The Bioinformatics Core goals are to (i) provide exceptional service in reproducible computational data analysis, (ii) educate the research community on current bioinformatics tools and techniques, (iii) foster long-term collaborations with the UCR research community and (iv) connect bioinformaticians on campus to promote the exchange of ideas and expertise. The Core provides project-specific consultation on experimental design and data analysis, development of novel analysis pipelines and workflow with special skills in the areas of genomics (e.g., Whole Genome- and Exome-seq), transcriptomics (e.g., RNA-seq, small RNA-seq, Ribo-seq), epigenomics (e.g., Methyl-seq, ATAC-seq), and system biology. To foster collaborations and educate researchers on analysis tools and techniques, the Core also provides hands-on bioinformatics training workshops and seminars to undergraduate and graduate students, post-docs, research scientists, and investigators. To promote the exchange of expertise and ideas in bioinformatics, the Core will host meet-ups/zoom sessions for specific methods and topics lead by novice and expert bioinformaticians. The fundamental goal of the Core is to provide first-rate computational analysis, pipelines, and workflows that will free the UCR investigators and research community to explore novel and exciting biological questions.