

Analyzing heterogeneous single cell ATAC data with *ArchR*

Slides prepared by Kevin MacPherson

scATAC-seq reveals chromatin landscape

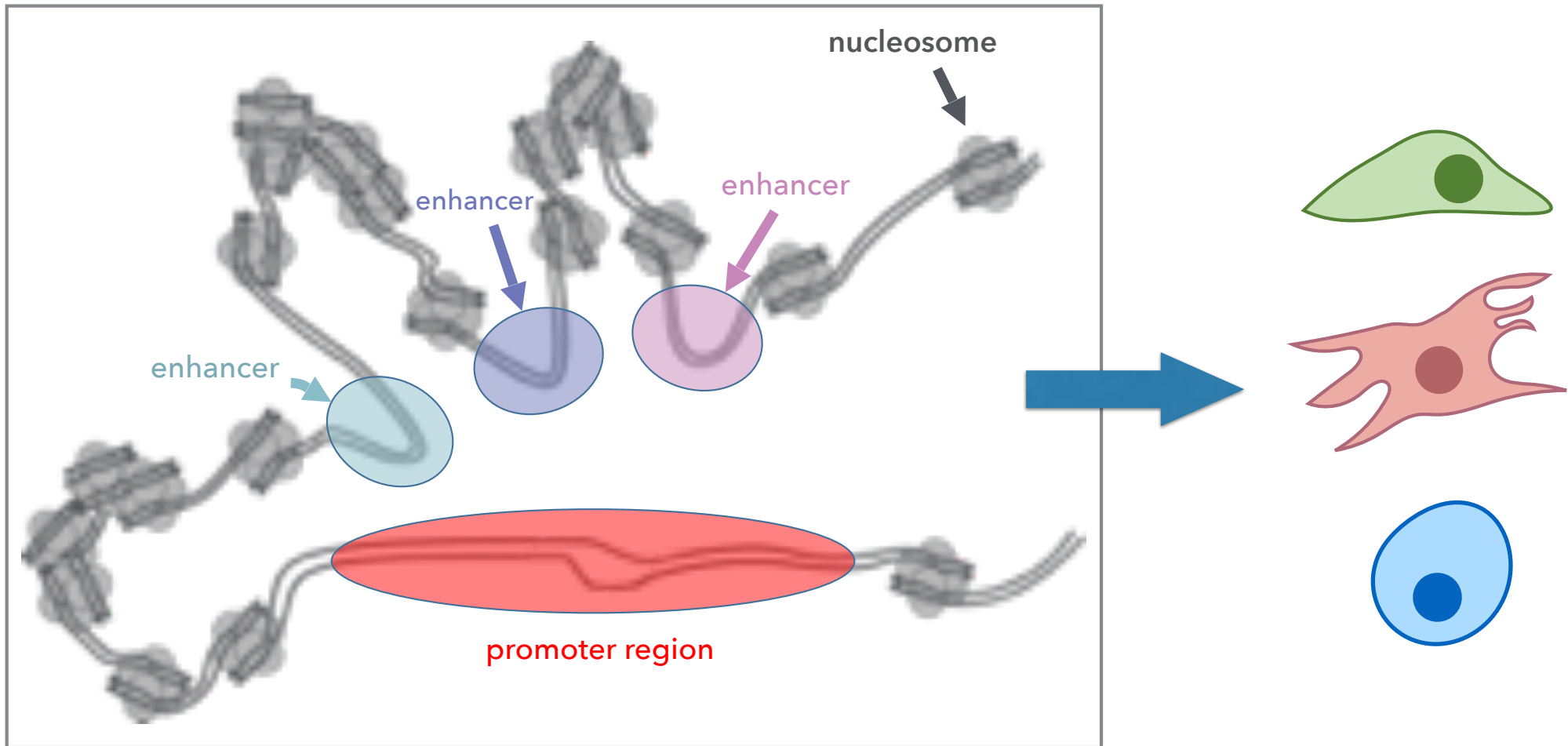
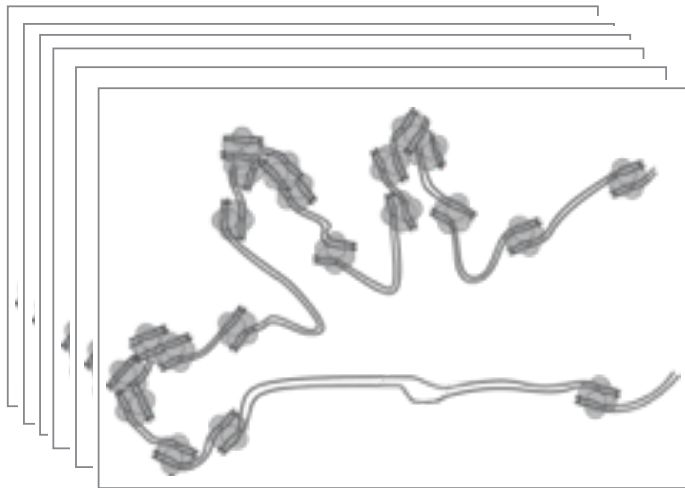
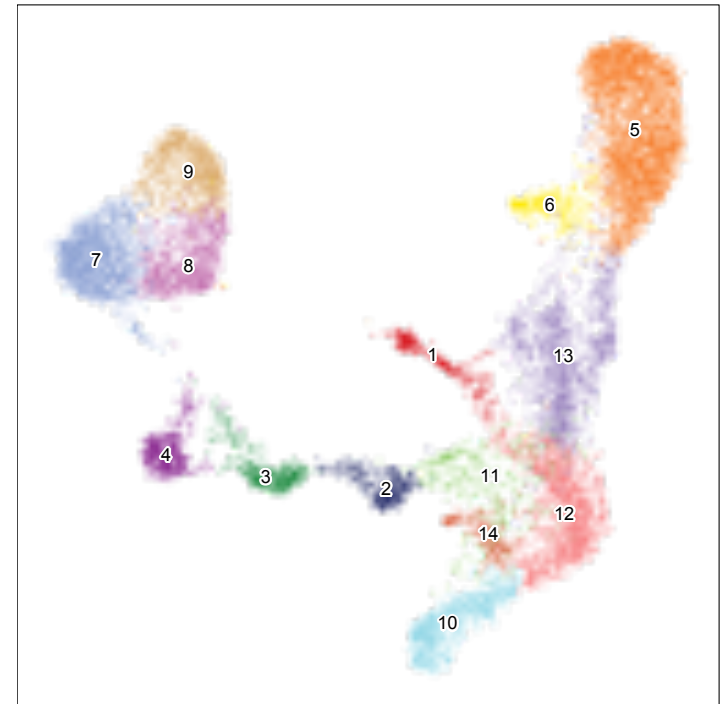


Figure courtesy of Ryan Mulqueen, PhD.

Heterogenous
Sample



Single cell ATAC profiles



Cell State Heterogeneity

<https://www.archrproject.com/articles/Articles/tutorial.html>

ArchR: Analysis of Regulatory Chromatin in R



ArchR: Analysis of Regulatory Chromatin in R

Read ATAC signal across genome



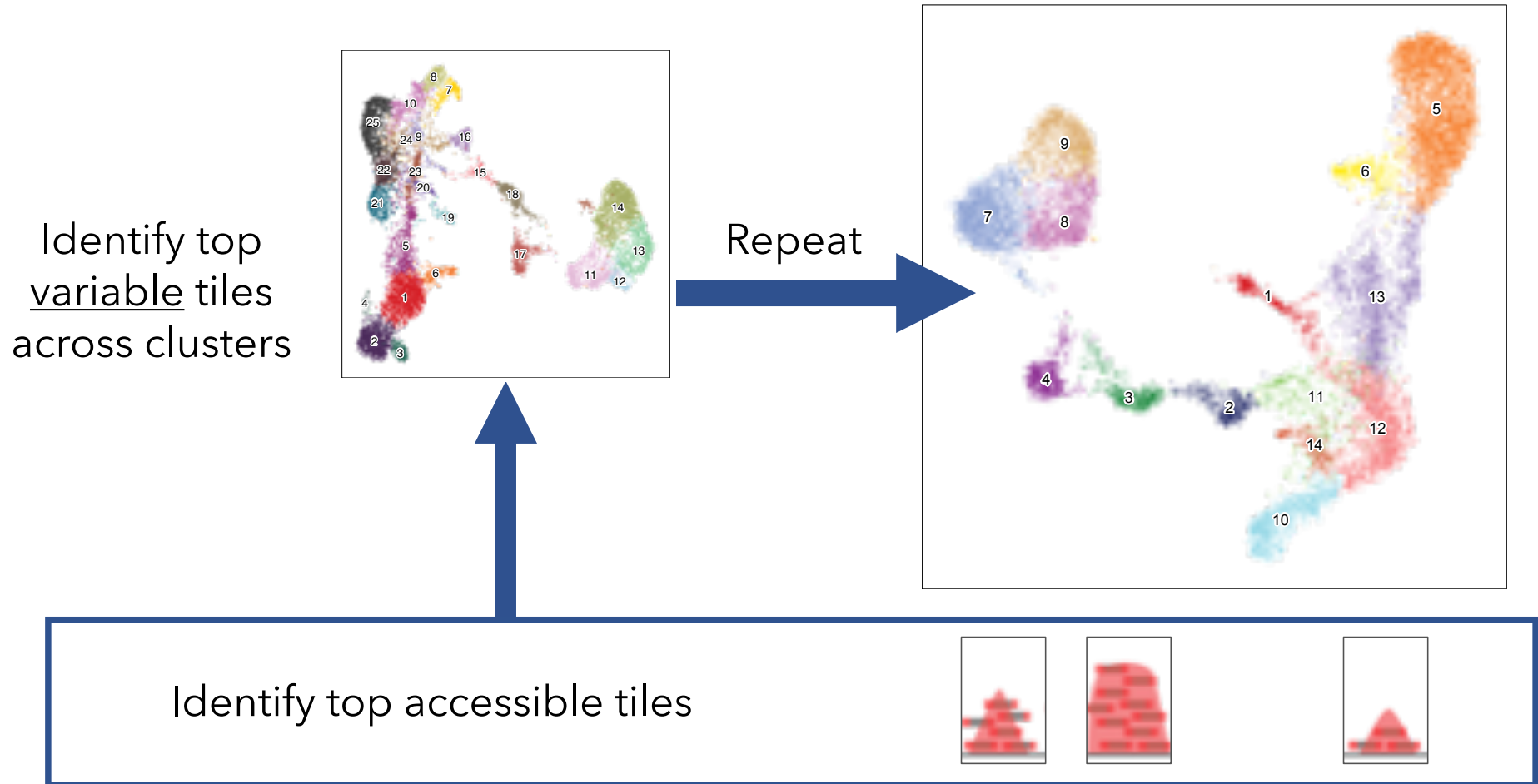
Split genome into 500 bp tiles



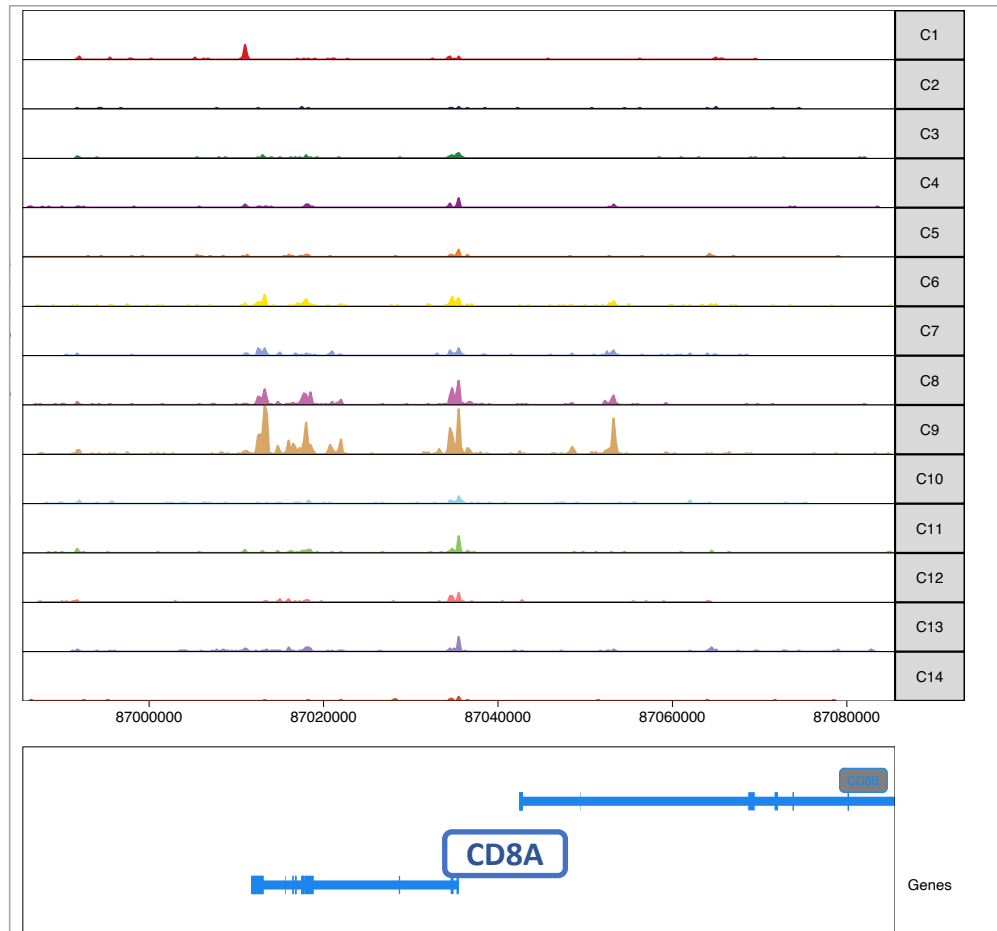
Identify top accessible tiles



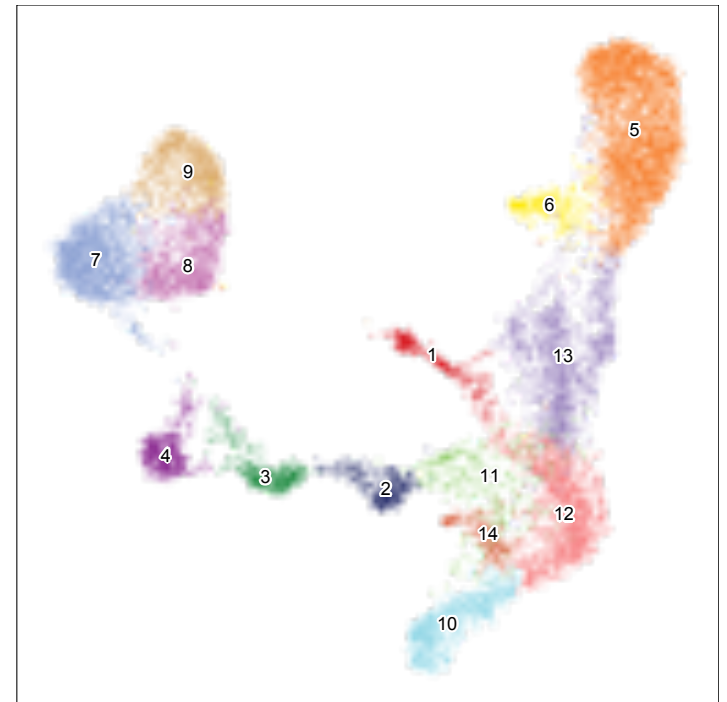
ArchR: Analysis of **R**egulatory **C**hromatin in **R**



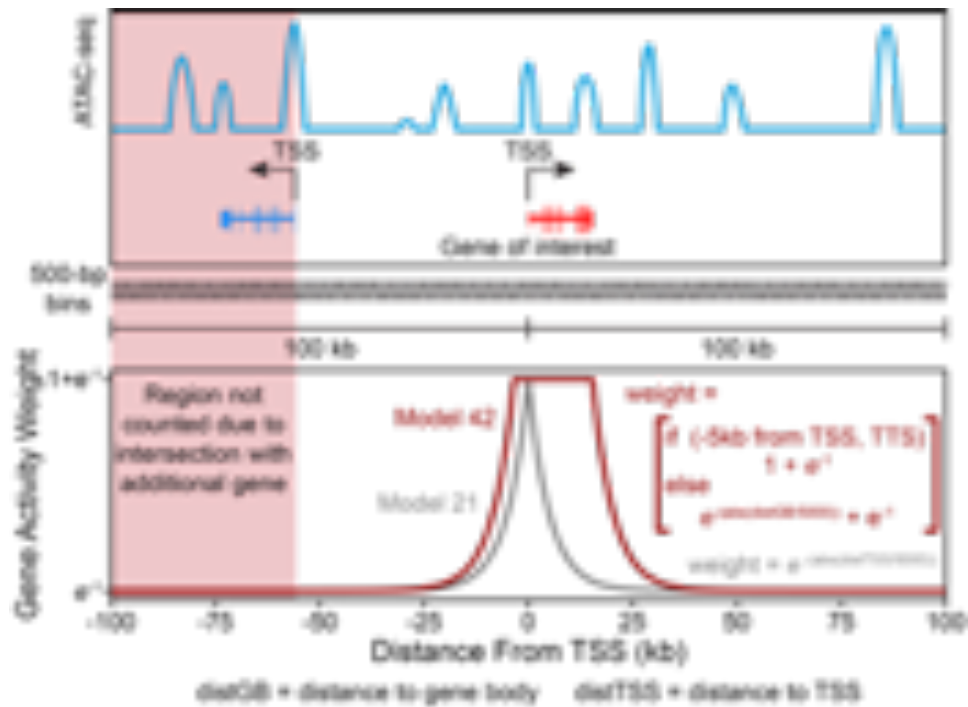
ArchR: Genome Browser View



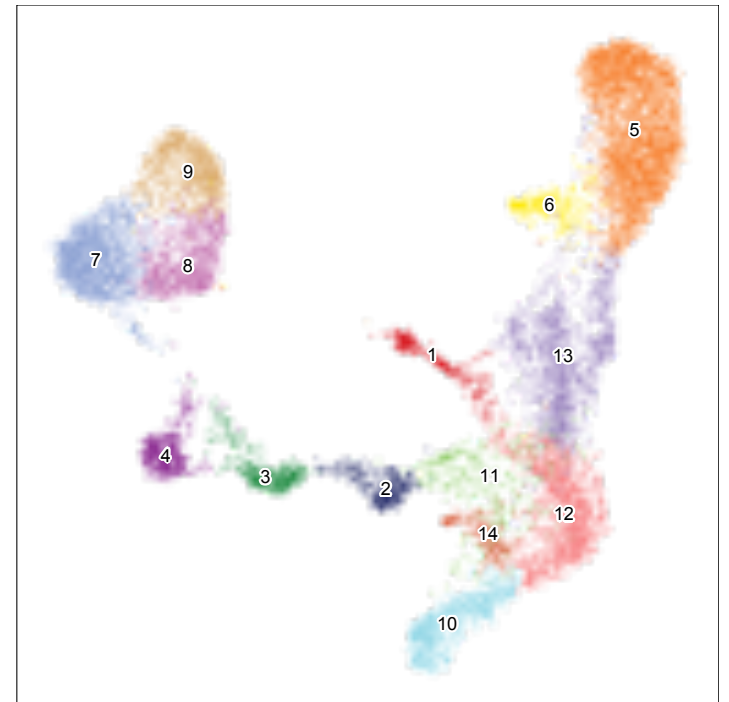
CD8⁺ T-cells in Cluster 9



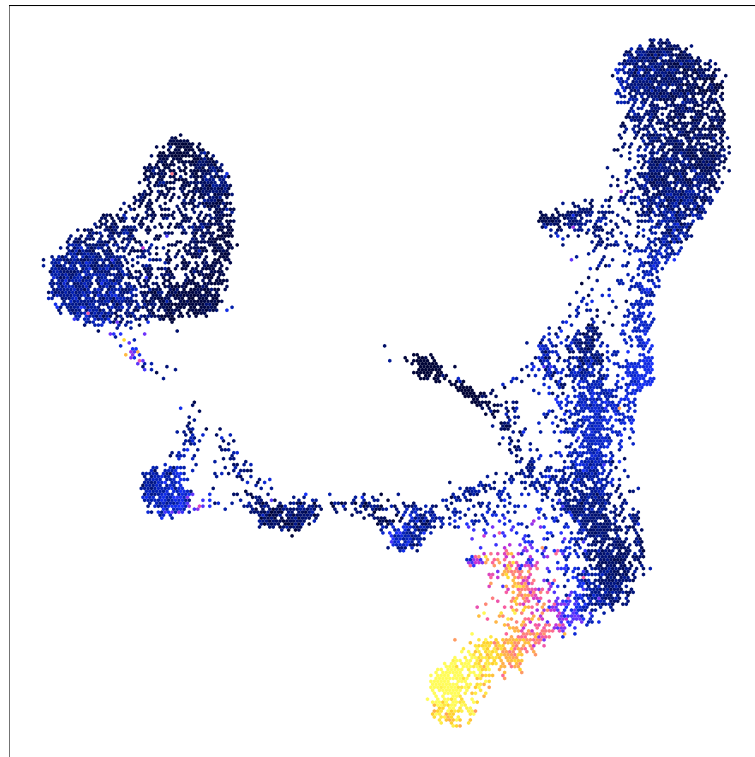
ArchR: Gene Accessibility Scoring



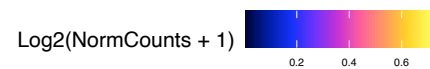
<https://www.archrproject.com/bookdown/calculating-gene-scores-in-archr.html>



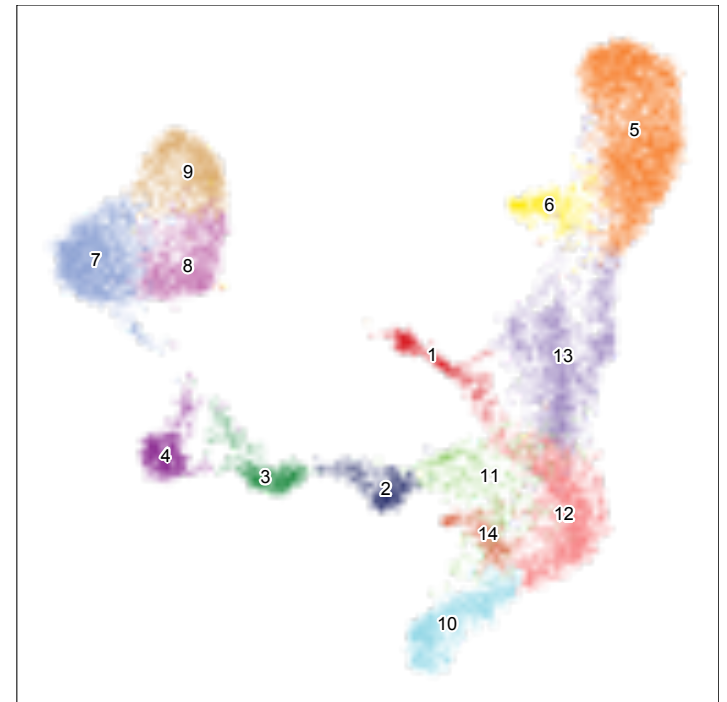
ArchR: Gene Accessibility Scoring



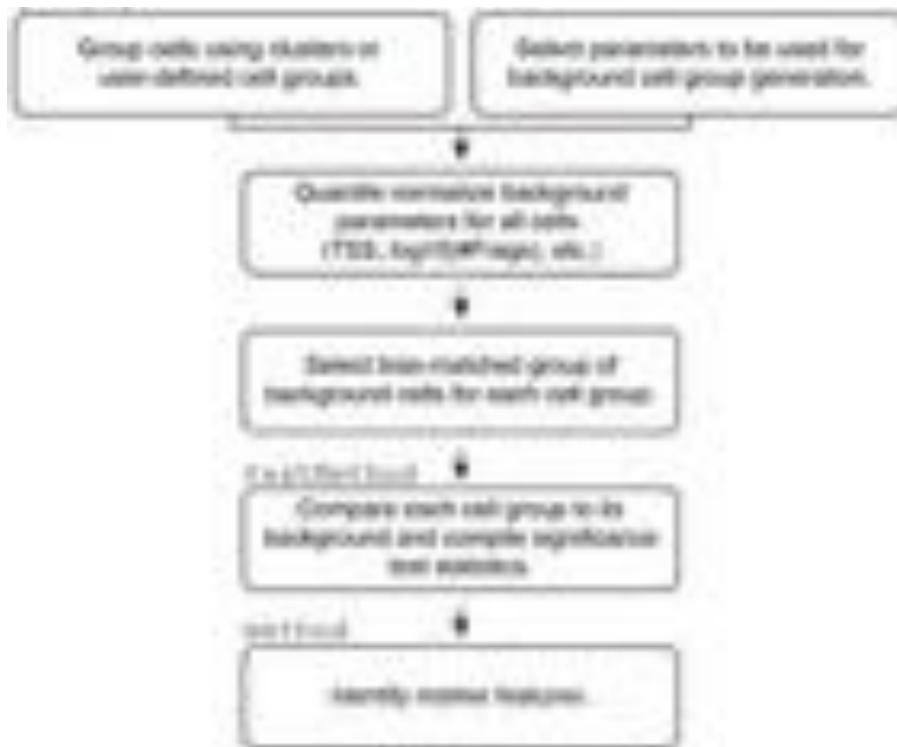
GATA1 Gene Score



Early Progenitor cells in Cluster 10

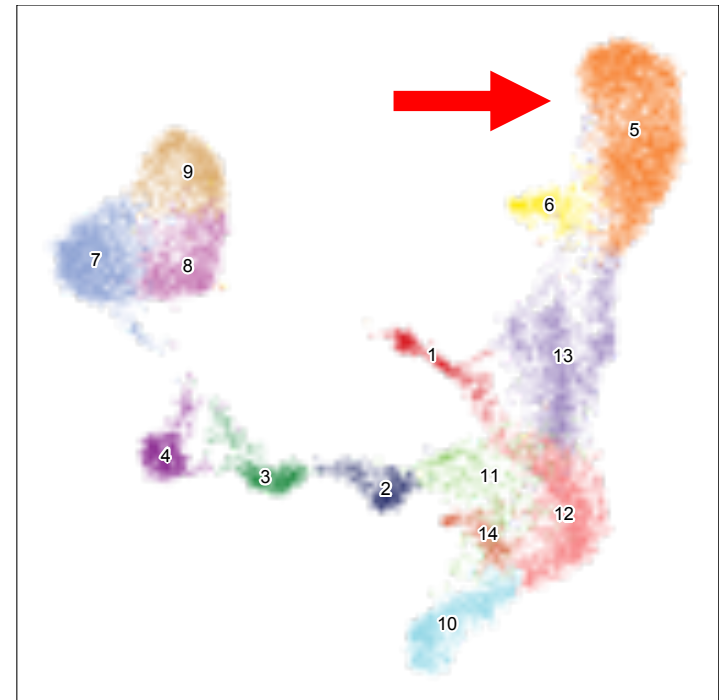


ArchR: Marker Gene identification

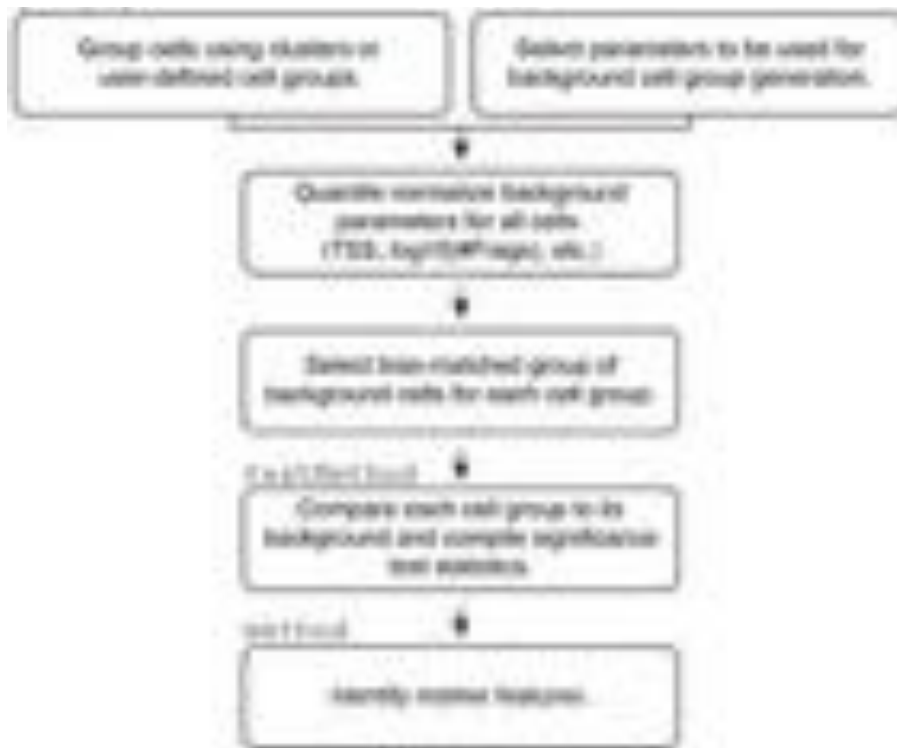


<https://www.archrproject.com/bookdown/identification-of-marker-features.html>

CD14 is an ArchR-called marker gene for Cluster 5

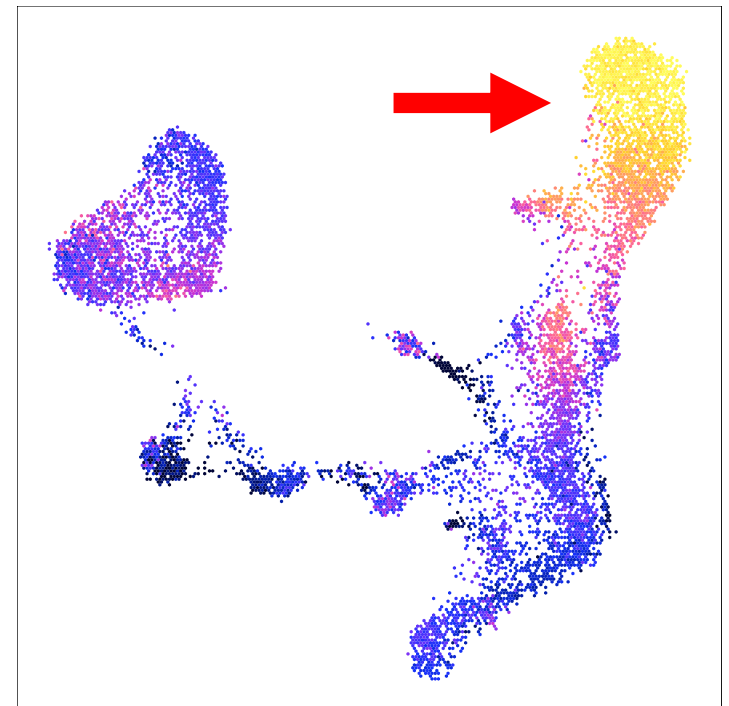


ArchR: Marker Gene identification

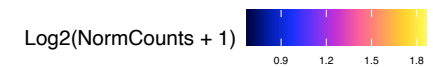


<https://www.archrproject.com/bookdown/identification-of-marker-features.html>

CD14 is an ArchR-called marker gene for Cluster 5



CD14 Gene Score



Peak-based analysis

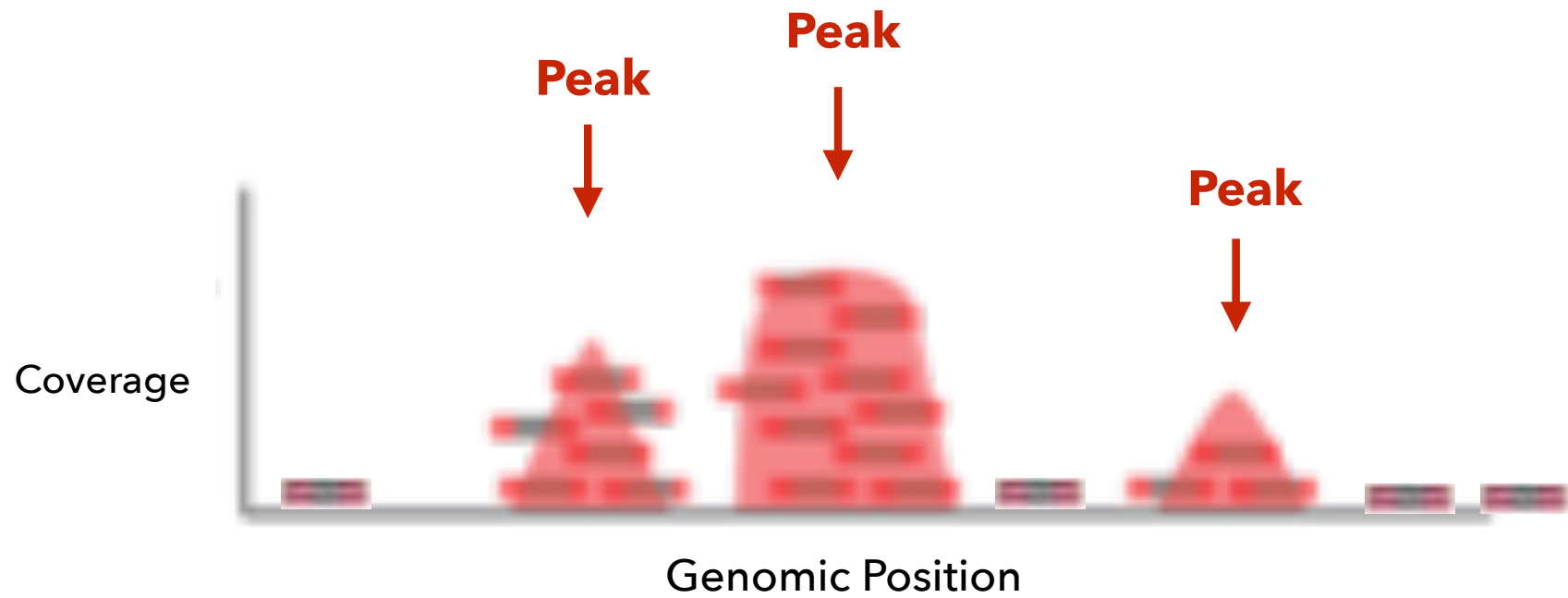
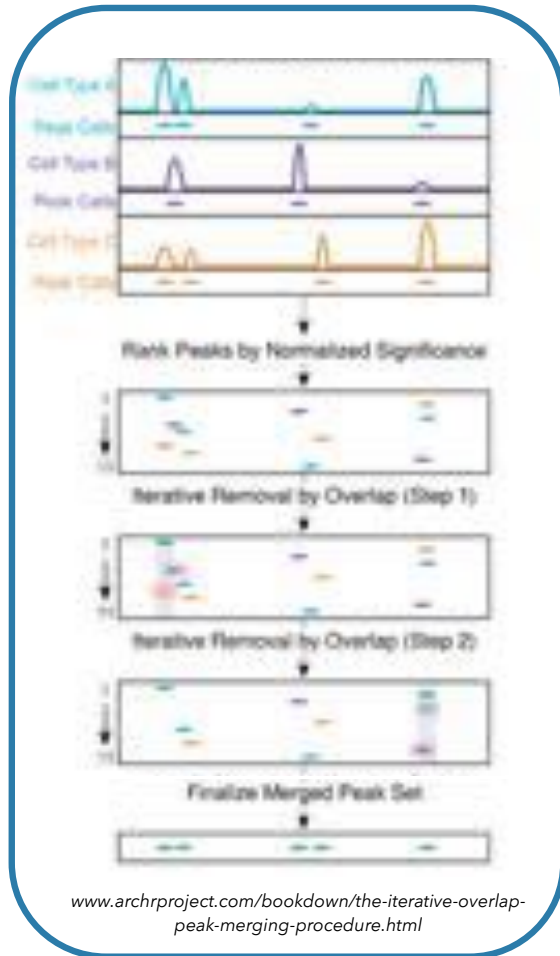
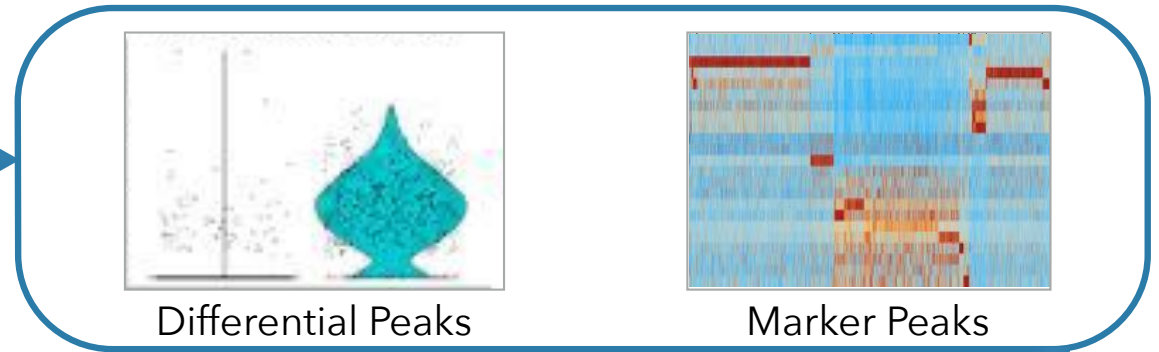


Figure courtesy of Ryan Mulqueen, PhD.

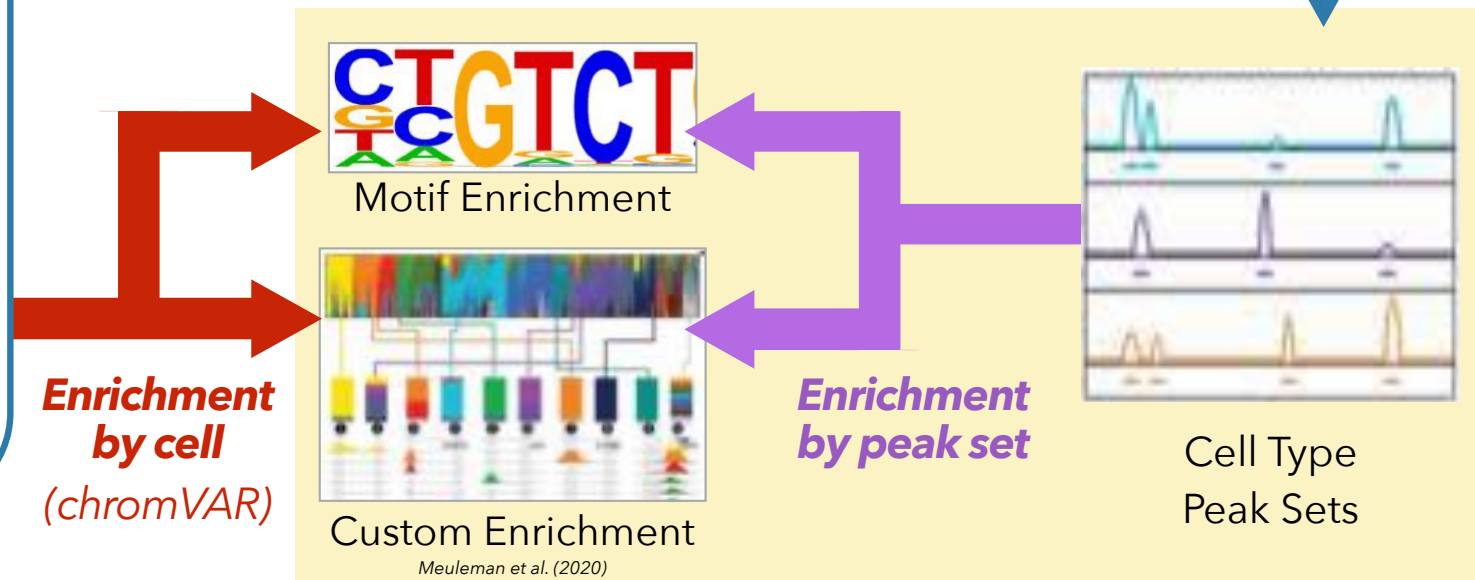
Peak Calling



Peak Testing



Feature Enrichment



Resources

ArchR tutorial & manual

- <https://www.archrproject.com/>

ArchR GitHub

- <https://github.com/GreenleafLab/ArchR>

ArchR publication

- Granja, J. M., Corces, M. R., *et al.* (2021). ArchR is a scalable software package for integrative single-cell chromatin accessibility analysis. *Nature genetics*, 53(3), 403–411.

Data used in this presentation:

- Granja, J. M., Klemm, S., *et al.* (2019). Single-cell multiomic analysis identifies regulatory programs in mixed-phenotype acute leukemia. *Nature biotechnology*, 37(12), 1458–1465.