Swiss Institute of Bioinformatics

BIOLOGY-INFORMED INTEGRATION AND VISUALIZATION OF MULTIOMICS DATA

Data overlapMatrix

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Learning outcomes

- What is overlapMatrix?
- Why do we need it?
- How to make it?

Multi-omics data snapshot

ATAC-seq
ChIP-seq

seqnames	start	end	strand	Symbol	distanceTSS	Group1	Group2
chr1	1	70	+	Gene1	5000	11	21
chr1	100	400	-	Gene1	5000	10	100
chr1	200	290	+	Gene3	2000	200	1000
chr2	300	500	-	Gene4	3000	400	1300
chr2	20	100	+	Gene5	20000	20	120
chr3	40	200	-	Gene6	40000	540	40
chr4	15	150	-	Gene7	150	1500	15

RNA-seq

Gene	Transcript	seqnames	start	end	Group1	Group2
Gene1	Transcript1	chr1	1	1000	100	0
Gene1	Transcript2	chr1	100	12000	0	110
Gene3	Transcript1	chr1	200	500	70	1000
Gene4	Transcript1	chr2	300	900	400	30
Gene5	Transcript1	chr2	20	2000	20	1
Gene6	Transcript1	chr3	40	4000	1	0
Gene7	Transcript1	chr4	15	150	0	0

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Differential analysis results

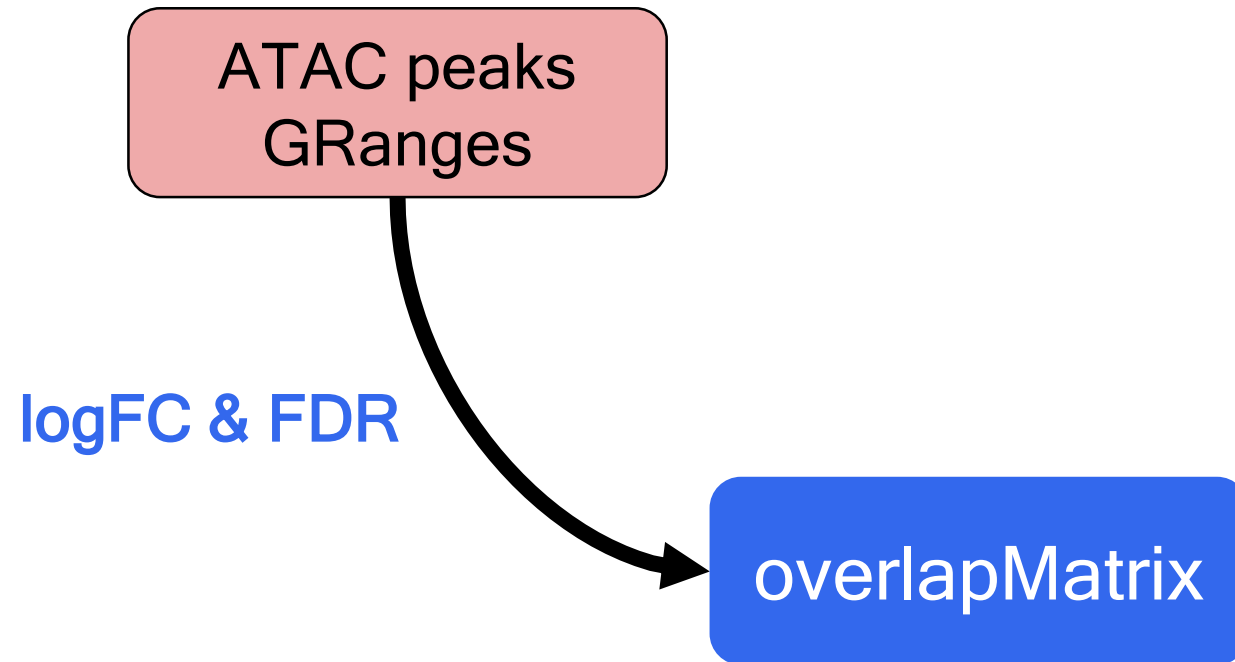| Assay	Analysis	Output
ATAC	Differential Accessibility	Statistically significant Peaks
ChIP	Differential Enrichment	Statistically significant Peaks
RNA	Differential Expression	Statistically significant Genes

Which assay to use as the anchor for overlaps?

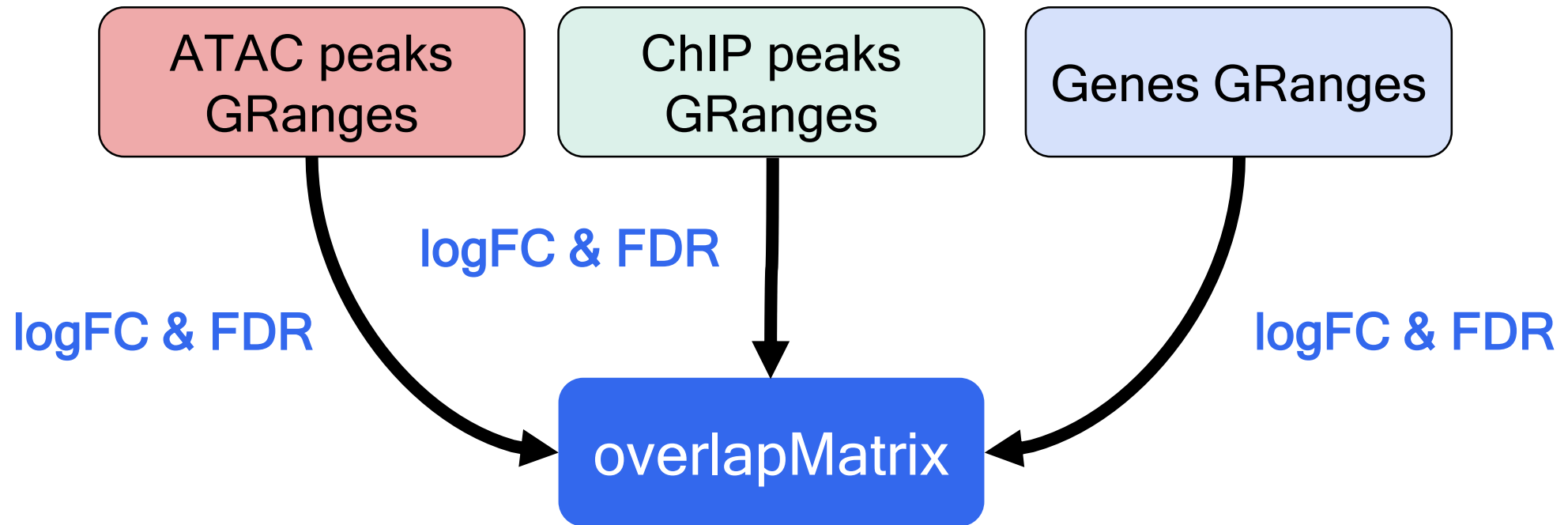1. RNA-seq

2. ChIP-seq

3. ATAC-seq

Which assay to use as the anchor for overlaps?

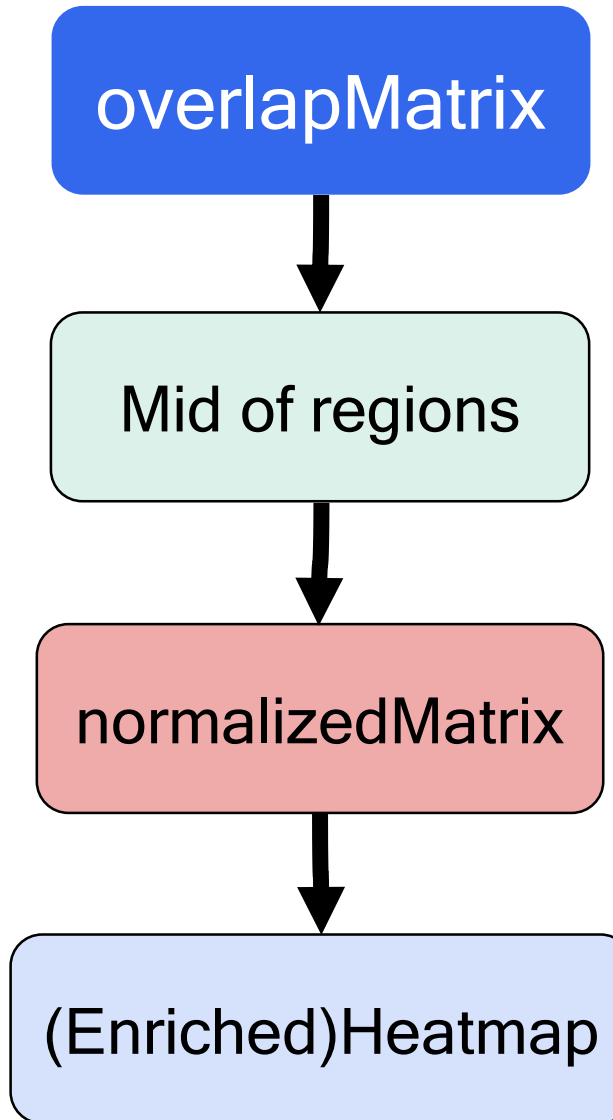| Assay	Measures	Pros	Cons	Anchor?	Why (or Why Not)
ATAC-seq	Chromatin accessibility	- Unbiased detection of open chromatin - High resolution - Captures regulatory regions	- Accessibility ≠ activity	**Yes**	Captures all potential regulatory regions; ideal for anchoring overlaps
ChIP-seq	Histone marks / TF binding	- Provides functional chromatin context - Captures specific modifications	- Lower resolution - Biased scope	No	Regions depend on the mark chosen; not comprehensive
RNA-seq	Gene expression	- Directly quantifies expression - Gene-level interpretation	- Lacks regulatory location info	No	Restrictive to mostly genes

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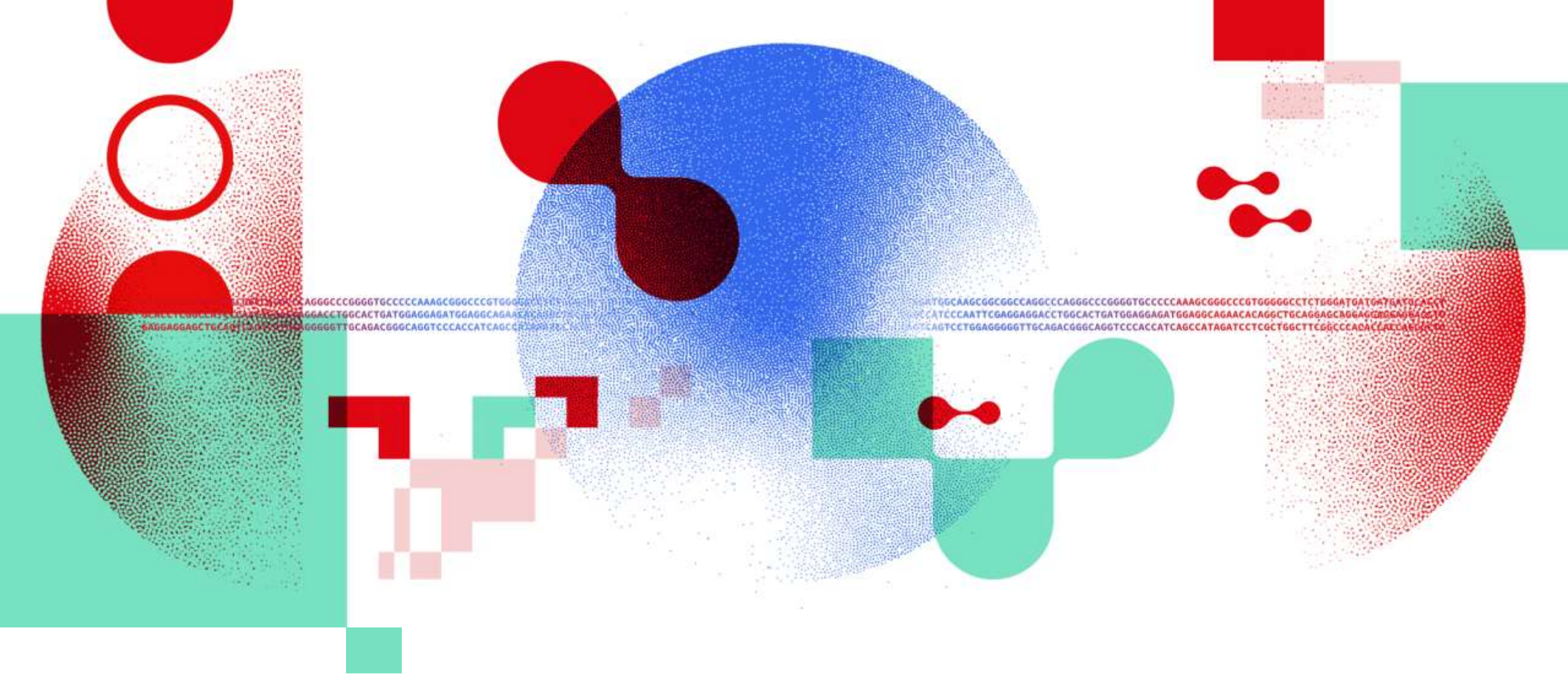# Pipeline for overlapMatrix

Pipeline for overlapMatrix

EnrichedHeatmap from overlapMatrix

Exercise 4

Thank you

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