



Seewiesen Colloquia

Speaker invited by: Baldwin Research Group

Thursday, December 08, 2016, 13h, in House 4, Lecture Room

Global brain analyses at cellular resolution using massively high-throughput single cell transcriptomics

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Understanding how brains vary across species or during disease necessitates defining and comparing cell types, the building blocks of neural circuits. Single-cell measurements of gene expression take advantage of the fact that cellular specialization is controlled transcriptionally, allowing an unbiased picture of intra- and inter-cell type variation. Due to the experimental noise, analyses with only hundreds or even thousands of measurements can be hard to interpret. Here we apply a system developed in our lab for massively high-throughput single-cell transcriptomics („Drop-seq“) to mouse and marmoset brains. Our first project has generated an atlas of cellular variation from the adult mice. This dataset consists of >750K single-cell transcriptomes from n=9 different brain regions. We illustrate this single-cell approach by comparing 28K interneurons and describe our ongoing efforts to compare brains across species and throughout development.

Who is Fenna Krienen?

- 2006 BA University of California, Berkeley, USA
- 2013 PhD (Psychology), Harvard University, USA
- 2014 Post-doc (Center for Advanced Study of Human Paleobiology), The George Washington University, USA
- 2015 - Post-doc (Genetics), Harvard Medical School, USA

Who is Arpiar Saunders?

- 2006 BA Swarthmore College, USA
- 2014 PhD (Neurobiology), Harvard Medical School, USA
- 2014 - Post-doc (Genetics), Harvard Medical School, USA

Selected publications:

- Macosko, E. Z., Basu, A., Satija, R., Nemes, J., Shekhar, K., Goldman, M., et al. (2015). Highly parallel genome-wide expression profiling of individual cells using nanoliter droplets. *Cell*, 161: 1202–1214.
- Saunders, A., Oldenburg, I. A., Berezovskii, V. K., Johnson, C. A., Kingery, N. D., Elliott, H. L., et al. (2015). A direct GABAergic output from the basal ganglia to frontal cortex. *Nature*, 521: 85-9
- Kozorovitskiy, Y*, Saunders, A*, Johnson, C. A., Lowell, B. B., & Sabatini, B. L. (2012). Recurrent network activity drives striatal synaptogenesis. *Nature*, 485: 646-650.
- Krienen, F.M., Yeo, B.T.T, Ge, T., Buckner, R.L., Sherwood, C.C. (2016). Transcriptional profiles of supragranular-enriched genes associate with corticocortical network architecture in the human brain. *Proceedings of the National Academy of Sciences USA*, 113: E469–E478.
- Buckner, R.L., Krienen, F.M. (2013). The evolution of distributed networks in the human brain. *Trends in Cognitive Sciences*, 17: 648-665.