

scPloidy: Infer ploidy of single cells (or nuclei) based on single-cell (or single-nucleus) ATAC-seq data

New R package!

Available from

- CRAN
- <https://github.com/fumi-github/scPloidy>

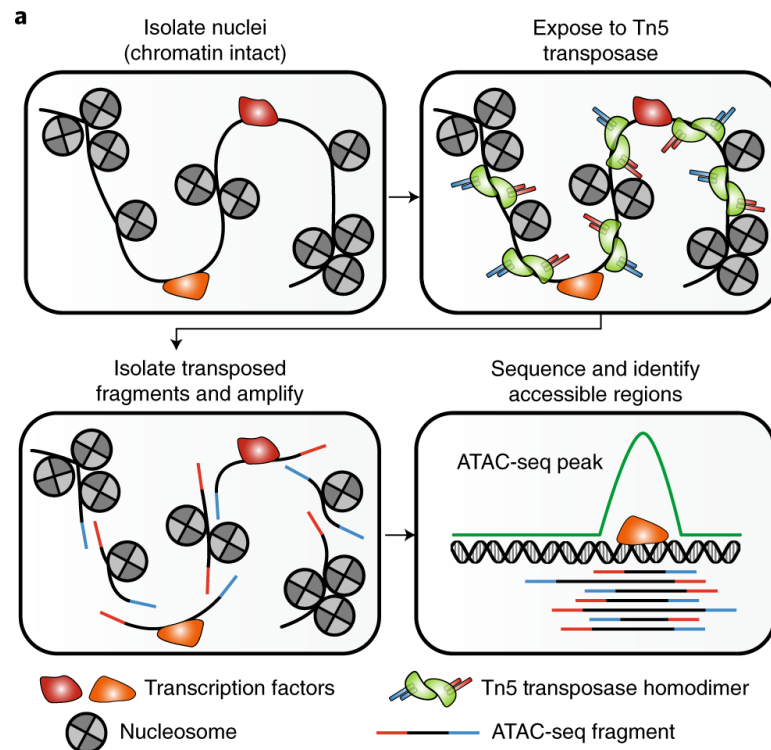


Background, Aim

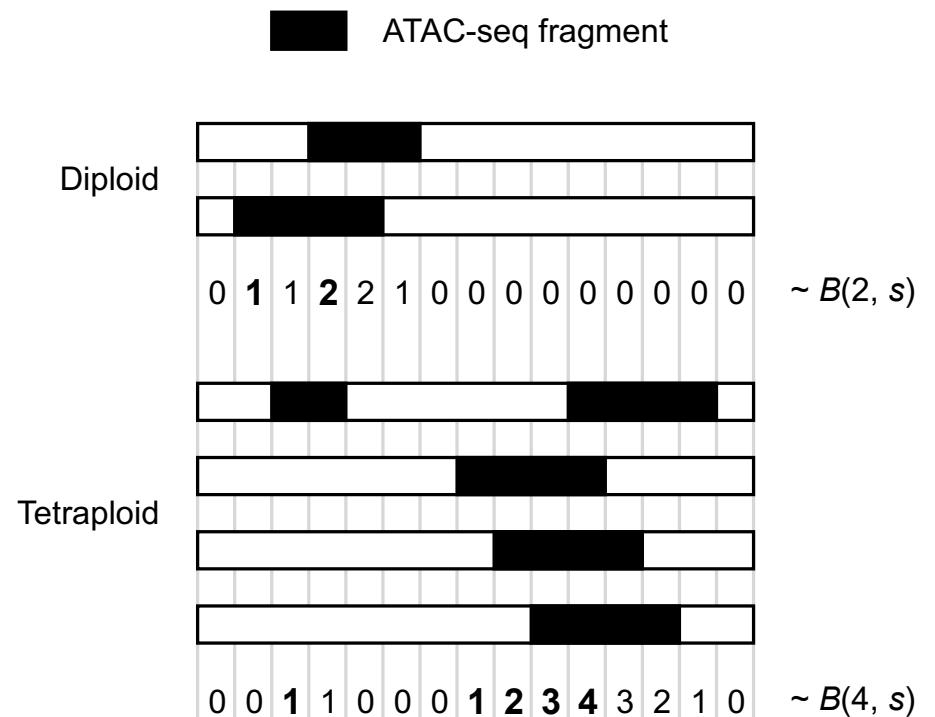
- Cells of different ploidy can constitute a tissue.
 - Hepatocyte: 2x, 4x, 8x
 - Cardiomyocyte: 2x, 4x
- Ploidy is related with cell function, damage, and regeneration.
- Standard experimental procedure is to stain DNA, separate by ploidy using a cell sorter, and perform single-cell analysis.
- If not sorted. **Infer ploidy based on ATAC-seq data.**

Methods

- ATAC-seq
 - Excise DNA fragments from open chromatin, and read by NGS.



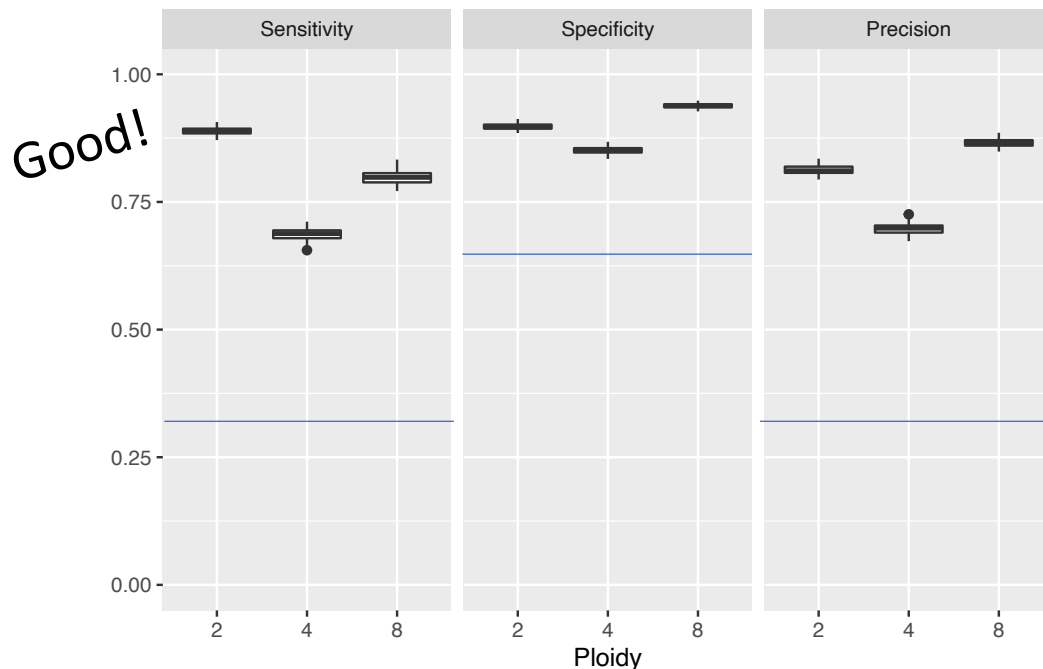
- Idea
 - In a diploid cell, # of DNA fragments derived from one specific locus is 0, 1 or 2.
 - If tetraploid, 0, 1, 2, 3 or 4.
 - Model by binomial distribution and infer ploidy.



Results

- Simulation

- From human peripheral blood mononuclear cells (diploid), generate a mixture of 2x, 4x, 8x (1521 each).



- Actual example

- Liver of a male rat (16 weeks old)
 - 4x, 8x should exist only in hepatocytes

# of nuclei	Prediction		
	2x	4x	8x
Hepatocyte	306	1427	593
Endothelial cell	457	125	0
Stellate cell	134	69	3
Macrophage	176	104	0
T, NK cell	81	40	0
B cell	38	18	1