# Cell types as building blocks of neural circuits

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Classification of neurons was a major preoccupation of Cajal, but later came to be viewed as a fairly boring enterprise. However, inability to define neuronal types has now emerged as a major bottleneck in analysis of neural circuits. Recent technical advances are improving the situation. We have applied one of them, high throughput single cell RNAseq, to the retina, the model system on which our research focuses. To generate a cell atlas, we obtain large numbers of transcriptomes, improve bioinformatic methods for analyzing the data, and match types defined molecularly to those defined by morphological and physiological criteria. The mouse retina (>100,000 cells profiled) appears to comprise around ~130 cell types and a more recently completed macaque retinal atlas (165,000 cells) comprises ~70 types. We are now beginning to use the atlases to probe retinal development, function and dysfunction in ways I will discuss: (1) Profiling retinal ganglion cells (RGCs) at earlier stages to learn how immature cells of a heterogeneous class diversify into ~45 types. (2) Analyzing RGCs following injury (optic nerve crush) or in disease models (glaucoma) to seek early transcriptional signatures that correlate with, and differences in the vulnerability of some RGC types to these insults. (3) Probing the evolution of cell types by profiling cells from several other vertebrates, including human, marmoset, chick, zebrafish, peromyscus, pig and ferret.

### Monday, May 27, 2019 04:00pm - 05:00pm

Raiffeisen Lecture Hall, Central Building

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