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SCHOOL OF PUBLIC HEALTH

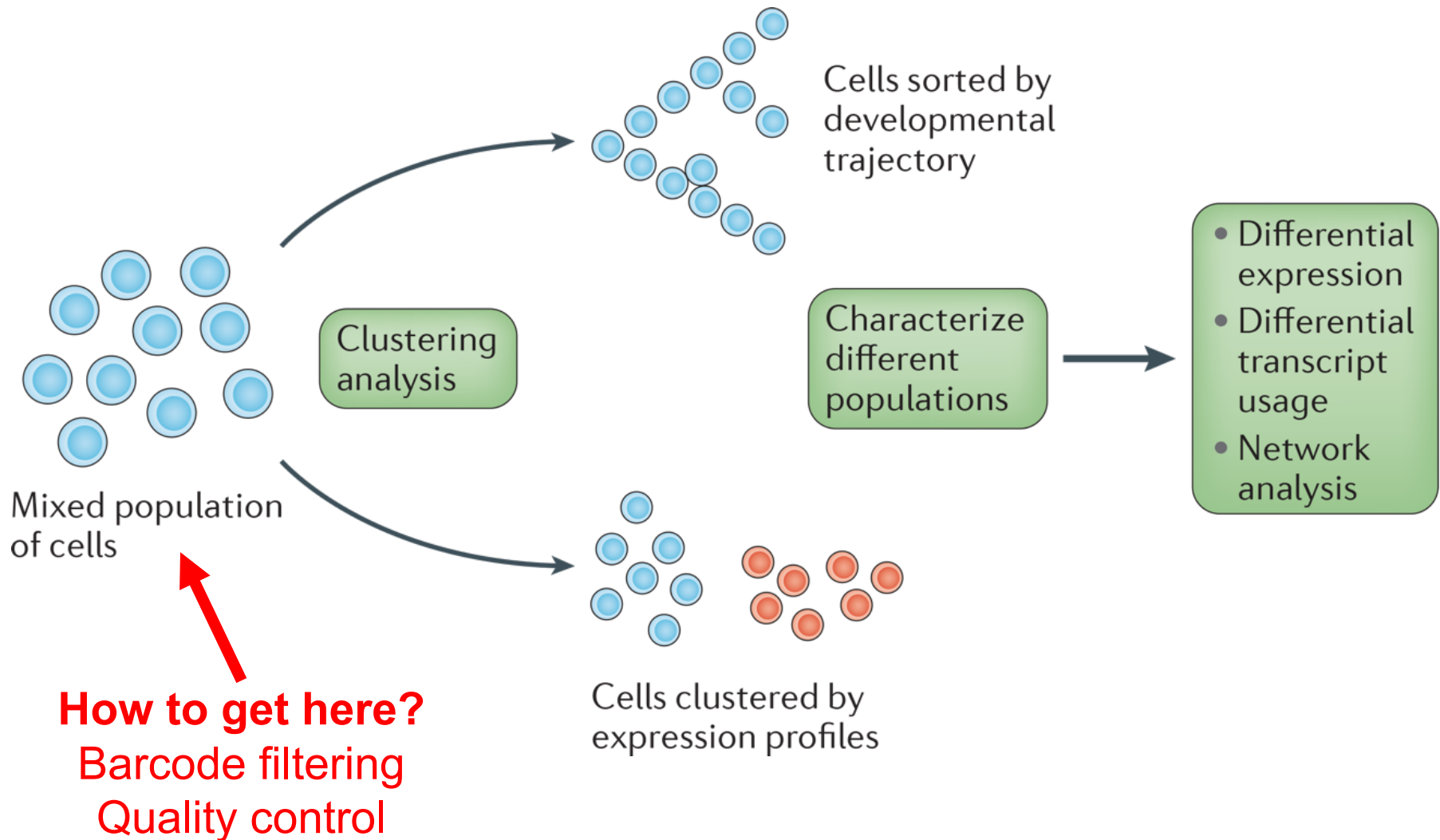
bcbioSinglecell: Import and analyze bcbio single-cell RNA-seq data

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July 26, 2017

<http://bioinformatics.sph.harvard.edu/bcbioSinglecell>

Cell population-level analysis facilitates cell type and differentiation cascade profiling



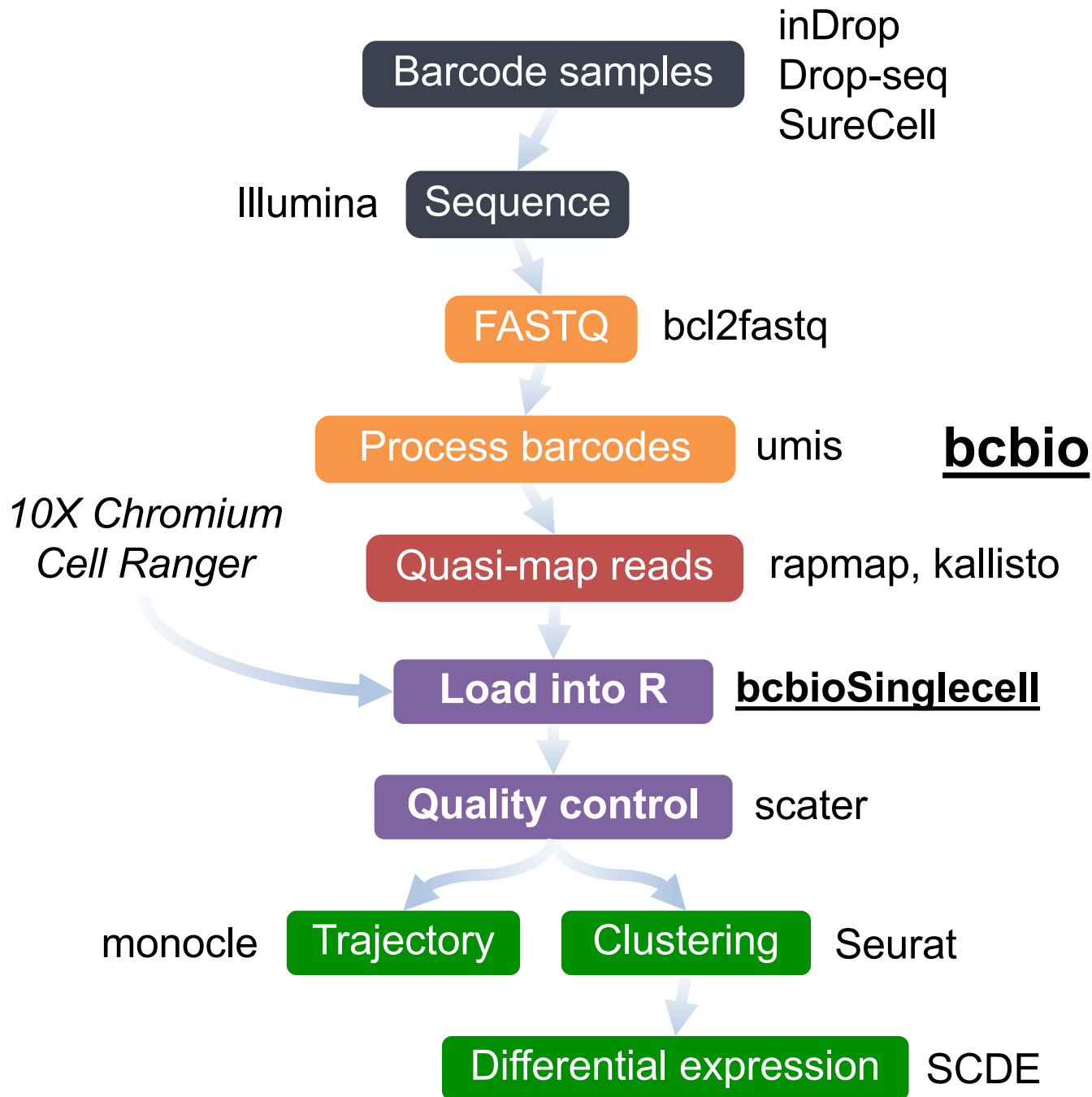


bcbio

- Native HPC support for single-cell RNA-seq analysis.
- Uses the [umis](#) package internally to process barcodes.
- Quantifies counts using either [rapmap](#) or [kallisto](#).
- Outputs transcript-level counts in MatrixMarket format.
- [bcbioSinglecell](#): R package interface to scRNA-seq data.
 - Automates sample import into R as a [SummarizedExperiment](#).
 - Saves counts as sparse matrix, using [Matrix](#) package.
 - Provides a number of quality control functions and [RMarkdown](#) templates for clustering workflows (e.g. [Seurat](#), [monocle](#)).
 - Data integration between Python and R!

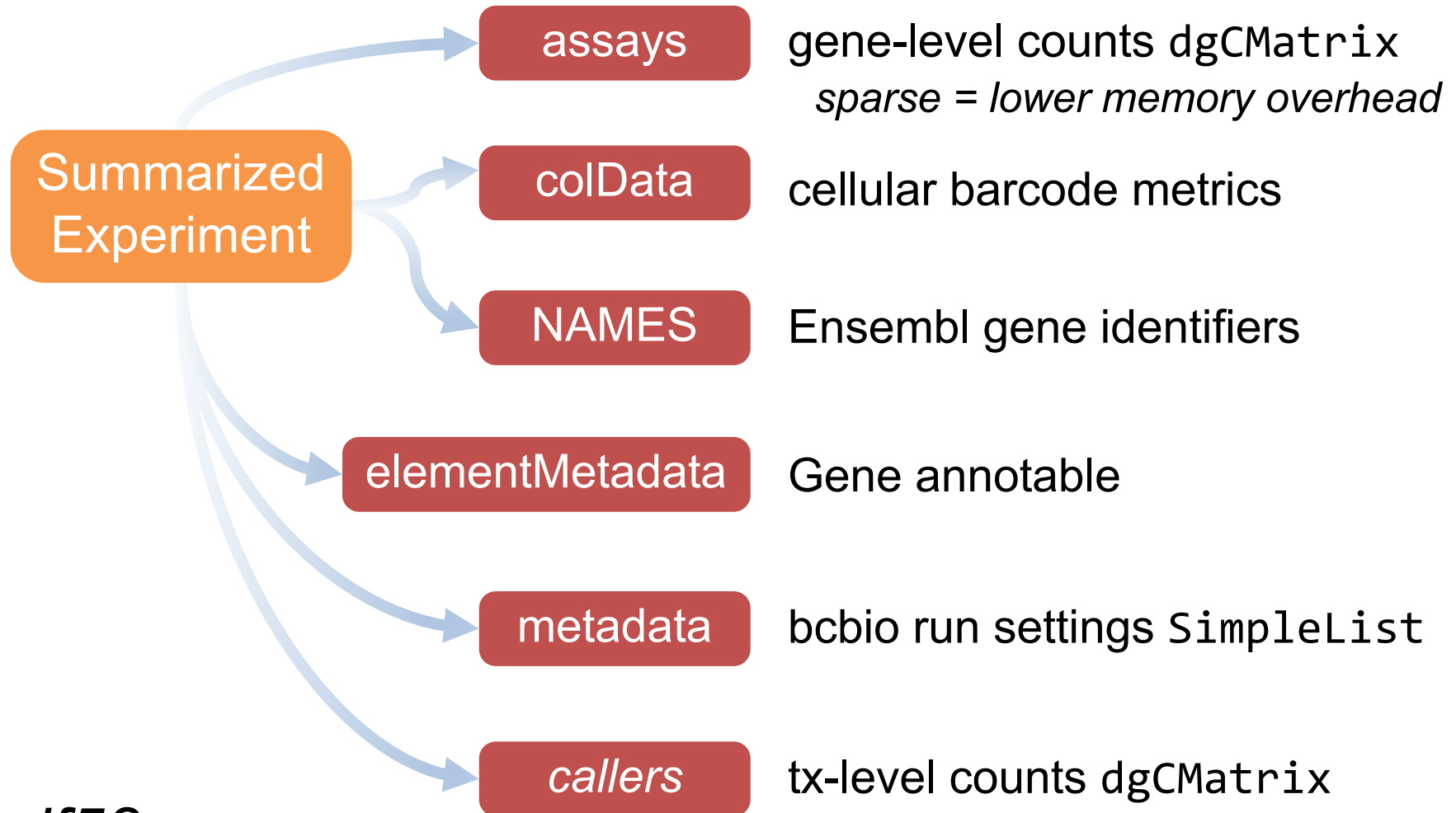
<https://bcbio-nextgen.readthedocs.io/>

<http://bioinformatics.sph.harvard.edu/bcbioSinglecell/>



bcbioSCDataSet S4 class

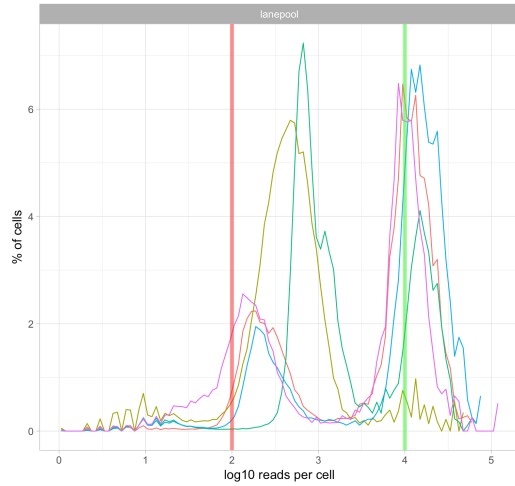
slotNames()



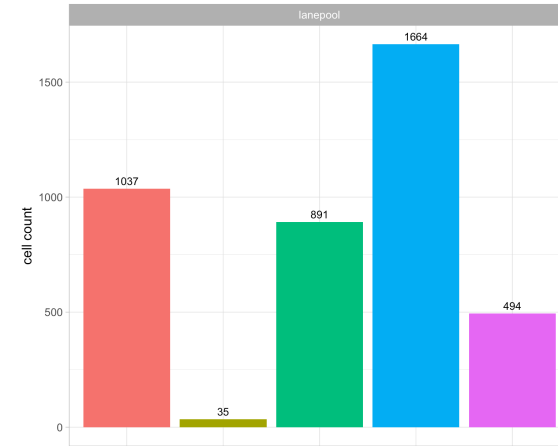
hdf5?

QC metrics and barcode filtering

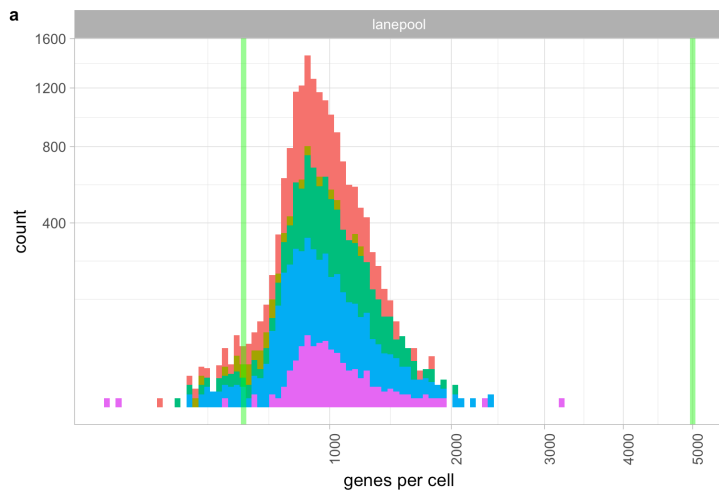
Reads per barcode



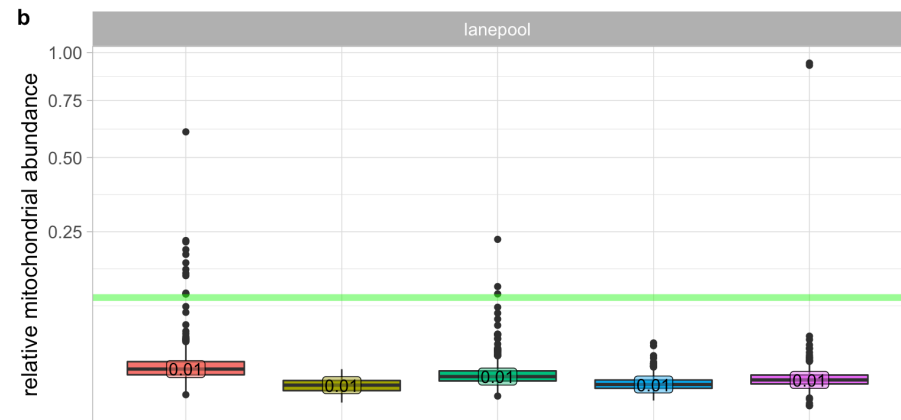
Cell counts



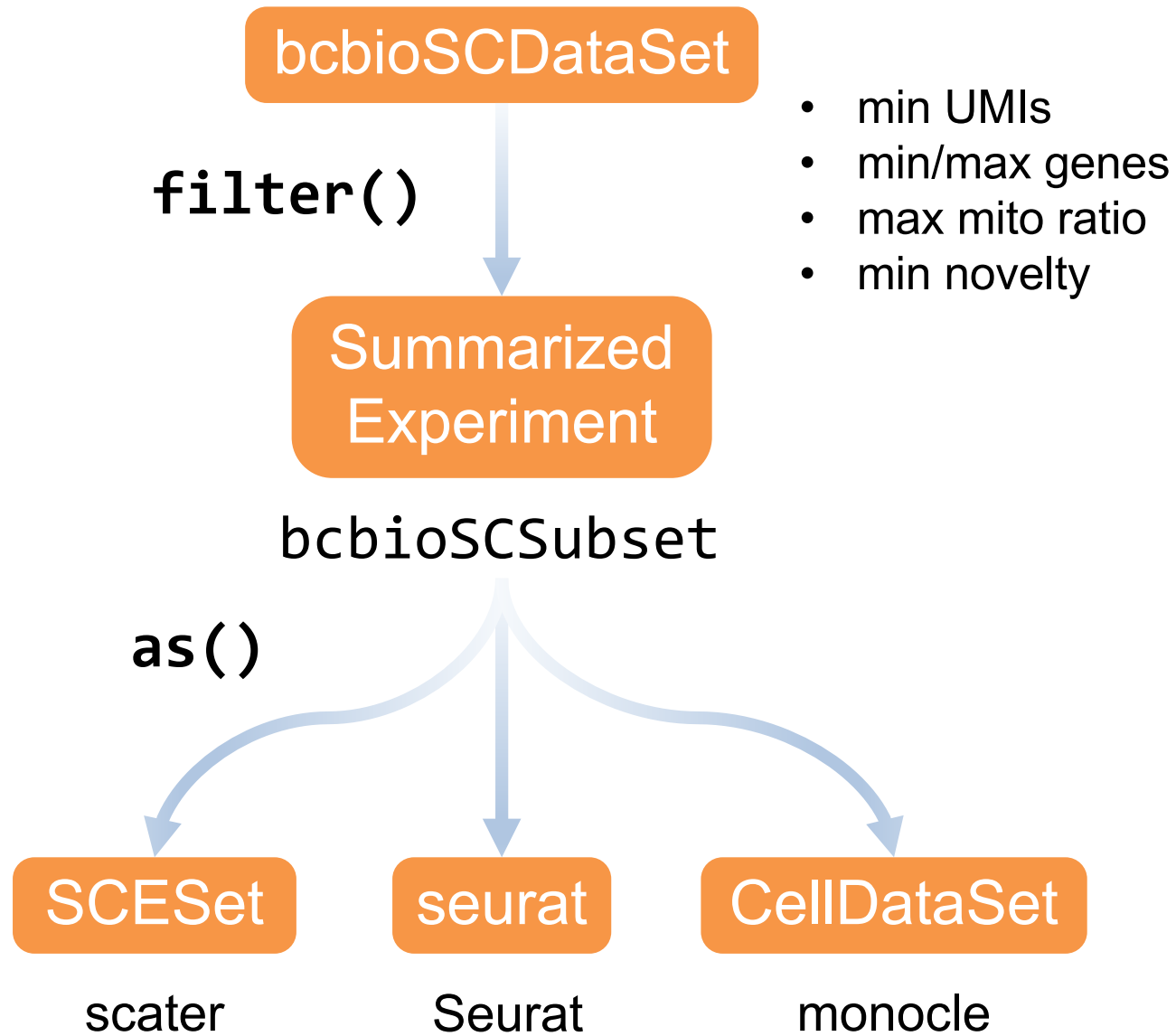
Gene detection



Mitochondrial abundance



bcbioSCSubset S4 class



Harvard Chan Bioinformatics Core



Shannan Ho Sui



John Hutchinson



Brad Chapman



Rory Kirchner



Meeta Mistry



Radhika Khetani



Mary Piper



Lorena Pantano



Michael Steinbaugh



Victor Barrera



Peter Kraft