

Webinar

Moving beyond the canonical dichotomy of drivers and passengers in cancer

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I will present our work on extending the canonical dichotomy of classifying cancer mutations as drivers and passengers. In this context, I will first present our work on identifying cancer drivers by integrating protein structure, protein motion, and cancer genomics data. Following this, I will present our work on the characterization of the non-driver (“passenger”) mutational landscape in thousands of cancer genomes. Here, we integrated genomic annotations and predicted functional impact scores to quantify the overall burdening of various elements in cancer genomes. We also showed how the overall functional burdening of different genomic elements correlates with patient survival time and tumor clonality. Finally, we observed statistical signals consistent with the notion that aggregated subsets of passenger variants - particularly those we predict to be functionally impactful- might confer weak selective effects.

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5:00 PM