

Swiss Institute of Bioinformatics

BIOLOGY-INFORMED MULTIOMICS DATA INTEGRATION AND VISUALIZATION

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

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





Differential analysis results

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



Identify the starting point

1. RNA-seq

2. ChIP-seq

3. ATAC-seq



ATAC-seq as a starting point

Target

seqnames	start	end	strand
chr1	1	70	+
chr1	100	400	-
chr1	200	290	+
chr2	300	500	-
chr2	20	100	+
chr3	40	200	-
chr4	15	150	-

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Gene7	Transcript1	chr4	15	150	0	0



Pipeline for overlapMatrix





Pipeline for overlapMatrix



Keeping all regions from ATAC-seq



EnrichedHeatmap from overlapMatrix





Exercise 4





Thank you

DATA SCIENTISTS FOR LIFE





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