Combi Seminar

Wednesday, 3.14.18 | 1:30 | Foege Auditorium



Dr. Georg Seelig

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Scaling single-cell transcriptomics with split-pool barcoding

Abstract: To facilitate scalable profiling of single cells, we developed Split Pool Ligation-based Transcriptome sequencing (SPLiT-seq), a single-cell RNA-seq (scRNA-seq) method that labels the cellular origin of RNA through combinatorial barcoding. SPLiT-seq is compatible with fixed cells or nuclei, allows efficient sample multiplexing and requires no customized equipment. We used SPLiT-seq to analyze 156,049 single-nucleus transcriptomes from postnatal day 2 and mouse brains and spinal cords. Over 100 cell types were identified, with gene expression patterns corresponding to cellular function, regional specificity, and stage of differentiation. Pseudo time analysis revealed transcriptional programs driving four developmental lineages, providing a snapshot of early postnatal development in the murine central nervous system. SPLiT-seq provides a path towards comprehensive single-cell transcriptomic analysis of other similarly complex multicellular systems.

Bio: Georg Seelig is an associate professor in the Paul G. Allen School of Computer Science and Engineering and the Department of Electrical Engineering at the University of Washington. He is an adjunct associate professor of bioengineering. He received his PhD in physics from the University of Geneva, Switzerland, and completed postdoctoral research in synthetic biology and DNA nanotechnology at Caltech. Seelig received a Burroughs Wellcome Foundation Career Award at the Scientific Interface in 2008, an NSF Career Award in 2010, a Sloan Research Fellowship in 2011, a DARPA Young Faculty Award in 2012, and an ONR Young Investigator Award in 2014.

Questions? Contact Brian Giebel at bgiebel@uw.edu or visit the Combi website at http://www.gs.washington.edu/news/combi.htm

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