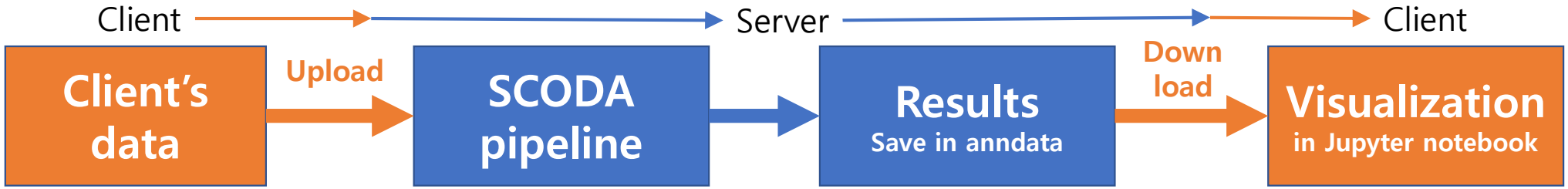
DKU MLBI LAB

SCODA pipeline
(Single-Cell Omics Data Analysis pipeline)



Supported format

1. Compressed 10x mtx files sets + (optional) meta data (csv file)
2. Compressed CSV (cell-by-gene matrix) + (optional) meta data (csv file)
3. Compressed h5ad file

Functions

1. Celltype annotation using HiCAT (v0.6.7)
2. DEG & GSA/GSEA per minor celltype
3. Inference of cell-cell interaction using CellPhoneDB (v2.1.7)
4. (optional) Tumor cell identification using InferCNV (v0.4.2) + icnv addon
5. More will be added soon

Results saved in anndata format (v0.8.0)

1. Celltype annotation in obs field
2. DEG & GSA/GSEA results for each celltype in uns field
3. CellPhoneDB results in uns field
4. (optional) Tumor cell identification results in obs field

Exploring the results

1. Use SCANpy & SCODA-viz package (open source)
2. Example Jupyter notebook provided
3. With a little bit of programming, users can get deeper insight into the data by comparing cells in different condition