Through extensive data analysis, our goal is to address core metastatic samples, we discerned specific cancer types/cancer novel CPGs. Second, after examining 250,000 primary and comprehensive understanding of tumour progression via our research is rooted in cancer genomics, systems biology, constructing dynamic protein-protein interaction networks. measuring variations in cancer fitness across cancer states, and by identifying novel cancer predisposition genes (CPGs), the context-dependent cancer fitness landscape. We do this considerably depending on the cellular context. In the Computational Cancer Genomics Lab, we strive to decipher clinical implications of our genomic findings.

Cancer state-specific fitness landscape

While metastasis is a primary factor for decreased survival rates among cancer patients, our comprehension of metastasis remains nascent in comparison to that of primary tumours. Building on our prior discoveries (Park et al., Nature Commun, 2021), we postulate that the optimal activity-fitness level of cancer genes varies based on the cancer’s state, such as primary versus metastatic tumours. By analysing 250,000 samples, we have identified 5 cancer types with notable differences and pinpointed 16 genes exhibiting distinct perturbations on the cancer states. These insights are pivotal for grasping the variances in cancer fitness across cancer states and could greatly enhance our understanding of treatment response disparities.

Identification of novel cancer predisposition genes (CPGs)

The roles of germline variants remain elusive and could be substantially underestimated. We presented compelling evidence indicating that Mendelian-disease associated genes could increase cancer risk similarly to CPGs. We proposed 4 potential classes of CPG-like OMIM genes that might indicate non-classical mechanisms of tumour progression (Song et al., Genome Medicine). In addition, we formulated a machine learning method that leverages comprehensive feature integration to pinpoint novel CPGs. Significantly, this will be the pioneering study to comprehensively predict previously unidentified CPGs.

RESEARCH HIGHLIGHTS

**Position-specific perturbed interaction network**

Protein interaction partners for a specific mutant protein can shift depending on the mutation location within the protein. Furthermore, we expect that the clinical responses of these mutations will differ based on the mutations. In 2023, in collaboration with M. Oren (Weizmann Institute of Science, Rehovot, Israel) and JS. Yang (CRAG, Barcelona, Spain), we initiated a project focusing on p53 mutations, supported by a Fundació Rumin Arques Award. This endeavour holds the potential to revolutionise network medicine by introducing an edge-specific treatment methodology.

**Performance of multi-omics beyond the classical CPGs**

Using samples from 250,000 patients, we have been advancing our understanding of cancer fitness across different states.

“`We identify novel CPGs by integrating multi-omics beyond the classical CPGs. Using samples from 250,000 patients, we have been advancing our understanding of cancer fitness across different states.”

**OVERVIEW**

Cancer is a multifaceted disease influenced by multiple factors. Moreover, the impact of genomic alterations varies considerably depending on the cellular context. In the Computational Cancer Genomics Lab, we strive to decipher the context-dependent cancer fitness landscape. We do this by identifying novel cancer predisposition genes (CPGs), measuring variations in cancer fitness across cancer states, and constructing dynamic protein-protein interaction networks. Our research is rooted in cancer genomics, systems biology, and network medicine. First, our findings aim to provide a comprehensive understanding of tumour progression via novel CPGs. Second, after examining 250,000 primary and metastatic samples, we discerned specific cancer types/cancer genes with distinct fitness levels based on their cancer states. Through extensive data analysis, our goal is to address core questions in cancer genetics and to explore the practical and clinical implications of our genomic findings.