1. Introduction	- Objectives - Computing requirements - Data	❖ Linux ❖ R ❖ wget
2. Data Pre-processing	- Merge technical replicate - Quality Control	❖ FastQC
3. Alignment	- Bowtie2 alignment - Duplicates - Fragment size	❖ Bowtie2 ❖ Samtools ❖ Picard
4. Filtering and Conversion	- Sam to bam - Bam to bed	❖ Samtools ❖ Bedtools
5. Spike-in Calibration	- Spike-in alignment - Scaling factor - ChIPseqSpikeInFree	❖ Bowtie2 ❖ Bedtools ❖ R: ChIPsewSpikeInFree
6. Peak Calling	- SEACR peak calling - MACS2 peak calling - % fragment in peaks	❖ SEACR ❖ MACS2 ❖ R: chromVAR
7. Visualization	- Genome browser - Heatmap	❖ Integrative Genome Viewer ❖ UCSC Genome Browser ❖ Deeptools
8. Differential Analysis	- DESeq2 - Peak x Sample matrix - Normalization - Differential detection	❖ R: DESeq2 ❖ R: GenomicRanges