



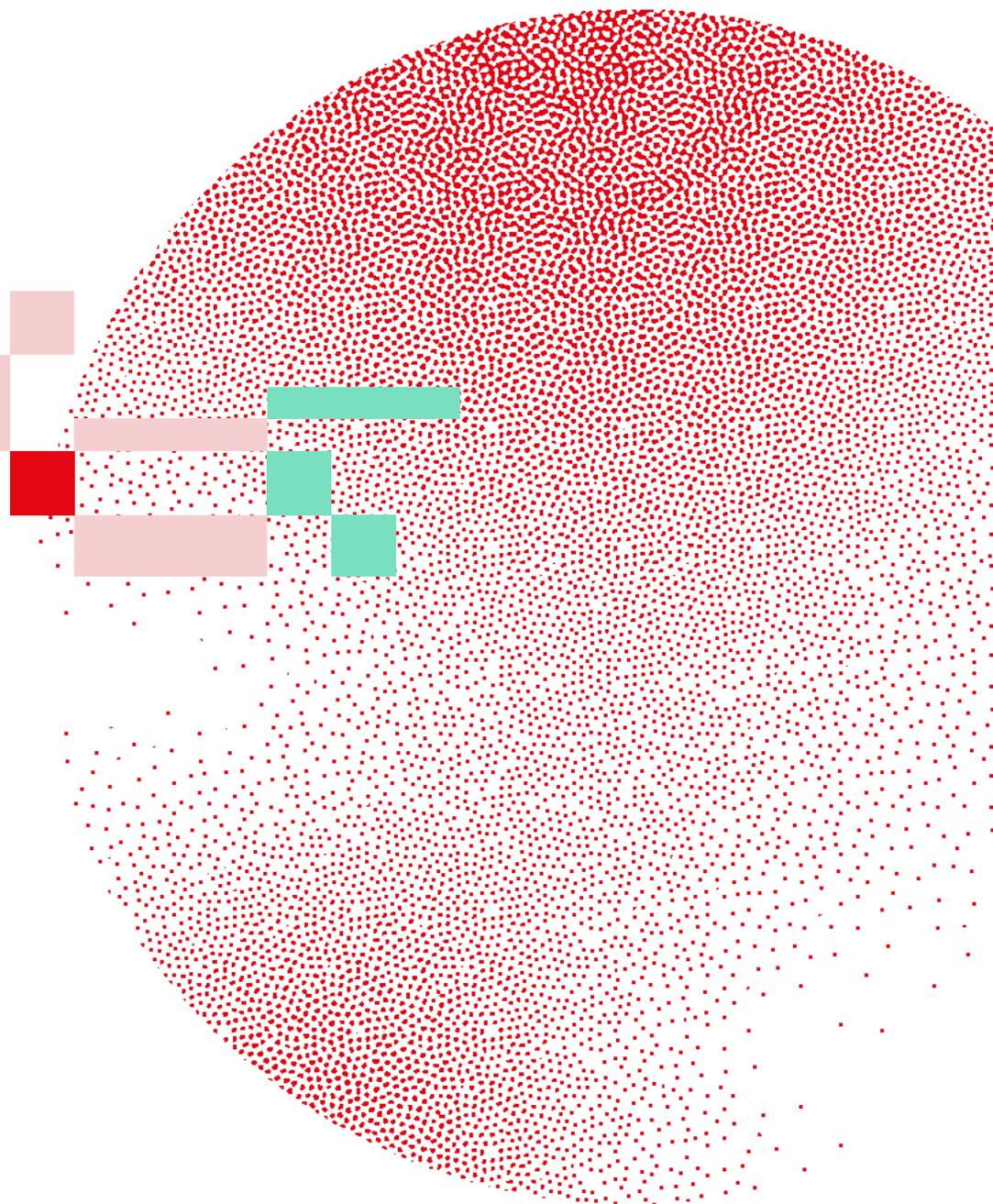
Swiss Institute of
Bioinformatics

BIOLOGY-INFORMED MULTIOMICS DATA INTEGRATION AND
VISUALIZATION

Integration of chromatin accessibility and gene expression data

Deepak Tanwar

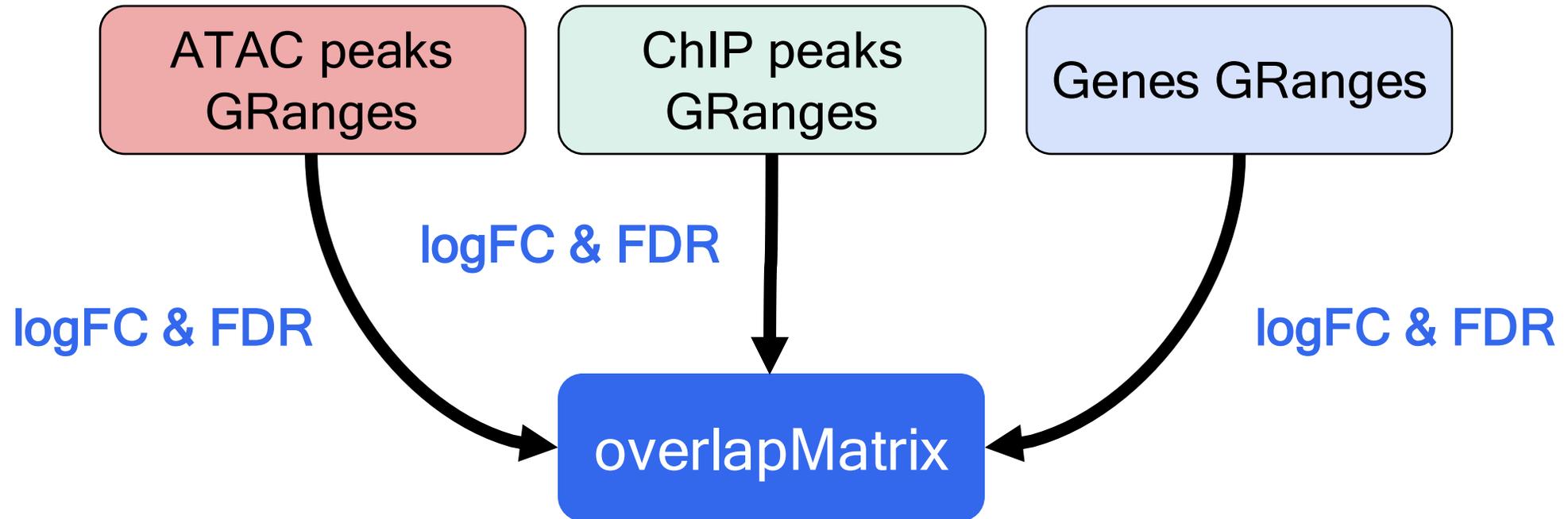
June 16-17, 2025



Learning outcomes

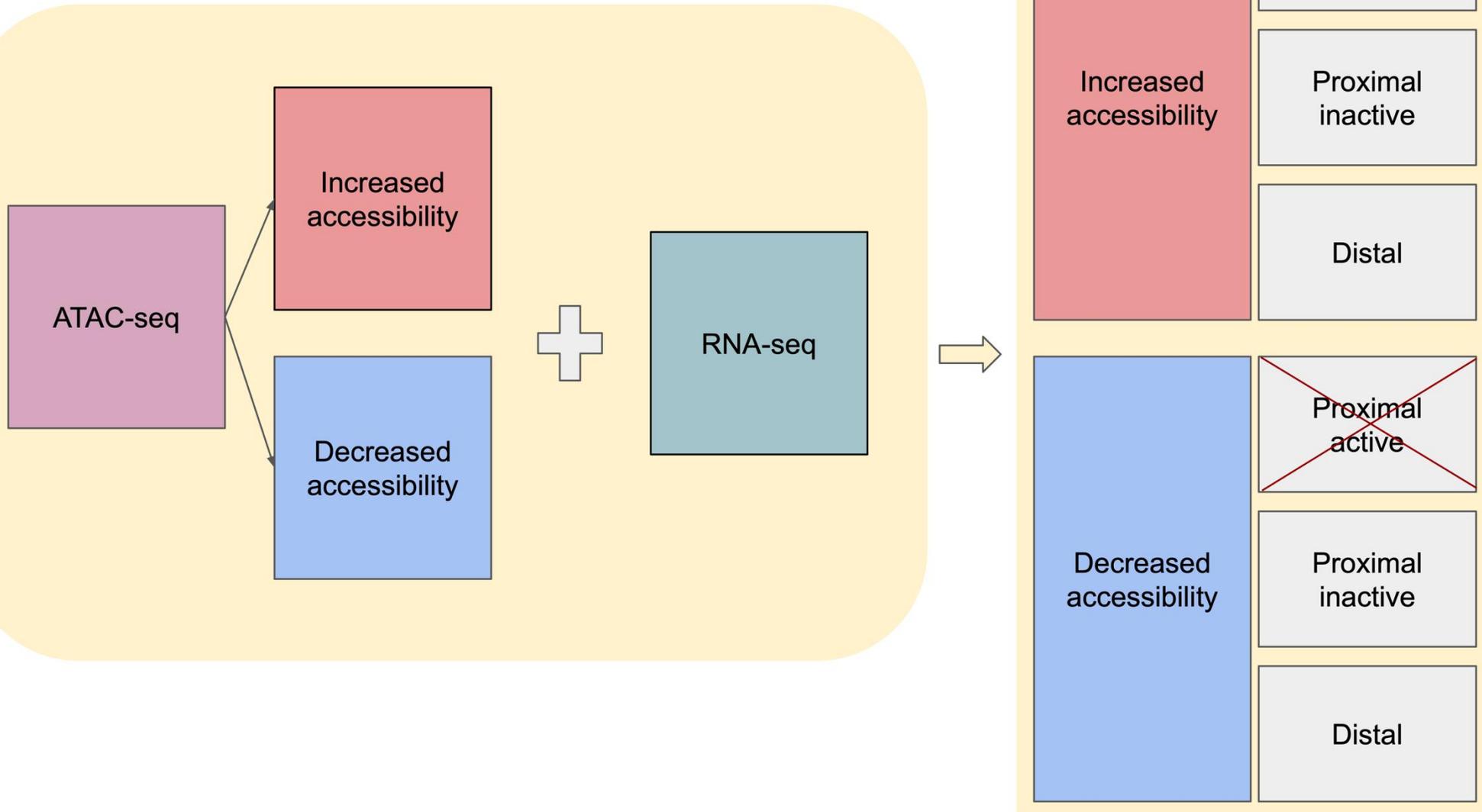
Interpreting integration of chromatin accessibility with gene expression

Pipeline for overlapMatrix

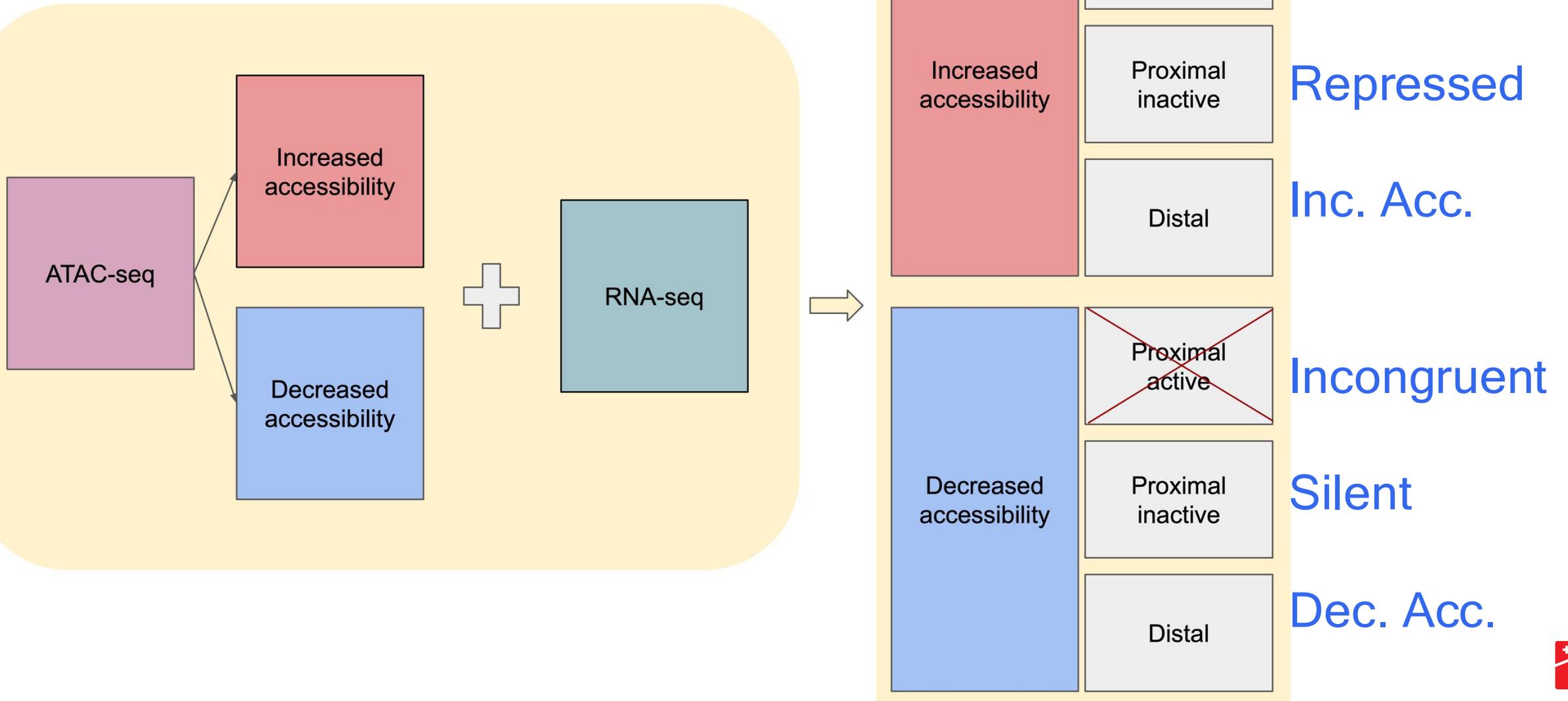


Keeping all regions from ATAC-seq

Integration of RNA-seq and ATAC-seq



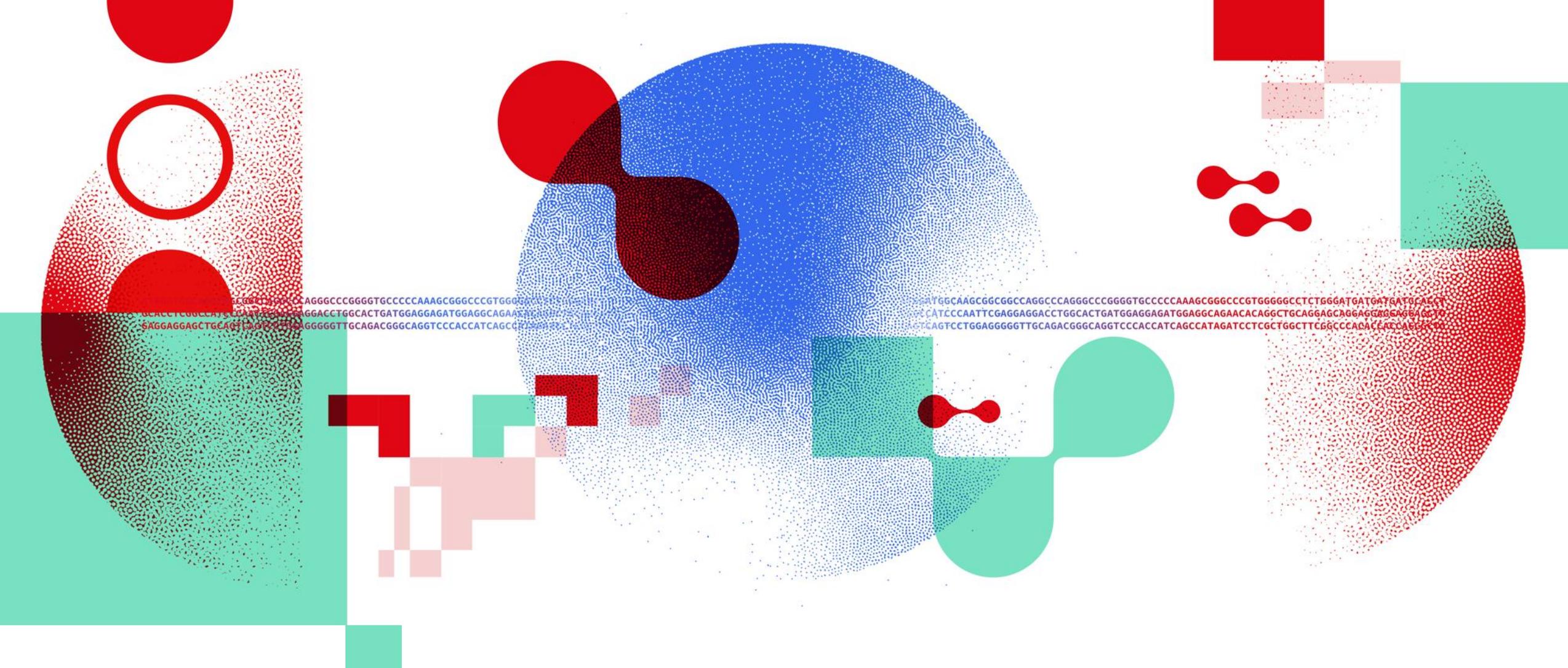
Integration of RNA-seq and ATAC-seq



Joint Interpretation of Chromatin Accessibility and Gene Expression

Category	ATAC-seq	RNA-seq	Interpretation
Active	↑	↑	Open chromatin & expressed gene → active regulatory element
Repressed	↓	↓	Closed chromatin & reduced gene expression
Inc. Acc.	↑	~ No change	Gained accessibility without expression → <i>primed</i> region?
Incongruent	↓	↑	Reduced accessibility but gene is expressed → <i>distal activation?</i>
Silent	↓	~ No expression	Closed chromatin & no transcription → inactive/silent
Dec. Acc.	↓	~ No change	Lost accessibility but RNA unchanged or not present?

Exercise 5



...AGGGCCCGGGTGCCCCAAAGCGGGCCGTGGG...
...GACCTCGCCATGCTAATG...GGACCTGGCACTGATGGAGGAGATGGAGGCAGAA...
...SAGGAGGAGCTGCAGT...AGGGGGTTGCAGACGGGCAGGTCACCATCAGCC...

...TGGCAAGCGGGCCAGGCCAGGGCCCGGGTGCCCCAAAGCGGGCCGTGGGGCCTCTGGGATGATGATGATGCACT...
...CATCCCAATTCGAGGAGGACCTGGCACTGATGGAGGAGATGGAGGCAGAACACAGGCTGCAGGAGCAGGAGGAGGAGGCT...
...TCAGTCCTGGAGGGGGTTGCAGACGGGCAGGTCACCATCAGCCATAGATCCTCGCTGGCTTCGGCCCAACACACAGGCT...

Thank you

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