

# Spatial Single Cell Analysis using oneAPI AI Analytics toolkit

By Abhishek Nandy Intel Software Innovator | oneAPI  
certified instructor

# Agenda

Applying the project to showcase that we are able to use medical imaging and we are future ready.

Using oneAPI AI Analytics toolkit we are able to write and develop performant code quickly and correctly.

# Important Terminologies

Transcriptional Profiling :- It is a process to identify a rare disease condition, ways to diagnose and also see the body responds to treatment

RNA Sequencing:-It is a sequencing technique which uses next generation sequencing to reveal the quality of RNA in biological sample at given moment, analyzing the continuously changing cellular structure.

Gene mutation:-It is process of change in a gene structure. Some mutations can lead to genetic disorders or illness

# What is Single Cell RNA?

Single-Cell RNA-Seq provides transcriptional profiling of thousands of individual cells.

It allows us to study gene expression.

Single Cell RNA allows to study gene mutation in rare diseases.

# Why use Squidpy

We will be porting Squidpy to Intel AI Analytics toolkit.

We will be porting Squidpy within Intel DevCloud.

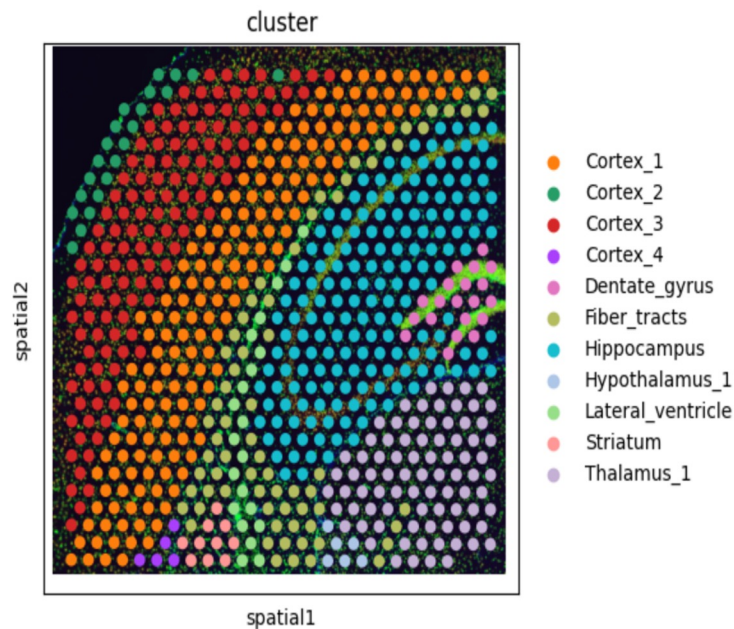
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# Porting Squidpy to Intel AI Toolkit

- We will be porting Squidpy to Intel AI Analytics toolkit.
- We will be porting Squidpy within Intel DevCloud.

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# Exploring Squidpy



Here are Images of Cluster data we have used using the spatial method.

It's an image of very high dimension data.

# Exploring Squidpy

image:0

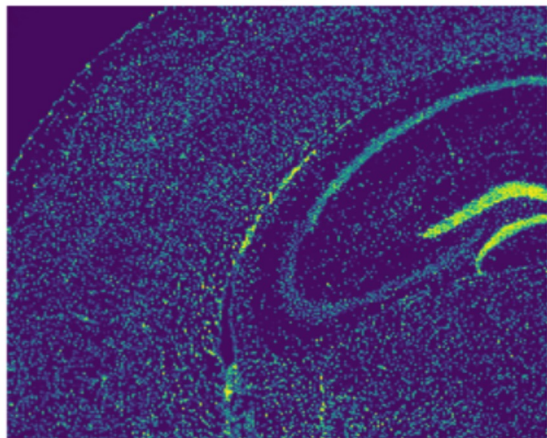


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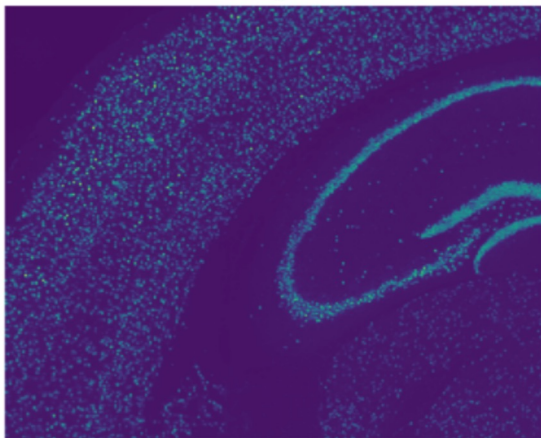
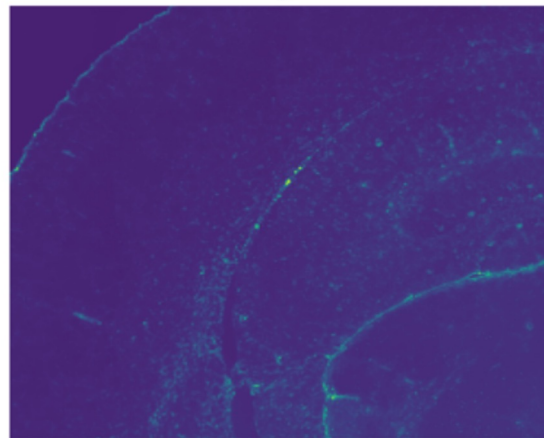


image:2





1.Spatial Dataset Import



2.Use Image container within  
DevCloud



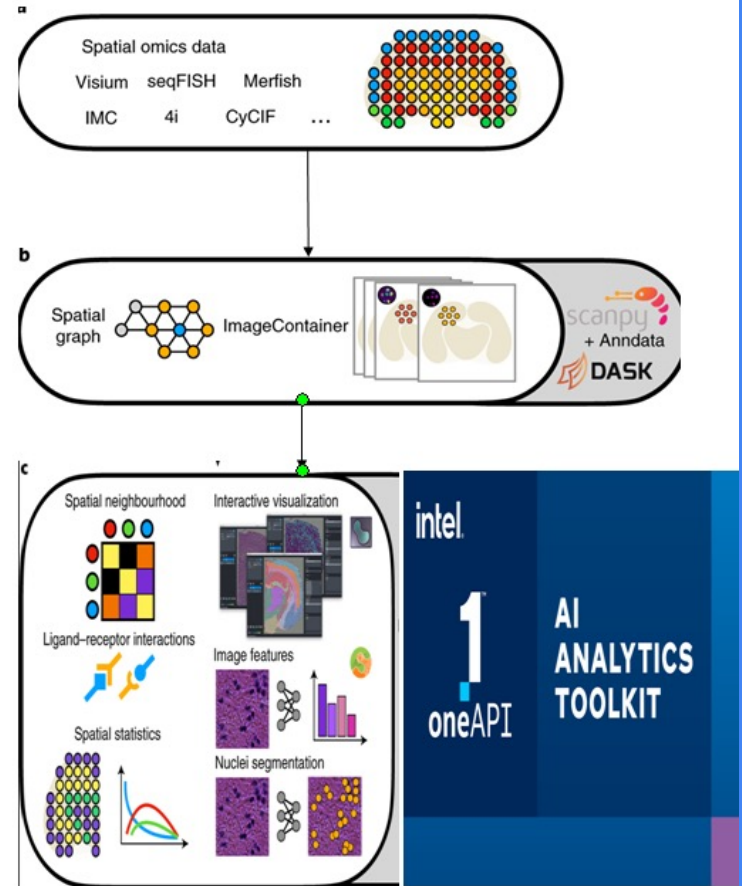
3.Interface to AI Analytics toolkit such as Intel Optimized  
Tensorflow



4.Analysis of Med image such Nuclei Segmentation,Ligand receptor

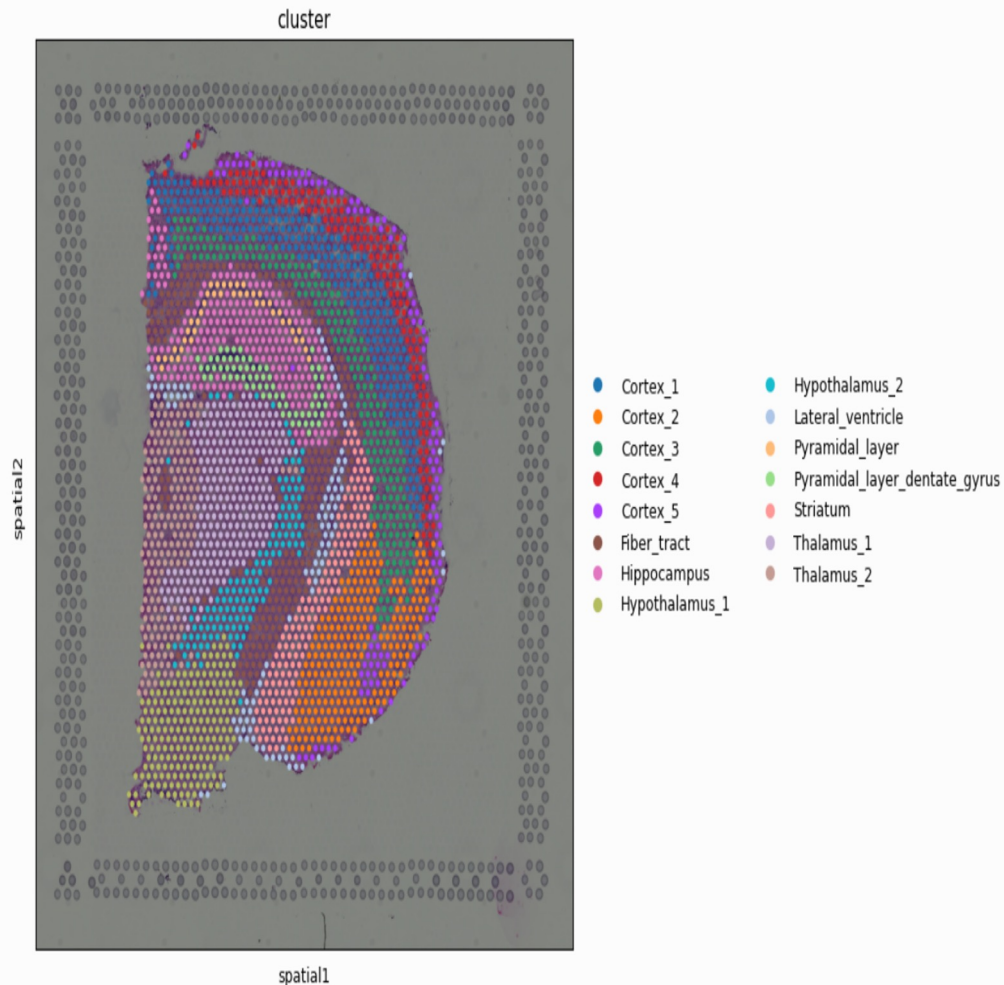
# Squidpy Flow

Complete flow of Squidpy



# Case Study Visium Data

Squidpy + Intel DevCloud  
+ Intel AI toolkit



# Steps

- Make sure we are logged into Intel DevCloud.
- We will be using Jupyter Notebook powered by Intel AI Analytics toolkit.
- We will install the Squidpy library using pip command.
- `pip install 'squidpy[interactive]'`

# Steps

- Make sure all the supporting libraries are ported.
- We load the preprocessed Data Set in this case visium dataset.
- We then use special function from squidpy to analyse the data.
- We emphasise on studying linkage on the dataset and find special patterns.

# Visualization

- We are able to study different kinds of datasets.
- Very useful in studying Medical Imaging data.
- We are able to analyse curated datasets from 10x genomics.
- Spatial statistics and graph analysis.

# Squidpy+Intel AIAnalytics toolkit + Intel DevCloud

- Optimized for different devices.
- Very useful in studying Medical Imaging data.
- We are able to analyse curated datasets from 10x genomics.
- We are able to do Spatial statistics and graph analysis.
- Worked with huge medical imaging datasets.

# Results

- We are able to analyse single cell RNA Data seamlessly.
- We are able to import high ordered gene data.
- We are able to express gene standards from 10x Genomics.
- We are able to find clustering of genes.



# Demo

Demo and code walkthrough on Intel DevCloud.

# Key Takeaway

- Using AI toolkit we are able to work with terabytes of data.
- We can study bulk genes in a genome structure.

# Key Takeaway in terms of Squidpy

- Build and analyze the neighborhood graph from spatial coordinates.
- Compute spatial statistics for cell-types and genes.
- Efficiently store, analyze and visualize large tissue images, leveraging skimage.
- Interactively explore anndata and large tissue images.

# Usefulness

- Understanding how Ligand Receptor works.
- How to find structural anomalies in single cell RNA.
- Effectively study parts of the image dataset.
- Very essential in studying rare diseases.

# Resources

- LinkedIn  
<https://www.linkedin.com/in/abhishek-nandy/>
- Intel oneAPI AI Analytics toolkit  
<https://rb.gy/1k5jzc>
- Single Cell RNA Analysis using Squidpy Project  
<https://rb.gy/4jnfj1>
- My YouTube Channel  
<https://rb.gy/vmdsbk>

Thank You!