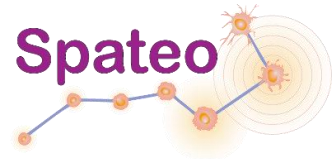


Spateo-viewer: the “Google earth” of spatial transcriptomics

Jiajun Yao
Aristotle ecosystem team

<https://github.com/aristoteleo/spateo-viewer>
<https://github.com/aristoteleo/spateo-release>



◆ Introduction

- What is Spateo-viewer?
- How does Spateo-viewer work?
- Why Spateo-viewer?

◆ Getting started

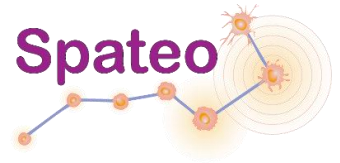
- Documentation
- Installation
- Usage

◆ Interactive-viewer

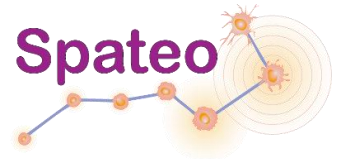
- Build 2D/3D spatial transcriptomics models
- Preprocess point cloud of single cells
- Reconstruct 3D meshes of tissue or organs
- Align serial slices of tissue or organs
-

◆ Static-viewer

- 2D/3D Tissue visualization
- Gene expression visualization
- Morphogenesis calculation and visualization
- Morphometric vector field animation
- Morphometric measurements
- Superior spatial transcriptomics models renderer
-



Introduction

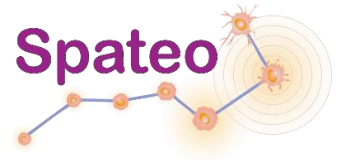


◆ What is Spateo-viewer?

- Spateo-viewer is the “Google earth” of spatial transcriptomics. Relying on a set of powerful libraries and tools in the Python ecosystem, such as Triage, PyVista, VTK, etc., it delivers a complete web application solution of creating convenient, vivid, and lightweight interface for 3D reconstruction and visualization of Spateo downstream analysis results. Currently, Spateo-viewer includes two major applications, interactive-viewer and static-viewer, which are respectively dedicated to the 3D reconstruction of spatial transcriptomics and the visualization of spatial transcriptomics analysis results.

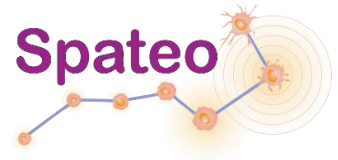
◆ How does Spateo-viewer work?

- Spateo-viewer is a lightweight and completely self-contained web application based on python, that can run either through a server or your local environment without network connection, thereby ensuring that Spateo-viewer can be used for visualization of spatial transcriptome data of any data size.

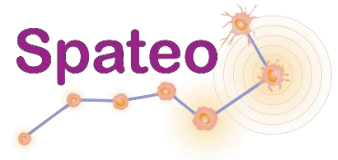


◆ Why Spateo-viewer?

- Spateo-viewer is a lightweight network application with few dependent packages and easy installation, which could be used in common systems such as Windows, Linux and MacOS.
- Spateo-viewer helps researchers with limited python programming skills to build and visualize 2D or 3D spatial transcriptomics models through an interactive web portal, and even perform downstream analysis of spatial transcriptomics data such as predicting organ morphogenesis trajectories.



Getting started



◆ Documentation

- <https://github.com/aristoteleo/spateo-viewer>
- <https://github.com/aristoteleo/spateo-viewer/blob/main/usage/StaticViewerUsage.md>
- <https://github.com/aristoteleo/spateo-viewer/blob/main/usage/InteractiveViewerUsage.md>
- <https://github.com/aristoteleo/spateo-release>
- <https://spateo-release.readthedocs.io/en/latest/tutorials/notebooks/tdr.html>

◆ Installation

- ① `git clone https://github.com/aristoteleo/spateo-viewer.git`
- ② `cd spateo-viewer`
- ③ `pip install -r requirements.txt`

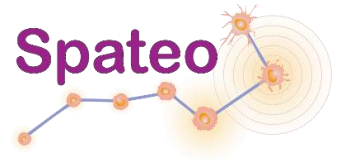
◆ Usage

Run Interactive-Viewer

- `python ./stv_interactive_app.py --port 1234`

Run Static-Viewer

- `python ./stv_static_app.py --port 1234`



Interactive-Viewer



2D/3D spatial transcriptomics models generator

DRAWER GUI

Active Model

Generate processed 2D/3D point cloud model and its anndata

Slices Alignment

Realignment of serial slices to build the 3D point cloud model

Mesh Reconstruction

Reconstruct the mesh model based on the 3D point cloud model

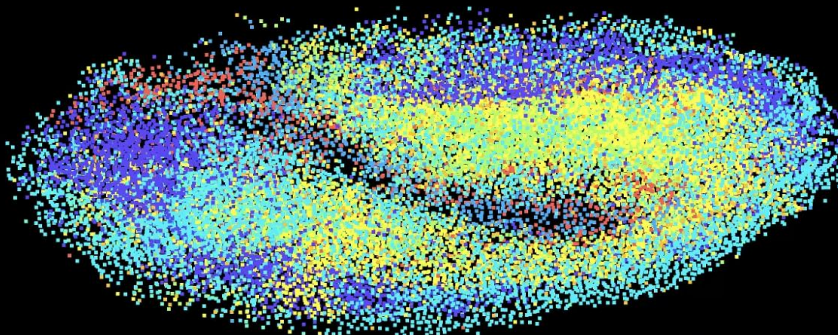
The logo of spateo-viewer and the switch of drawer

Useful widget for customizing data upload

TOOLBAR GUI

Some useful widgets for clipping active model:

- Toggle mouse function between viewing model and clipping model
- Reset active model to the original active model
-



CONTAINER GUI

Model could be translated, scaled, and rotated freely



Build 2D/3D spatial transcriptomics models

Active Model

Scalars

anno_ti...

ColorMap

Erdc Rai...

Picking Group

CNS

Overwrite the Active Model

X

Active Model Output

Anndata Output

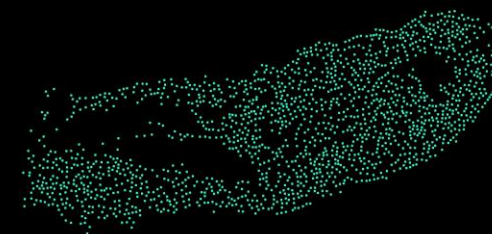
Visibility of Active Model

👁

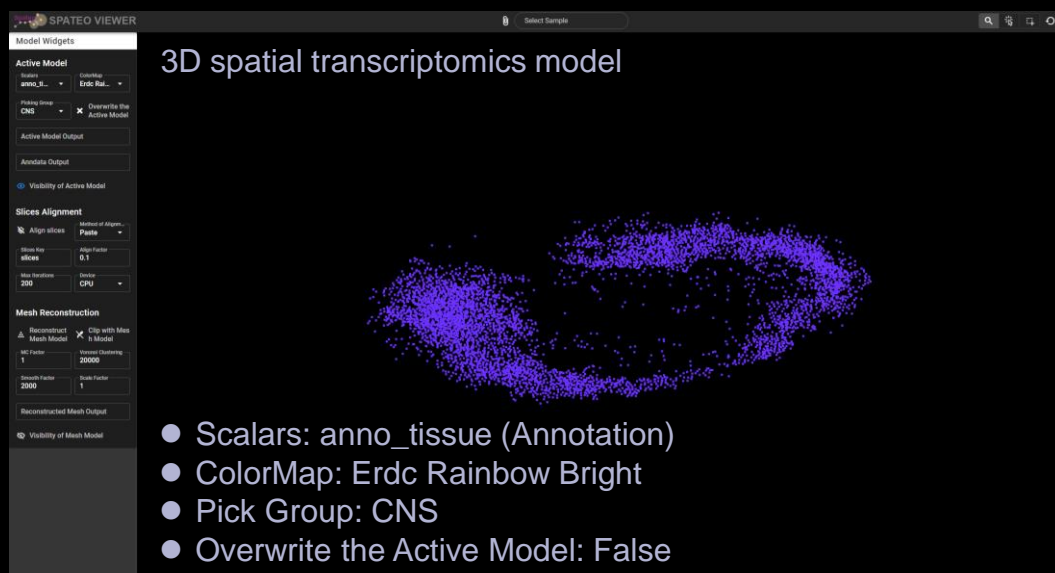
- **Scalars:** The key that stores information in `anndata.obs`.
- **ColorMap:** Name of the matplotlib colormap to use when mapping the scalars.
- **Pick Group:** One or more subtypes can be extracted from the original active model based on the information contained in `Scalars`.
- **Overwrite the Active Model:** If the `Overwrite the Active Model` is on, multiple models can be extracted from the original active model.
- **Active Model Output:** File name of the active model. If the file name ends with `vtk`, the active model will be automatically saved to the `./stv_model` folder.
- **Anndata Output:** File name of the anndata object. If the file name ends with `h5ad`, the anndata object will be automatically saved to the `./stv_model` folder.



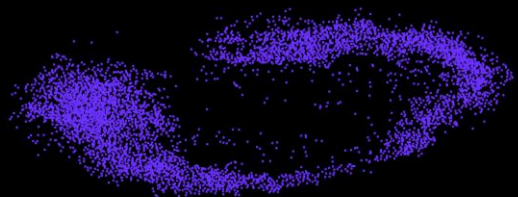
2D spatial transcriptomics model



- Scalars: slices
- ColorMap: Erdc Rainbow Bright
- Pick Group: E8-10_b_S13
- Overwrite the Active Model: False



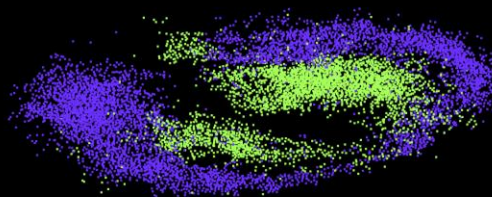
3D spatial transcriptomics model



- Scalars: anno_tissue (Annotation)
- ColorMap: Erdc Rainbow Bright
- Pick Group: CNS
- Overwrite the Active Model: False



Multiple 3D spatial transcriptomics models



- Scalars: anno_tissue (Annotation)
- ColorMap: Erdc Rainbow Bright
- Pick Group: CNS and midgut
- Overwrite the Active Model: True



Preprocess point cloud of single cells

Active Model

Scalars

anno_ti...

ColorMap

Erdc Rai...

Picking Group

CNS

✕

Overwrite the Active Model

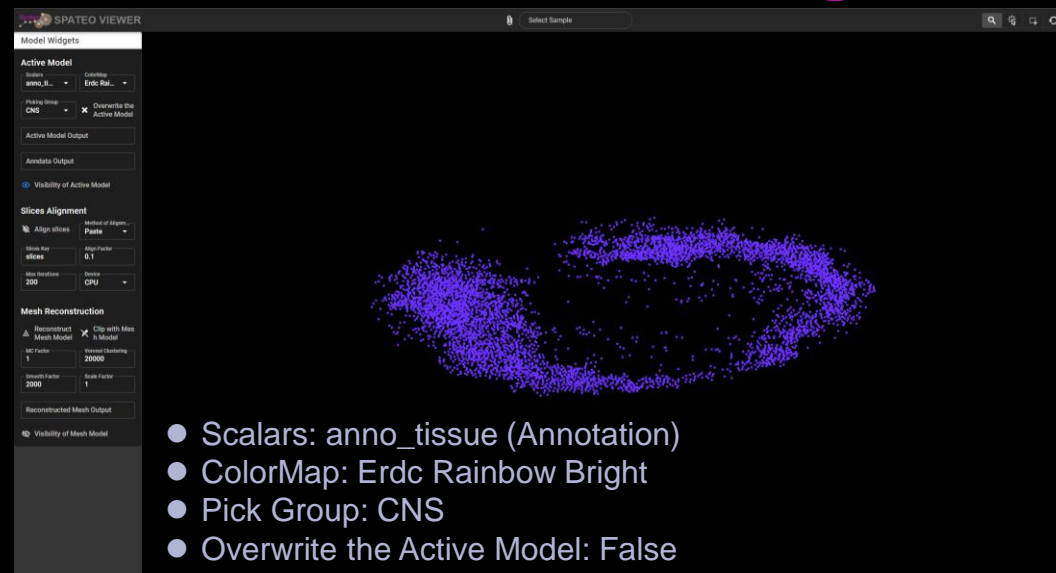
Active Model Output

Anndata Output

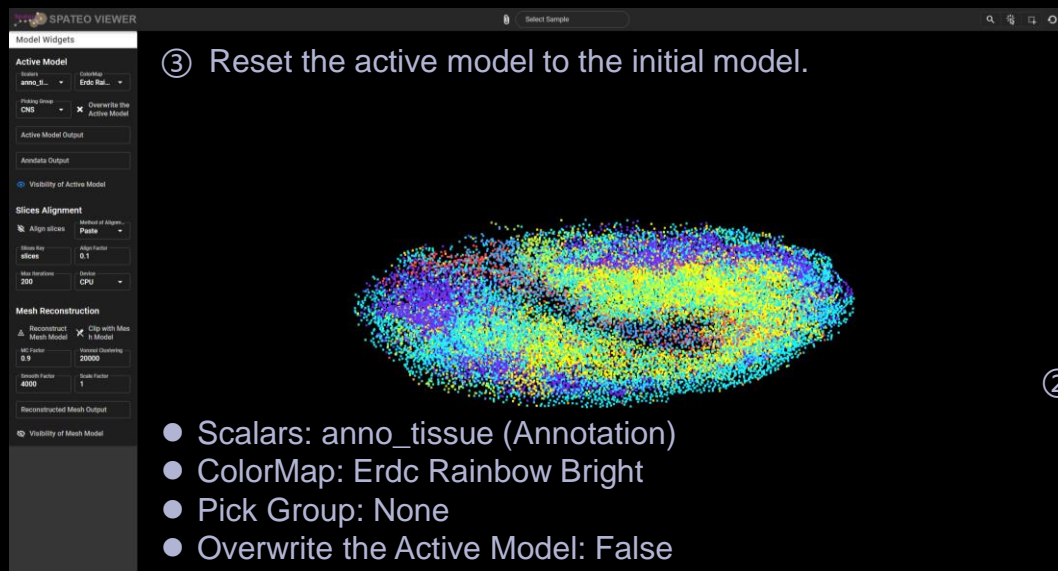
👁

Visibility of Active Model

- **Scalars:** The key that stores information in `anndata.obs`.
- **ColorMap:** Name of the matplotlib colormap to use when mapping the scalars.
- **Pick Group:** If the key in Scalars that stores non-numeric information, the Pick Group includes all categories.
- **Overwrite the Active Model:** If the `Overwrite the Active Model` is on, multiple models can be visualized simultaneously.
- **Active Model Output:** File name of the active model. If the file name ends with `vtk`, the active model will be automatically saved to the `./stv_model` folder.
- **Anndata Output:** File name of the anndata object. If the file name ends with `h5ad`, the anndata object will be automatically saved to the `./stv_model` folder.

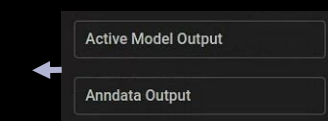


- Scalars: anno_tissue (Annotation)
- ColorMap: Erdc Rainbow Bright
- Pick Group: CNS
- Overwrite the Active Model: False

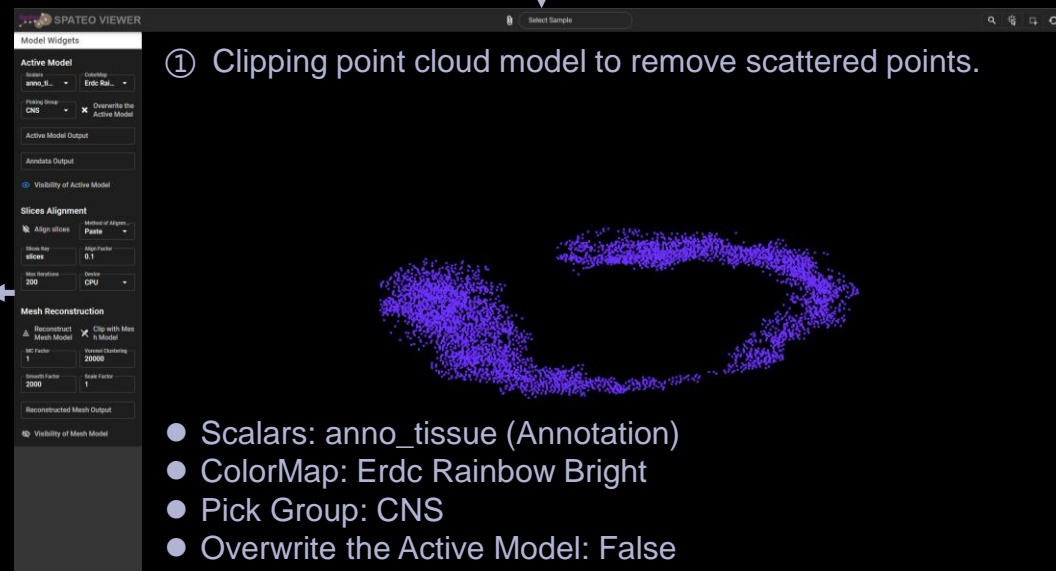


③ Reset the active model to the initial model.

- Scalars: anno_tissue (Annotation)
- ColorMap: Erdc Rainbow Bright
- Pick Group: None
- Overwrite the Active Model: False



② Saving clipped point cloud model and its anndata object.




① Clipping point cloud model to remove scattered points.


- Scalars: anno_tissue (Annotation)
- ColorMap: Erdc Rainbow Bright
- Pick Group: CNS
- Overwrite the Active Model: False



Mesh reconstruction

Mesh Reconstruction

 Reconstruct Mesh Model

 Clip with Mesh Model


MC Factor
1

Voronoi Clustering
20000

Smooth Factor
5000

Scale Factor
1

Reconstructed Mesh Output

 Visibility of Mesh Model

- **Reconstruct Mesh Model:** Open mesh reconstruction.
- **Clip with Mesh Model:** Clipping active model with mesh model.
- **MC Factor:** The most critical hyperparameter in the reconstruction method in the range of 0 to 2.
- **Voronoi Clustering:** Number of Voronoi clustering.
- **Smooth Factor:** Number of iterations for Laplacian smoothing.
- **Scale Factor:** The scale by which the model is scaled.
- **Reconstructed Mesh Output:** File name of mesh model. If the file name ends with `vtk`, the mesh model will be automatically saved to the `./stv_model` folder.



① Mesh reconstruction.

→ Reconstructed Mesh Output →
② Saving mesh model.



③ Clipping active model with mesh model.



Slices alignment

Slices Alignment

Align slices

Method of Alignment

Paste

Slices Key

Align Factor

slices

0.1

Max Iterations

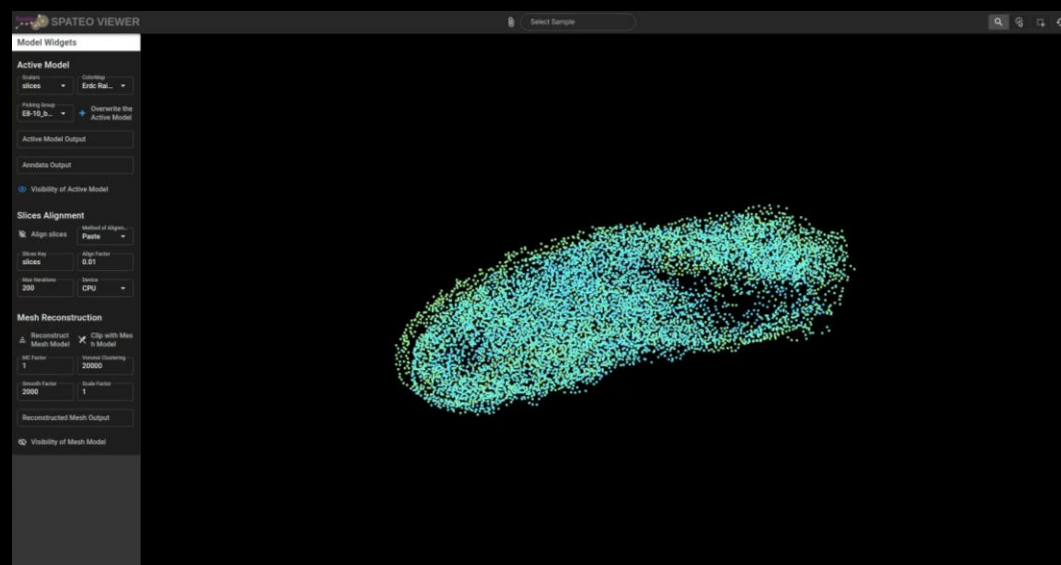
Device

200

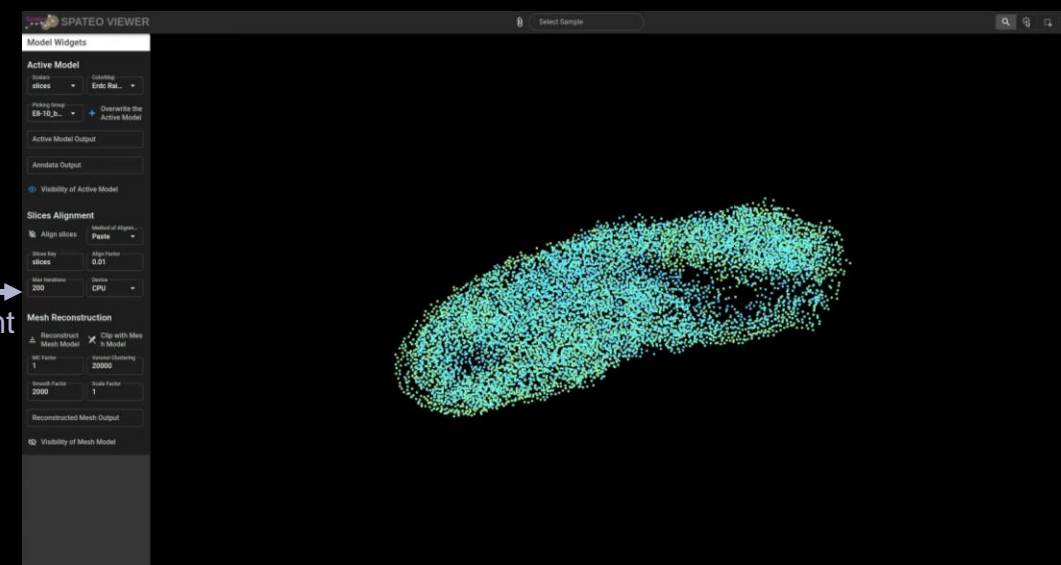
CPU

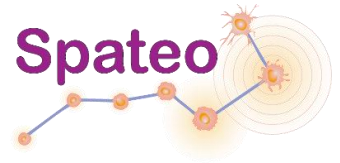
- **Align slices:** If the `Align slices` is on, re-align the slices in the active model.
- **Method of Alignment:** The method used to realign the series slices. Currently we support Paste¹, Morpho².
- **Slices Key:** The key in `anndata.obs` that corresponds to the slice names.
- **Align Factor:** The most critical hyperparameter in the alignment method.
 - If the alignment method is Paste, it represents alpha, which is the Alignment tuning parameter. When ``alpha = 0`` only the gene expression data is taken into account, while when ``alpha = 1`` only the spatial coordinates are taken into account. Recommended setting from 0.01 to 0.1.
 - if the alignment method is Morpho, it represents max_outlier_variance. Reduce the spatial variance to decrease Gaussian tails to achieve robustness to partial alignment. Lower means less robust, but more accurate. Recommended setting from 1 to 50.
- **Max Iterations:** The maximum number of iterations for alignment.
- **Device:** Equipment used to run the program.

1. Zeira, R., Land, M., Strzalkowski, A. et al. Alignment and integration of spatial transcriptomics data. Nat Methods 19, 567–575 (2022).
2. Qiu, X. et al. Spateo: multidimensional spatiotemporal modeling of single-cell spatial transcriptomics. BioRxiv 2022.12.07.519417 (2022).



① Slices Realignment





Static-viewer



Superior spatial transcriptomics models renderer

DRAWER GUI

GitTree

Toggle active model and model visibility

ModelCard

Optimize model visualization or calculate model morphogenesis

OutputCard

Output screenshot or animation

The logo of spateo-viewer and the switch of drawer

Useful widget for customizing data upload

TOOLBAR GUI

Some useful widgets:

- Theme toggle
- Background toggle
- Rendering mode toggle
- Main model Visibility toggle
- Bounding box toggle
- Ruler toggle
- Axis toggle
- Camera angles reset
-

SPATEO VIEWER

PC_Embryo
PC_CNS
PC_Midgut
PC_Muscle
PC_SalivaryGland
PC_Amnioerosa
Mesh_Embryo
Mesh_CNS
Mesh_Midgut
Mesh_Muscle
Mesh_SalivaryGland
Mesh_Amnioerosa

Active Model

POINT CLOUD **MORPHOGENESIS**

Scalars
anno_tissue Picking Group

Add Legend Add Group Reload Model

Coords spatial Matrices X

Color None Colormap Set3_r

Opacity

Ambient

Point Size

Output Widgets

Screenshot Generation

Screenshot Output (PNG or PDF)

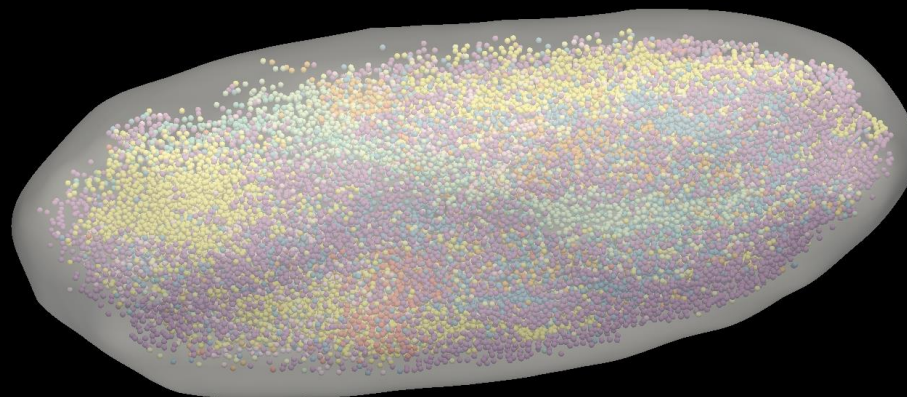
Animation Generation

Animation N Points 50 Animation Framerate 10

Animation Output (MP4)

CONTAINER GUI

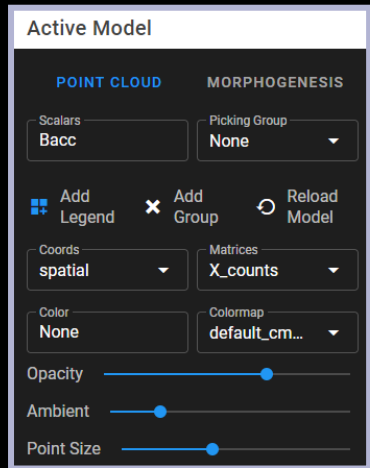
Model could be translated, scaled, and rotated freely



- CNS
- amnioerosa
- epidermis
- hemolymph
- midgut
- muscle
- salivary gland
- trachea
- yolk

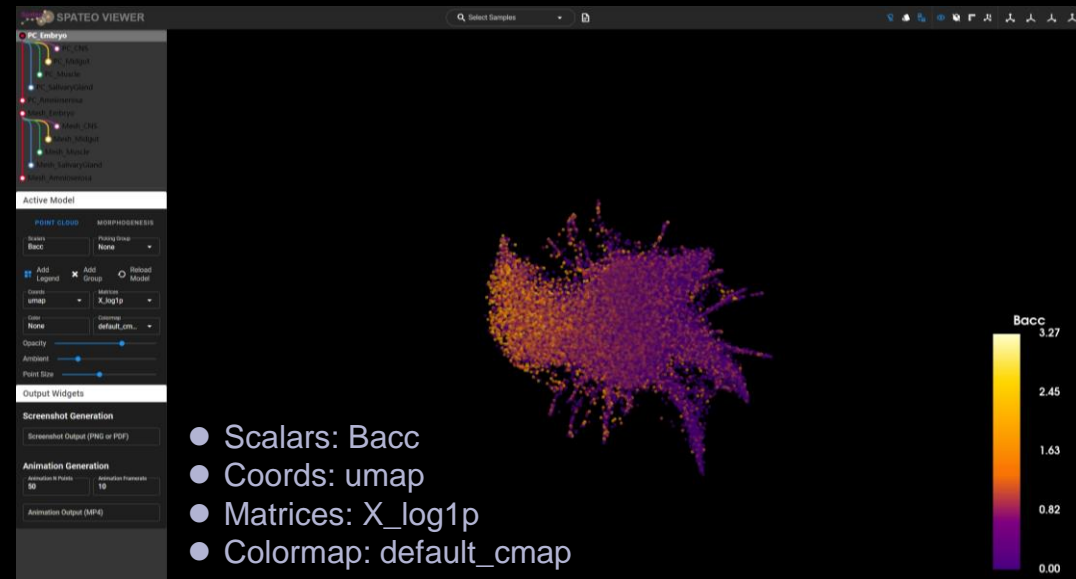
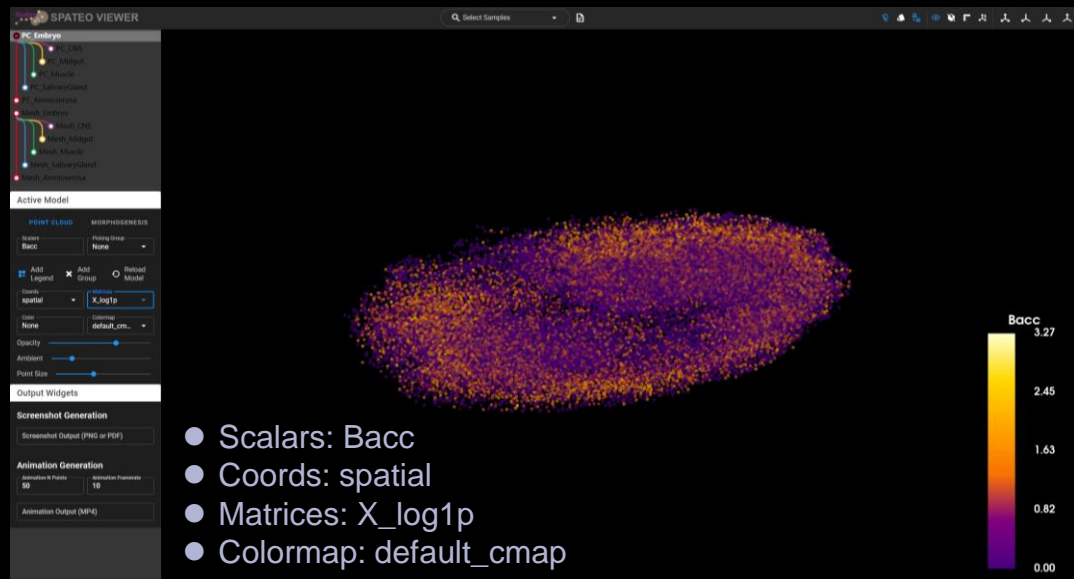
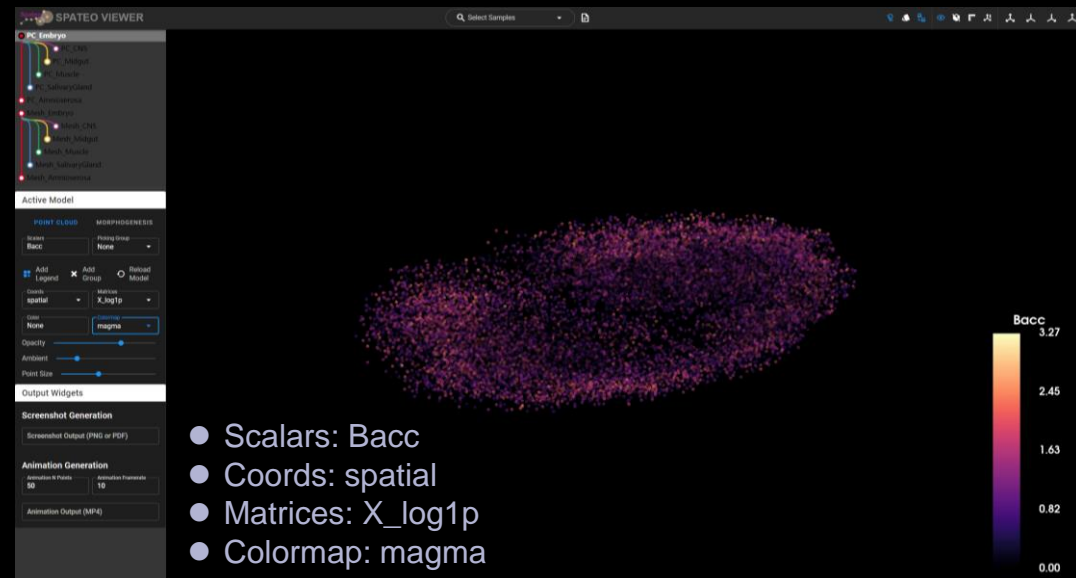


Gene expression visualization



PC ModelCard

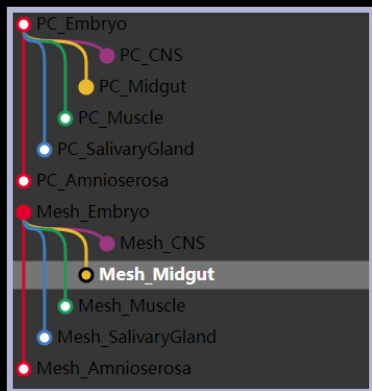
- **Scalars:** Name of the gene to be visualized.
- **Add Legend:** Add the legend corresponding to the current `Scalars` in the GUI.
- **Coords:** Model coordinate name. `spatial` represents the spatial coordinates in the reality, and `umap` represents the spatial coordinates in the umap dimensionality reduction space.
- **Matrices:** Toggle gene expression matrices, including all matrices contained in anndata.
- **Colormap:** Name of the matplotlib colormap to use when mapping the `Scalars`.
- **Opacity:** Opacity of the model in the range of 0 to 1.
- **Ambient:** The amount of light in the range of 0 to 1.
- **Point Size:** Point size of any nodes in the dataset plotted in the range of 0 to 20.



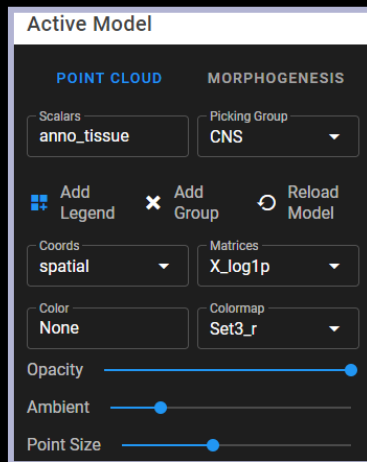
Users can conveniently choose genes to be visualized in the whole embryo model or in any one or more tissues.



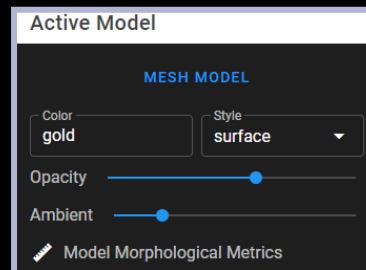
Tissues visualization



Toggle active model and model visibility

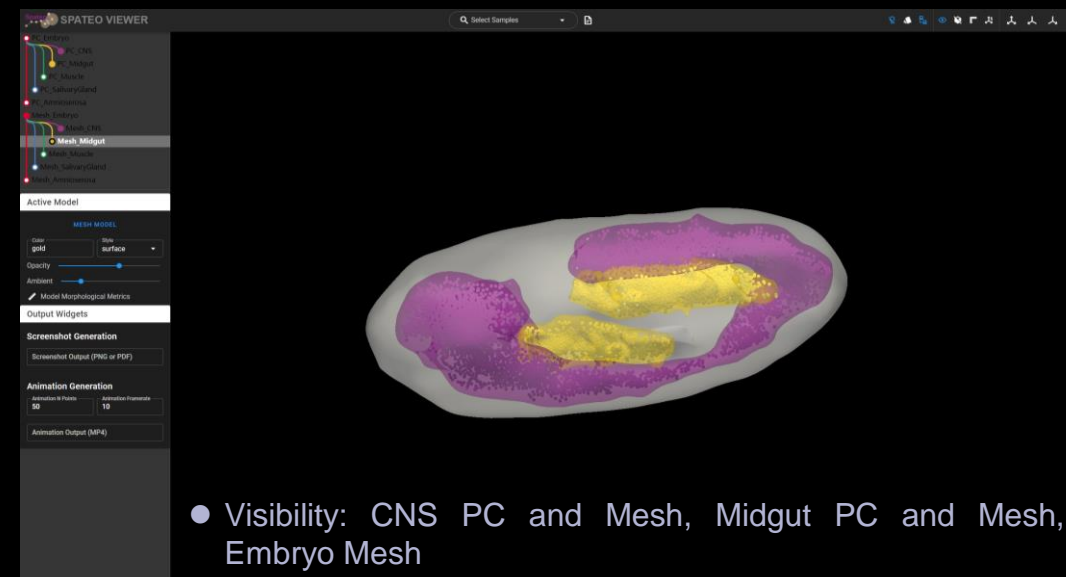


PC ModelCard

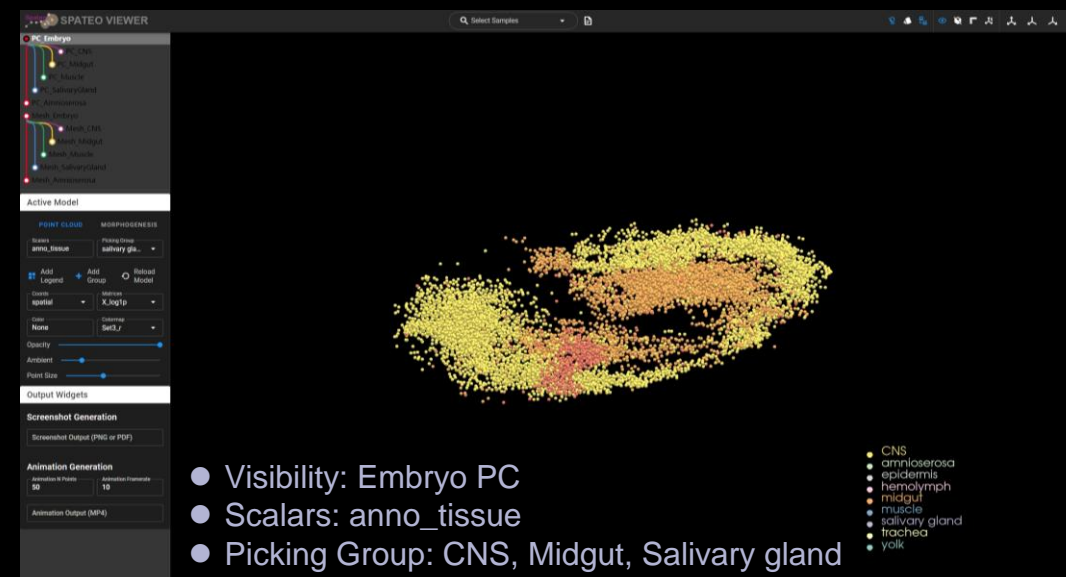


Mesh ModelCard

- **Scalars:** None or the annotation key in the anndata.obs.
- **Picking Group:** One or more subtypes can be extracted from the original active model based on the information contained in `Scalars`.
- **Add Group:** If the `Add Group` is on, multiple models can be extracted from the original active model.
- **Reload Model:** Reset the active model to the original active model.
- **Color:** The color of the active model if `Scalars` is None.
- **Colormap:** Name of the matplotlib colormap to use when mapping the `Scalars`.
- **Style:** Visualization style of the model, including `points`, `surface` and `wireframe`.
- **Opacity:** Opacity of the model in the range of 0 to 1.
- **Ambient:** The amount of light in the range of 0 to 1.



- Visibility: CNS PC and Mesh, Midgut PC and Mesh, Embryo Mesh



- Visibility: Embryo PC
- Scalars: anno_tissue
- Picking Group: CNS, Midgut, Salivary gland

Users can conveniently choose tissue models to be visualized.



Morphogenesis visualization

Active Model

POINT CLOUD

MORPHOGENESIS

Calculate the Morphogenesis

Uploaded Target Anndata

Target Anndata

drosophila_E8_9h_midgut_annd...

Mapping Factor

0.001

Morphofield Factor

3000

Morphopath Length

10000

Morphopath Sampling

500

Morphofield Visibility

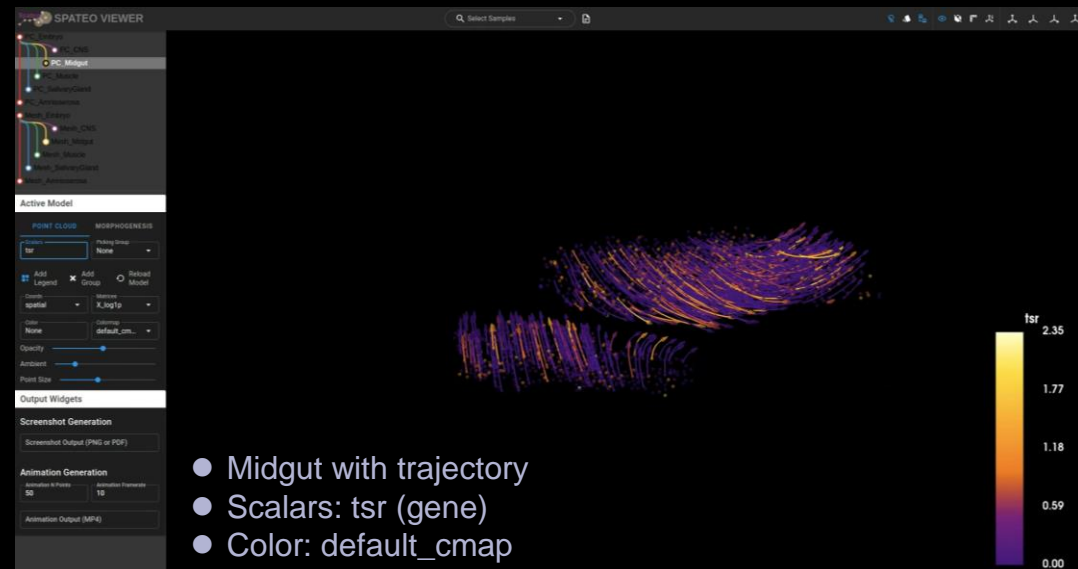
Morphopath Visibility

Morphogenesis Animation Output (...)

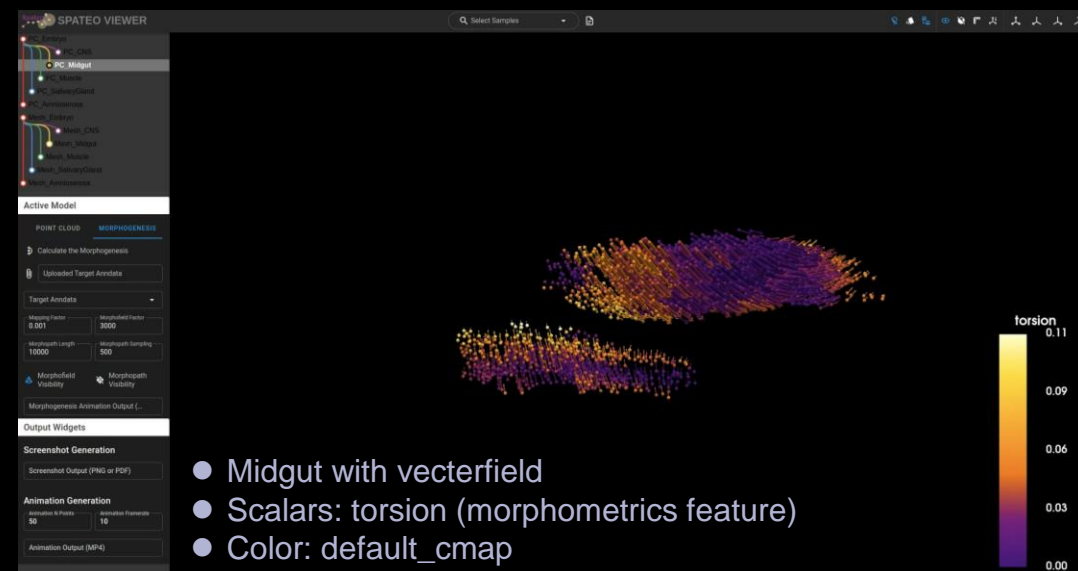
- **Calculate the Morphogenesis:** If `Target Anndata` is not None, calculate the morphogenesis of the active model.
- **Uploaded Target Anndata:** Upload the spatial transcriptomics data of the next stage corresponding to the active model.
- **Target Anndata:** Select the next stage data for calculating morphogenesis.
- **Morphofield Visibility:** Toggle Morphofield visibility.
- **Morphopath Visibility:** Toggle Morphopath visibility.

● Morphometrics features:

1. acceleration: the time derivative of the velocity;
2. torsion: the degree of twisting;
3. curl: a quantity measuring the degree of rotation at a given point in the morphometric vector field;
4. curvature: the derivative of the unit tangent vector;
5. Each of them have real physical meanings.

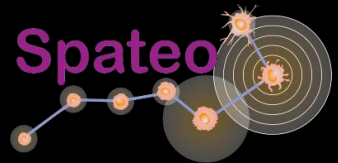


- Midgut with trajectory
- Scalars: tsr (gene)
- Color: default_cmap



- Midgut with vectorfield
- Scalars: torsion (morphometrics feature)
- Color: default_cmap

Users can calculate the morphogenesis and visualize the morphometrics features.



Morphogenesis visualization

Active Model

POINT CLOUD

MORPHOGENESIS

Calculate the Morphogenesis

Uploaded Target Anndata

Target Anndata

drosophila_E8_9h_midgut_annd...

Mapping Factor

0.001

Morphofield Factor

3000

Morphopath Length

10000

Morphopath Sampling

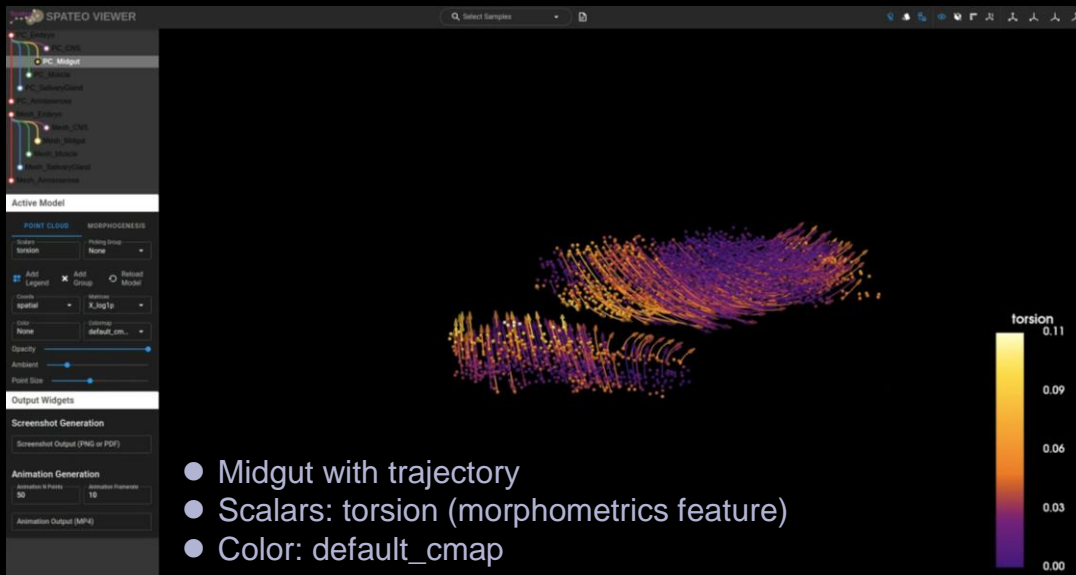
500

Morphofield Visibility

Morphopath Visibility

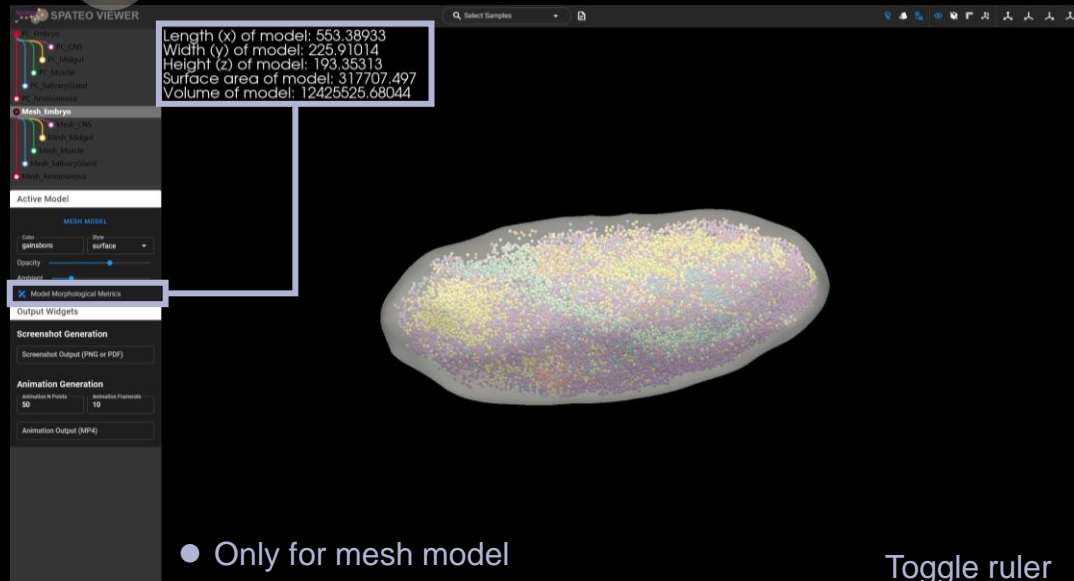
Morphogenesis Animation Output (...)

- **Morphogenesis Animation Output:** File name of Animation. If the file name ends with `mp4`, the animation will be automatically saved to the `./stv_image` folder.

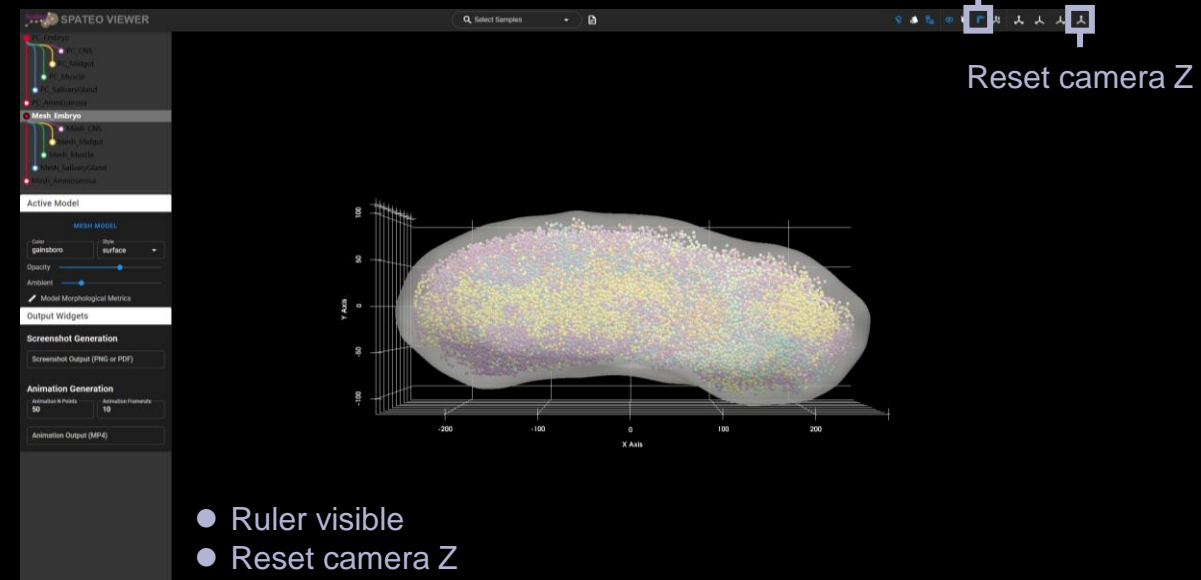
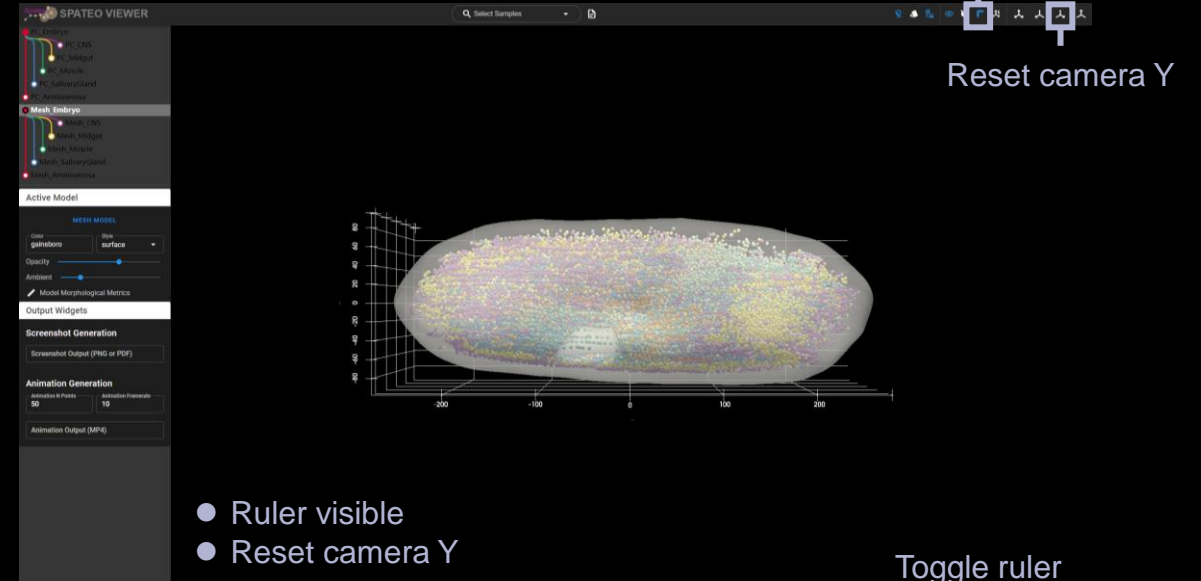
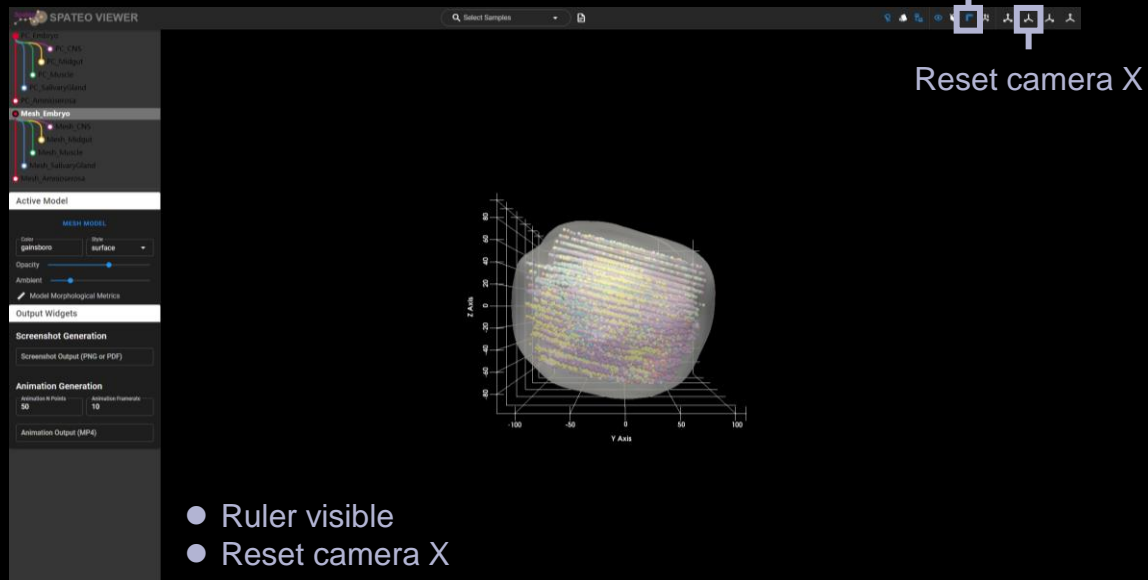




Morphometric measurements



Toggle ruler



Users can measure the morphological feature such as length, surface area and volume of the reconstructed 3D model of organ/embryo.



Image or animation generation/saving

Output Widgets

Screenshot Generation

Screenshot Output (PNG or PDF)

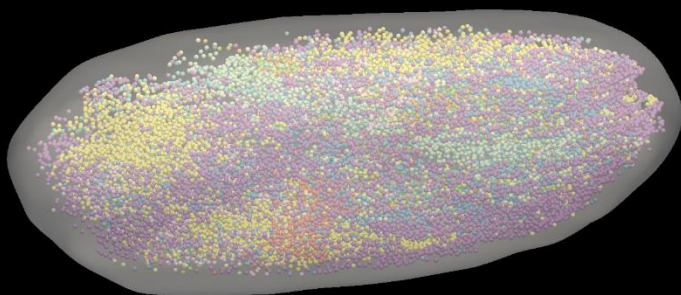
Animation Generation

Animation N Points
50

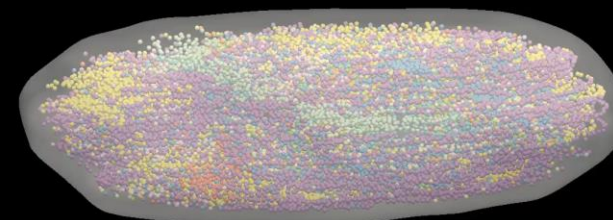
Animation Framerate
10

Animation Output (MP4)

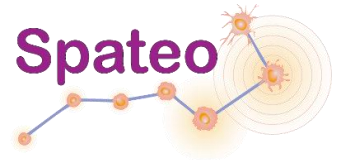
- **Screenshot Output:** File name of Screenshot. If the file name ends with `png` or `pdf`, the image will be automatically saved to the `./stv_image` folder.
- **Animation N Points:** Number of points on the orbital path in the animation.
- **Animation Framerate:** Frames per second in the animation.
- **Animation Output:** File name of Animation. If the file name ends with `mp4`, the animation will be automatically saved to the `./stv_image` folder.



● Screenshot



● Animation



Questions / Discussions

<https://github.com/aristoteleo/spateo-viewer/issues>

yaojiajun2021@gmail.com