Capasso

**Decoding Pediatric Neuroblastoma Through Multi-Omic and Single-Cell Bioinformatics**

This research project investigates how inherited genetic predispositions interact with somatic alterations to drive neuroblastoma, a pediatric cancer, using large-scale genomic data and advanced bioinformatics. We apply computational algorithms to analyze single-cell RNA sequencing, whole-exome and whole-genome sequencing (short and long reads), genome-wide association studies (GWAS), and epigenomic data to identify both inherited and acquired molecular changes involved in tumor development.

Our integrative approach focuses particularly on non-coding mutations that disrupt transcription factor binding, combining these analyses with ATAC-seq, Hi-C, and DNA methylation data to uncover mechanisms underlying tumor progression. Long-read sequencing data further enhance the detection of complex structural variants and non-coding regulatory alterations that are often missed by short-read methods, providing a more comprehensive view of the genomic landscape. Additionally, single-cell transcriptomic analysis enables us to characterize gene expression heterogeneity and identify causal genes that promote cellular survival and treatment resistance after chemotherapy.

Ultimately, this project aims to translate genomic insights—derived through comprehensive bioinformatic analyses of large-scale genomic and epigenomic data—into clinically relevant biomarkers for risk stratification and to inform the development of personalized therapies for children with neuroblastoma.