<div align="center">sceExplorer:</div>

Raw data:

- Input: Count matrix/ .f5 file/ 10X files/ .rds object and annotation file
- Output: .rds object (SingleCellExperiment class)

QC filter (SingleCellExperiment):

- Input: .rds object
- Output: filtered data

Normalization:

- Input: QC-filtered data
- Output: Normalized counts

Highly Variable Gene Selection:

- Input: Normalized counts
- Output: VGcounts

Dimension Reduction:

   i.   Linear:

- Input: VGcounts
- Output: PCA

   ii.   Non-Linear:

- Input: PCA
- Output: Umap/tSNE

Clustering:

- Input: PCA/Umap/tSNE
- Output: Clusters

Batch Correction:

   i.   Correction on Expression Matrix

- Input: VGcounts
- Output: BEVGcounts
  - ♦ Dimension Reduction:
    - o Linear:
      - ▪ Input: BEVGcounts
      - ▪ Output: BEPCA

   ii.   Correction on Dimension Reduction

- Input: counts
- Output: BEPCA

Non-Linear:

- Input: BEPCA
- Output: Umap/tSNE

Clustering:

- Input: BEPCA/Umap/tSNE
- Output: Clusters

DEG Analysis:

- Input: Raw counts and comparison vector
- Output: DEG table

<u>Cell Type Annotation</u>:
- Input: Count Matrix and clusters
- Output: Cell type

<u>Cell Development</u>:
- Input: Cell Type
- Output: Cell Development