

Swiss Institute of Bioinformatics

BIOLOGY-INFORMED MULTIOMICS DATA INTEGRATION AND VISUALIZATION

# Integration of multi-omics data

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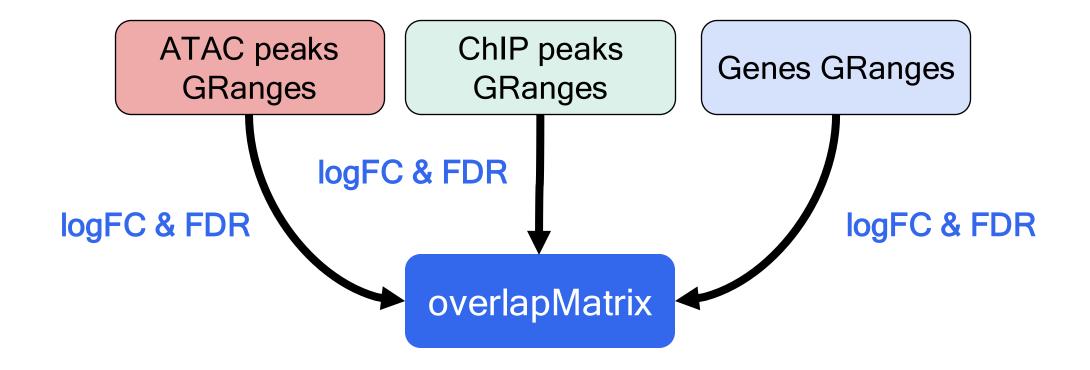


#### Learning outcomes

Interpreting integration of chromatin accessibility, histone modifications and gene expression



#### Pipeline for overlapMatrix



## Keeping all regions from ATAC-seq



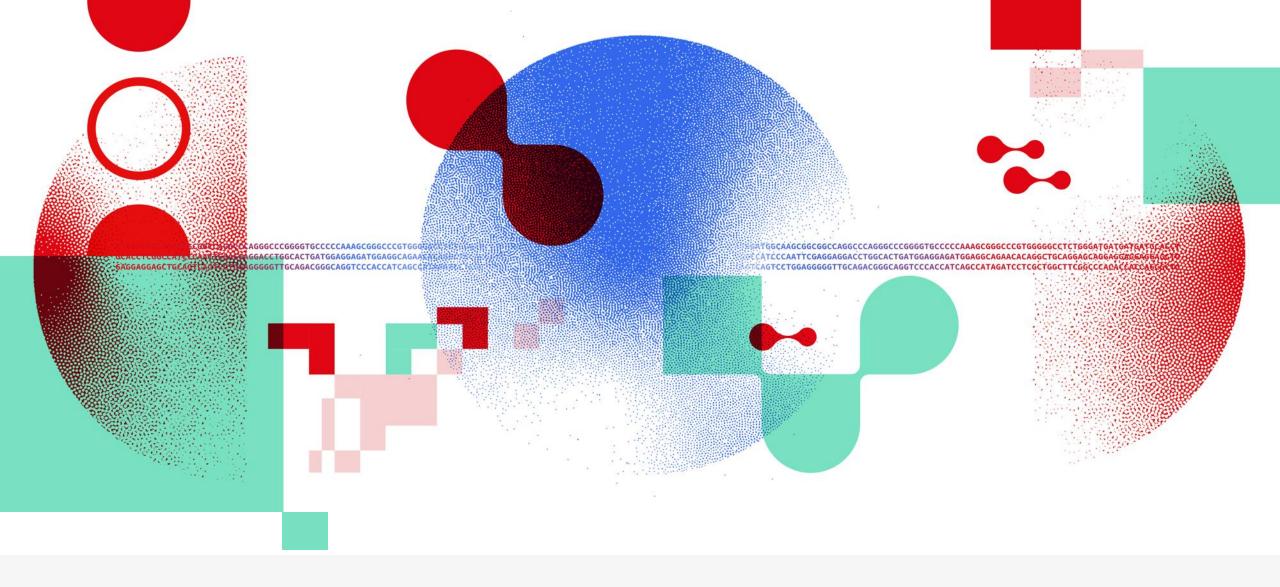
### Regulatory regions from multi-omics data

Category	ATAC	H3K4me1	H3K27ac	H3K4me3	H3K27me3	RNA	Dist. to TSS
Gained Enhancers	<b>↑</b>	<b>↑</b>	<b>↑</b>	none	-	<b>↑</b>	>2500 bp
Lost Enhancers	<b>↓</b>	<b>↓</b>	<b>↓</b>	none	-	<b>\</b>	>2500 bp
Active Promoters	<b>↑</b>	_	<b>↑</b>	<b>↑</b>	<b>-</b>	<b>↑</b>	<2500 bp
Repressed Promoters	<b>↓</b>	_	<b>↓</b>	<b>↓</b>	<b>↑</b>	<b>↓</b>	<2500 bp



## Exercise 6





## Thank you

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