



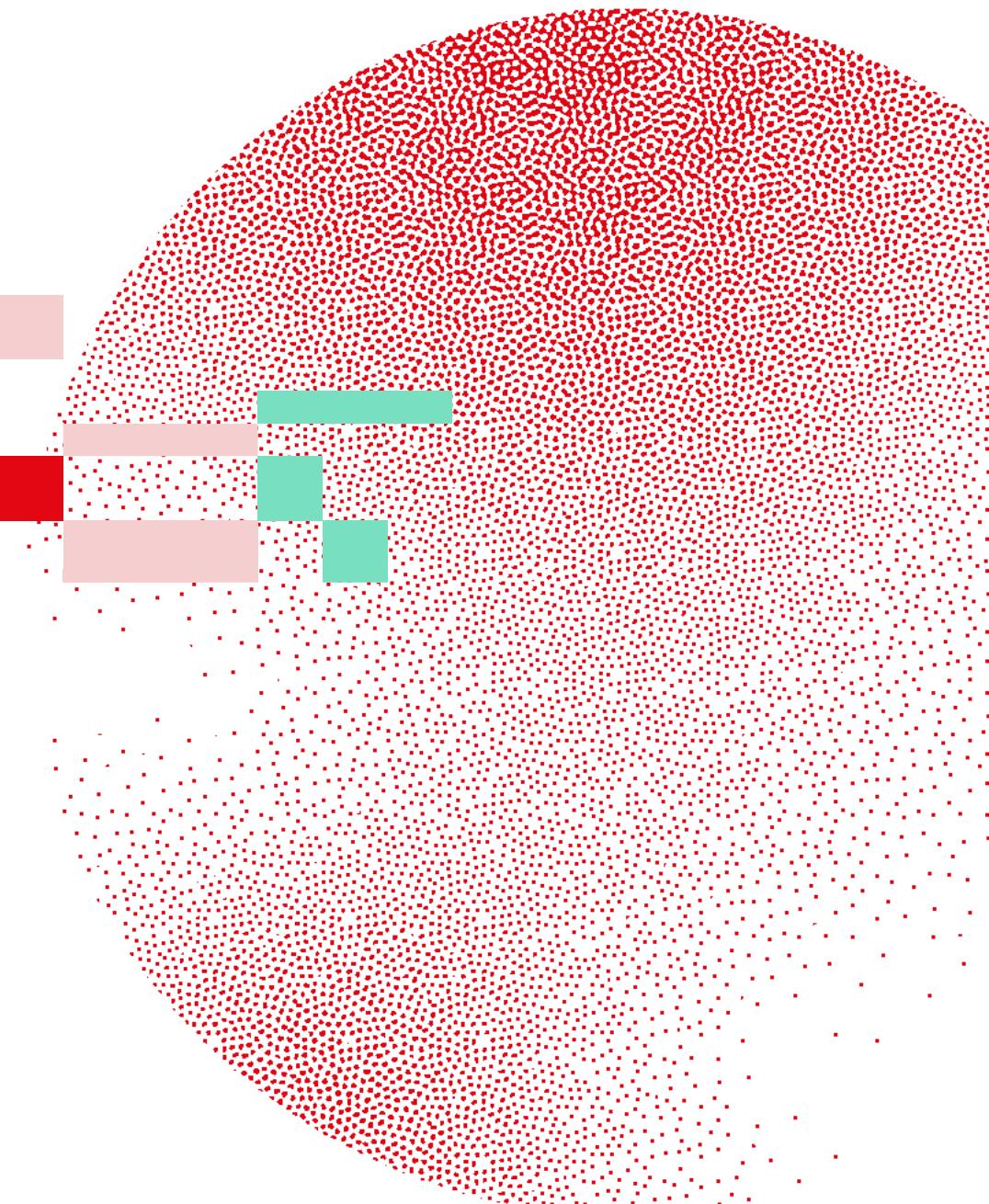
Swiss Institute of
Bioinformatics

BIOLOGY-INFORMED INTEGRATION AND VISUALIZATION OF
MULTIOMICS DATA

Normalization and Visualization

Deepak Tanwar

February 17-19, 2026



Learning outcomes

- Information from multi-omics datasets
- Heatmap vs EnrichedHeatmap
- Methods for normalizing data in the target regions

ATAC-seq data snapshot

To assess genome-wide chromatin accessibility.

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

How can you visualize the ATAC-seq data?



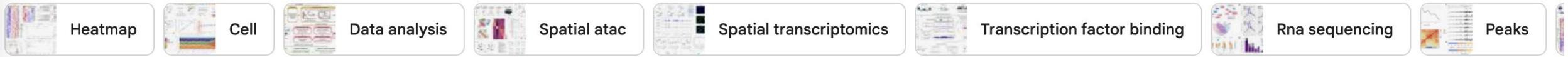
atac seq visualization



AI Mode All Images Videos Forums Short videos Web More ▾

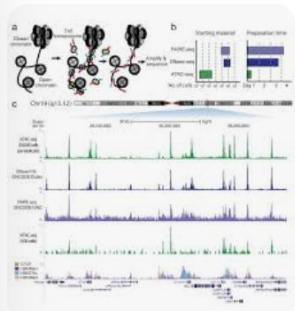
Tools ▾

Saves

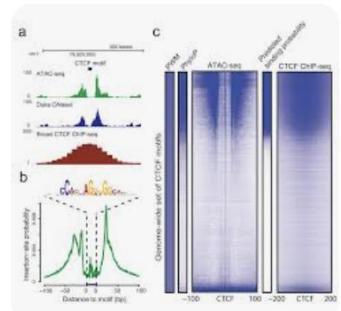


See detailed insights & Compare multiple related Papers for : "atac seq visualization"

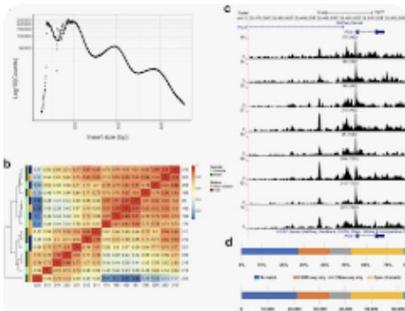
Compare insights



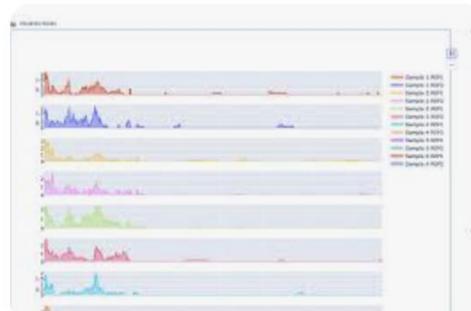
Galaxy Training!
Hands-on: ATAC-Seq ...



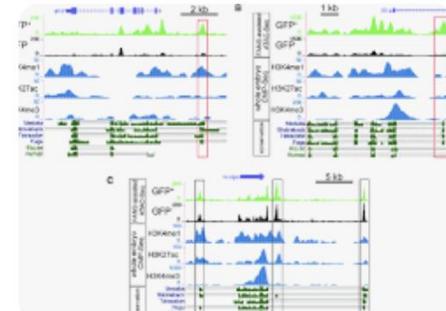
seandavi.github.io
ATAC-Seq with Biocondu...



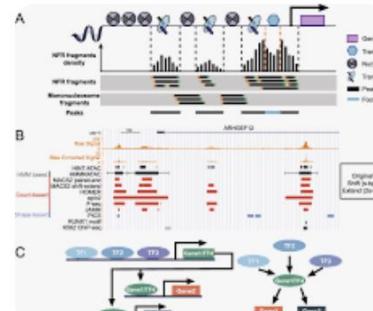
Nature
open chromatin in pancreatic isl...



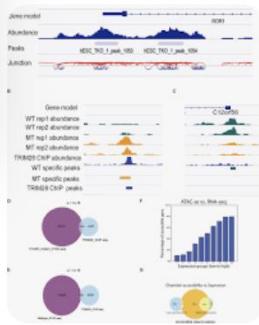
LatchBio
Interactive Tools for ATAC-seq Analysis



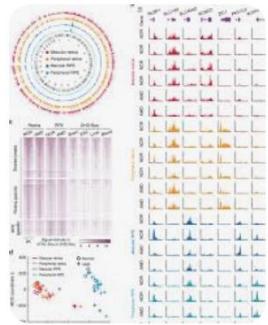
ResearchGate
Mapping of ATAC-Seq Reads at Kn...



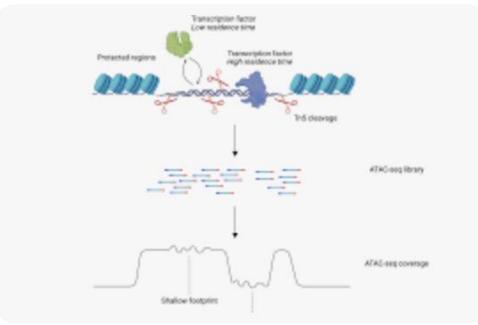
Springer Link
ATAC-seq data analysis | Ge...



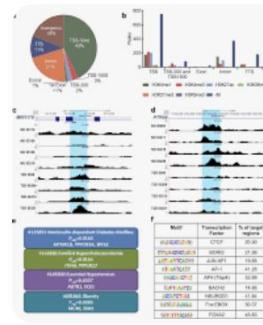
ResearchGate
Visualization of AT...



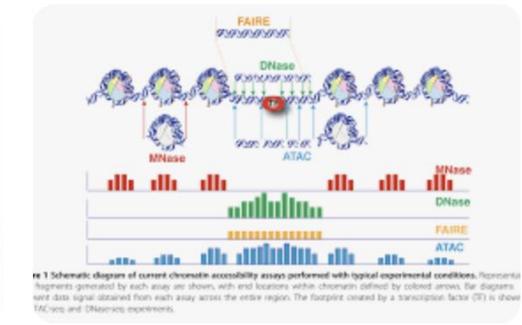
Nature
ATAC-Seq analysis...



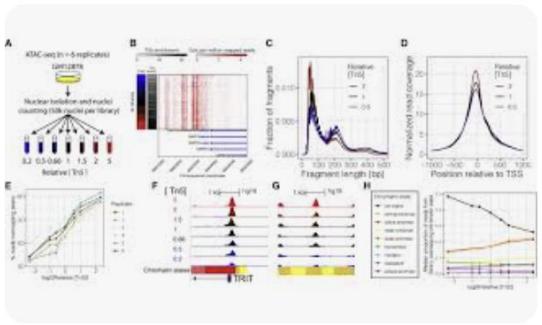
BioRender.com
Digital footprinting with ATAC-seq ...



APExBIO
ATAC-seq



Yiwei Niu
ATAC-seq data analysis: from FASTQ t...



Cell Press
ATAC-Seq Data with ataqv: Cell ...

ChIP-seq data snapshot

To investigate the interaction between proteins and DNA

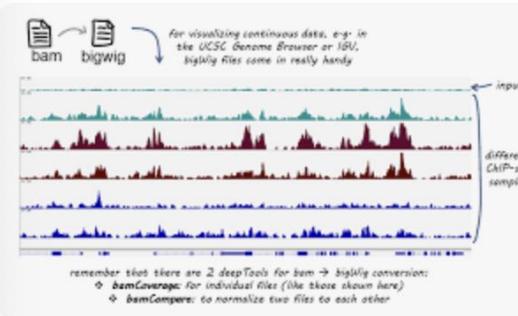
seqnames	start	end	strand	Symbol	distanceTSS	Group1	Group2
chr1	11	70	+	Gene1	5000	11	21
chr1	200	400	-	Gene1	5000	10	100
chr1	100	290	+	Gene3	2000	200	1000
chr2	100	500	-	Gene4	3000	400	1300
chr2	50	100	+	Gene5	20000	20	120
chr3	40	200	-	Gene6	40000	540	40
chr4	5	150	-	Gene7	150	1500	15

How can you visualize the ChIP-seq data?

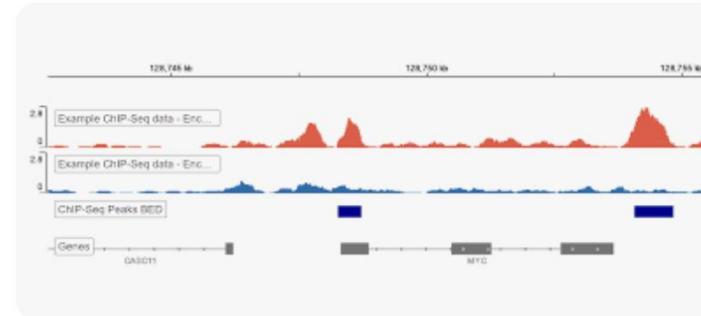


See detailed insights & Compare multiple related Papers for : “chip seq visualization”

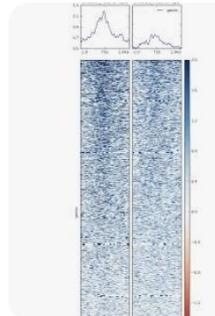
[Compare insights](#)



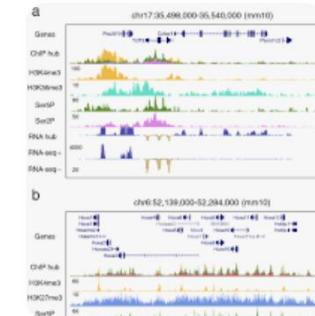
[GitHub Pages](#)
Visualization of peaks | Introduction ...



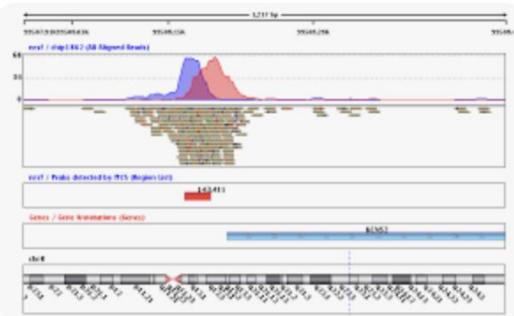
[Basepair](#)
ChIP-Seq Analysis Tutorial - Basepair



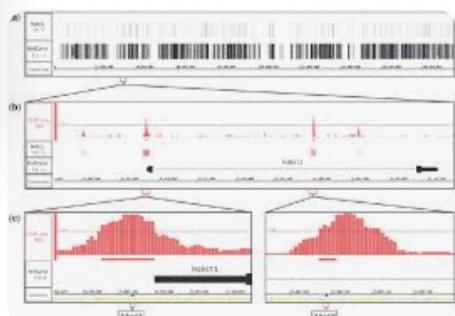
[GitHub Pages](#)
Visualization of pe...



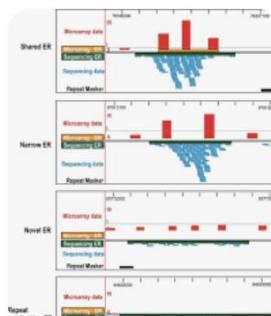
[Nature](#)
Productive visualizatio...



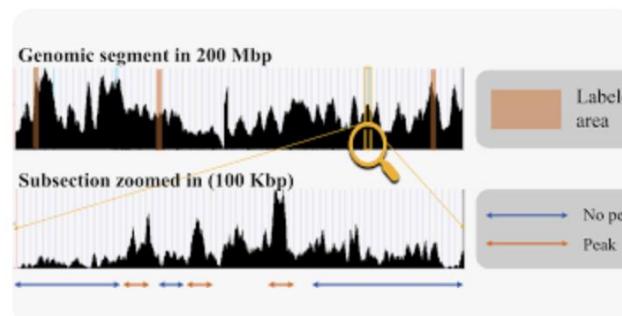
[NGS Strand NGS](#)
ChIP-Seq| Strand NGS



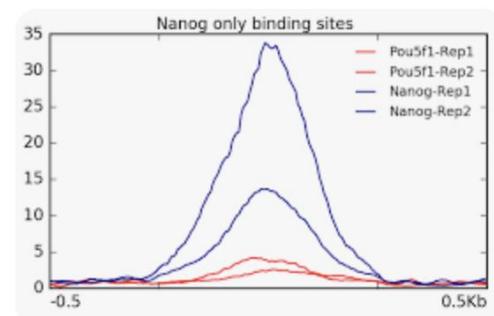
[ResearchGate](#)
Visualizing ChIP-Seq data. (a) MAC...



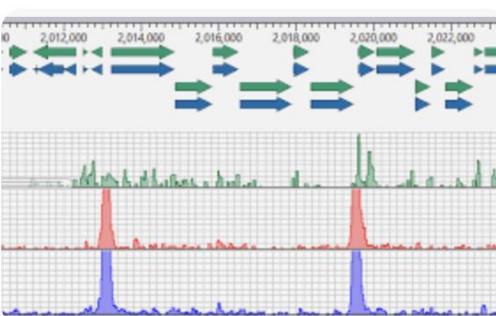
[ResearchGate](#)
ChIP-seq data for H...



[Nature](#)
CNN-Peaks: ChIP-Seq peak detection ...



[GitHub Pages](#)
Visualization of peaks | Introduction ...



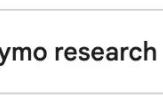
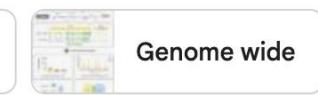
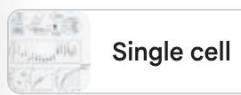
[dnastar](#)
ChIP-Seq Data Analysis Workflow | DNA...

WGBS data snapshot

To determine the methylation state of the genome.

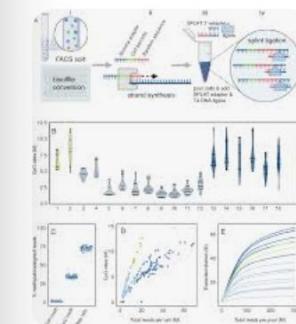
seqnames	start	end	strand	Symbol	distanceTSS	Group1	Group2
chr1	1	1	+	Gene1	5000	1.0	0.0
chr1	100	100	-	Gene1	5000	0.0	0.0
chr1	200	200	+	Gene3	2000	0.7	1.0
chr2	300	300	-	Gene4	3000	0.4	0.3
chr2	20	20	+	Gene5	20000	0.2	0.1
chr3	40	40	-	Gene6	40000	1.0	1.0
chr4	15	15	-	Gene7	150	0.0	1.0

How can you visualize the WGBS data?

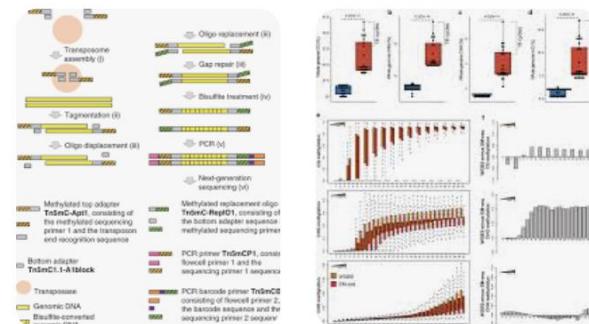


See detailed insights & Compare multiple related Papers for : "wgbs seq visualization"

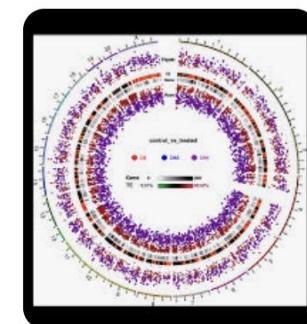
[Compare insights](#)



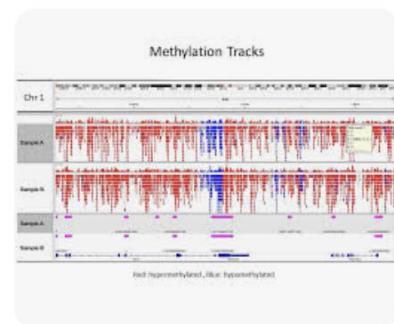
[Nature](#)
single cell WGBS lib...



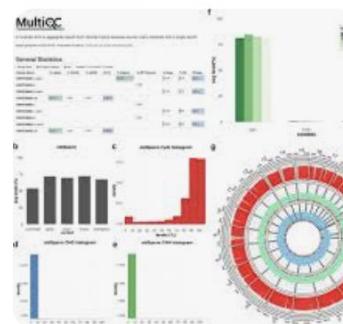
[ResearchGate](#)
T-WGBS library pre...



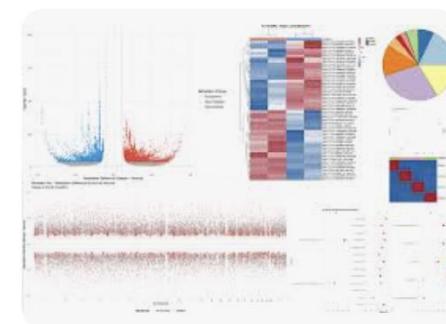
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methylation levels be...



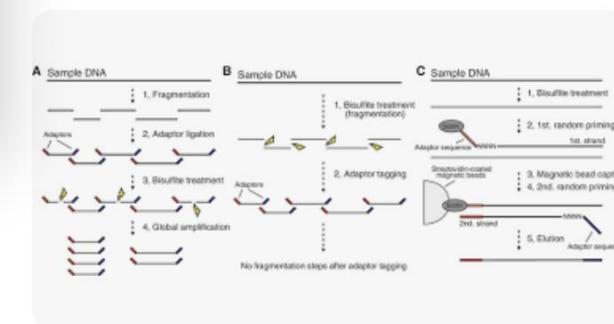
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Whole Genome Bisulfite Sequ...



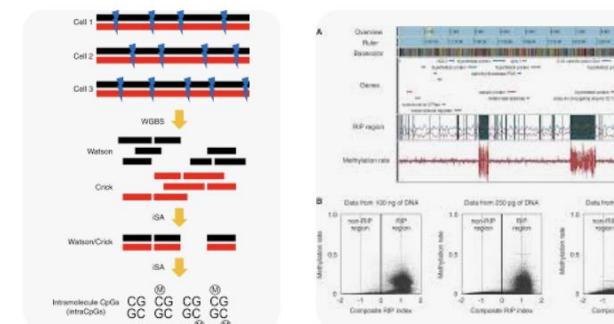
[Springer Link](#)
whole-genome bisulfite se...



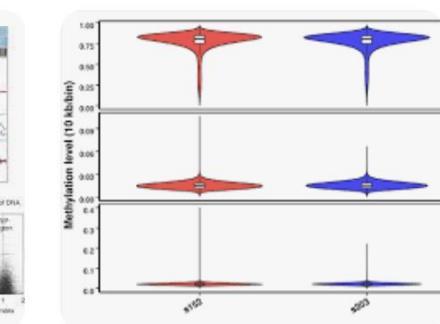
[NGS Learning Hub](#)
How To Analyze DNA Methylation ...



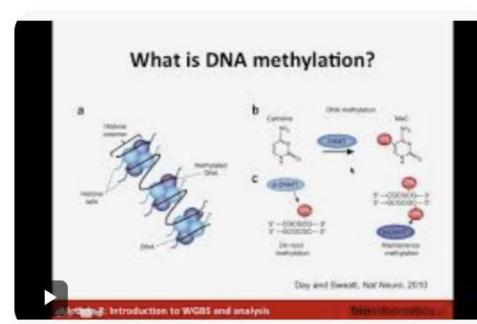
[ResearchGate](#)
WGBS and PBAT. (A) Schematic of the ...



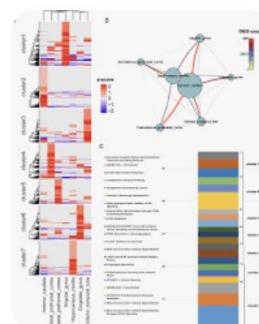
[Nature](#)
Resolution of the D...



[EpigenTek](#)
Whole Genome Bisulfite Sequ...



[YouTube](#)
Introduction to WGBS and Analysis - Y...



[Frontiers](#)
Gene Expression a...

RNA-seq data snapshot

To analyze expression across the transcriptome.

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

How can you visualize the RNA-seq data?

AI Mode

All

Images

Videos

Forums

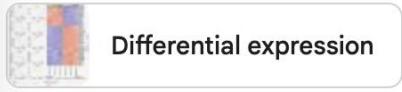
Short videos

Web

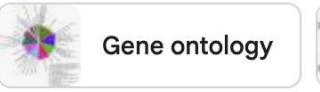
More ▾

Tools ▾

Saves



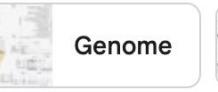
Differential expression



Gene ontology



Single cell



Genome



Alignment



Analysis



Bulk



Volcano



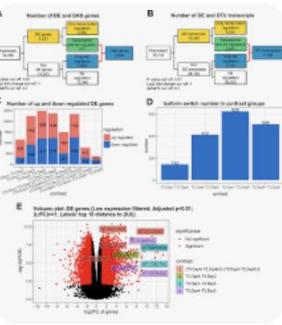
Tpm



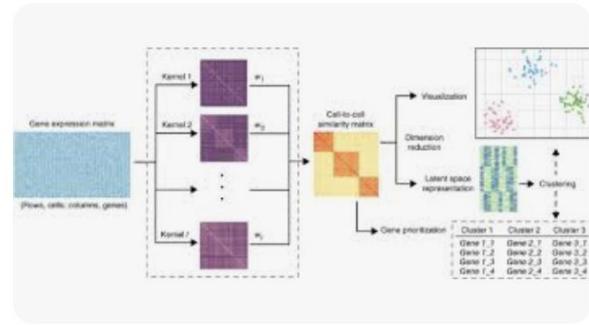
See detailed insights & Compare multiple related Papers for : "rna seq visualization"

[Compare insights](#)


Posit Community
rnaseqDRaMA - RNAseq data ...



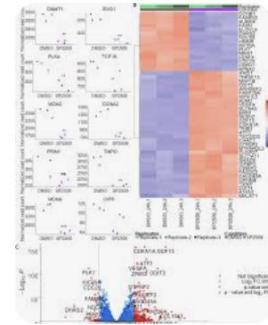
r⁶ ResearchGate
visualization outputs f...



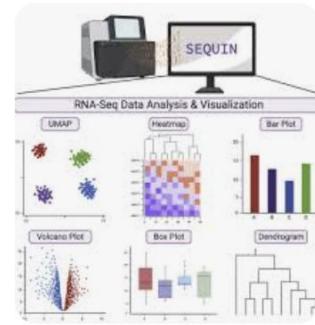
Nature
analysis of single-cell RNA-seq data ...



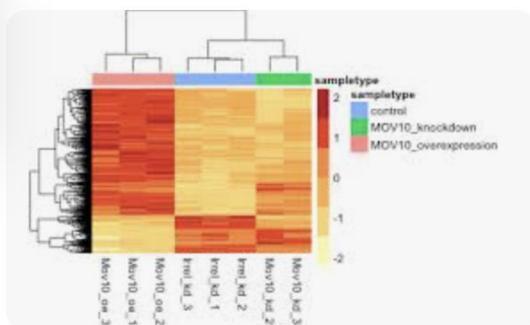
Elucidata
Bulk RNA-seq Data Visualization Tools



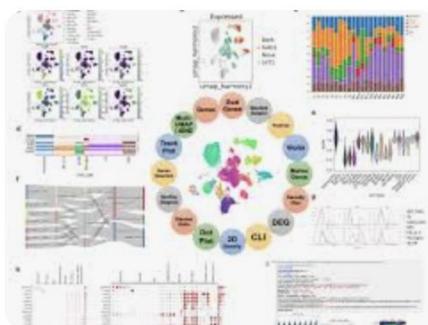
Springer
RNA-seq data | B...



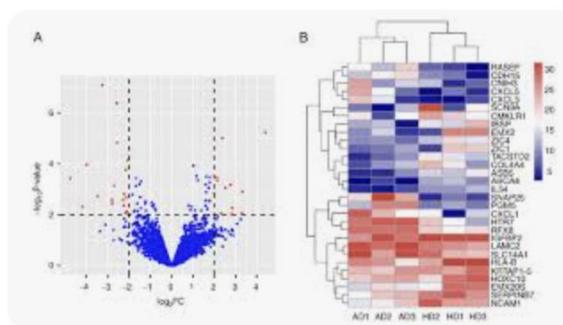
ScienceDirect.com
RNA-seq data ...



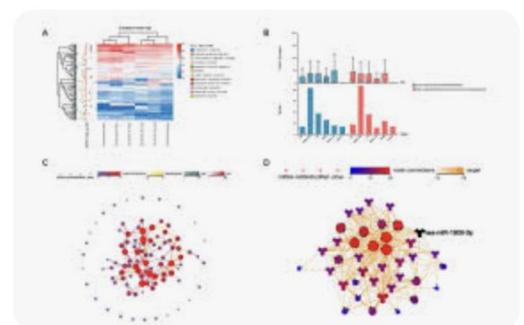
GitHub Pages
RNA-seq visualizations | Training-modules



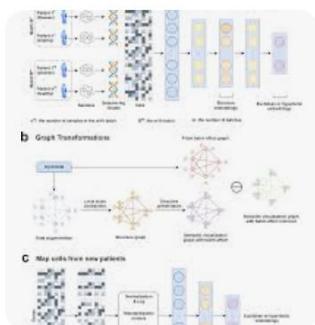
BioInfoRx
BxGenomics - RNA-Seq data anal...



r⁶ ResearchGate
Visualization of DEGs between AD-MSCs ...

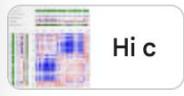


RNA-Seq Blog
Intuitive RNA Data Visualization ...



Nature
single-cell RNA-Seq pro...

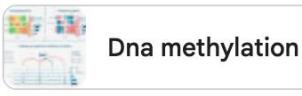
How can you visualize ATAC-seq, ChIP-seq,
WGBS, and RNA-seq data together?



Hi c



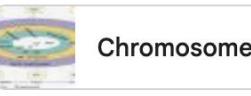
Epigenetics



Dna methylation



Data



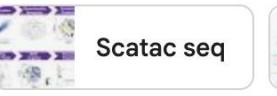
Chromosome



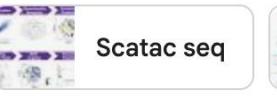
ScRNA-seq analysis



Epigenomics



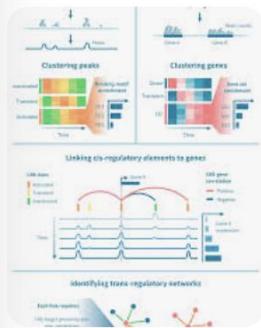
Single cell



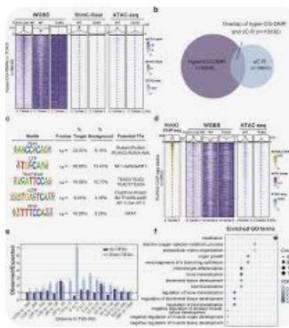
Scatac seq

See detailed insights & Compare multiple related Papers for : "atac seq, chip seq, wgb, rna seq: multiomics visualization"

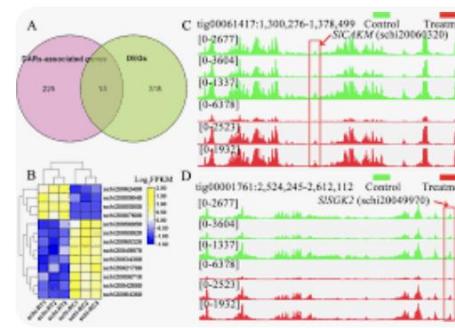
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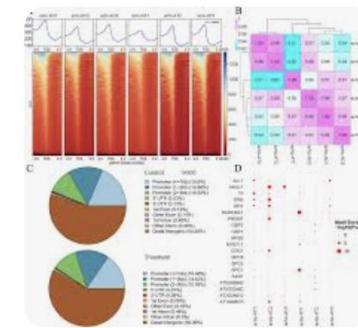
G Geneva Technologi...
RNA-seq and ChIP-seq data ...



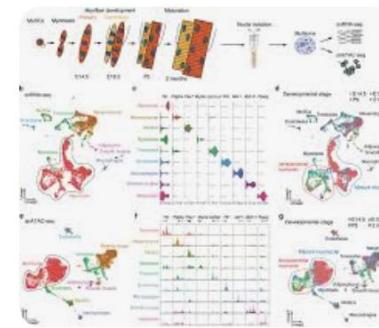
R ResearchGate
RNA-seq, WGBS, 5h...



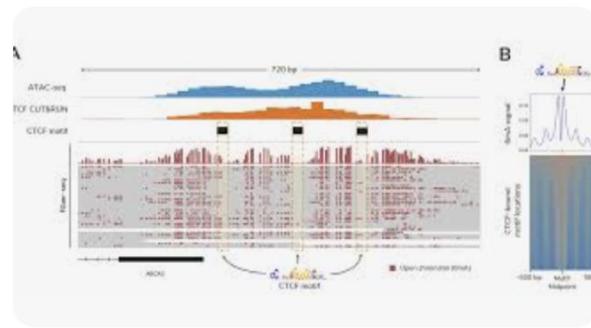
Springer Link
ATAC-seq and RNA-seq ...



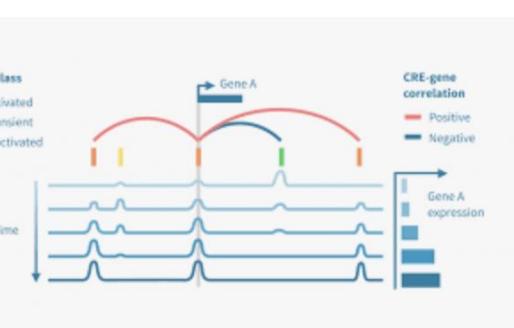
Springer Link
ATAC-seq and RNA-seq ...



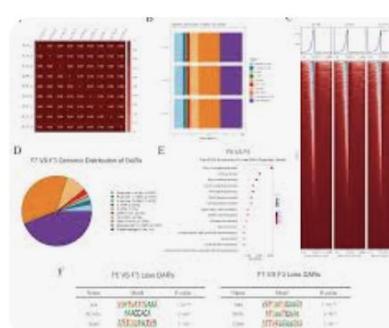
R ResearchGate
Multi-omics single nucleus R...



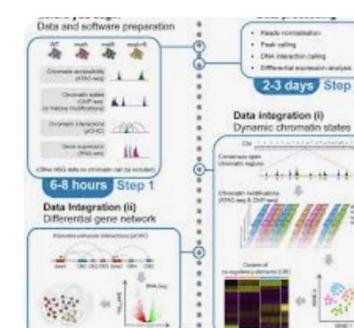
EpiCypher
Fiber-seq 101: A Multiomic Assay That ...



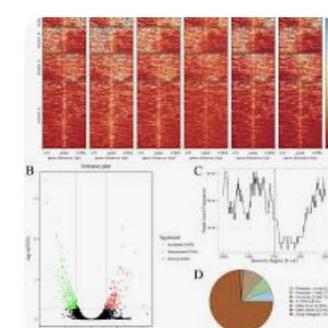
G Geneva Technologies
RNA-seq and ChIP-seq data ...



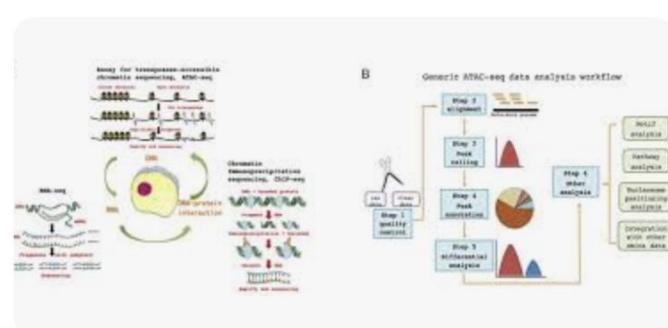
MDPI
ATAC-seq and RNA-seq Analysis...



STAR Protocols - Cell Press
chromatin remodeling ...



Springer Link
ATAC-seq and RNA-seq ...

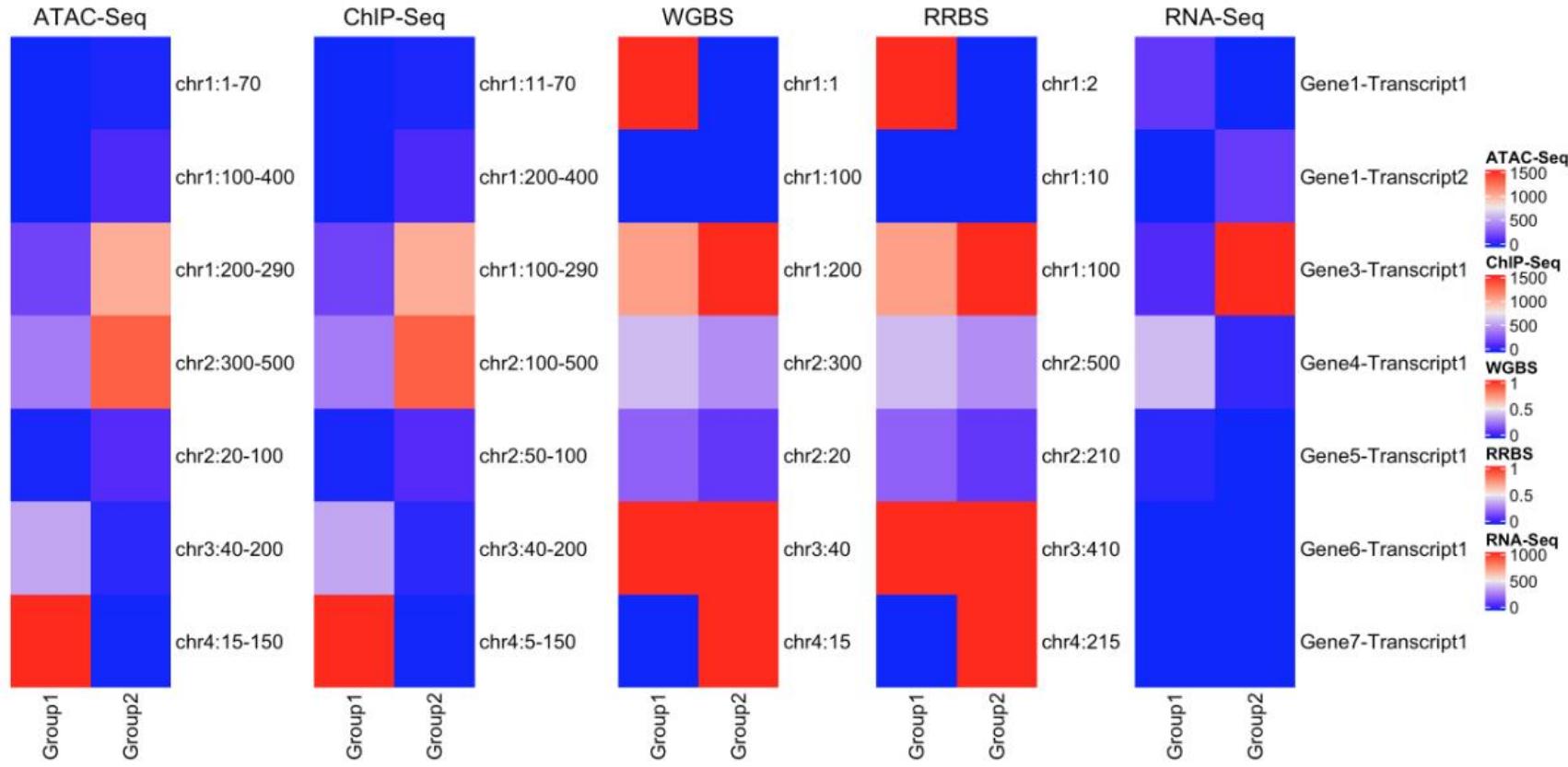


R ResearchGate
Principles and workflow of ATAC-seq ...

What is the best way to visualize these data together?

These tables have 100's of 1000's of rows

Heatmaps?



How to properly integrate these data?

Let's say, we want to look around 200bp of TSS!

TSS
(target)

	seqnames	position	strand
Gene_1	chr21	13	+
Gene_2	chr21	46	+
Gene_3	chr21	78	+
Gene_4	chr21	10	+
Gene_5	chr21	45	+

How to properly integrate these data?

Let's say, we want to look around 200bp of TSS!

TSS
(target)

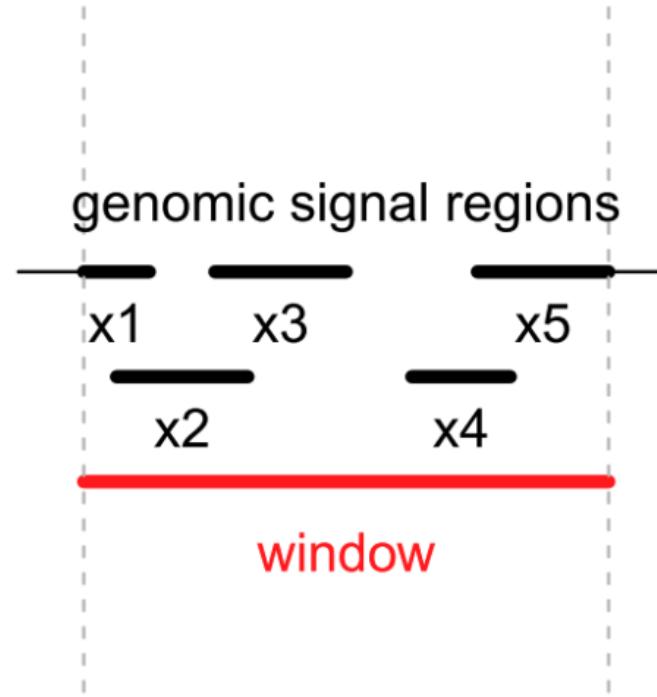
	seqnames	position	strand
Gene_1	chr21	13	+
Gene_2	chr21	46	+
Gene_3	chr21	78	+
Gene_4	chr21	10	+
Gene_5	chr21	45	+

ChIP-Seq data
(genomic signal)

	seqnames	start	end	strand	Group1
	chr21	11	70	+	11
	chr21	200	400	-	10
	chr21	100	290	+	200
	chr21	100	500	-	400
	chr21	50	100	+	20

Averaging methods to summarize the signals

Averaging model



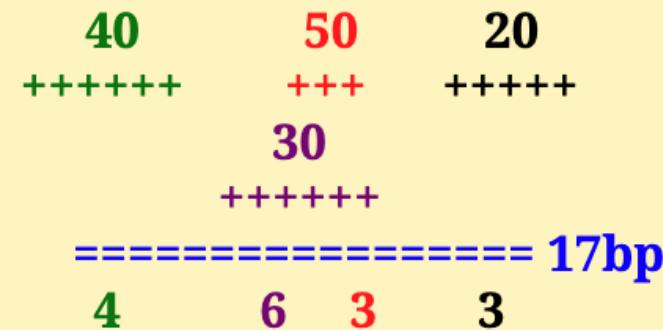
The **red line** represents one window in the target regions or in the flanking regions when normalizing genomic signals to target regions. **Black lines** represent genomic signals that overlap to the given window.

Averaging methods to summarize the signals

absolute

$$v_a = \frac{\sum_{i=1}^n x_i}{n}$$

Calculates the **mean** value from all signal regions regardless of their width.



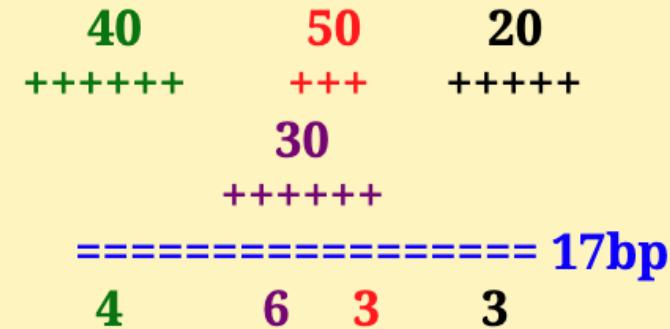
4bp not overlapping to any region

$$v_a = \frac{40 + 30 + 50 + 20}{4}$$

Averaging methods to summarize the signals

weighted

$$v_w = \frac{\sum_{i=1}^n x_i w_i}{\sum_{i=1}^n w_i}$$



Calculates the **mean** value from all signal regions **weighted by the width of their intersections**.

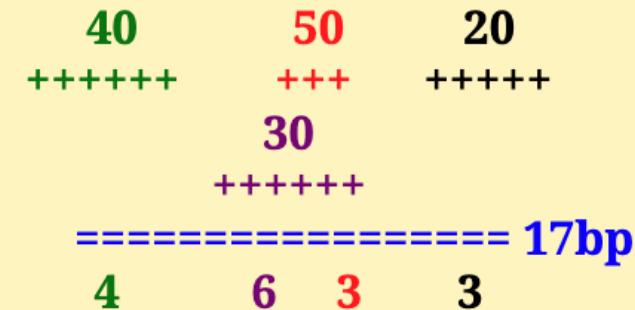
4bp not overlapping to any region

$$v_w = \frac{40 \times 4 + 30 \times 6 + 50 \times 3 + 20 \times 3}{4 + 6 + 3 + 3}$$

Averaging methods to summarize the signals

WO

$$v_{w0} = \frac{\sum_{i=1}^n x_i w_i}{W + W'}$$



Calculates the **weighted mean** between the intersected and un-intersected parts.

$$(W = \sum_{i=1}^n w_i),$$
$$(W' = \sum_{i=1}^n w'i)$$

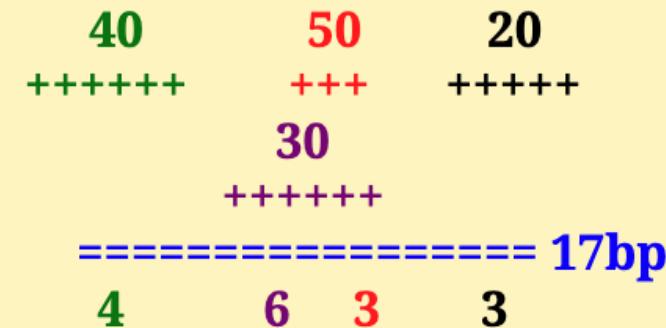
4bp not overlapping to any region

$$v_{w0} = \frac{40 \times 4 + 30 \times 6 + 50 \times 3 + 20 \times 3}{4 + 6 + 3 + 3 + 4}$$

Averaging methods to summarize the signals

coverage

$$v_c = \frac{\sum_i^n x_i w_i}{L}$$



The **mean signal averaged by the width of the window**. L is the **width of the window itself**.

4bp not overlapping to any region

$$v_c = \frac{40 \times 4 + 30 \times 6 + 50 \times 3 + 20 \times 3}{17}$$

How to use these methods?

Gu *et al.* BMC Genomics (2018) 19:234
<https://doi.org/10.1186/s12864-018-4625-x>

BMC Genomics

SOFTWARE

Open Access



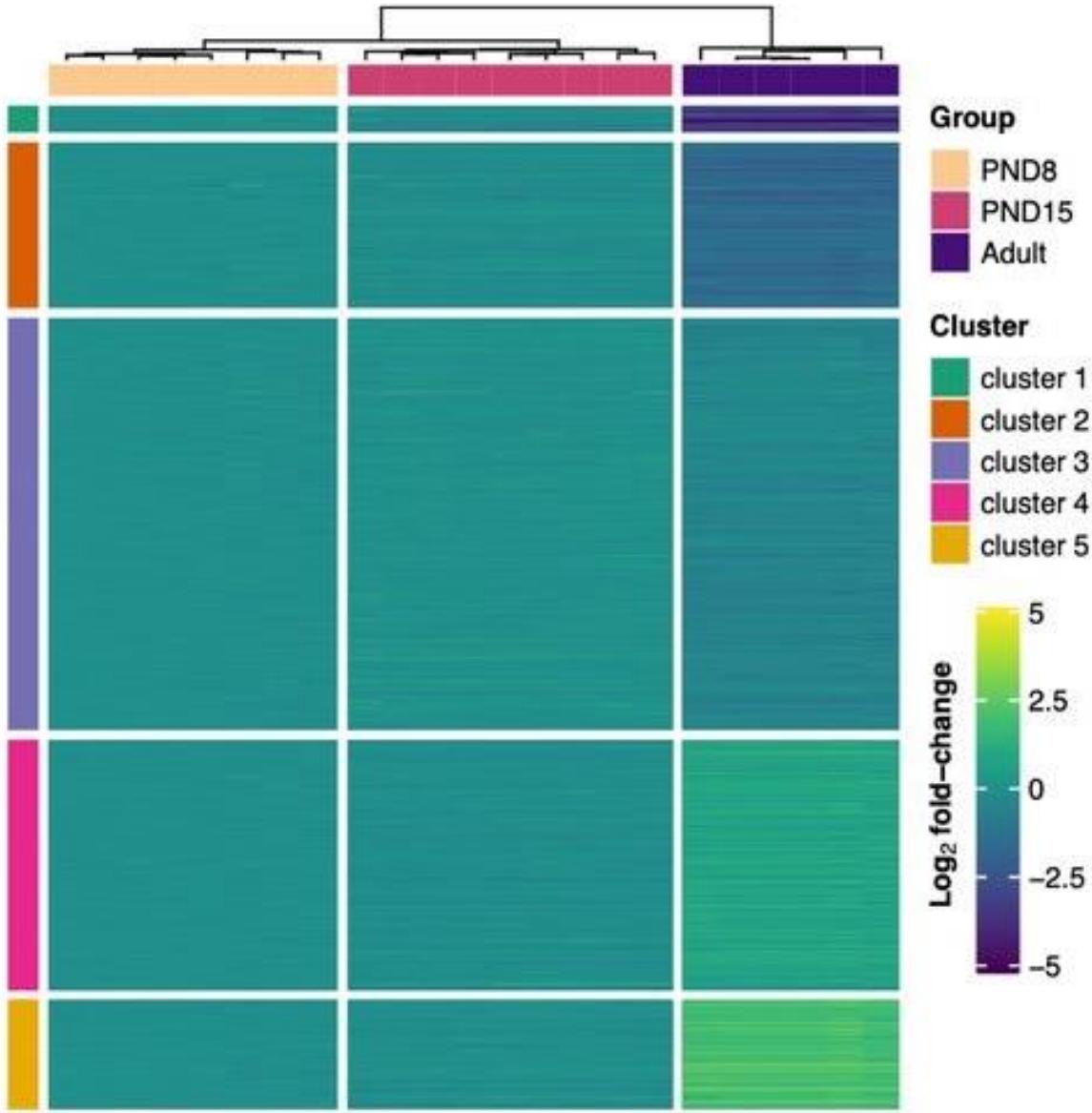
EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations

Zuguang Gu^{1,2*}, Roland Eils^{1,2,3}, Matthias Schlesner¹ and Naveed Ishaque^{1,2}

Which method to be used for different data?

Assay	Signal Representation	Recommended mean_mode	Key Considerations
ATAC-seq	Peaks (binary)	"coverage"	Shows fraction of window covered by peaks.
	Coverage (numeric)	"w0"	Averages signal intensity, weighted by overlap. Good for BigWig data.
ChIP-seq	Peaks (binary)	"coverage"	Shows fraction of window covered by peaks.
	Coverage (numeric)	"w0"	Averages signal intensity, weighted by overlap. Good for BigWig data. Set <code>empty_value = 0</code> (or background).
WGBS	CpG methylation (numeric)	"absolute"	Averages methylation values of individual CpG sites within the window. Crucial to set value_column . Highly recommend <code>smooth = TRUE</code> and <code>empty_value = NA</code> for better visualization due to sparse CpG distribution.

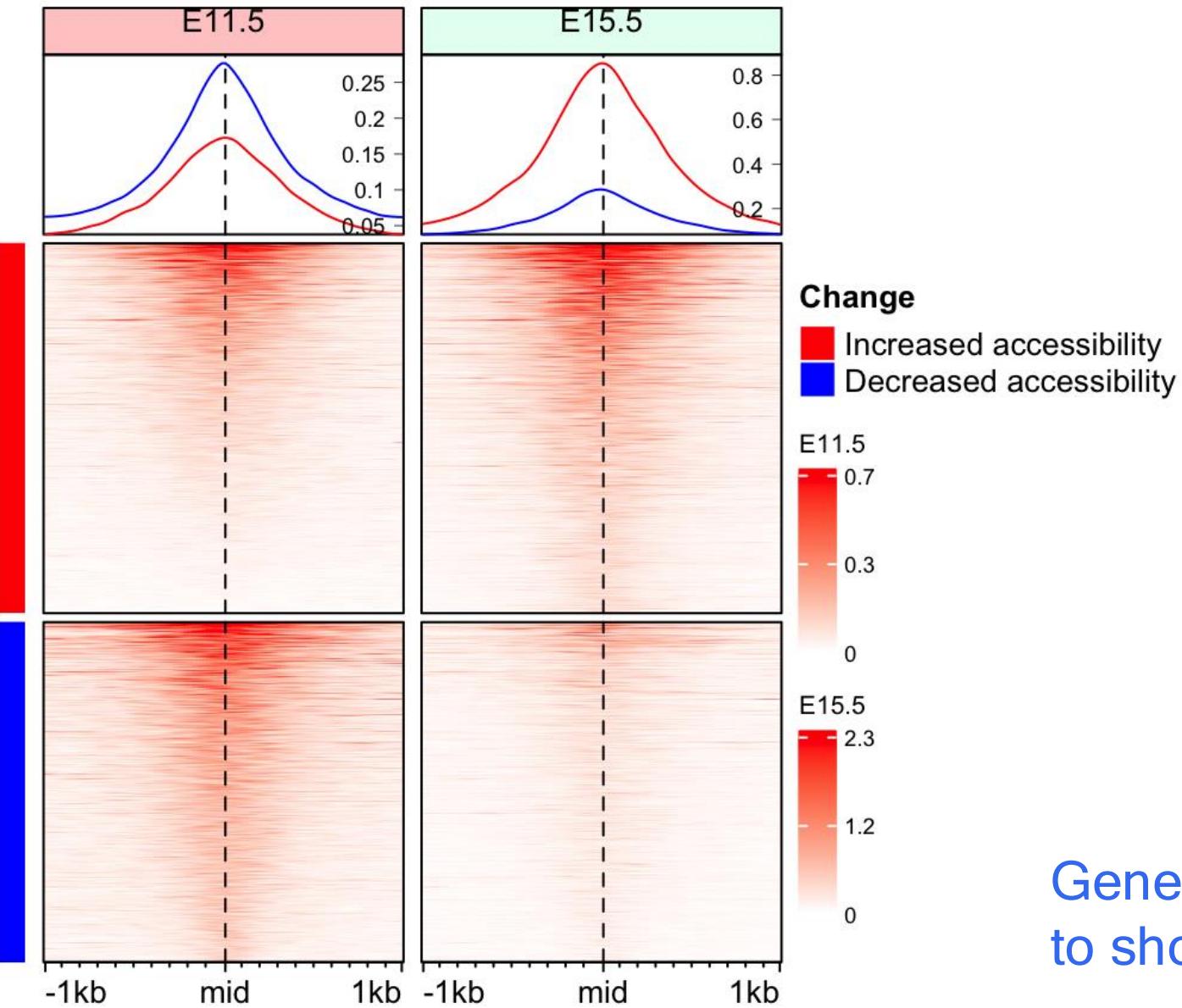
Understanding Heatmap



Heatmap

- Matrix
- Color
- Rows
- Rows annotation
- Columns
- Columns annotation
- Color scale
- Clustering
- Rows and columns order

Understanding EnrichedHeatmap

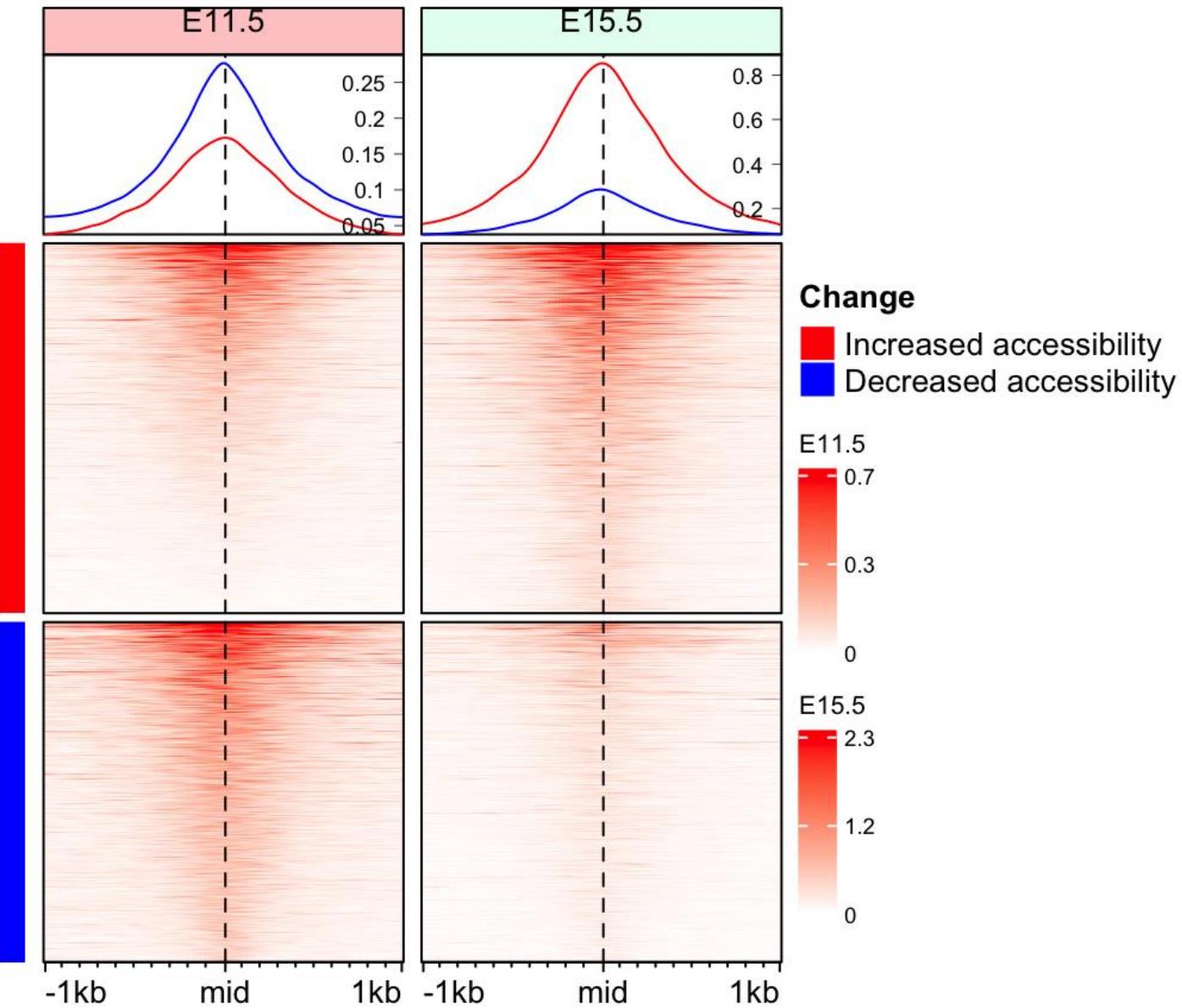


EnrichedHeatmap

- Matrix
- Color
- Rows
- Rows annotation
- Profile plot
- Columns title
- Color scale
- Rows order
- Axis

Generally, replicates are merged into one to show average differences

Understanding EnrichedHeatmap

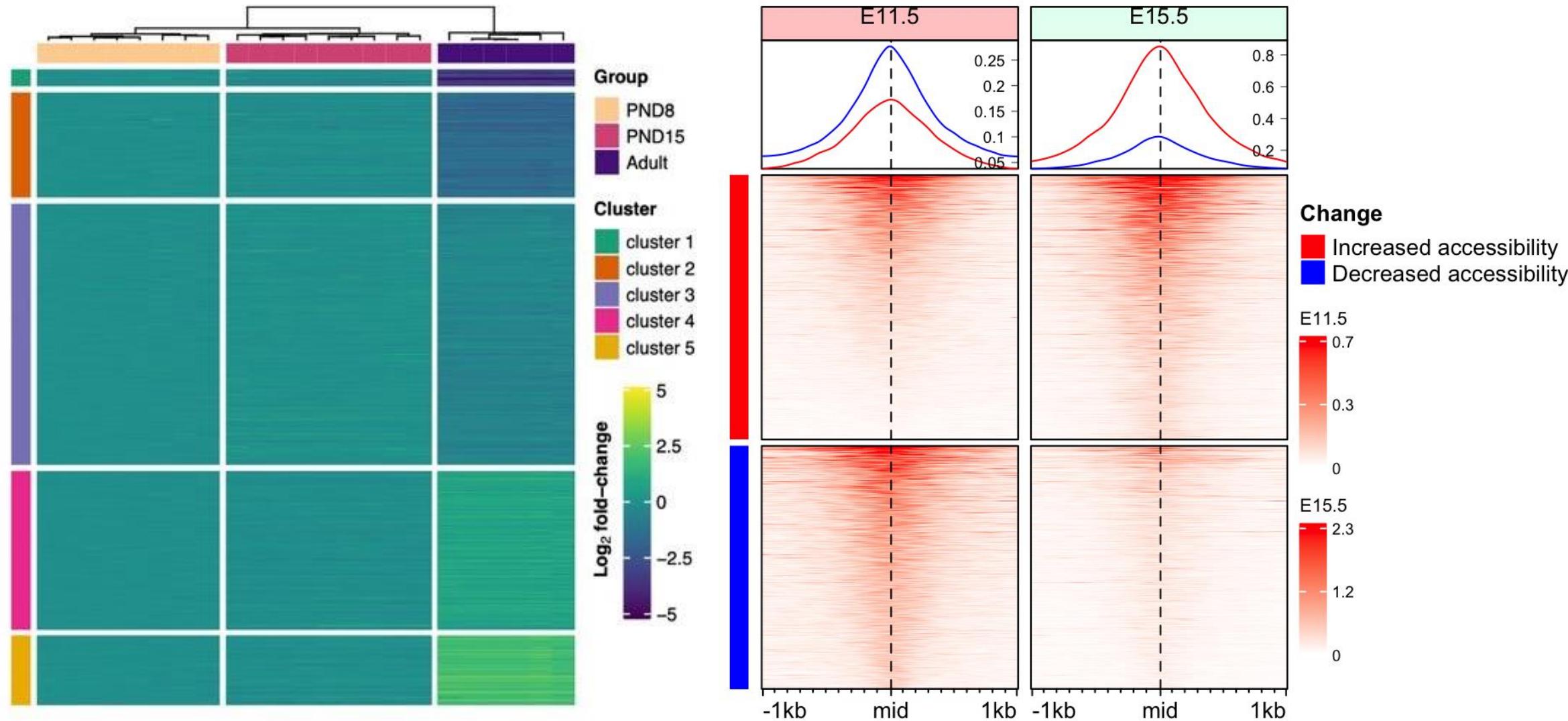


E15.5

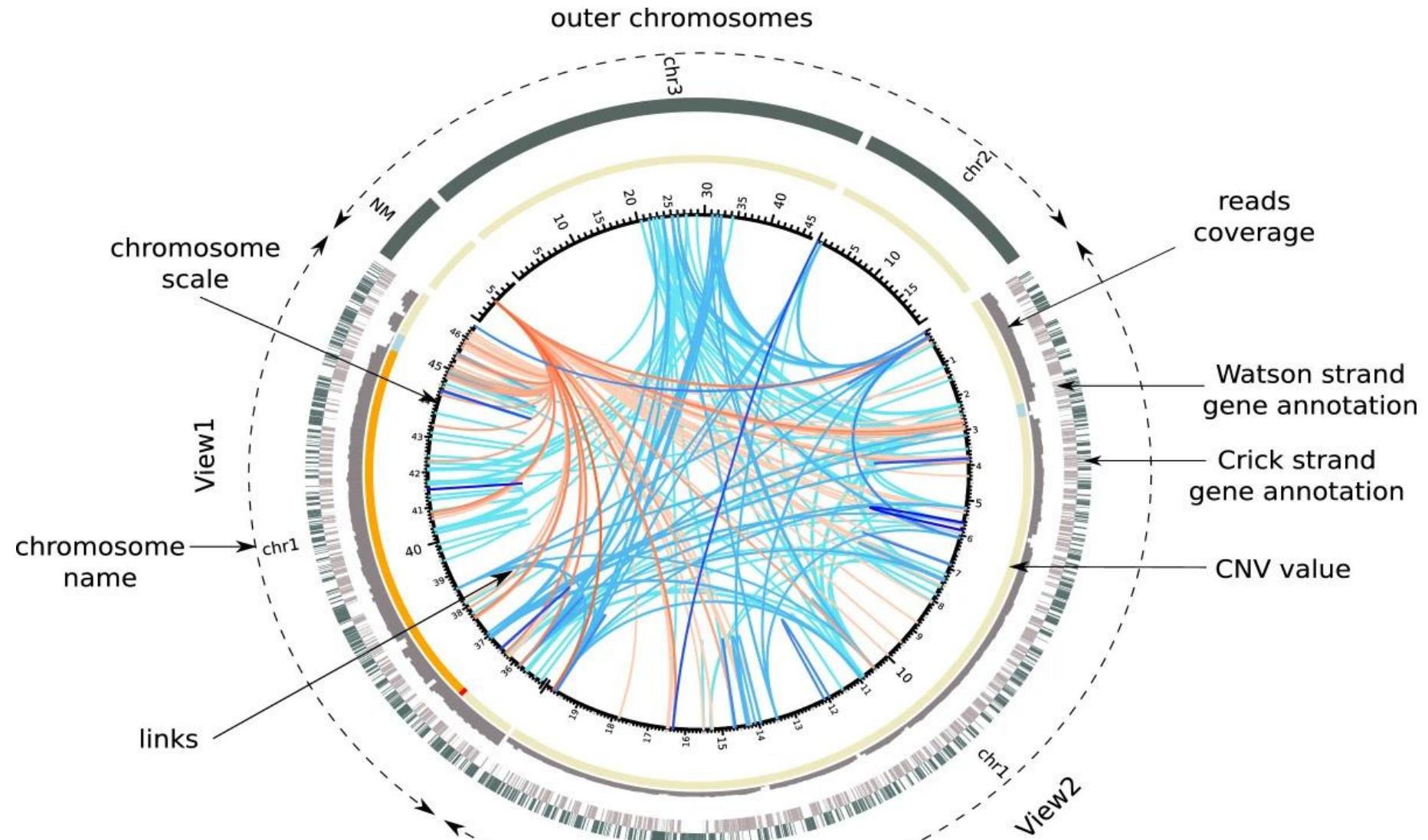
- Color scale: 0 - 2.3
- Profile plot scale: 0-0.8

Why?

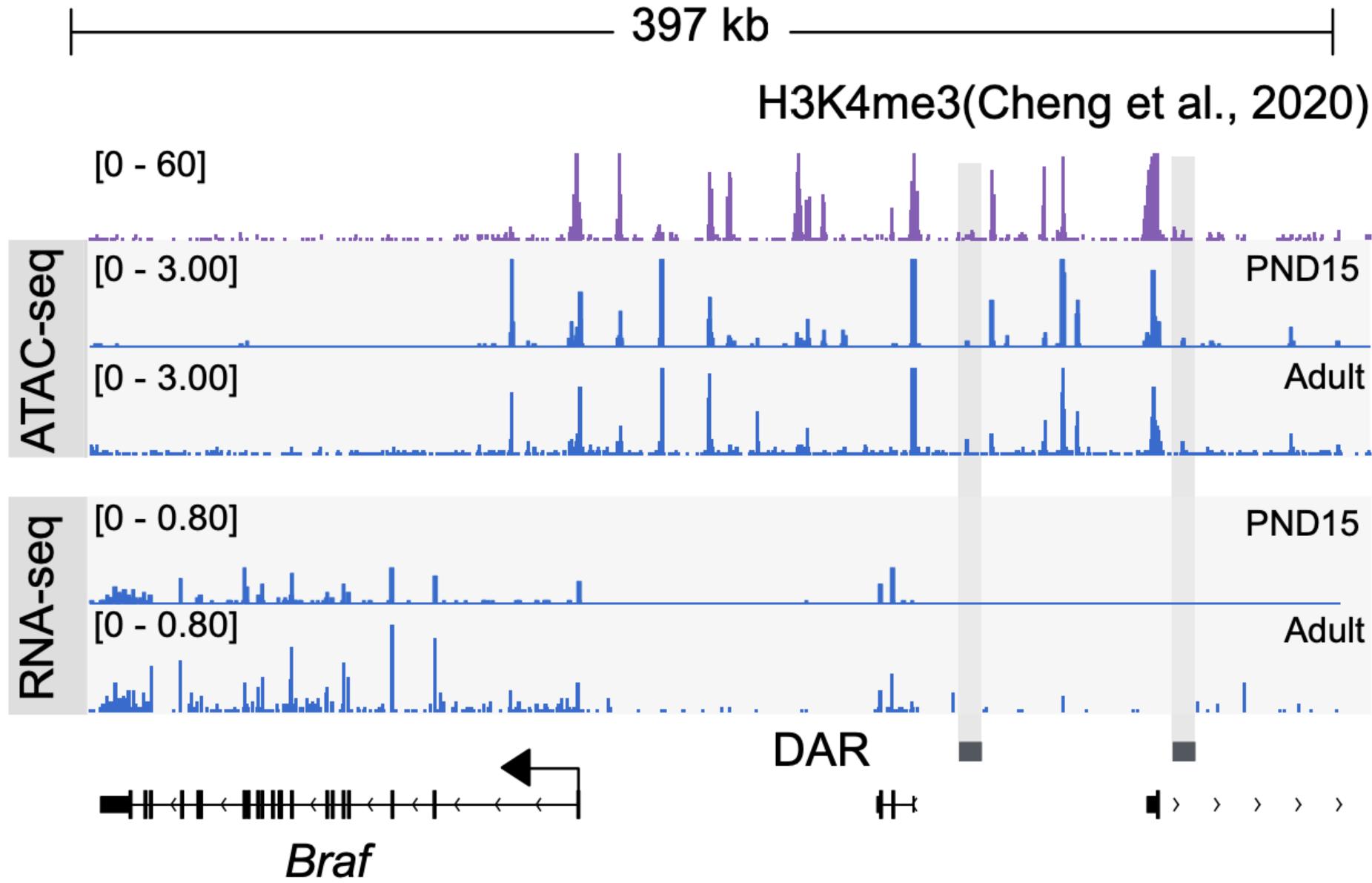
Best way to represent complex data. Other ways?



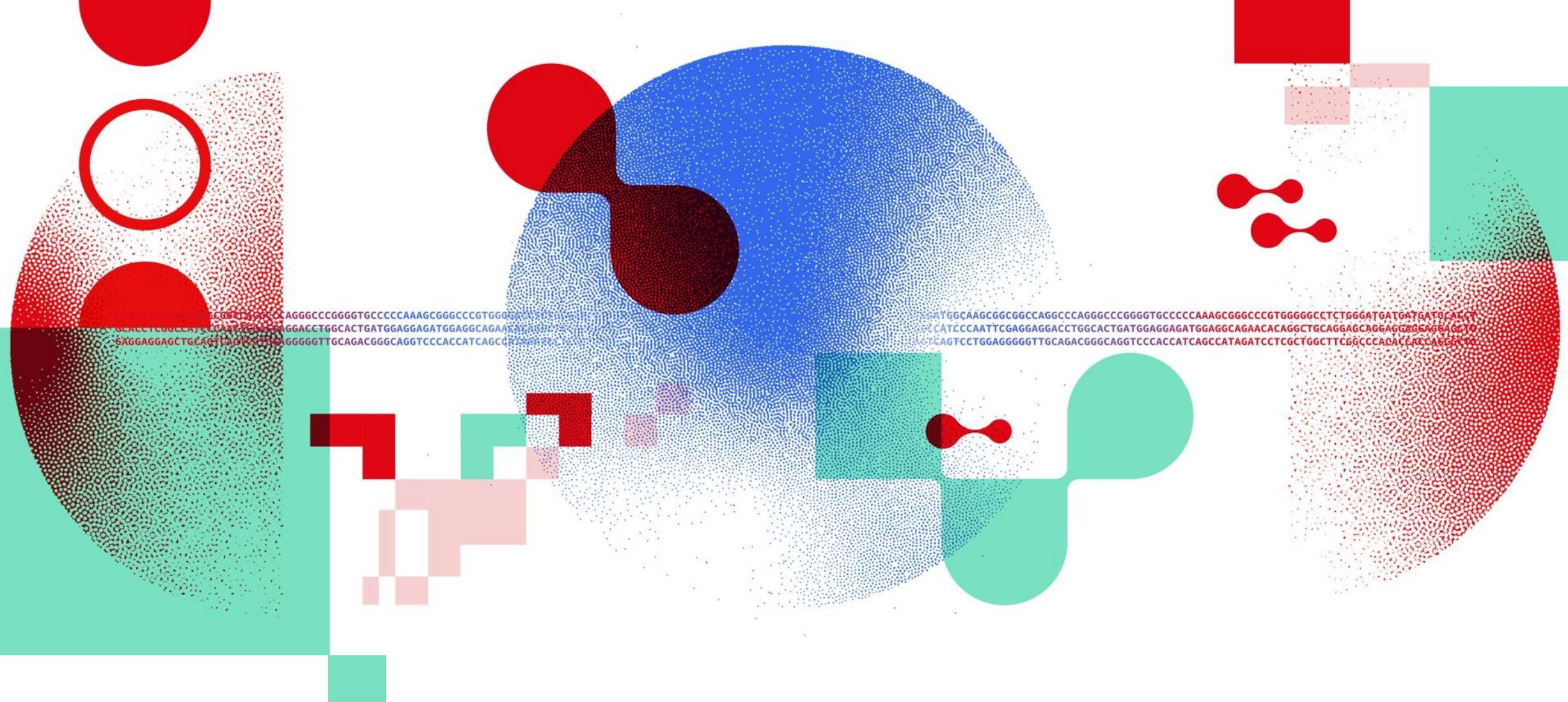
Circos



Genomic snapshots



Exercise 2 & 3



Thank you

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