



Swiss Institute of
Bioinformatics

BIOLOGY-INFORMED INTEGRATION AND VISUALIZATION OF
MULTIOMICS DATA

Dataset and data structure

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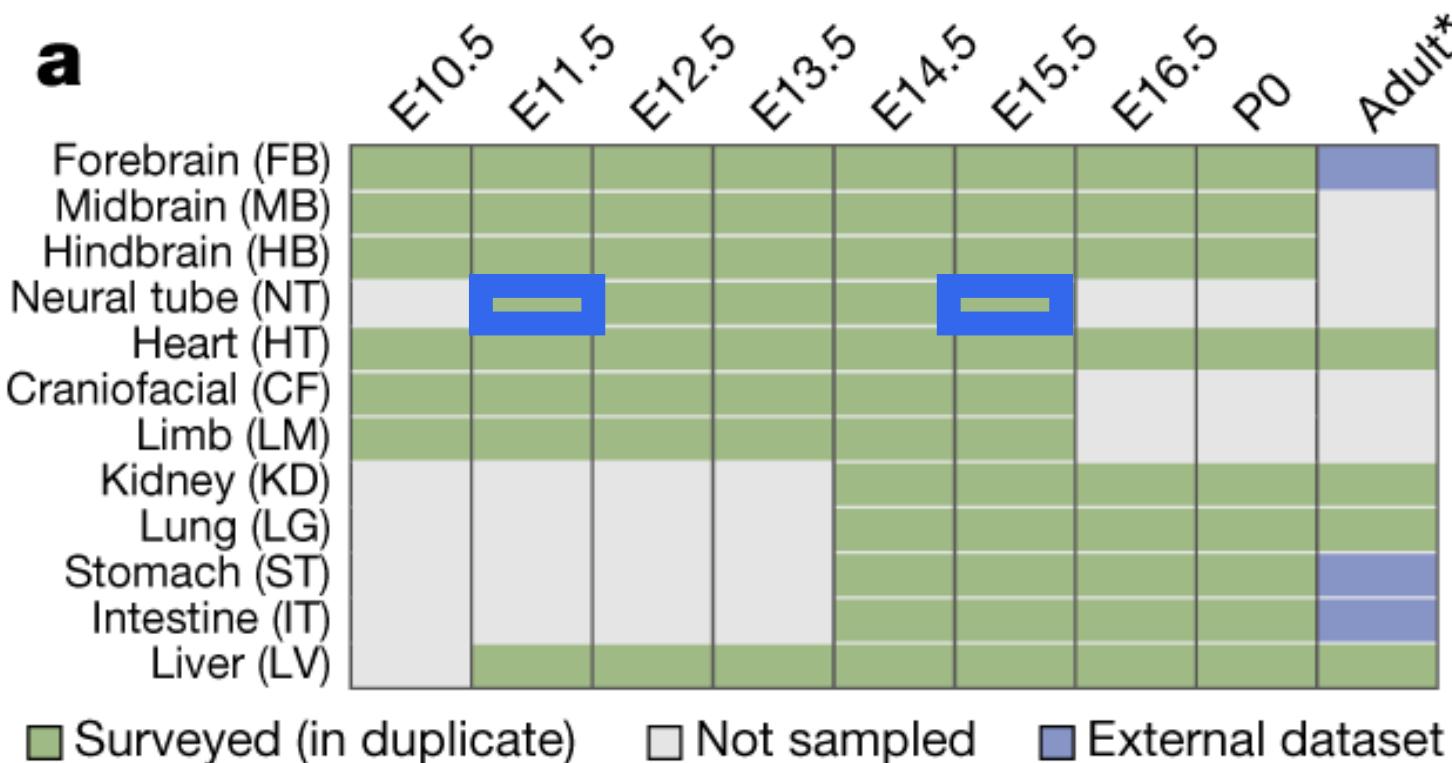
February 17-19, 2026



Learning outcomes

- Know about the datasets used in this course
- Introduction to data structures:
 - SummarizedExperiment
 - GRanges

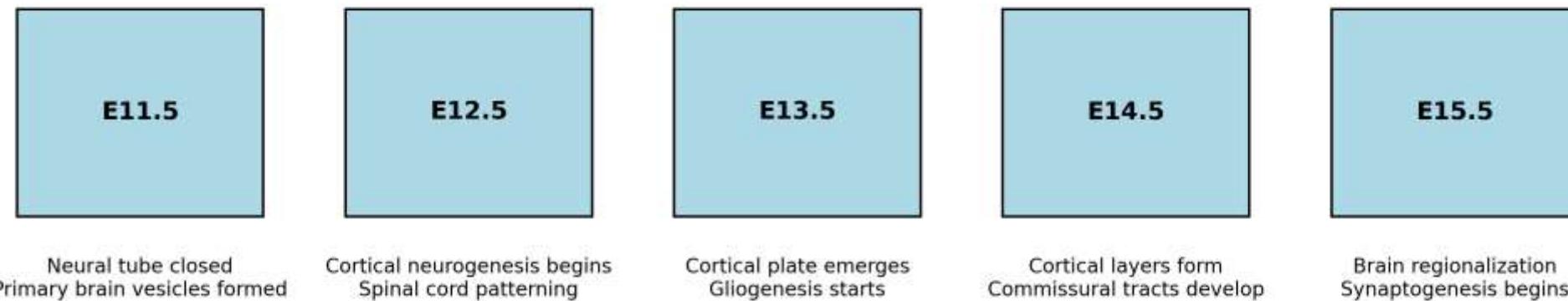
Dataset for the course



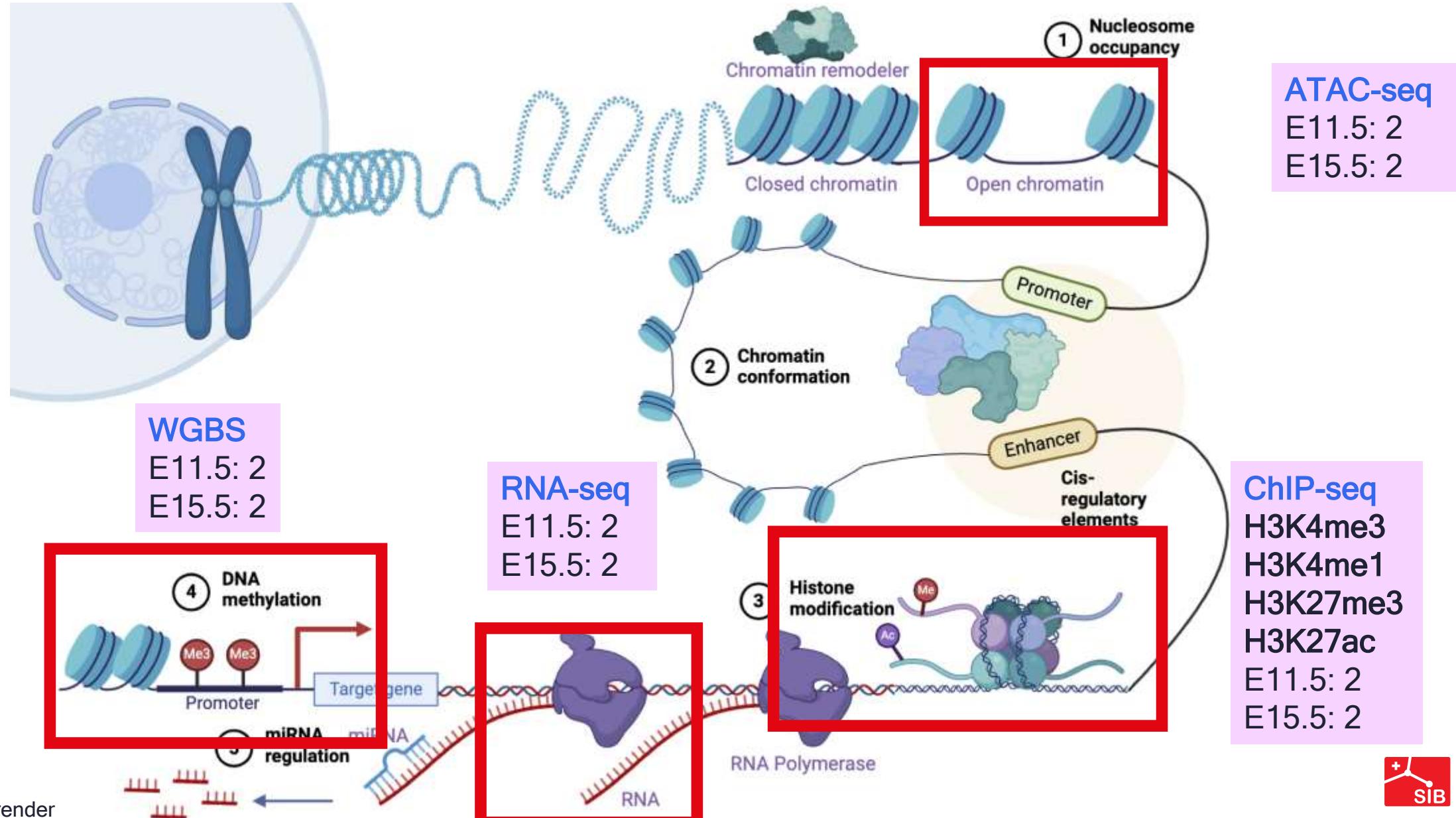
Neural tube development in mouse

In mouse embryonic development, the neural tube is a crucial structure that forms the central nervous system, encompassing the brain and spinal cord.

Neural Plate Development in Mouse (E11.5-E15.5)



Multiomics datasets from mouse neural tube development



Gene expression data in a data.frame

	Condition
Sample1	Control
Sample2	Treatment
Sample3	Treatment

	GeneType
GeneA	Transcription Factor
GeneB	Kinase
GeneC	Receptor

	Sample1	Sample2	Sample3
GeneA	5.2	6.0	5.5
GeneB	3.8	4.1	3.9
GeneC	7.1	6.8	7.3

data.frame: rownames

	GeneType
GeneA	Transcription Factor
GeneB	Kinase
GeneC	Receptor

	Sample1
GeneA	5.2
GeneB	3.8
GeneC	7.1

	Condition
Sample1	Control
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	Sample1	Sample2	Sample3
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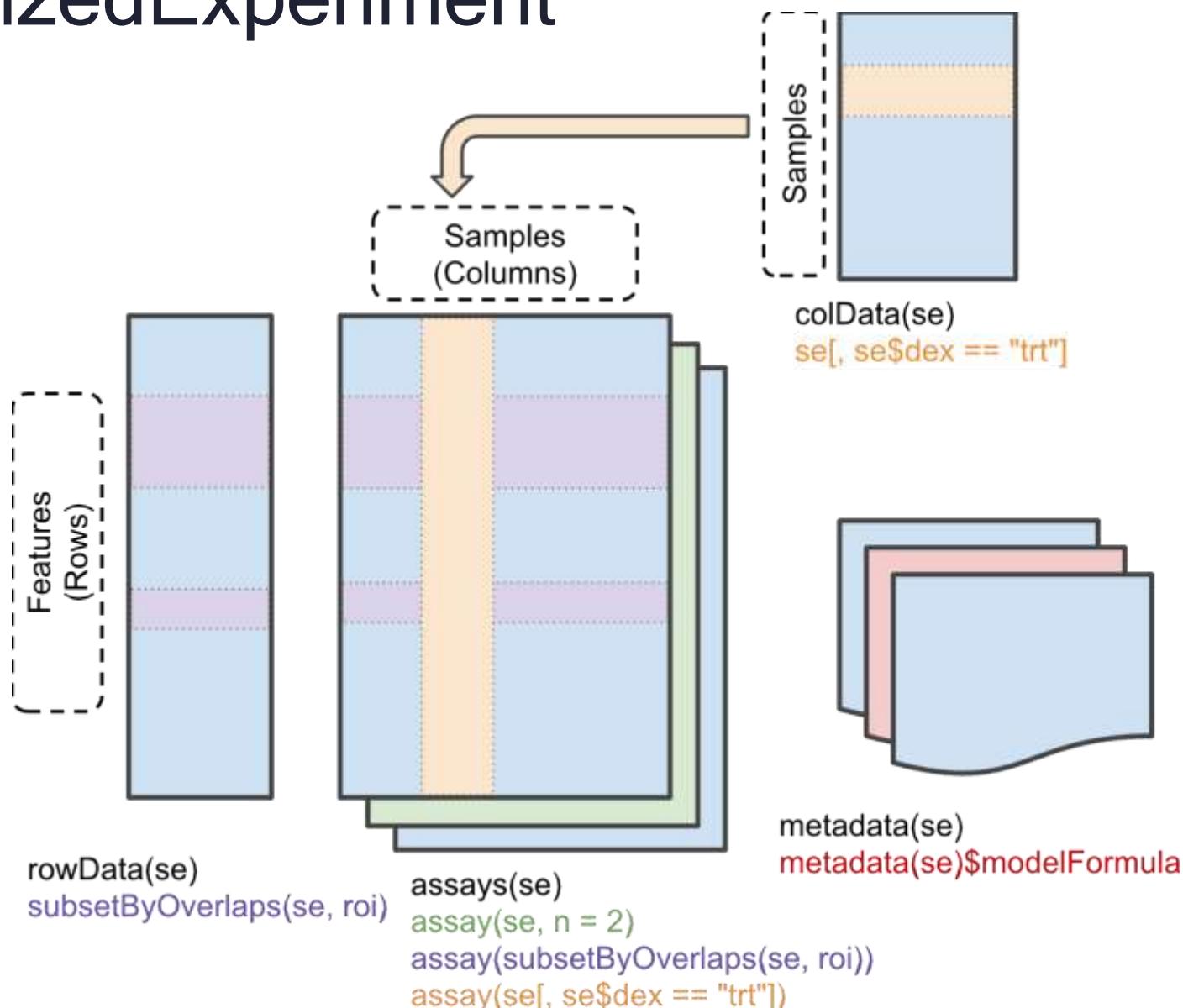
data.frame: colnames

GeneType	
GeneA	Transcription Factor
GeneB	Kinase
GeneC	Receptor

	Sample1	Sample2	Sample3
GeneA	5.2	6.0	5.5
GeneB	3.8	4.1	3.9
GeneC	7.1	6.8	7.3

	Condition
Sample1	Control
Sample2	Treatment
Sample3	Treatment

SummarizedExperiment



Data format for ATAC/ ChIP sequencing data

Condition	
Sample1	Control
Sample2	Treatment
Sample3	Treatment

	Chr	Start	End
Peak1	chr1	1000	1500
Peak2	chr2	2000	2500
Peak3	chr3	3000	3500

	Sample1	Sample2	Sample3
Peak1	120	130	125
Peak2	85	90	88
Peak3	200	210	205

Genomic Ranges snapshot

```
> gr = exons(TxDb.Hsapiens.UCSC.hg19.knownGene); gr
```

GRanges with 289969 ranges and 1 metadata column:

	seqnames	ranges	strand	exon_id
[1]	chr1	[11874, 12227]	+	1
[2]	chr1	[12595, 12721]	+	2
[3]	chr1	[12613, 12721]	+	3
...
[289967]	chrY	[59358329, 59359508]	-	277748
[289968]	chrY	[59360007, 59360115]	-	277749
[289969]	chrY	[59360501, 59360854]	-	277750

seqinfo: 93 sequences (1 circular) from hg19 genome

GRanges

```
length(gr); gr[1:5]  
seqnames(gr)  
start(gr)  
end(gr)  
width(gr)  
strand(gr)
```

DataFrame

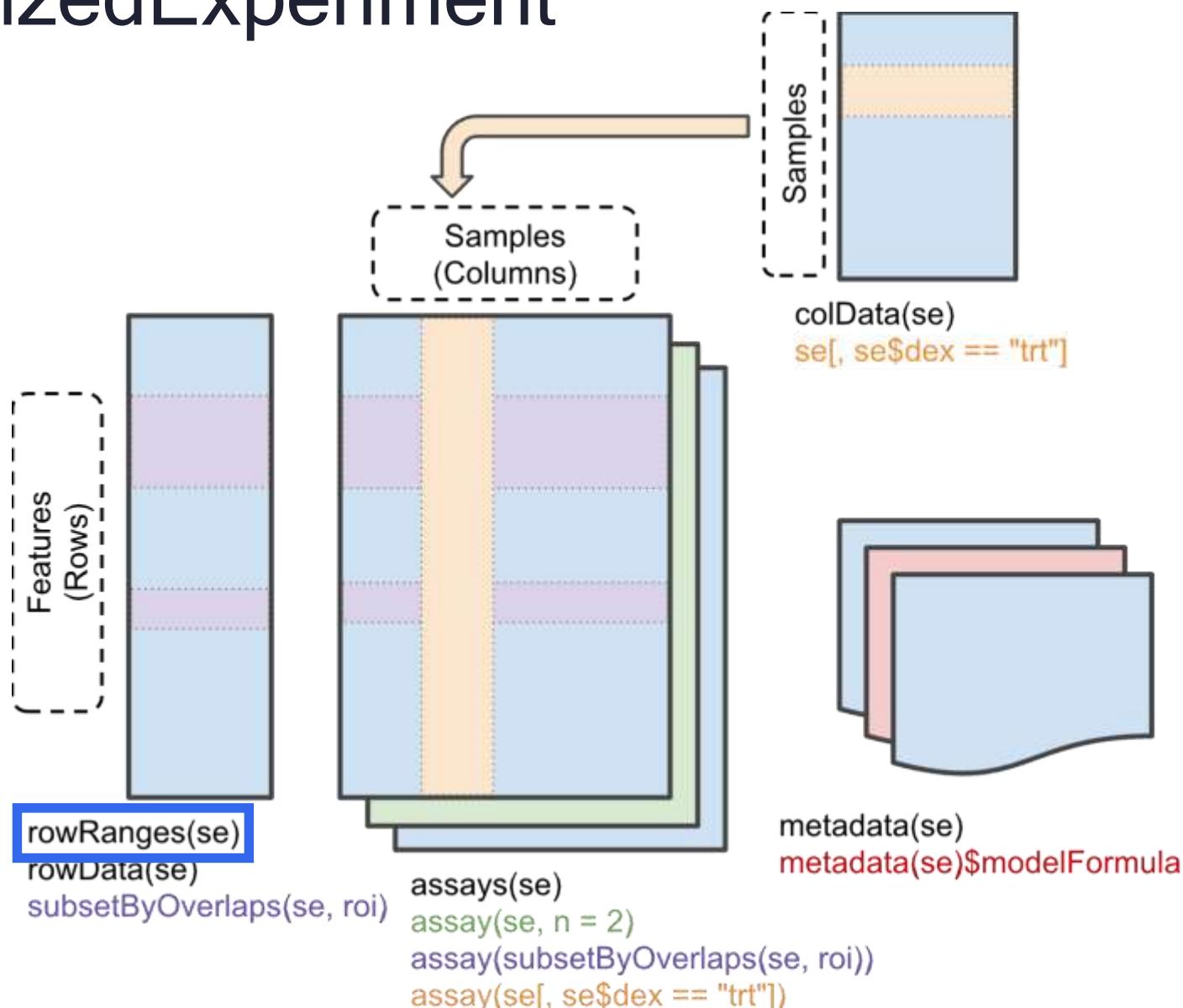
```
mcols(gr)  
gr$exon_id
```

SqInfo

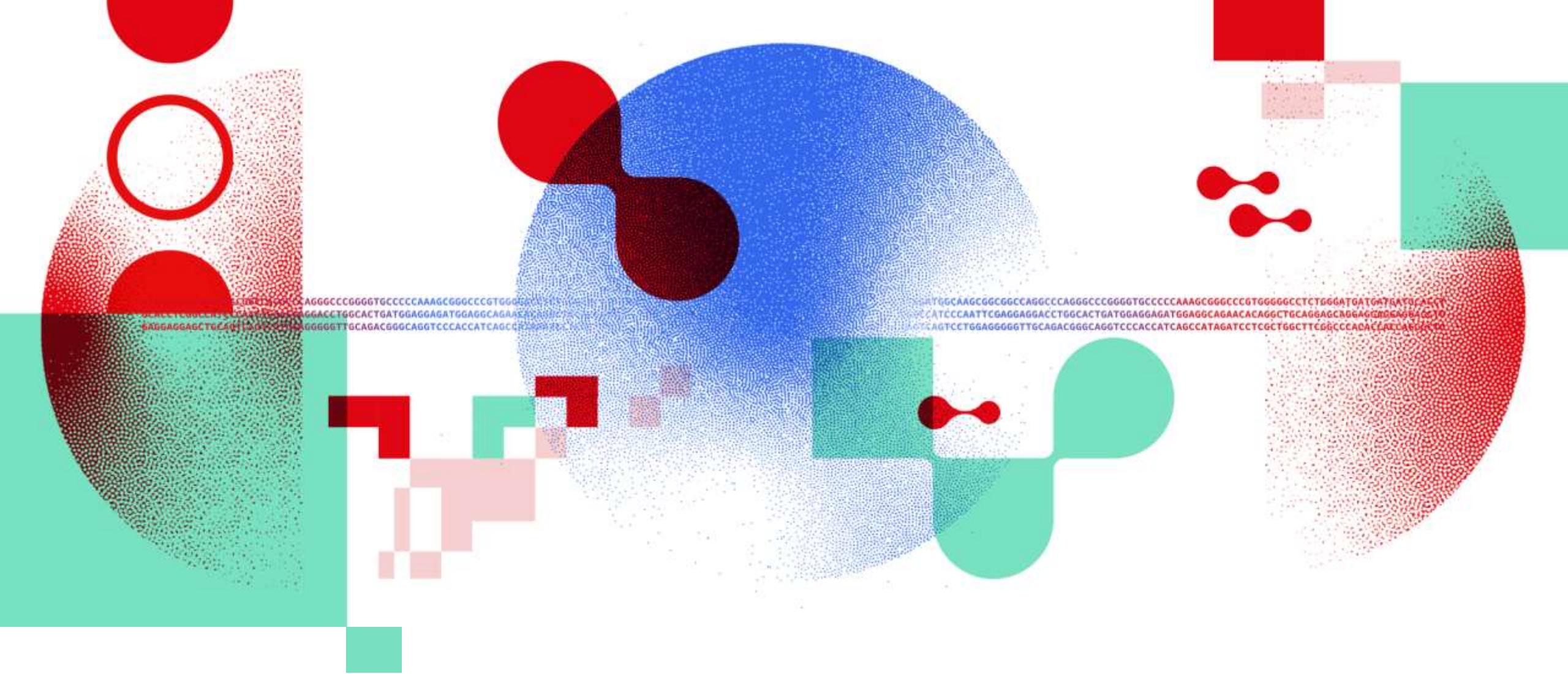
```
seqlevels(gr)  
seqlengths(gr)  
genome(gr)
```



SummarizedExperiment



Exercise 1



Thank you

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