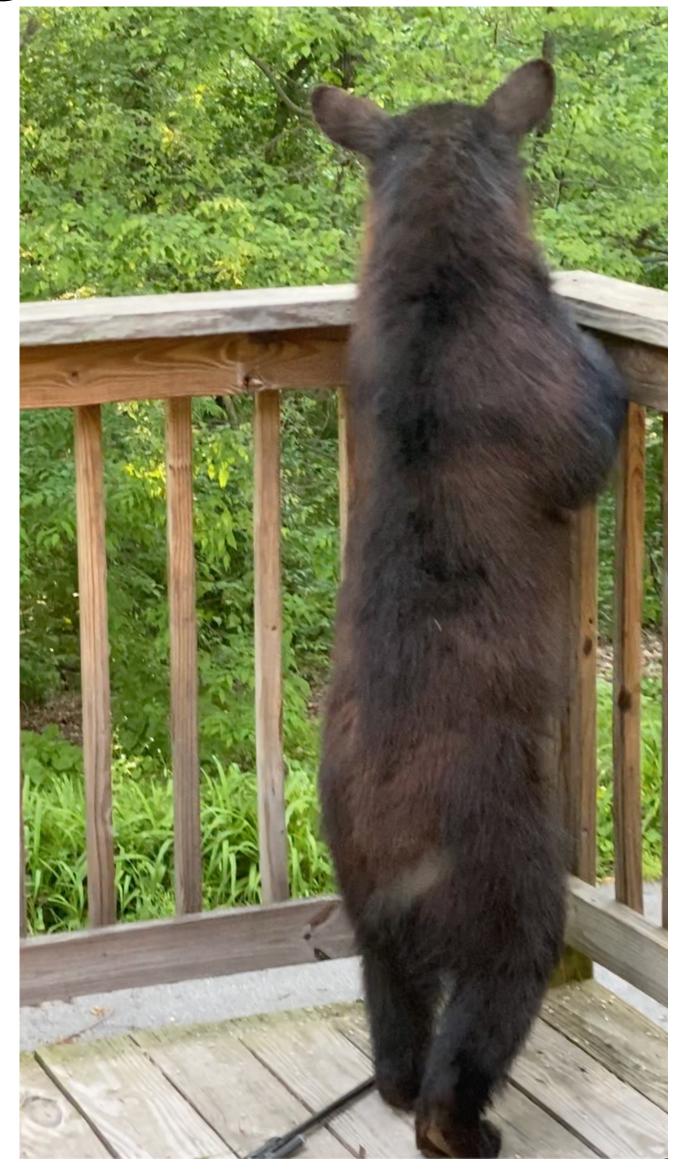
Day 3: Comparative and Phylogenomic Inferences

- How we can use our consensus sequence from our raw reads to mapped reads or de novo assembly?
- Comparative Genomics: The study of genomes within and between taxa to better understand structure, organization and biological function.
- Evolutionary Genomics: The study of how genes and genomes change over time.
- Phylogenomics: Tree-based Inferences of evolutionary histories of related taxa.



Phylogenomic Analyses of Host Species

- Evolutionary history of species
- Population structure and phylogeography
- Historic and ongoing patterns of migration and gene flow
- Genetic diversity within and between genomes
- Detection of Inbreeding
- Detection of hybridization
- Endangered or relic species, subspecies and populations

Applications

• Identification of genes involved in disease resistance and progression



- Definition of patterns of evolution and selection within targeted genes
- Identification of variants linked with disease pathogenicity in host
- Predictive effects of pathogen emergence in naïve host populations or species