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# SCODA pipeline

(Web-based single-cell Omics Data Analysis pipeline)

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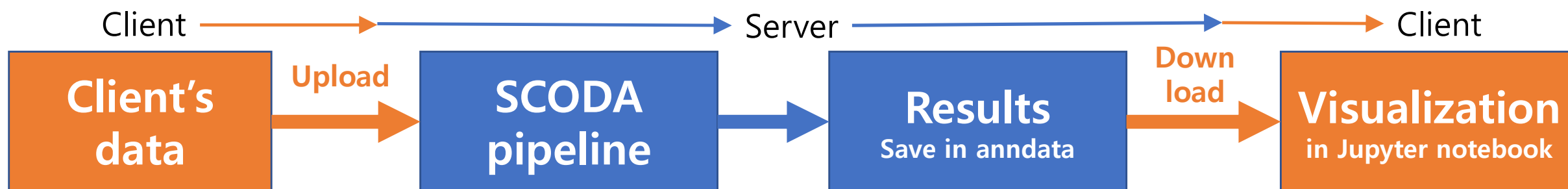
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# What is SCODA?

- ❑ Automated one-stop computing service for **Single-Cell (transcript)Omics Data Analysis** (single-cell RNA-seq)
- ❑ Especially useful for
  - In-vivo Tissue/tumor micro environment (TME) study.
  - Immune cell profiling in, for example, autoimmune disease & cancer
- ❑ Simply uploading your count data, you get **standardized functional analysis results in ten-minutes or so** (depending on your data size)
- ❑ Results include
  - High precision **cell-type annotation** (major-type, minor-type and subset)
  - Condition specific **DEG and GSA** results per-cell-type
  - Possible **cell-cell interactions** between different cell-types per-condition
  - CNV estimates and **tumor-cell identification** results

# SCODA pipeline overview

## (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

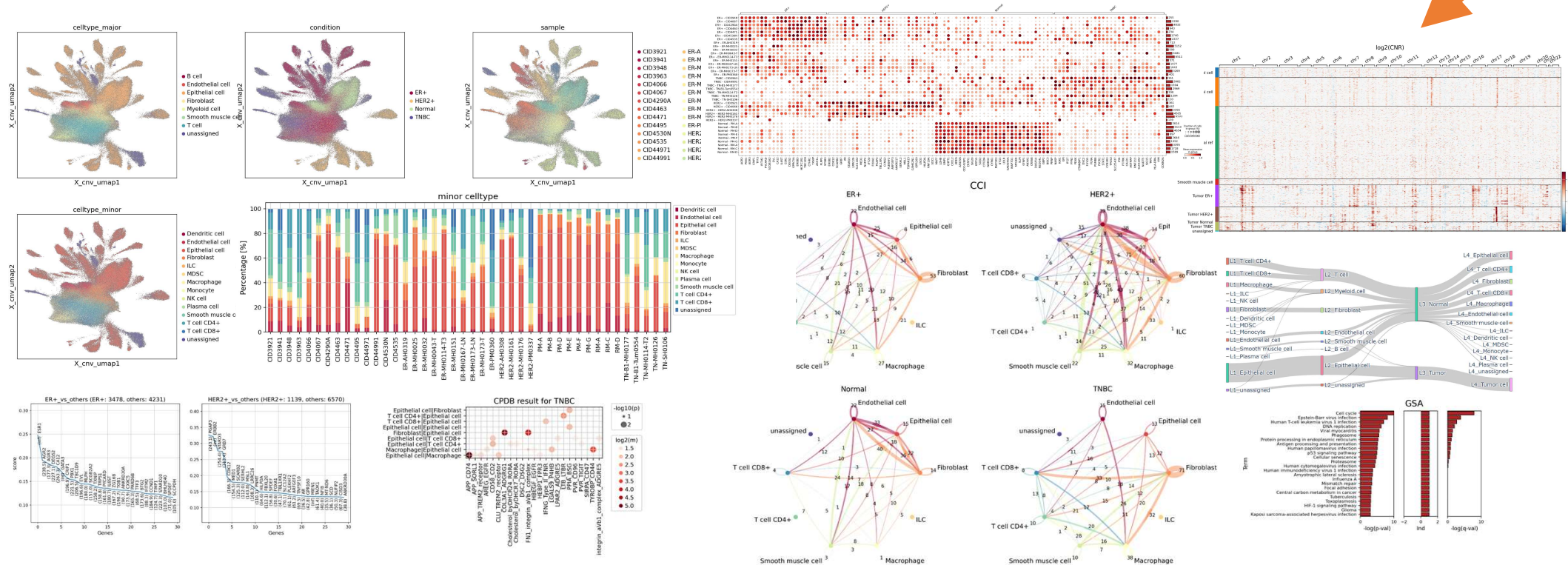
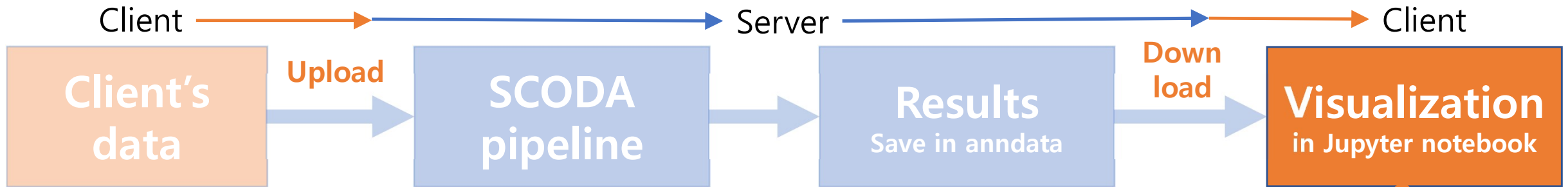
### Results saved in anndata format (v0.8.0)

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

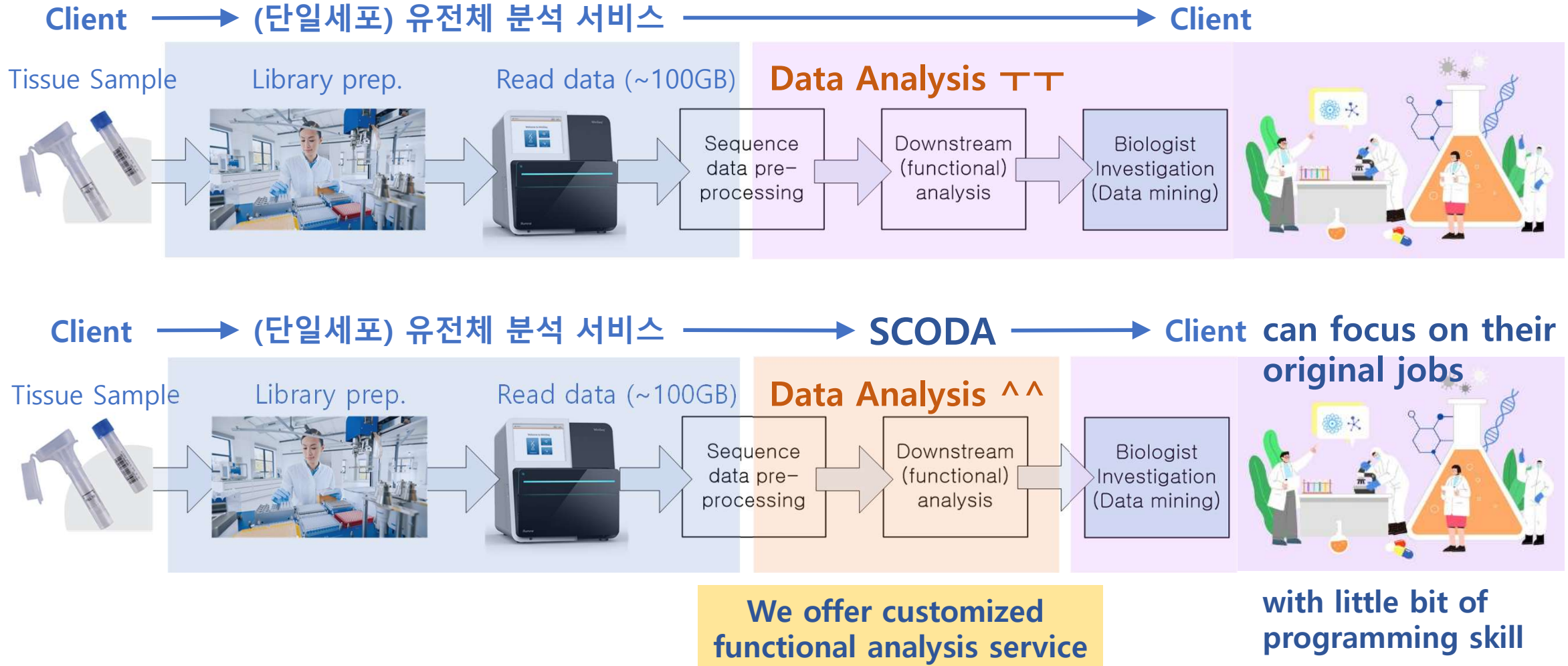
### Exploring the results

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

# SCODA-viz: visualization lib. (free open source)



# Why SCODA ?



# How to use SCODA?

- ❑ With your raw datasets (e.g., CellRanger v3 count data)
  1. Go to SCODA home <https://mlbi-lab.net> to upload and get results.
  2. Get Jupyter notebook to explore the results: [https://github.com/combio-dku/scoda\\_explorer](https://github.com/combio-dku/scoda_explorer)
  3. Mine the SCODA results in Jupyter notebook on your own computer (or in Google Colab)
- ❑ Contact: [mlbi.dku@gmail.com](mailto:mlbi.dku@gmail.com) for any inquiries or online workshop for using SCODA-viz



# Why SCODA?

- ❑ Trend in bio/medical research: convergence of data science & bio/medicine.
- ❑ Requires complicated communications between biologist and informatician.
- ❑ SCODA is an **automated one-stop computing service** using **verified, standardized functional analysis tools** for single-cell omics data.
- ❑ With SCODA, you don't need to spend your time to do something that are not your field of expertise, e.g.,
  - for complicated computing environment setup
  - develop pipelines to preprocess your datasets
- ❑ Can accelerate the research with single-cell RNA-seq data.
- ❑ **The only thing you need is a little-bit of programming skill**, e.g., handling data frame, for your own data mining.
- ❑ It provides you with a much higher degree of freedom for your research.

# What is SCODA?

- ❑ The computing server accepts 10x mtx format (CellRanger v3 output), csv or anndata formatted h5ad file (optionally with meta data)
- ❑ SCODA pipeline **utilizes verified, suitably licensed (or free) open source SWs** (HiCAT v0.6.12, CellPhoneDB v2.1.7, InferCNV v0.4.2, anndata v0.8.0)
- ❑ **Free visualization library** is provided for your own data mining (using scanpy, seaborn, matplotlib packages)
- ❑ **You only need a little bit of programming skill** (in python or R) **to explore the SCODA results by yourself.**
- ❑ Small group workshop (training) for data mining is available.
- ❑ **With SCODA, you can focus more on your original jobs!!! (i.e., biology and/or medical research)**