Dissecting protein and RNA dysregulation in cancer using high-resolution omics

Cancer and other human diseases are inherently complex, requiring high-resolution methods to effectively discover disease mechanisms and potential cures. Current investigation approaches involve multi-modal, high-resolution techniques such as genome-wide, single-cell, and spatially resolved omics. These methods generate data of unprecedented volume and heterogeneity. Our research mission addresses this challenge by focusing on developing and applying the dedicated computational strategies required to handle these complex datasets. By combining cutting-edge high-throughput proteomics and RNA omics analyses with a pan-disciplinary approach, we aim to ultimately unravel the precise protein and RNA molecular mechanisms underlying dysregulation in cancer and other human diseases.