SciLifeLab

Single cell exercise

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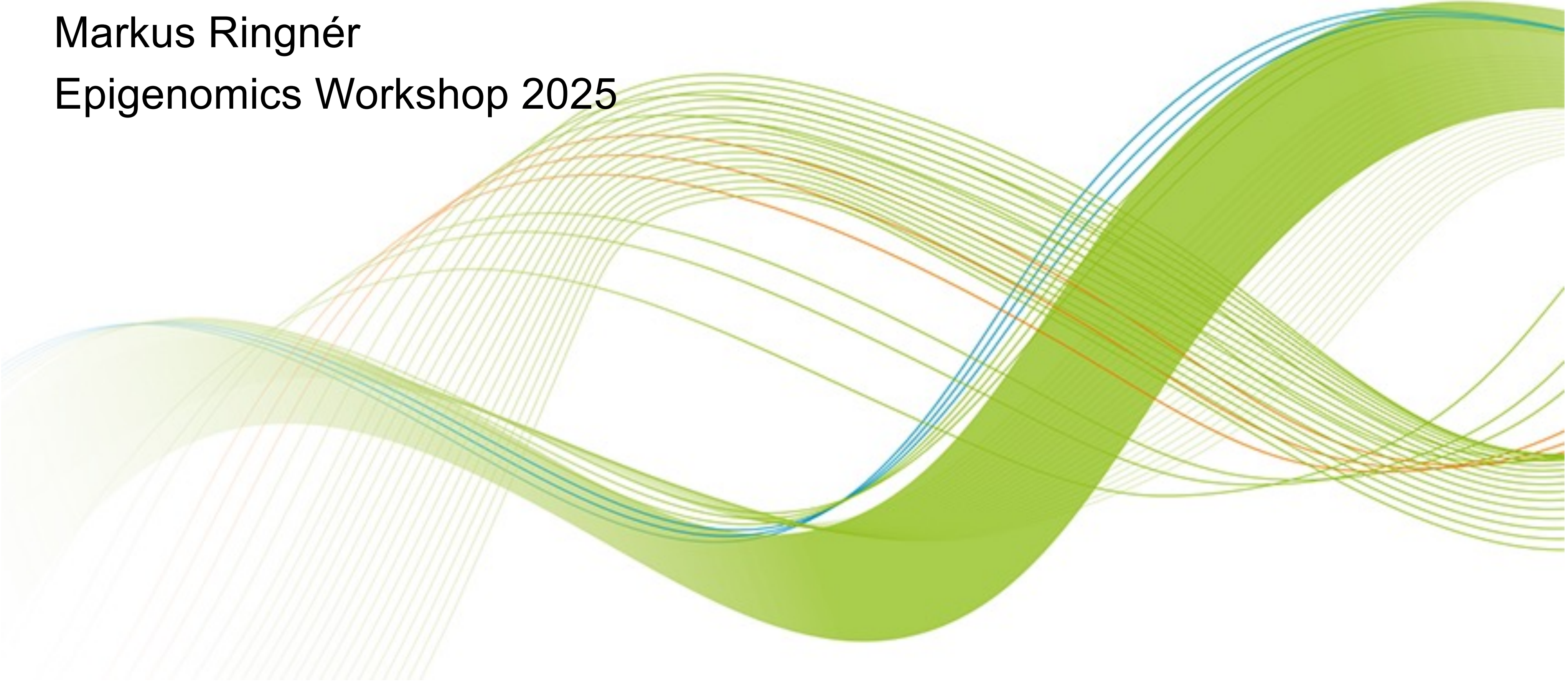

Single cell exercise

- **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 (around 10 mins) to run

Practical things

- All these are R exercises
- The single cell exercise can be run in three ways
    - On Uppmax using modules. **Recommended.** No setting up, everything is already installed. Should work without problems, but you need an Uppmax account.
    - On uppmax, using containers. Good for reproducibility. Also a good option if Rstudio is slow using ssh
    - On your laptop. You need to install R and all packages. Also you need around 13Gb to run the single cell exercise.

- Read instructions, then ask us!