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Brain development at single-cell resolution: retracing the origins of pediatric brain tumors

LE JEUDI 27 JUIN 2019 À 12 H 30

Conjointement avec le Département de biochimie, de microbiologie et de bio-informatique et CERVO

Pavillon Charles-Eugène-Marchand, salle Hydro-Québec (1210)

Childhood brain tumours have suspected prenatal origins. To identify vulnerable developmental states, we generated a single-cell transcriptome atlas of >60,000 cells from embryonal pons and forebrain, two major tumour locations. We derived gene signatures for 200 distinct cell populations and defined regional cellular diversity and differentiation dynamics. Projection of bulk and single-cell tumour transcriptomes onto this dataset allowed us to identify the lineage of origin for several tumor types. Importantly, single-cell tumour profiles reveal highly defined cell hierarchies mirroring transcriptional programs of the corresponding normal lineages. Our findings identify impaired differentiation of specific neural progenitors as a common mechanism underlying these pediatric cancers and provide a rational framework for future modeling and therapeutic interventions.

Lunch et breuvages seront offerts.

**SVP confirmer votre présence sur : <https://doodle.com/poll/4g5wdg8zqikm34hv>
avant le mercredi 26 juin, 10 h**

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