

# 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