Computational and Quantitative Biology Lecture Series

Wednesday
February 16, 2022
15.00 (GMT+1)

The seminar will be held on line. Please register at https://bit.ly/3sqj4uJ
You will receive an invite with the link to the seminar.
Visit https://cqb.dieti.unina.it/index.php/events for the event series.

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Computational analysis of cancer genomes

Somatic mutations are the driving force of cancer genome evolution. Given the evolutionary principles of cancer, one effective way to identify genes involved in cancer is by tracing the signals left by the positive selection of driver mutations across tumours. We analyze thousands of tumor genomes to generate a compendium of cancer genes across tumor types (http://www.intogen.org). Most mutations identified in tumors in cancer genes are mutations of unknown significance. The mutations observed in thousands of tumors, --natural experiments testing their oncogenic potential replicated across individuals and tissues-- may be exploited to identify driver mutations in cancer genes. From these mutations, we extract features that describe the mechanism of tumorigenesis of each cancer gene and tissue and use those to build machine learning models that effectively identify driver mutations. With those models we perform in silico saturation mutagenesis to outline blueprints of potential driver mutations in cancer genes. These blueprints support the interpretation of newly sequenced patients' tumors and the study of the mechanisms of tumorigenesis of cancer genes across tissues.

Finally, by analyzing more than 3500 whole-genomes of treated metastatic patients we uncovered the mutational footprints (or mutational signatures) of commonly used cancer treatments. These signatures allowed us to measure the mutational toxicity of these treatments across patients and organs.

Nuria Lopez-Bigas is an ICREA Research Professor at the Institute for Research in Biomedicine and associate professor at the University Pompeu Fabra. She leads the Biomedical Genomics lab (http://bbglab.irbbarcelona.org), focused on the study of cancer from a genomics perspective. The group combines strong expertise in biology and bioinformatics. Lopez-Bigas lab has developed pioneer computational methods to identify cancer genes from the pattern of somatic mutations, and has analyzed more than 28000 tumor genomes to generate a catalog of cancer genes across tumor types (http://www.intogen.org). They have also developed a highly used tool (http://www.cancergenomeinterpreter.org) to annotate cancer driver mutations and biomarkers of drug response in individual tumors.
The group is also interested in understanding the mutational processes that lead to the accumulation of mutations in tumor cells. A major recent contribution from the lab is the discovery that DNA-bound proteins interfere with the nucleotide excision repair machinery, leading to increased rate of DNA mutations at the protein binding sites. They have also discovered that germline and somatic mutation rate follows a 10.3 bp periodicity in nucleosome covered regions. They demonstrated that this is caused by DNA damage and repair acting differently depending on the orientation of the DNA minor groove around nucleosomes. And more recently they have described mutational footprints of cancer therapies.
Her work has been recognized with awards such as the prestigious Banc de Sabadell Award for Research in Biomedicine, the Catalan National Award for Young Research Talent and the Career Development Award from the Human Frontiers Science Program Organization.

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