CCBIO seminar (BMED380)

SCAN ME

Thursday, December 15, 14:30 at the BBB, Auditorium 4

Using somatic mutations to reconstruct the life histories of normal and cancer cells

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From fertilization onwards, individual cells of the human body continuously experience DNA damage and accumulate somatic mutations. As mutations in the genome are reliably passed on to a cell's progeny, the somatic genome of a cell becomes a record of its life history and a means to infer its relationship to any other cell of the same individual. In essence, somatic mutations connect all cells together into one large phylogenetic tree of human development with the zygote at the root. Besides recording the cell division, migration and differentiation of early development, somatic mutations can also delineate aberrant, premalignant expansions and shed light on the evolution of a cancer in response to treatment.

In this seminar, I will discuss the surprising insights that we have recently gained by using somatic mutations as natural lineage markers. Covering the timescale from early development to cancer evolution, I will present my findings on (i) patterns of embryogenesis in the human body[1] and placenta[2], (ii) early precursor clones to Wilms tumor[3], a childhood kidney cancer, and (iii) a surprising case of lineage switch leukemia in response to CAR-T cell therapy[4].

References

1. Coorens THH, Moore L *et al*. Extensive phylogenies of human development inferred from somatic mutations. *Nature* 597, 387-392(2021).
2. Coorens THH, Oliver TRW *et al*. Inherent mosaicism and extensive mutation of human placentas. *Nature* 592, 80–85 (2021).
3. Coorens THH *et al*. Embryonal precursors of Wilms tumor. *Science* 366, 1247–1251 (2019).
4. Coorens THH *et al*. Clonal origin of lineage switch leukaemia following CAR-T cell and blinatunomab therapy. *In preparation*

Chair: Camilla Krakstad <camilla.krakstad@uib.no>, Dept. of Clinical Medicine