**Classes:**

**filt\_neurons:**

**Parent class: none**

**Child classes: bc\_neurons**

Essential fields (we should construct these fields when we generate filt\_neurons, during data processing. Leave things that are not generated blank at this point, e.g. CCF, clustid, etc.):

* .id
* .pos
* .pos40x
* .expmat
* .genes
* slice
* clustid
* clustname
* subclass
* CCF
* CCFparentname
* CCFano
* metadata

Obsolete (keep for now, but probably remove in the future):

* angle
* depth

**bc\_neurons:**

**Parent class: Filt\_neurons**

**Child classes: bc\_rabies\_neurons, bc\_barseq\_neurons**

Essential fields:

* dom\_bc
* dom\_bc\_count
* all\_bc
* all\_bc\_count

**bc\_rabies\_neurons:**

**Parent class: bc\_neurons**

**Child classes: none?**

Essential fields:

* is\_starter
* is\_presyn
* RG\_count
* matched\_presyn
* matched\_presyn\_count
* curation

(What to do with rolony level data? Both genes and barcodes)

**Methods:**

**Generating datasets:**

* make\_neurons (used during image processing to generate filt\_neurons)
* assign\_cluster\_labels
* assign\_CCF
* make\_conn\_neurons

**Manipulating datasets:**

* subset\_neurons
* combine\_neurons (need to check if two datasets are compatible (how to handle repeated cell ids? How should slice numbers be handled? We probably should allow handling of multiple datasets, but then how to deal with different gene panels and metadata?)

**Analysis:**

* plot\_cells (plot raw images of cells)
* plot\_slices (plot color-coded cells on slices, options to color code by various things)
* plot\_umap (plot color-coded umap, options to color code by various things)
* various qc plots (genes/cell+reads/cell)
* expand\_bc (expand bc\_neurons to get a list of neuron-bc pairs with counts)
* eval\_starter\_coverage (rabies specific)
* eval\_starter\_spread (rabies specific, but might be useful for barseq with modifications).
* calc\_min\_hamming\_dist (calculate min hamming distance among a list of barcodes?)
* plot\_type\_enrichment?
* plot\_subclass\_enrichment?
* Roi-based analyses?

**General helpers:**

* get\_folders (also used in image processing, probably should belong there)
* unzip\_files (same as above)
* convert\_filenames (same as above)