



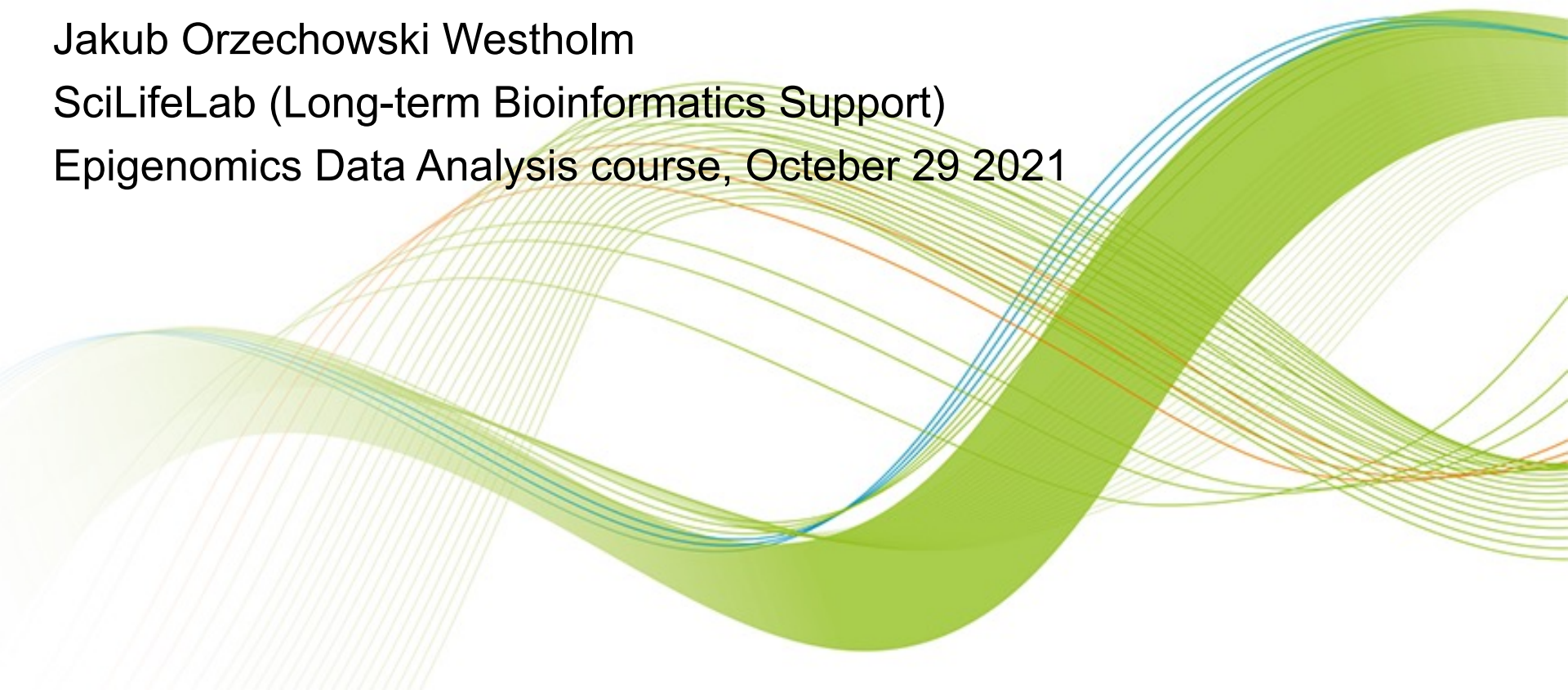
SciLifeLab

Single cell and data integration exercises

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SciLifeLab (Long-term Bioinformatics Support)

Epigenomics Data Analysis course, October 29 2021



- **Single cell ATAC-seq**
 - Learn to process single cell ATAC-seq data:
 - QC, filter cells
 - Normalization, clustering, visualization
 - Motif analysis
 - Find differentially accessible regions
 - Integration with RNA-seq data
 - Quite advanced exercise, may take a while
 - Some steps take a while (5-10 mins) to run



- **Genomic overlaps**
 - Learn to:
 - Manipulate genomic ranges
 - Compute overlaps between data sets
 - Check if those overlaps as statistically significant
 - Quite basic exercise

- All these are R exercises
- The single cell exercise can be run in two ways
 - With singularity. A bit complicated to set up, but “sure to work”
 - With Uppmax modules. Easier to set up, but less stable (last year this worked for around 75% of students).
- The exercise on genomic regions should run without problems using Uppmax modules.
- (If you run these exercises on your local computer, you will have to install all packages yourselves. This is not hard, but takes a while.)
- [Read instructions](#), then ask us!





**KEEP
CALM
AND
GOOD
LUCK**