

This is to certify that
Samuel Carleial Fernandes
has successfully taken part in

Epigenomics Data Analysis: from bulk to single cell

Held Online, 25-29 October 2021

The course consisted of lectures, exercises and group discussions. The following subjects were covered in the lectures and exercises:

- Data processing and analyses for differential methylation with Illumina EPIC arrays and Bisulfite-seq
- Methylation methods and technologies
- ChIP-seq and ATAC-seq data processing and analysis principles incl. peak calling, peak (in)dependent quality metrics, differential binding/accessibility analysis; motif enrichment
- Peaks annotations and functional analysis
- Quantative ChIP-seq methods
- ChIP-seq alternatives with ChIC, CUT&Run and CUT&Tag
- Introduction to Nextflow and nf-core epigenomics pipelines
- Single cell methods for epigenomics
- Data integration

Examination:

Active participation during lectures, group sessions and practical exercises

The course was arranged by the National Bioinformatics Infrastructure Sweden (NBIS) at Science for Life Laboratory (SciLifeLab).

29 October 2021



Agata Smialowska, PhD
National Bioinformatics Infrastructure Sweden
Science for Life Laboratory
Stockholm University

Signature page

This document has been electronically signed
using eduSign.

eduSign