



Swiss Institute of
Bioinformatics

BIOLOGY-INFORMED INTEGRATION AND VISUALIZATION OF
MULTIOMICS DATA

Integration of chromatin accessibility and gene expression data

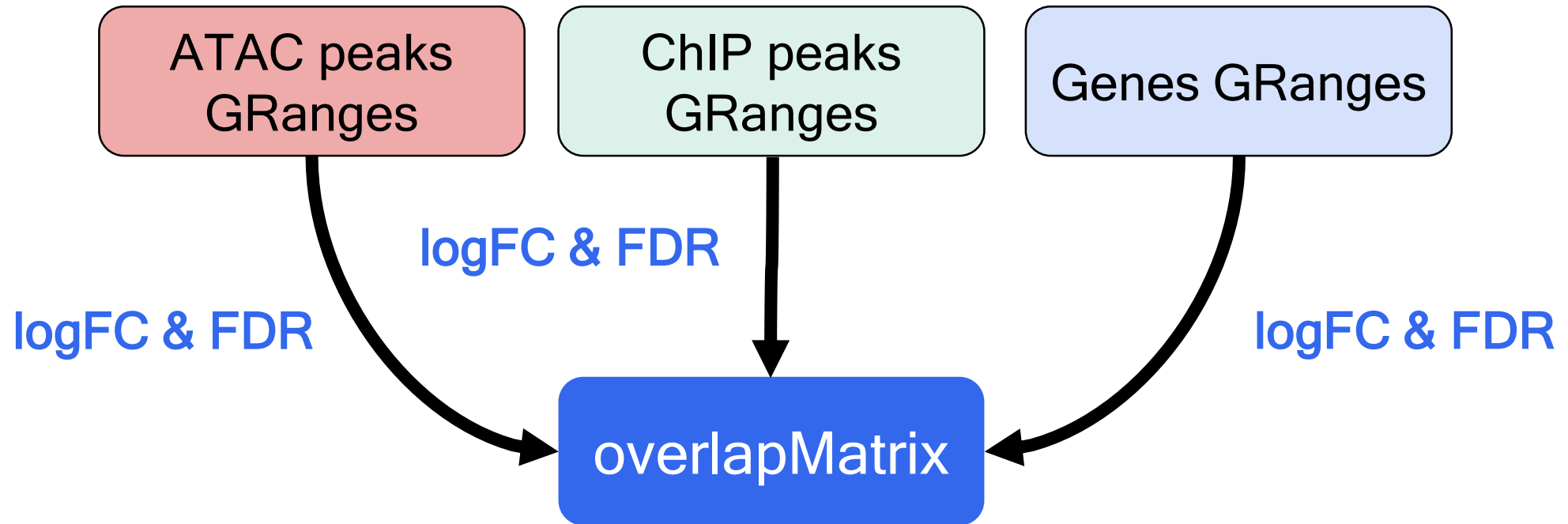
Deepak Tanwar

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Learning outcomes

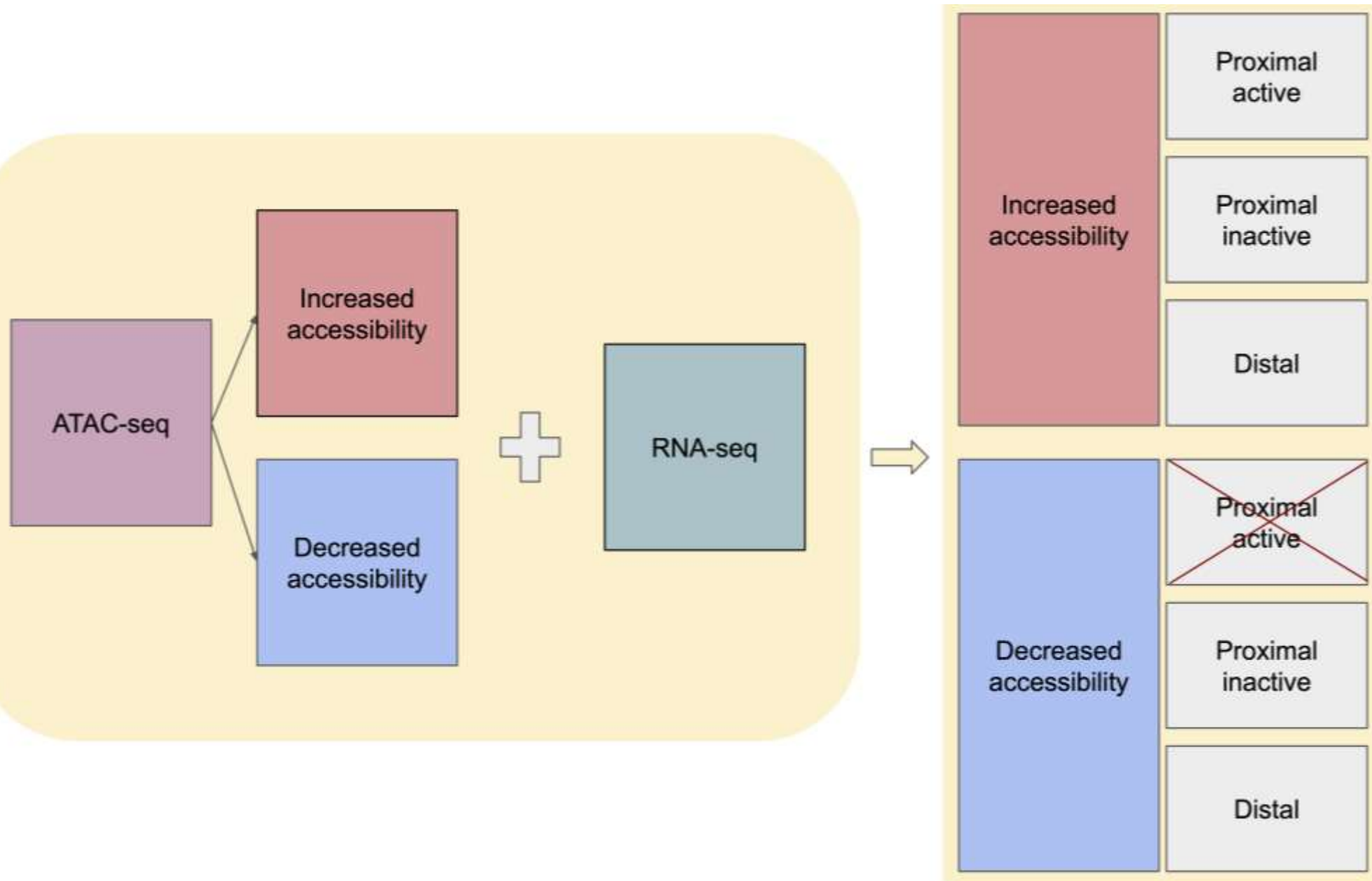
Interpreting integration of chromatin accessibility with gene expression

Pipeline for overlapMatrix

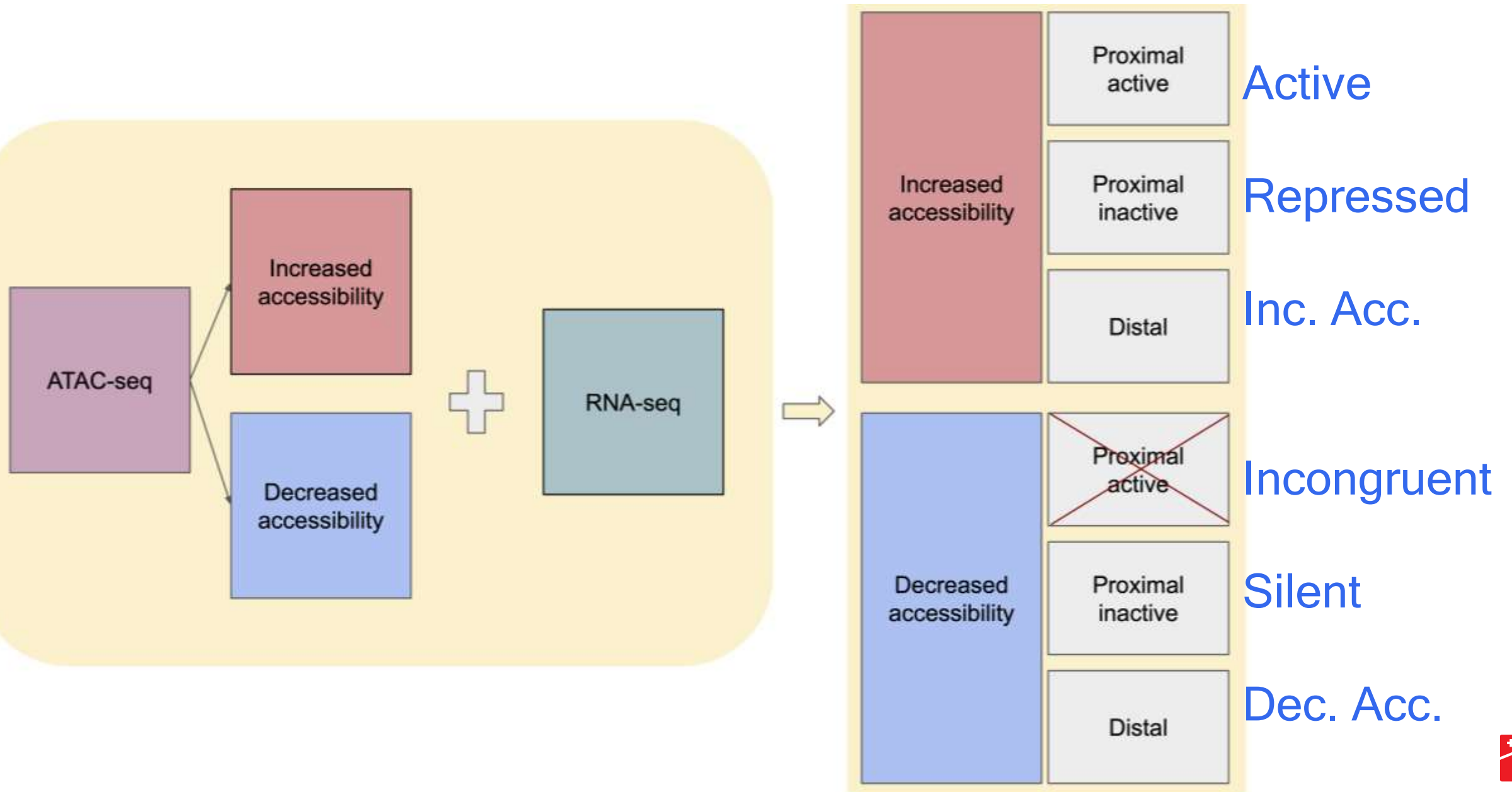


Keeping all regions from ATAC-seq

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

