CIRCUS: Detecting circular patterns in scRNA and CITESeq data
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Project scope: There is an increasing number of multimodal single-cell RNA sequencing (scRNASeq) data available. In this project we are using CITE-Seq and RNA seq data, where we use surface marker expression in combination with gene expression data to see if we can detect fluctuating patterns (circles) in the RNA. You will have access to our collaboration partners data.

Project learning objectives:
- Get familiar with single cell RNA seq processing
- Test the hypothesis that we can correlate protein and RNA abundance in a circular pattern
- Use graph algorithm for Hamiltonian path detection
- Make a nice graphical representation

Project outline:
- Learn single cell data processing
- Find a suitable library to efficiently detect Hamiltonian circles on k-nn graphs.
- Verify if there is a correlation and make nice plot
- Find other datasets to confirm individual findings
- Write the report.

Project requirements:
- Python
- Interest in Molecular biology
- At least one Monkey