Applied Computational Genomics

Phenotype

Microbiome

Metabolome

Transcriptome

Epigenome

Genome

Genetics

UNIVERSITY OF SOUTH FLORIDA
A PREEMINENT RESEARCH UNIVERSITY

GENOMICS PROGRAM
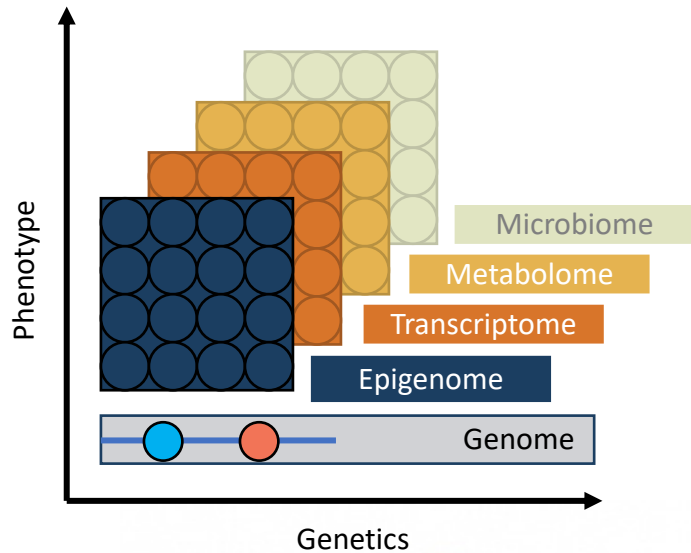
OBJECTIVE

Sequencing DNA is no longer the bottleneck, rather, the bottleneck is the computational analysis and also interpretation. This course is an introduction to computational genomics, emphasizing the fundamentals of next-generation sequencing (NGS) analysis. The participants will be provided with end-to-end hands-on training, along with an introduction to basic concepts in using popular tools and techniques for genome, transcriptome, epigenome, and microbiome.

Hands-on Skills/Tools taught:

1. Necessary Linux and R command line for NGS analysis
2. Beautiful data visualization with R
3. Sequencing quality control tool for NGS: FastQC
4. RNA-Seq analysis: HISAT, Cufflink, Cuffdiff, DEseq
5. Gene ontology analysis
6. NGS read aligner: BWA, Bowtie
7. ChIP-Seq peak calling: Macs2
8. 16S rRNA analysis: DADA2
9. Protein structure visualization: PyMOL