



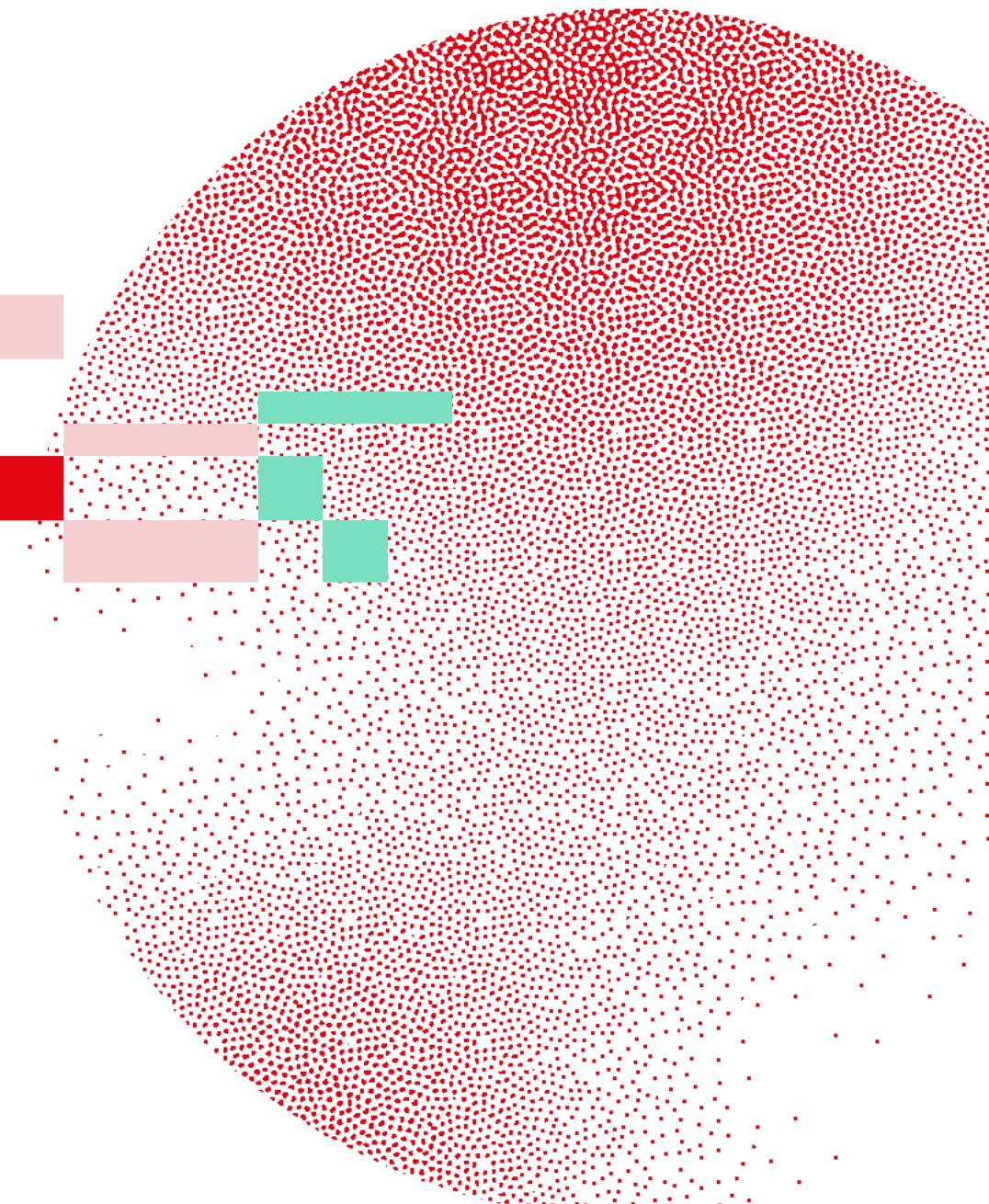
Swiss Institute of  
Bioinformatics

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?

AI Mode

All

Images

Videos

Forums

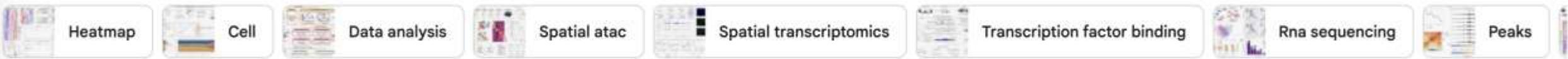
Short videos

Web

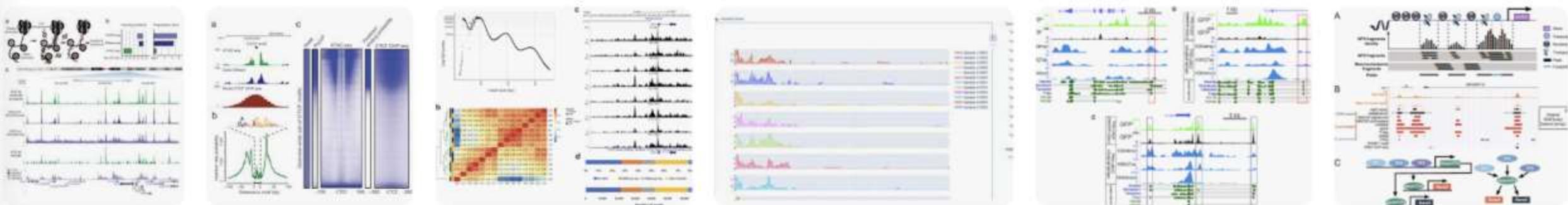
More

Tools

Saves



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

[Compare insights](#) 

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

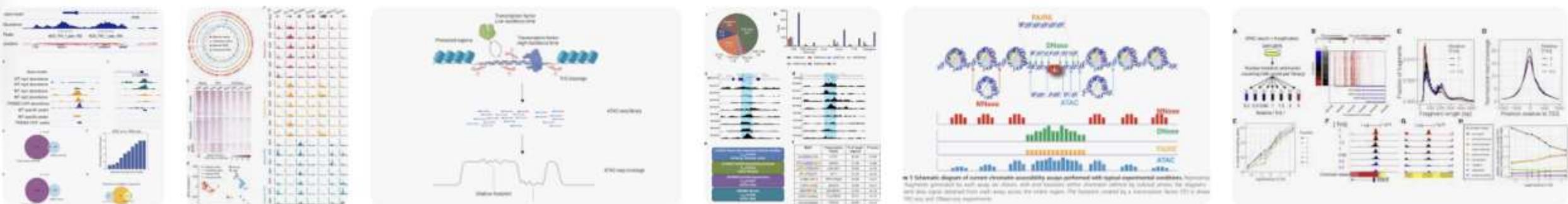
seandavi.github.io  
ATAC-Seq with Biocondu...

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?

AI Mode

All

**Images**

Videos

Forums

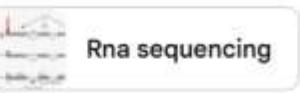
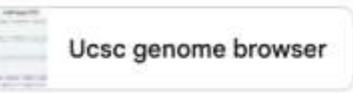
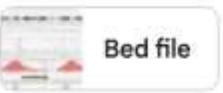
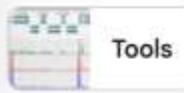
Short videos

Web

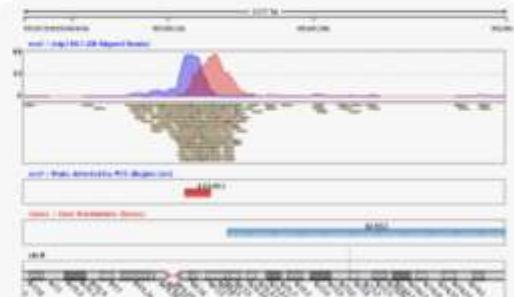
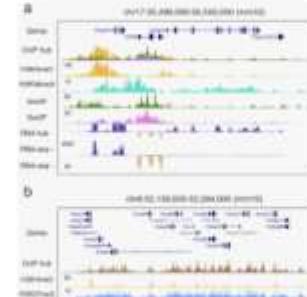
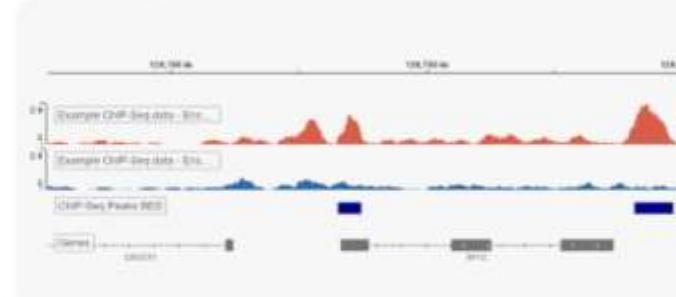
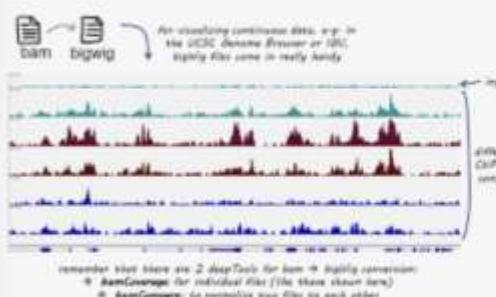
More

Tools

Saves



See detailed Insights & Compare multiple related Papers for : "chip seq visualization"

[Compare insights](#) 

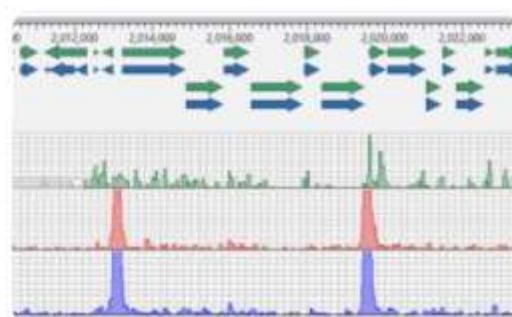
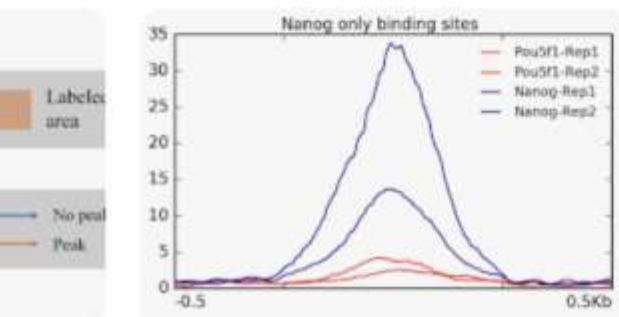
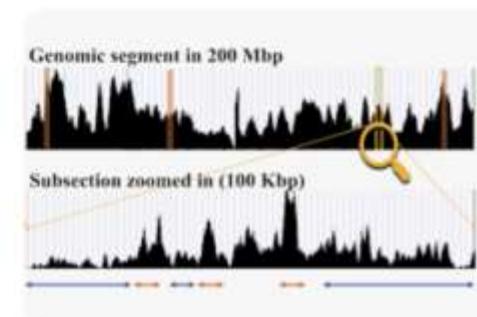
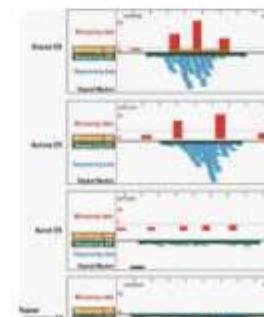
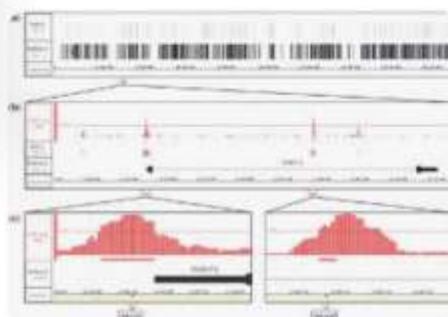
GitHub Pages  
Visualization of peaks | Introduction ...

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?

AI Mode

All

Images

Forums

Short videos

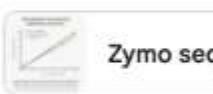
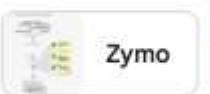
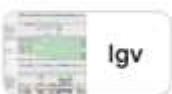
Web

Flights

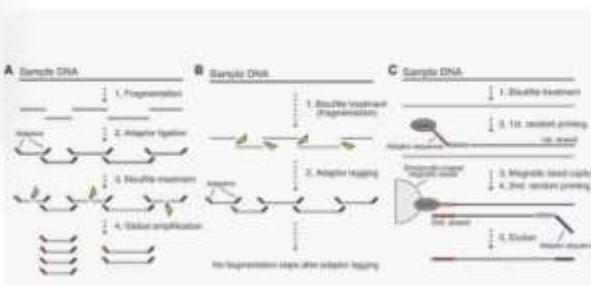
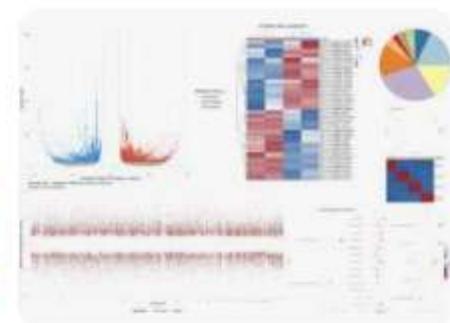
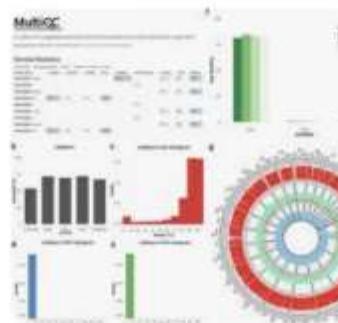
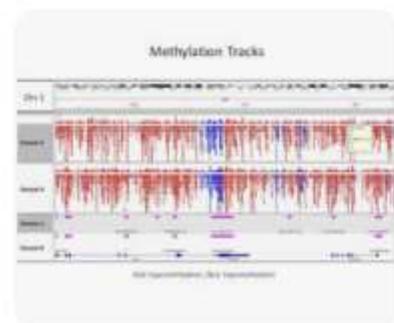
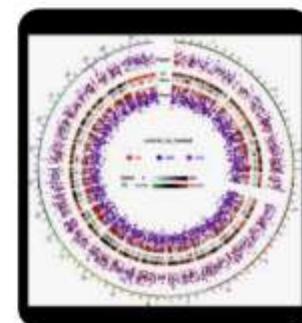
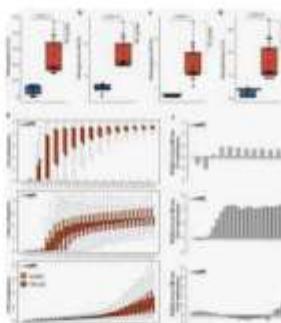
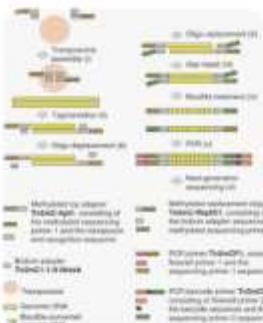
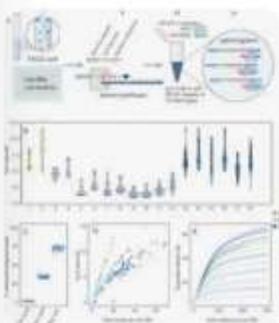
More

Tools

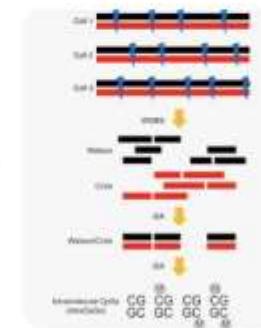
Saves



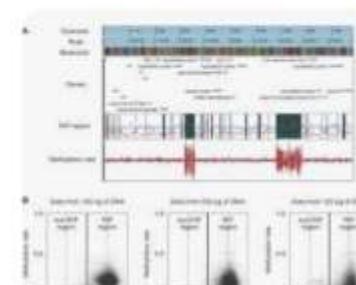
See detailed insights & Compare multiple related Papers for : "wgbs seq visualization"

[Compare insights](#) 

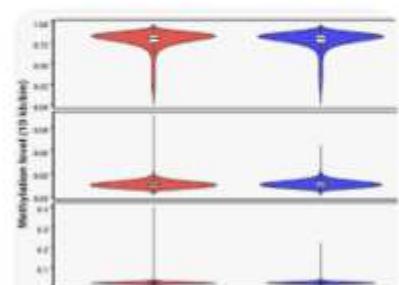
ResearchGate  
WGBS and PBAT. (A) Schematic of the ...



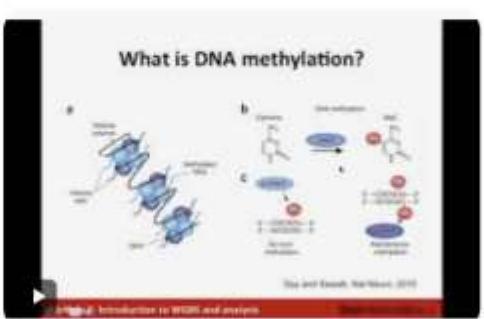
Nature  
Resolution of the D...



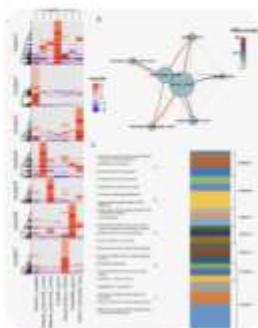
ResearchGate  
WGBS of N. crassa by PB...



Novogene  
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?

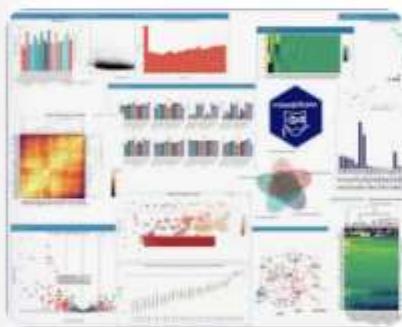
AI Mode All Images Videos Forums Short videos Web More

Tools

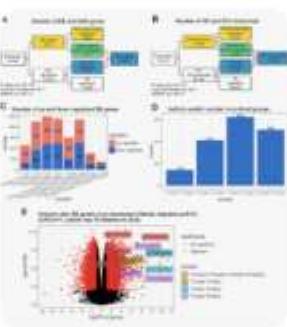
Saves



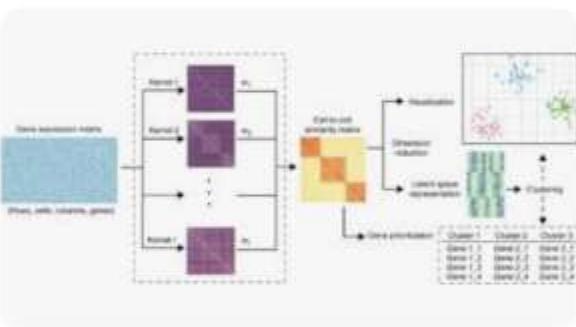
See detailed insights & Compare multiple related Papers for : "rna seq visualization"

[Compare insights](#)


● Posit Community  
rnaseqDRaMA - RNAseq data ...



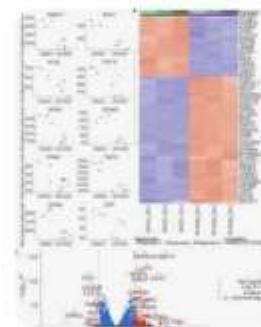
● ResearchGate  
visualization outputs f...



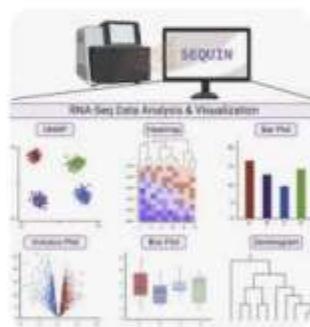
● Nature  
analysis of single-cell RNA-seq data ...



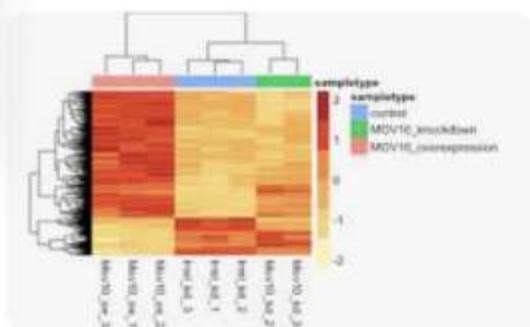
● Elucidata  
Bulk RNA-seq Data Visualization Tools



● Springer  
RNA-seq data | B...



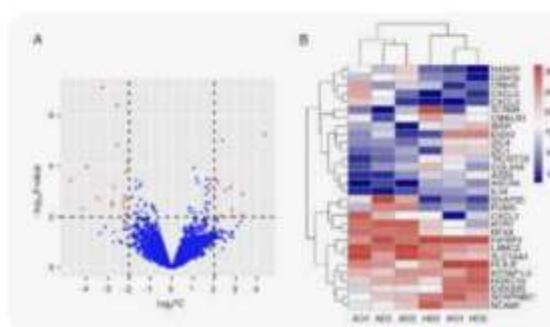
● ScienceDirect.com  
RNA-seq data ...



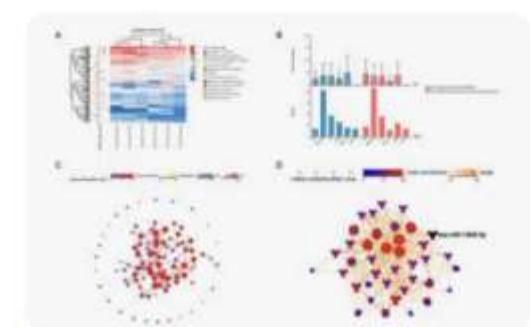
● GitHub Pages  
RNA-seq visualizations | Training-modules



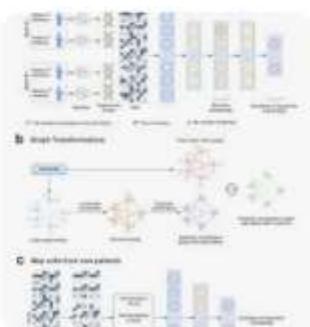
● BioInfoRx  
BxGenomics - RNA-Seq data anal...



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

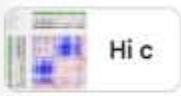


● RNA-Seq Blog  
Intuitive RNA Data Visualization ...



● Nature  
single-cell RNA-Seq pro...

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



Hi c



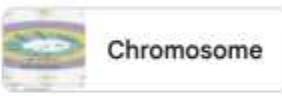
Epigenetics



Dna methylation



Data



Chromosome



Scrna seq analysis



Epigenomics



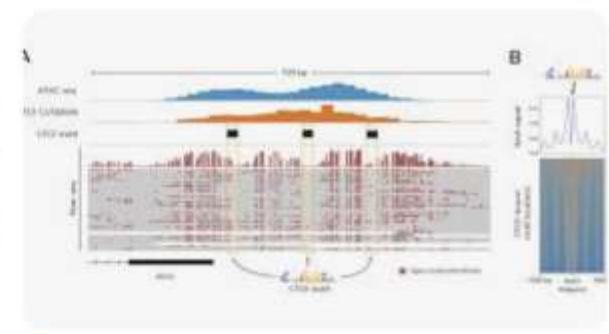
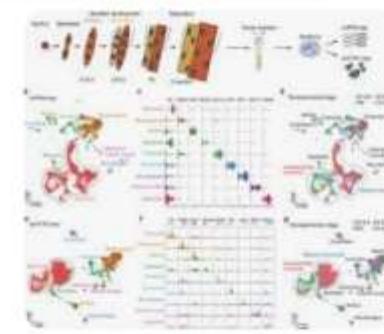
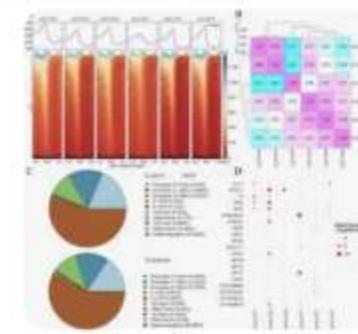
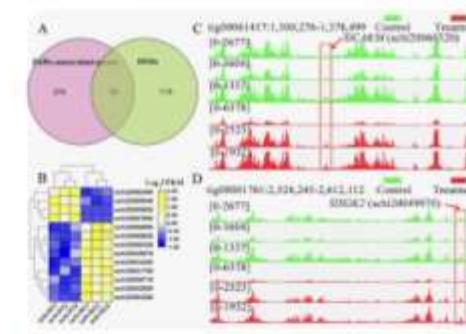
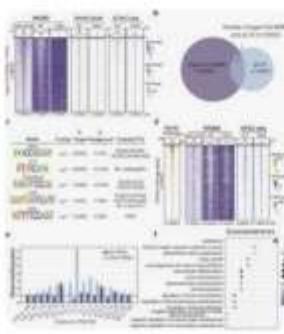
Single cell



Scatac seq



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

[Compare insights](#)


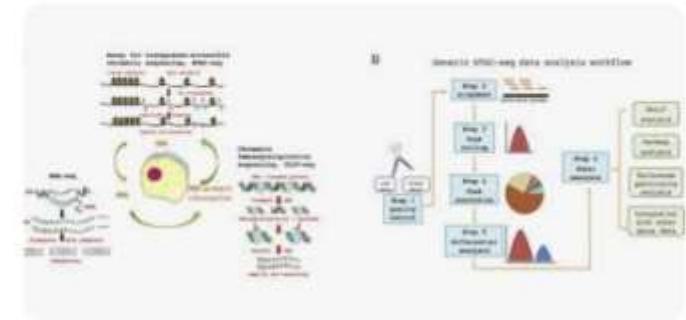
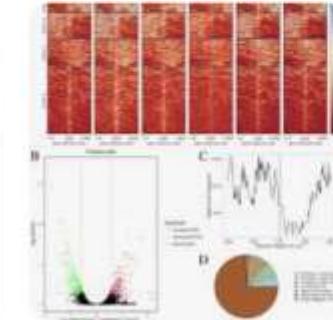
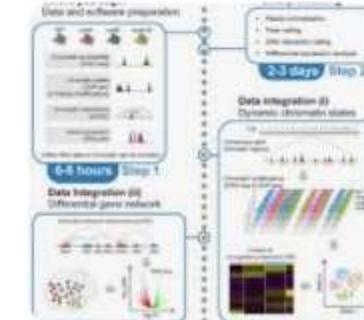
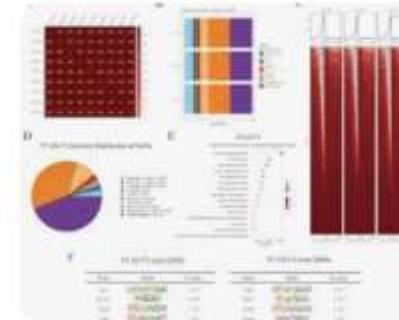
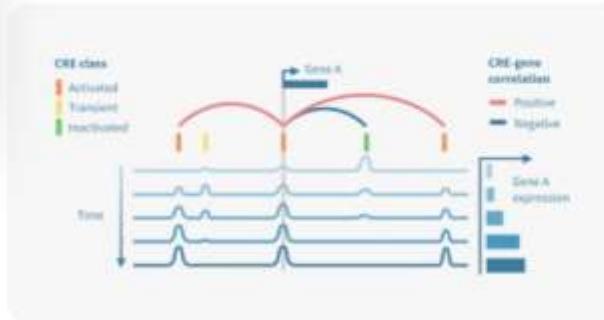
Geneva Technologi...  
RNA-seq and ChIP...

R<sup>2</sup> ResearchGate  
RNA-seq, WGBS, 5h...

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

R<sup>2</sup> ResearchGate  
Multi-omics single nucleus R...

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



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

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

STAR Protocols - Cell Press  
chromatin remodeling ...

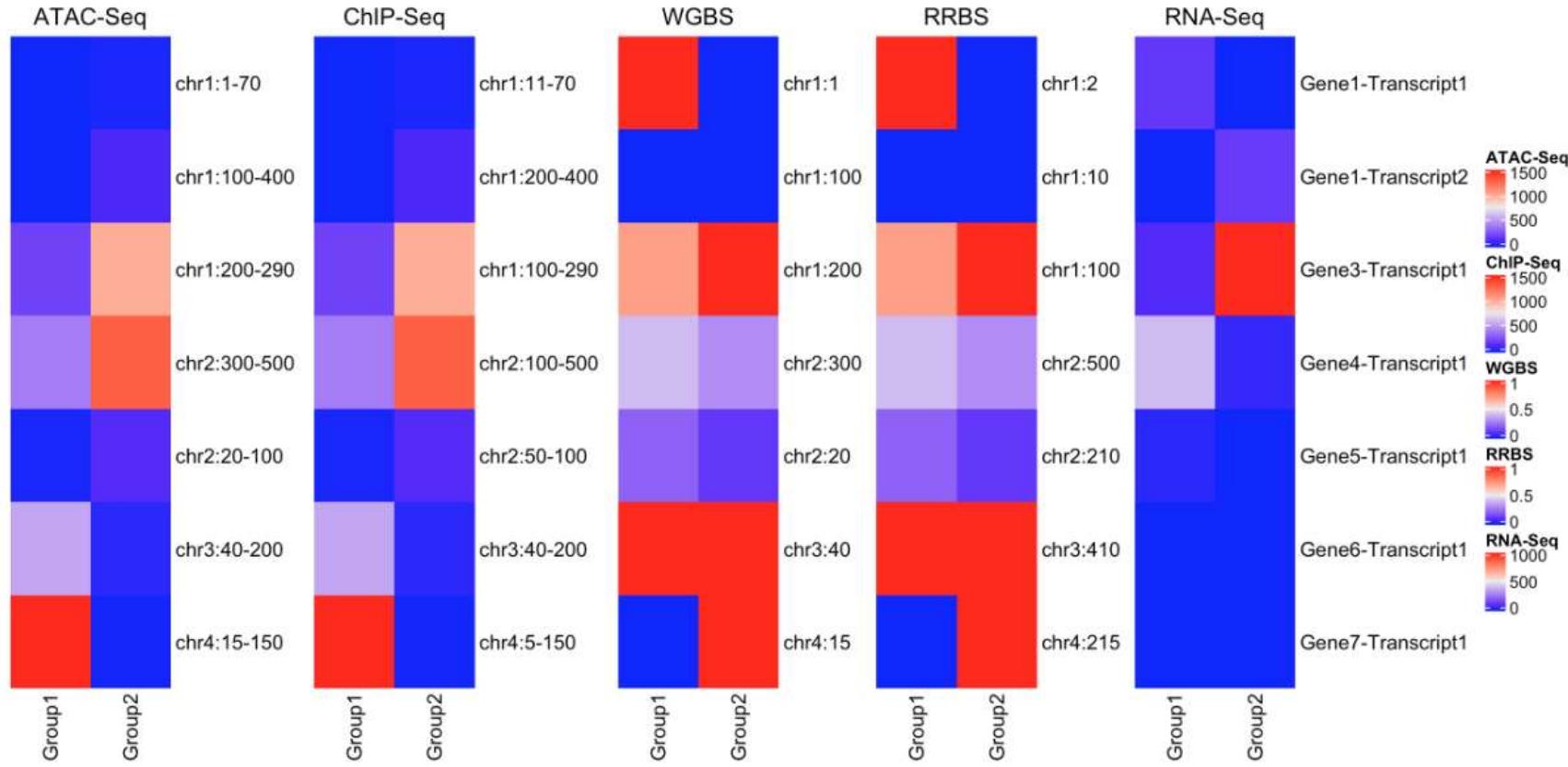
Springer Link  
ATAC-seq and RNA-seq ...

ResearchGate  
Principles and workf low 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)

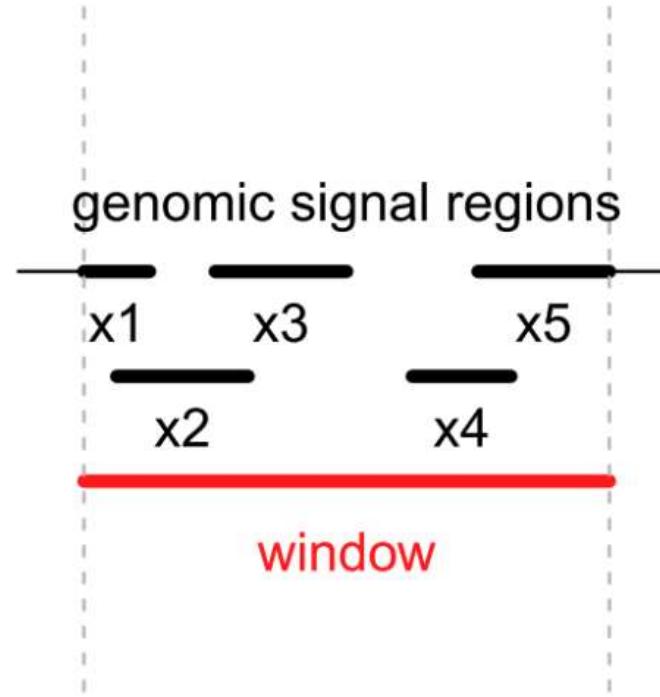
	seqnames	position	strand
Gene_1	chr21	13	+
Gene_2	chr21	46	+
Gene_3	chr21	78	+
Gene_4	chr21	10	+
Gene_5	chr21	45	+

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



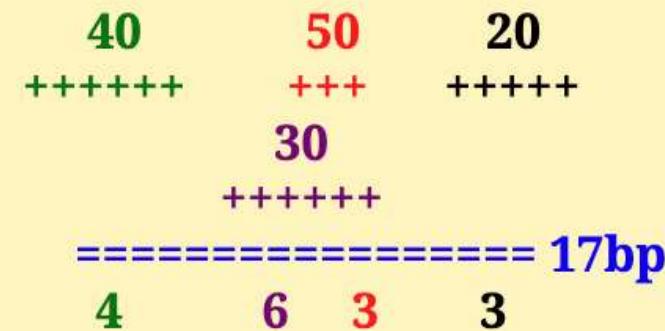
The **red line** represents one window in the target regions or in the flanking regions when normalizing genomic signals to target regions. **Black lines** represent genomic signals that overlap to the given window.

# 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.



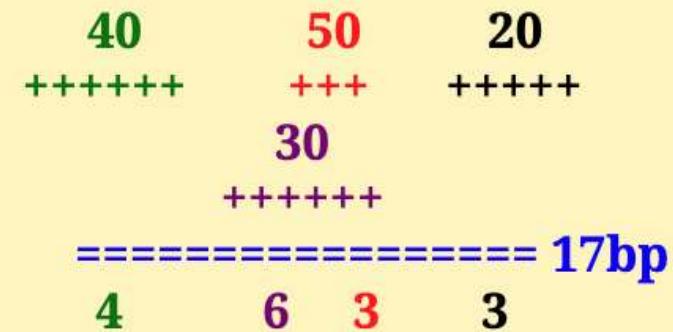
**4bp** not overlapping to any region

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

# 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

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

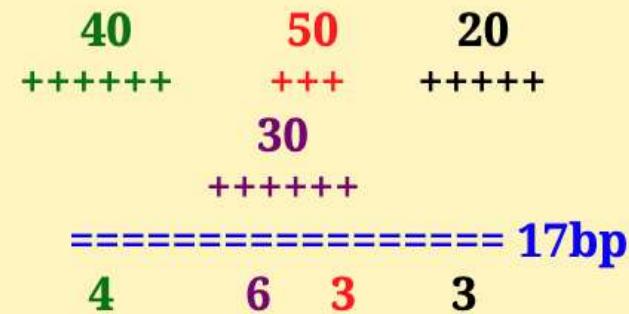
# Averaging methods to summarize the signals

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.

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



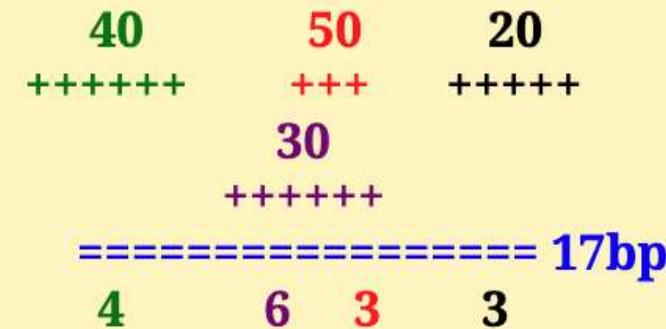
**4bp not overlapping to any region**

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

# 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



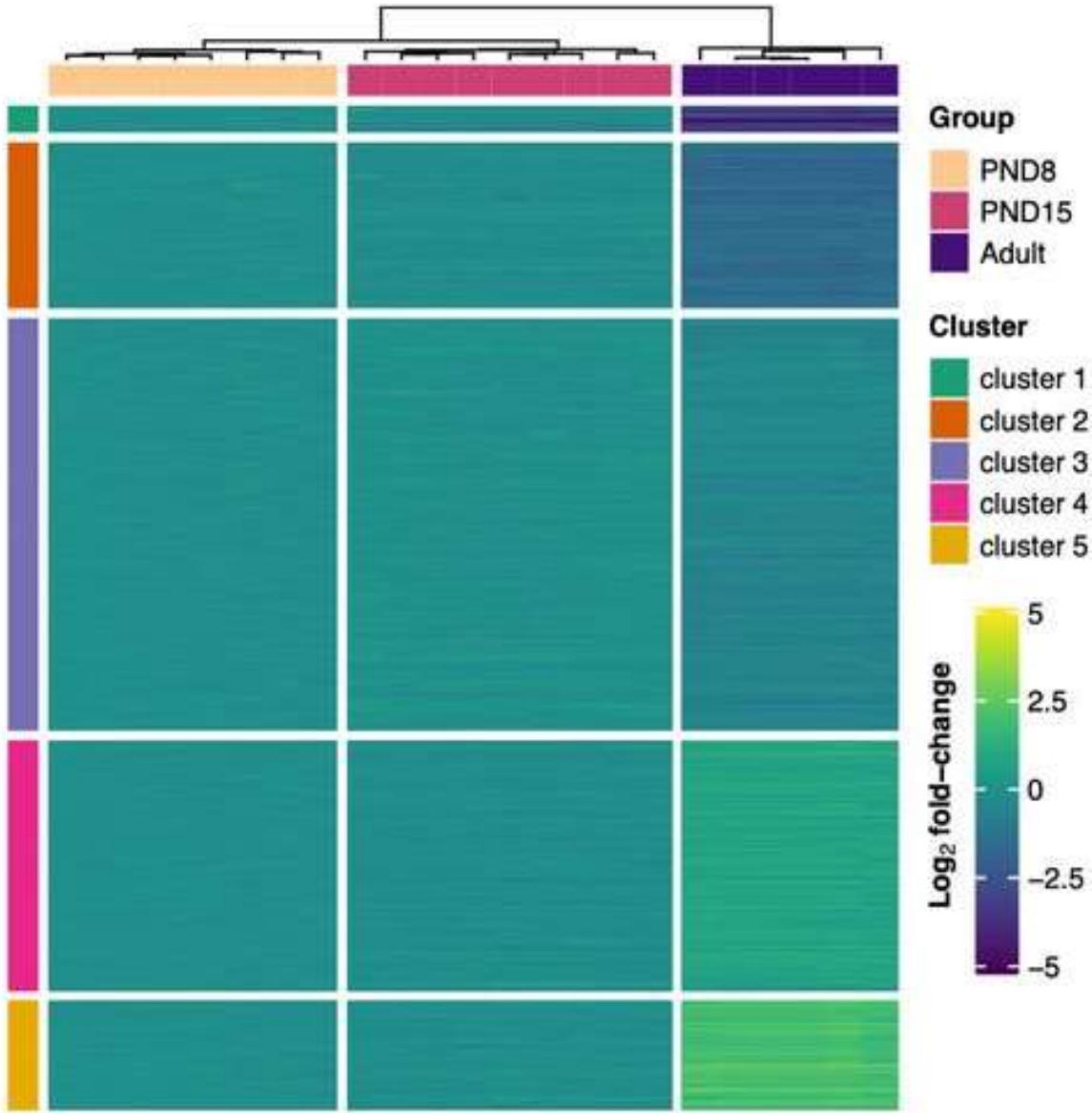
## EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations

Zuguang Gu<sup>1,2\*</sup>, Roland Eils<sup>1,2,3</sup>, Matthias Schlesner<sup>1</sup> and Naveed Ishaque<sup>1,2</sup>

# 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. <b>Crucial to set value_column</b> .  <b>Highly recommend <code>smooth = TRUE</code> and <code>empty_value = NA</code> for better visualization due to sparse CpG distribution.</b>

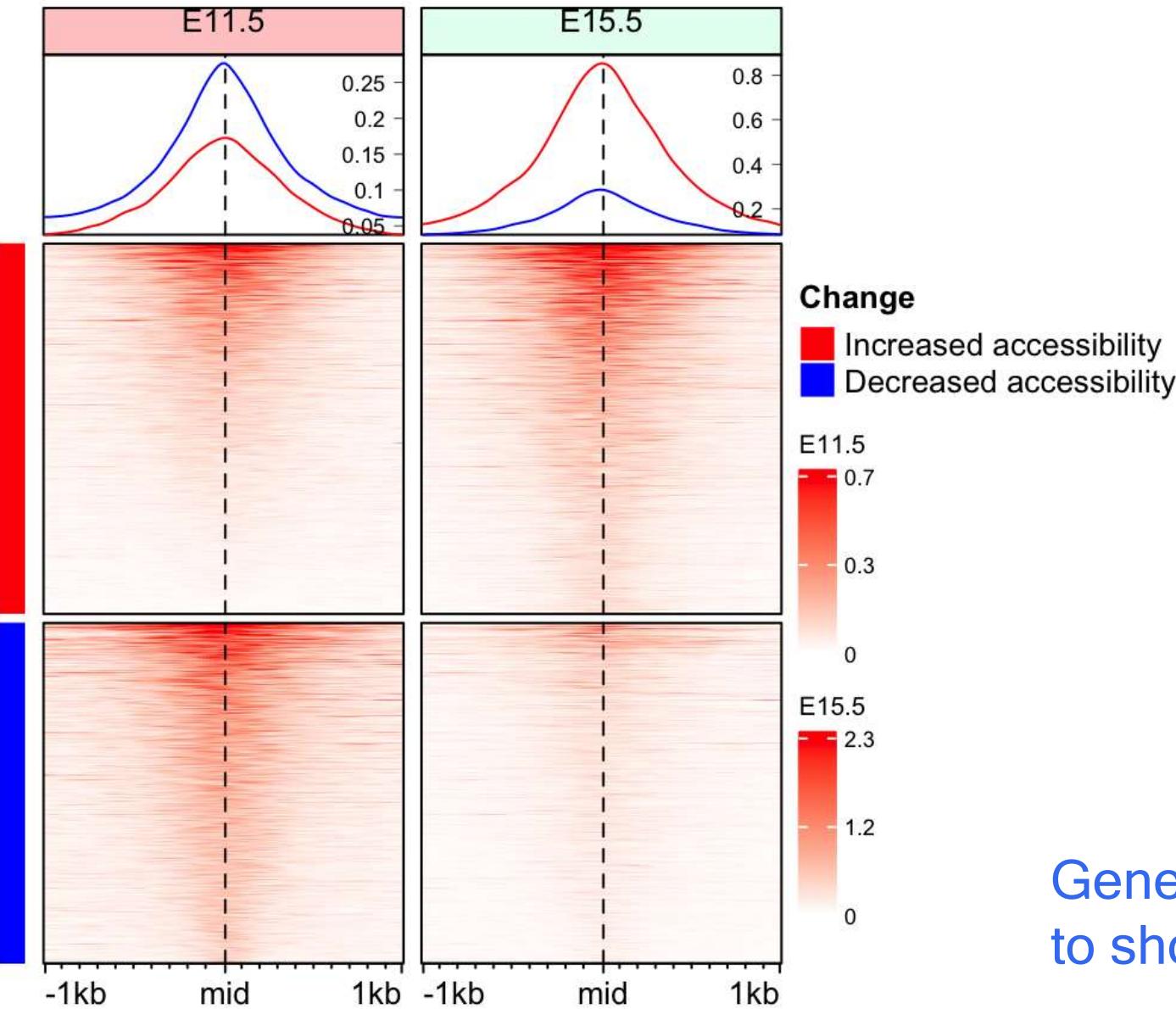
# Understanding Heatmap



## Heatmap

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

# Understanding EnrichedHeatmap

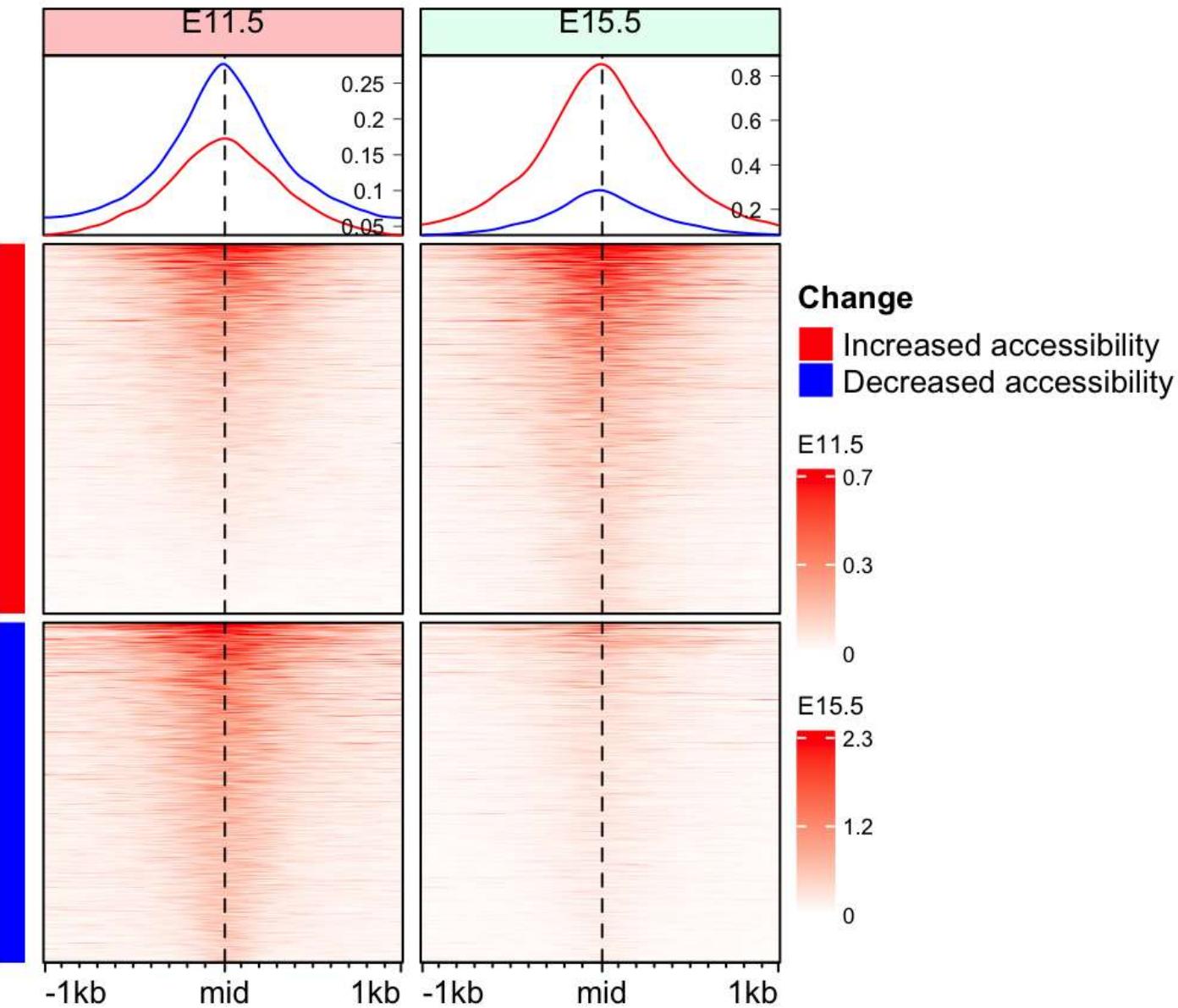


## EnrichedHeatmap

- 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

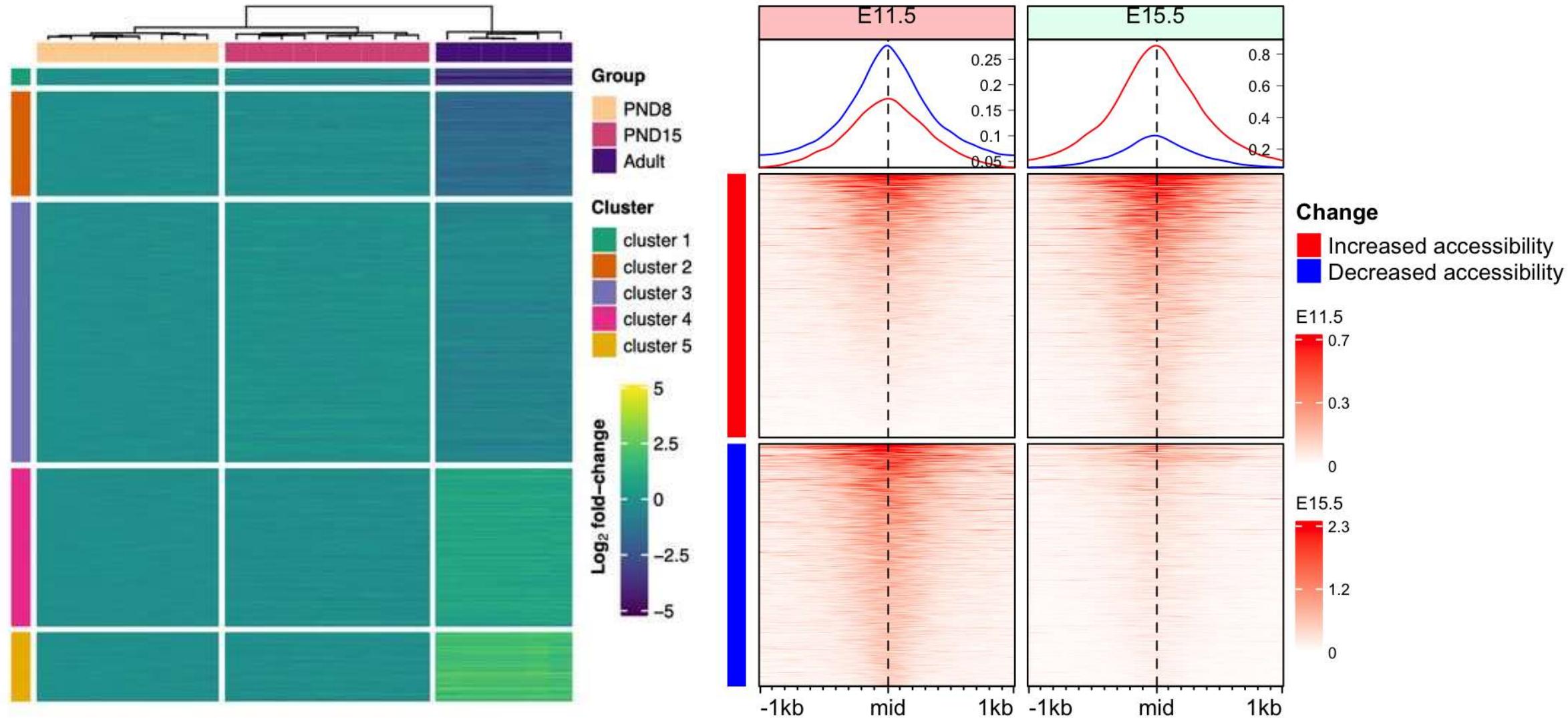


E15.5

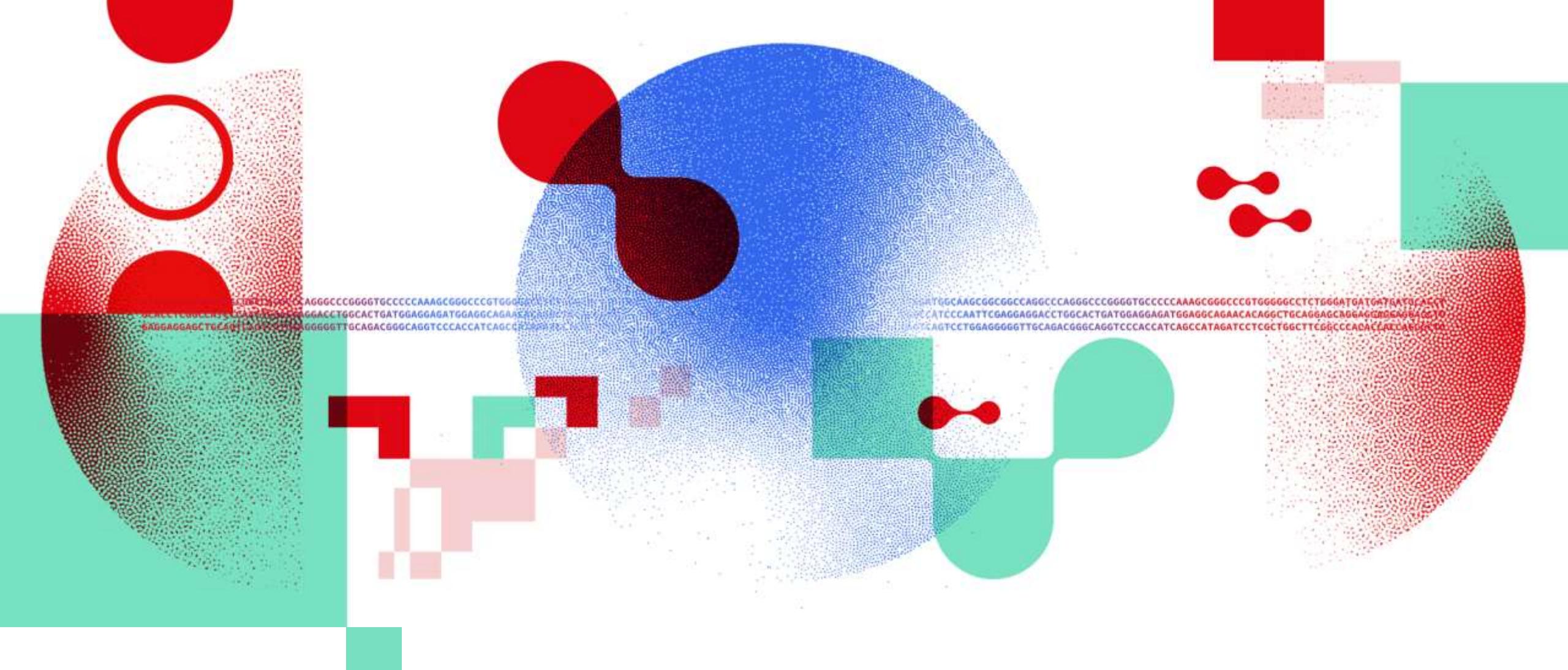
- Color scale: 0 - 2.3
- Profile plot scale: 0-0.8

Why?

# Best way to represent complex data. Other ways?



# Exercise 2 & 3



# Thank you

DATA SCIENTISTS FOR LIFE  
[sib.swiss](http://sib.swiss)