

ChIP-seq Data Analysis and Translational Applications

HDAC1 regulated chromatin landscape and transcriptional dependencies in CLL



Abstract: Over the past ten years, with the introduction of next generation sequencing (NGS), bioinformatics has become an integral part of the translational research. NGS technology has been utilized to perform broad range of experiments to identify DNA alterations, quantify RNA, study chromatin structure and protein-DNA interactions for whole genome. Analysis, annotation, interpretation and integration of NGS data, started to bring a new angle to many research projects.

In this presentation, I will briefly introduce ChIP-seq data analysis, then, will focus on integration of multiple datasets in the direction of the biological question. I will walk you through a project where I analyzed and integrated different types of ChIP-seq data to study **HDAC1 regulated chromatin landscape and transcriptional dependencies in chronic lymphocytic leukemia (CLL)**. In this project we identified a critical role for HDAC1 in establishing the transcriptional dependencies essential for survival in CLL by profiling HDAC1 with BRD4, H3K27Ac superenhancers, H4K9Ac, chromatin accessibility signatures, Pol2 measurements and expression signatures to generate a regulatory chromatin landscape.

About the Speaker: Dr. Gulcin Ozer is a research assistant professor in the Department of Biomedical Informatics at The Ohio State University Wexner Medical Center (OSUWMC) and a senior advisor for the Biomedical Informatics Shared Resource (BISR). Her research focuses on development and application of computational and bioinformatics methods to address problems in biomedical research. She have a robust expertise in analysis and interpretation of high-throughput high dimensional biological data including RNA-sequencing, exome-sequencing, ChIP-sequencing, ATAC-sequencing, whole genome re-sequencing, as well as microarray, and NanoString data. Dr. Ozer works closely with Division of Hematology on analysis and integration of various types of sequencing data generated to understand genomic foundations of hematologic and lymphoid malignancies, as well as clonal evolution and resistance to treatment. Dr. Ozer received her doctoral degree in Biophysics (Computational Biology and Bioinformatics track) from Ohio State University, a master's degree in Biophysics from Gaziantep University in Gaziantep, Turkey, and a bachelor's in computer engineering from Bogazici University in Istanbul, Turkey. Dr. Ozer has authored or co-authored 48 peer-reviewed publications.

H. Gulcin Ozer, PhD
Friday, September 4th, 11:00am-12:00pm
Carmen Zoom