

Bioinformatics Interest Group (BIG) Lecture

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H 52



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Chromosomal instability and copy-number evolution in cancer

Intra-tumour heterogeneity (ITH) is the main driver of resistance development in the clinic and the greatest impediment to targeted cancer therapies. Large-scale consortia such as PCAWG and the TRACERx have assembled vast amounts of genetic, transcriptomic, and epigenetic data to map out ITH across human cancers. Machine learning and data science approaches now start to provide in-depth insights into the evolution of many human malignancies with the prospect of predicting and preventing the evolution of resistant subclones on a per patient level.

Chromosomal instability (CIN), a hallmark of many tumours and a key characteristic separating healthy from cancerous tissue, thereby plays a central role in generating ITH. CIN describes the ability of tumours to generate and tolerate extensive somatic copy-number alterations (SCNA) and genomic rearrangements. Besides its immediate clinical relevance, SCNA variability also forms a rich source of genetic variation that can be exploited for reconstructing tumour evolution in the patient in retrospective studies.

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