scRNA-seq clustering and trajectory inference

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Registration link:

Hours of instruction: 2

Prerequisites:

- ∉ a basic knowledge of python programming concepts

- ∉ Install scanpy, scvelo, and sklearn packages

Summary:

Clustering methods allow researchers to identify subpopulations and explore the heterogeneity of single-cell data. This Bootcamp will introduce three clustering strategies, K-means based clustering, hierarchical clustering, and shared-nearest-neighbour-based clustering. Trajectory inference approaches can computationally infer the order of single-cells along developmental trajectories. The gene expression level and spliced/unspliced mRNA trajectory inference methods will be introduced at this Bootcamp.

Contents:

I. **Module 1 (70 mins)**
   a. Recap: dimensional reduction methods (5 mins)
      i. Principal Components Analysis
   b. Clustering methods (40 mins)
      i. K-Means based methods
      ii. Hierarchical clustering methods
      iii. Shared-nearest-neighbour methods
   Hands on (25 mins)

10 mins break

II. **Module 2 (40 mins)**
   a. Trajectory inference (25 mins)
      i. Gene expressional level inference
      ii. RNA velocity and trajectory inference
   Hands on (15 time)