

Bioinformatics for epigenomics

Two-day course

Professional advanced training for HBO and university teachers and researchers.

This two-day course provides a **practical introduction** to the analysis and interpretation of analyzing epigenetic editing induced effects in epigenomics and RNA-seq data, using a real multi-omics dataset throughout.



This course is funded by
Epi-Guide-Edit.

Participants will work with sequencing data from DNA methylation, chromatin accessibility, protein–DNA interactions, and gene expression, gaining insight into how these layers contribute to **the effect of epigenetic editing**.

The course combines lectures, hands-on exercises, and reproducible analysis workflows in R, enabling participants to understand both the experimental context and the computational steps required to move from **raw data to biological interpretation**.

When: Wednesday September 30 & Thursday October 1, 2026

Location: Hugo R. Kruytgebouw (Z.409), Utrecht, Netherlands

Costs: €50 (incl. 2 lunches, dinner on SEP 30 is optional for €30)

Registration: [Please register here](#) or scan the QR-code.

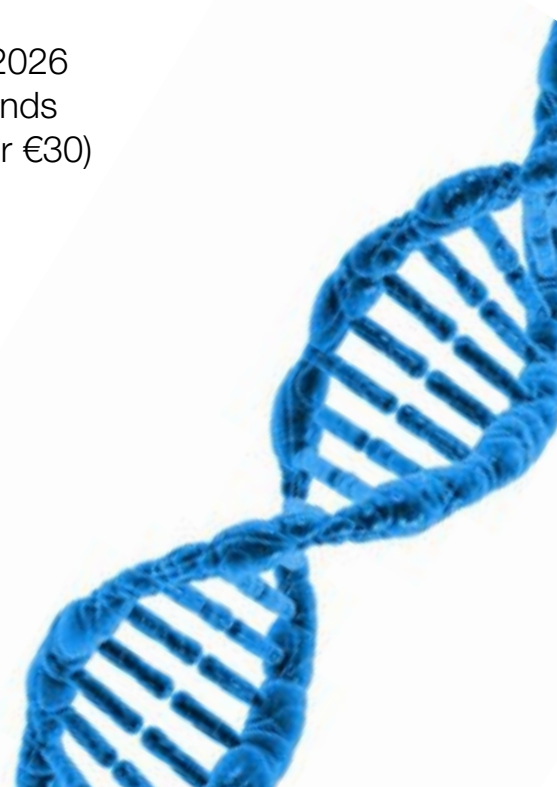


Registration deadline is September 11, 2026.

Questions?

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Programme

Register here:



Day 1

09:30 - 12:30

Lecture: Introduction to epigenomics and epigenetic editing

Lecture: Methylome sequencing

Hands-on: Working with methylome sequencing data

Guest lecture of research case

12:30 - 13:30 Lunch

13:30 - 17:00

Lecture: Introduction to ATAC-seq and ChIP-seq

Hands-on: Working with ChIP-seq and ATAC-seq data

Lecture: Introduction to RNA-seq

Lecture: The use of public (web-based) analysis tools

Hands-on: Working with public tools for gene set analysis

Dinner (optional)



Day 2

09:30 - 12:30

Lecture: Gentle introduction to R

Hands-on: Creating visuals with R, dplyr and ggplot2

Lecture: Statistical analysis of RNA-seq data

Hands-on: Working with R and DESeq2

Guest lecture of RNA-seq study

12:30 - 13:30 Lunch

13.30 - 17:00

Lecture: Introduction to biological interpretation of gene sets

Hands-on: Working on gene sets

Lecture: The use of ChatGPT and similar tools for biological analysis

Hands-on: Working with AI tools

Wrap-up / Q&A



Who should attend:

This course is primarily intended for teachers in HBO and university environments. The focus during the course will be on working with example data files and exercises that can be translated into a curriculum for students. The course is also useful for graduate students, postdoctoral researchers, and other life scientists who generate or plan to generate sequence-based omics data and want to better understand how these experiments are designed, analyzed, and interpreted. Ideally, participants should have some background in molecular or cellular biology and affinity with data driven research. Programming skills are not required for this course.

Please note, registration deadline is September 11, 2026.

Contact: Wynand Alkema, w.b.l.alkema@pl.hanze.nl / Biwen Wang, b.wang@pl.hanze.nl