BIOLOGY-INFORMED INTEGRATION AND VISUALIZATION OF MULTIOMICS DATA

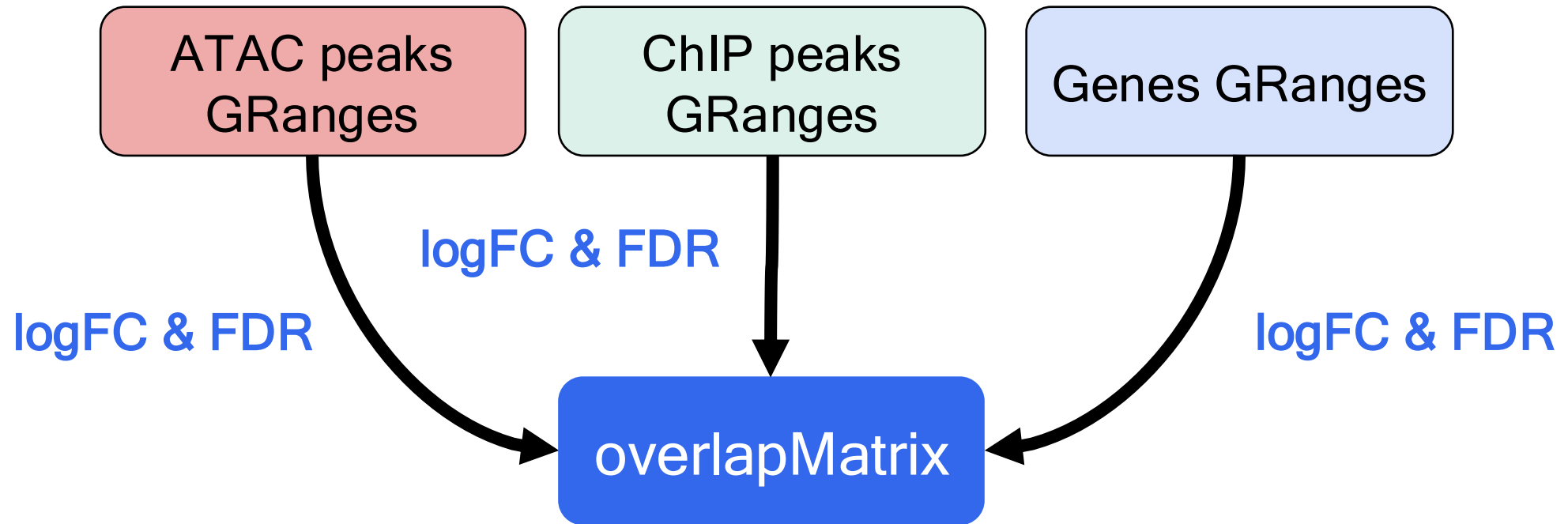# Integration of chromatin accessibility and gene expression data

Deepak Tanwar
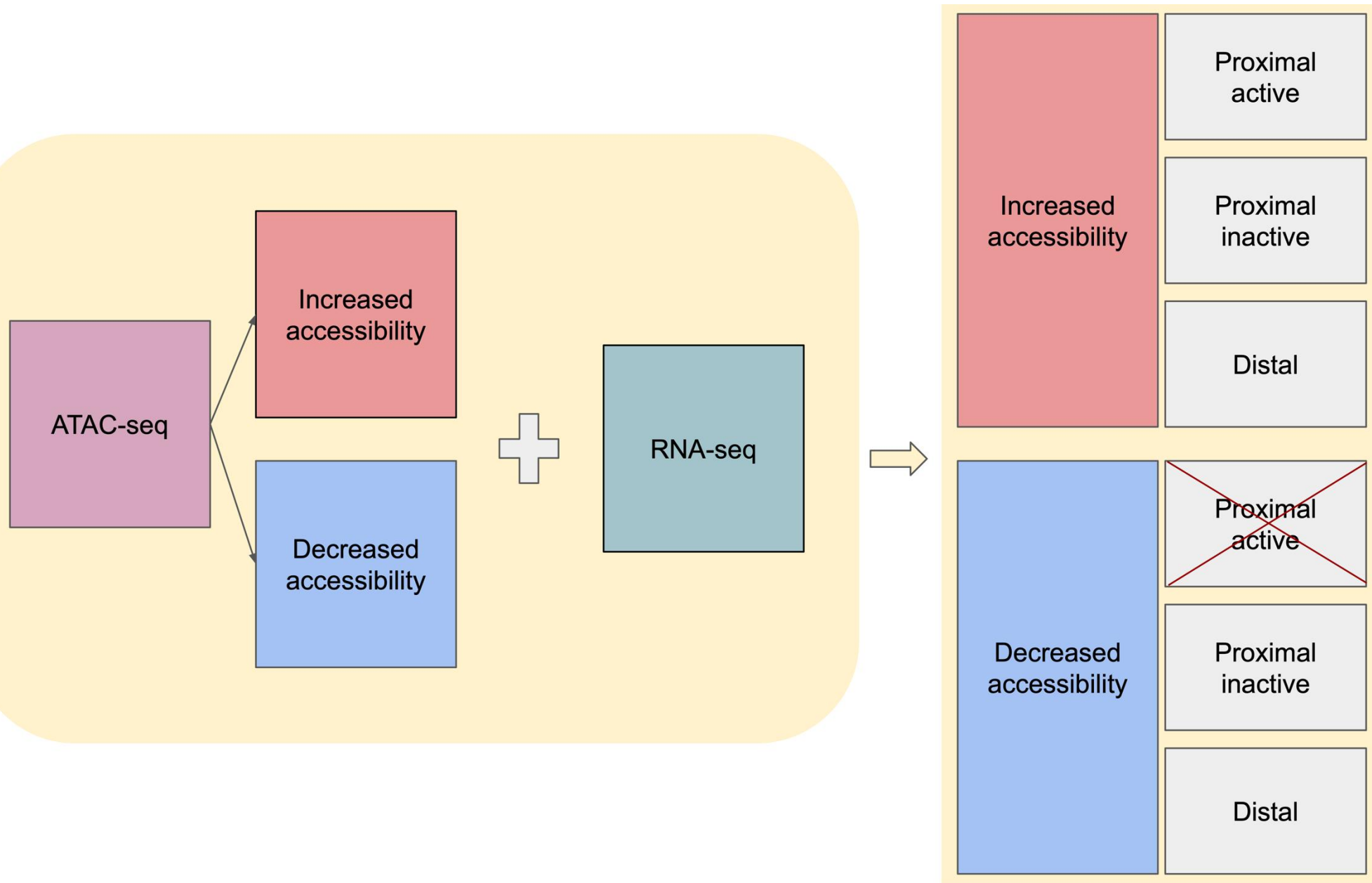
February 17-19, 2026

Learning outcomes

Interpreting integration of chromatin accessibility with gene expression
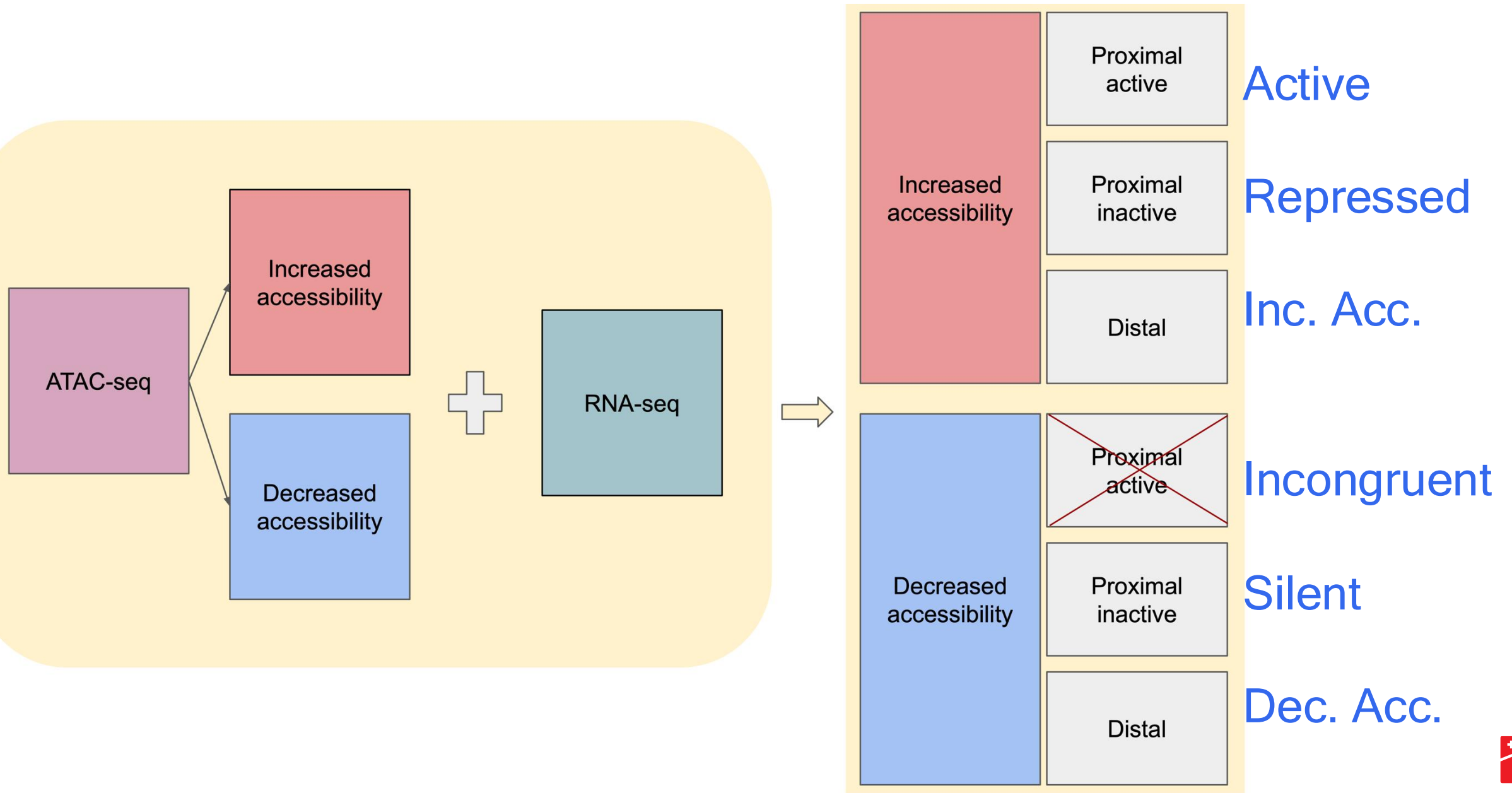
Pipeline for overlapMatrix
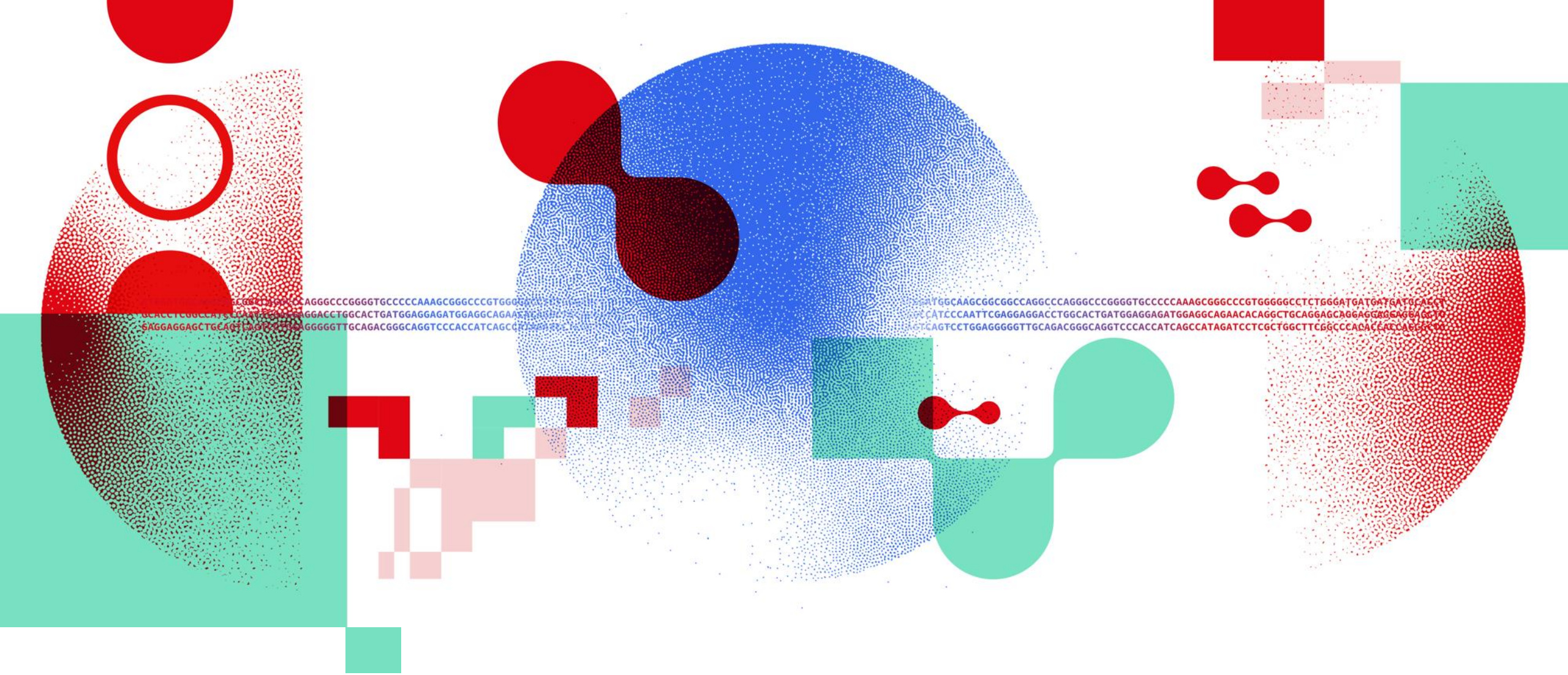
Integration of RNA-seq and ATAC-seq

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Joint Interpretation of Chromatin Accessibility and Gene Expression

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

SIB

Exercise 5

Thank you

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