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Translating cancer proteogenomics data into biological and clinical insights

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Advancements in high-throughput omics technologies have provided an unprecedented opportunity for cancer studies. At the same time, advanced technologies have led to an increasing gap between data generation and our ability to interpret the vast amount of interconnected data. My lab develops and uses integrative bioinformatics approaches that help translate omics data into biological and clinical insights. In this talk, I will briefly introduce our established computational workflow for cancer proteogenomics data analysis[1]. I will use data generated by the National Cancer Institute's Clinical Proteomic Tumor Analysis Consortium (CPTAC) on HPV-negative head and neck squamous cell carcinoma (HNSCC) as an example to demonstrate the utility of proteogenomics data in driving therapeutic hypothesis generation for precision oncology[2]. I will also present our efforts on improving phosphoproteomics data analysis[3] and making proteogenomics data accessible and useful to non-computational biologists[4, 5].

References

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