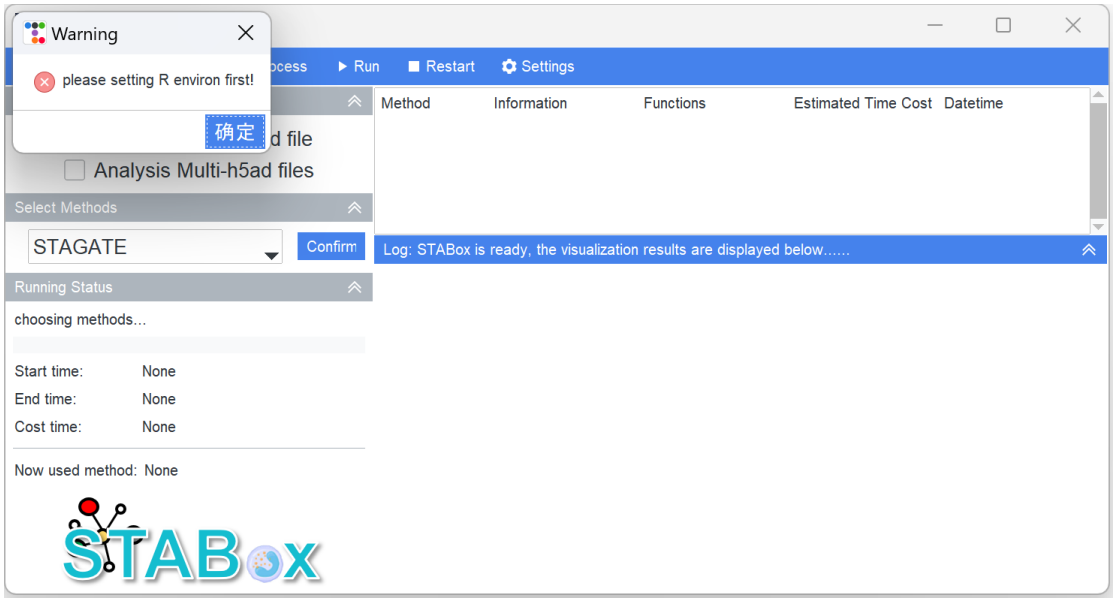
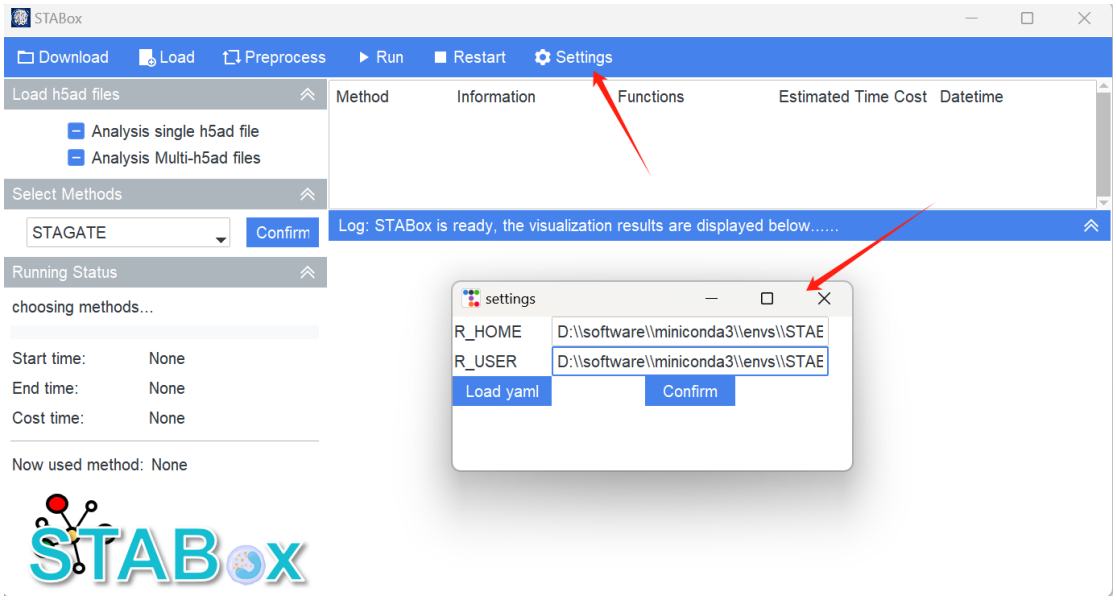
# R environment setting

If run successfully, you will launch the following GUI:

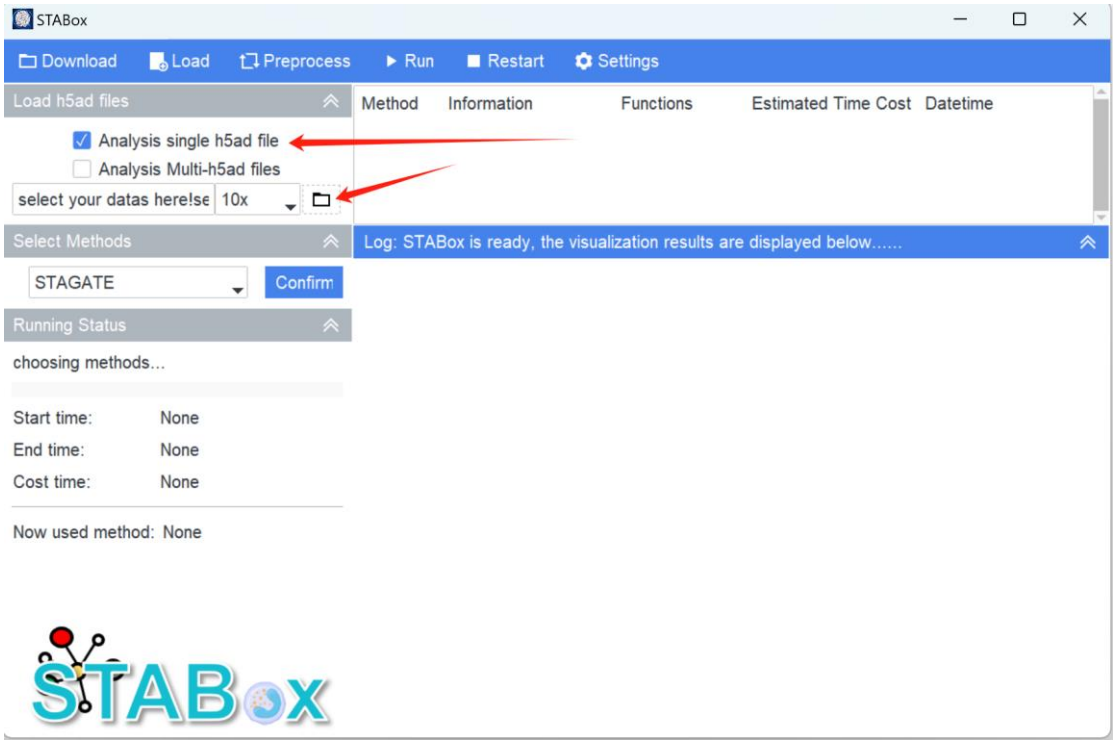



When running STABox for the first time, please specify the installation path of the R environment:
R_HOME: D:\\software\\miniconda3\\envs\\STABox\\lib\\R
R_USER: D:\\software\\miniconda3\\envs\\STABox\\Lib\\site-packages\\rpy2

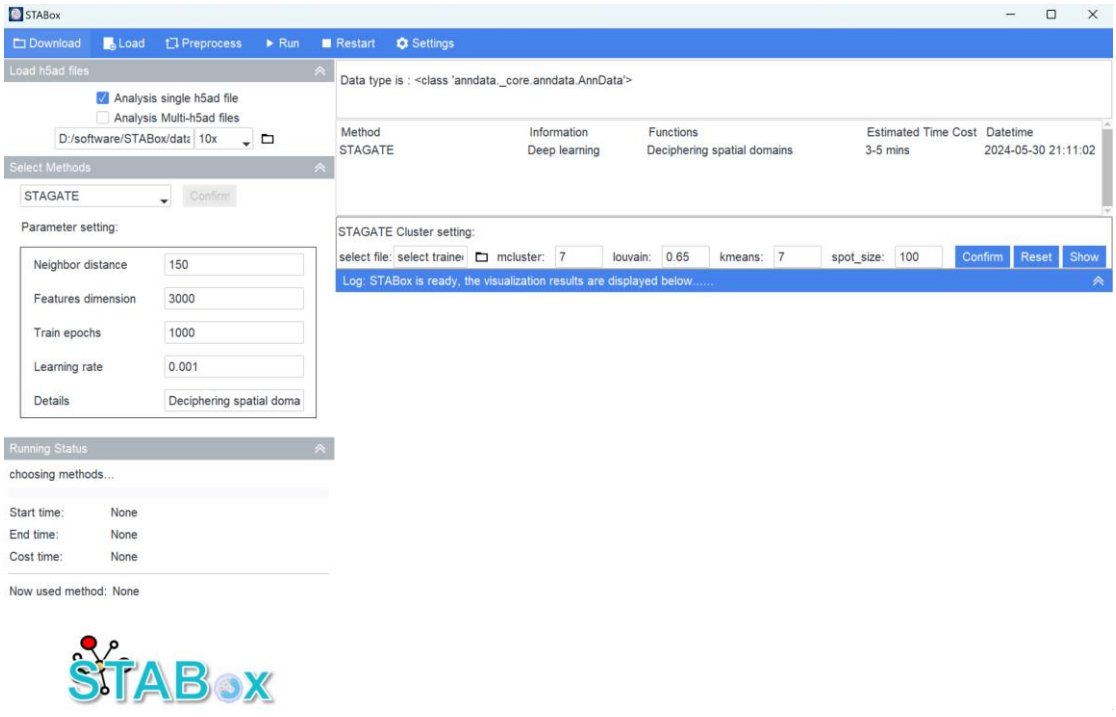


# Running STAGATE

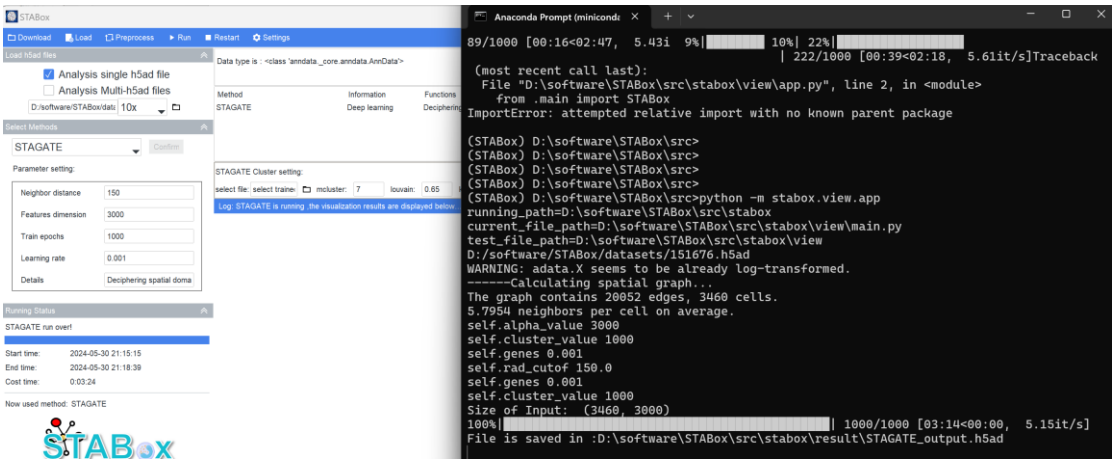
Firstly, we need to specify the pre-processed h5ad file path, then select STAGATE method and click “Confirm”.



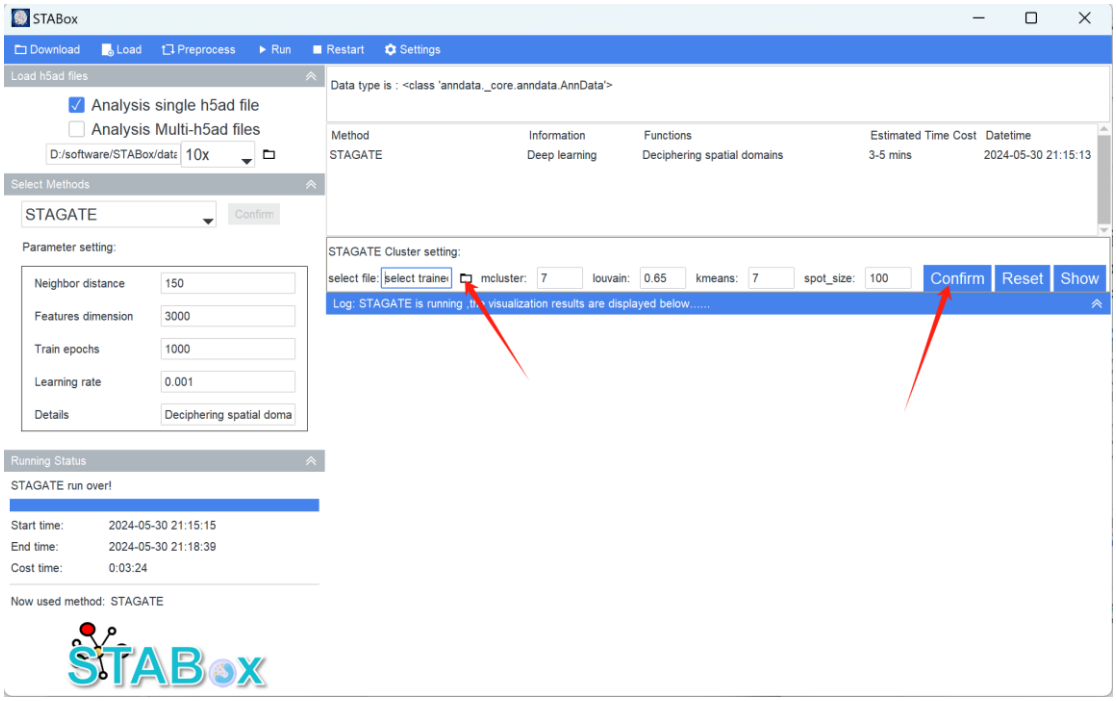

Next, we need to set the training parameters of the STAGATE model, and then click “Run” to start the training process.



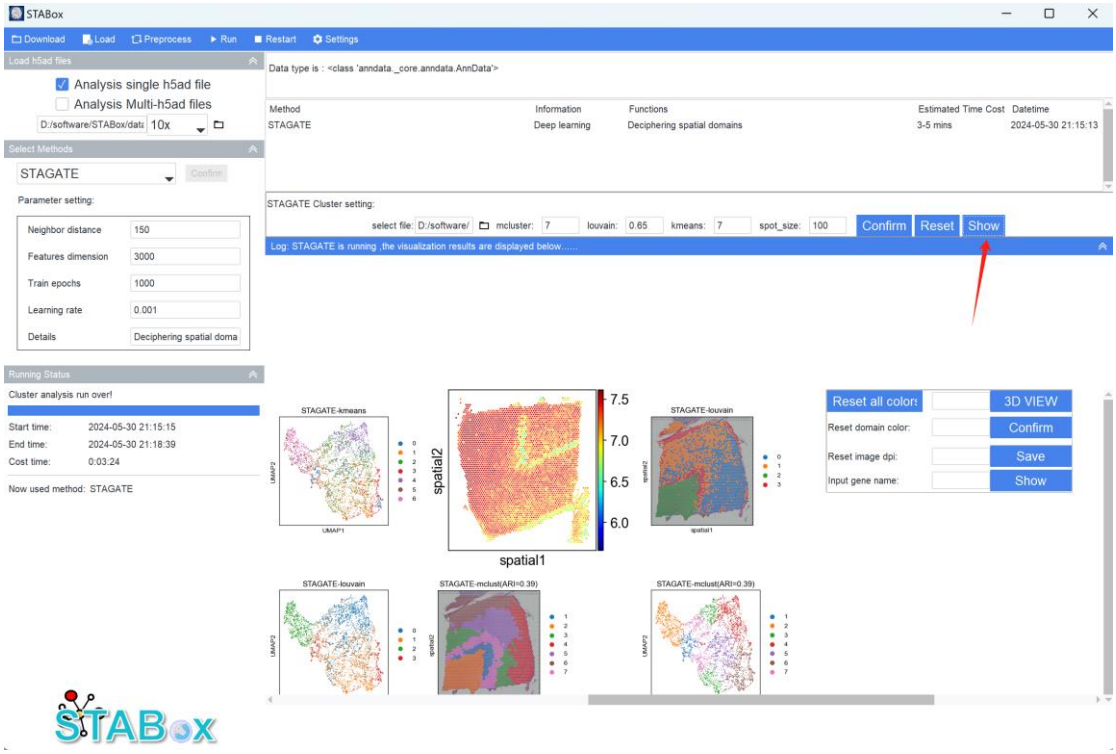
During the model training process, we can monitor the training progress by checking the command line window. The results are stored at D:\software\STABox\src\stabox\result\STAGATE_output.h5ad, and we can find this path from the print history from the command window.



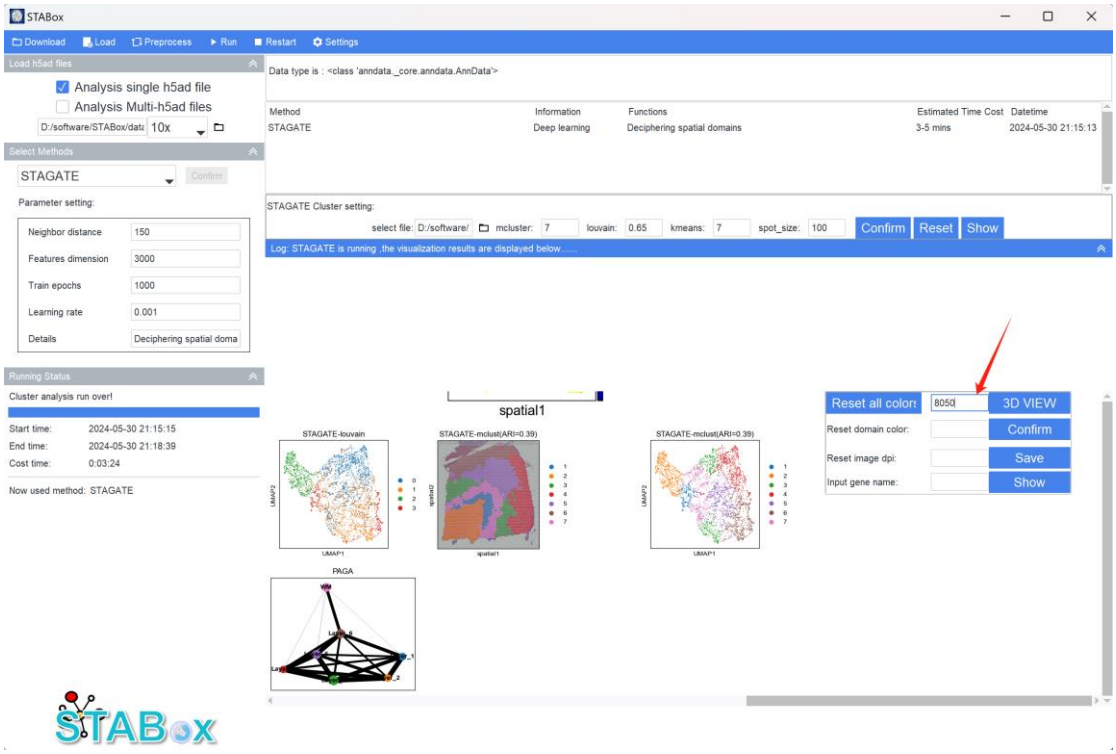

Next, we import the h5ad file with running results, and run the three clustering methods: mclust, Louvain, and kmeans. Then, click “Confirm” to start the clustering process.

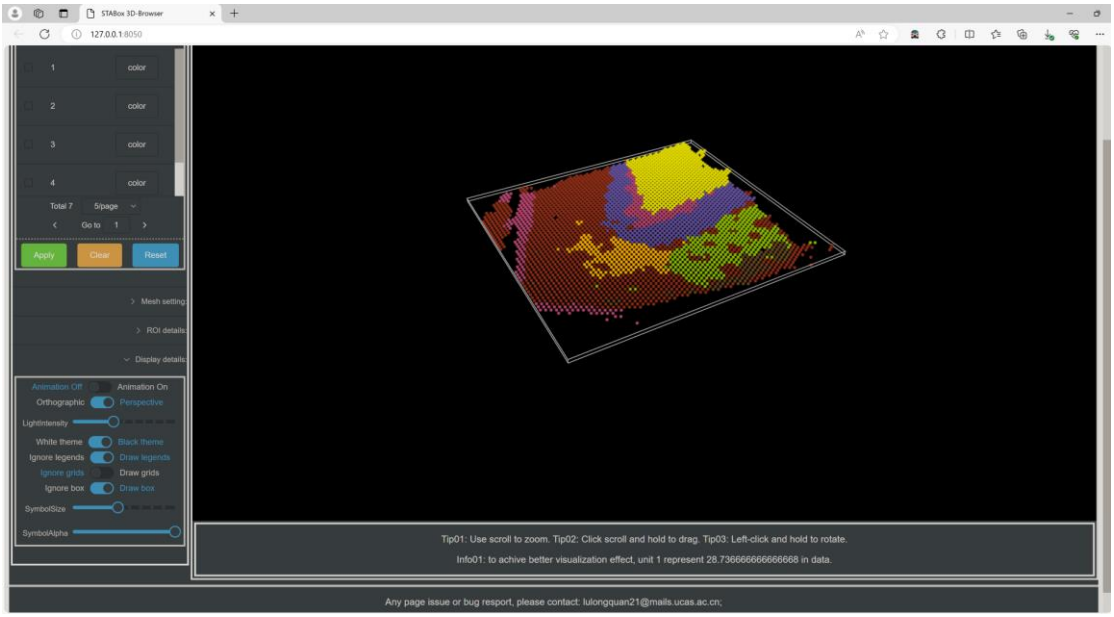



When running finished, click “Show” to display the results of dimensionality reduction, clustering, and trajectory inference as follows:



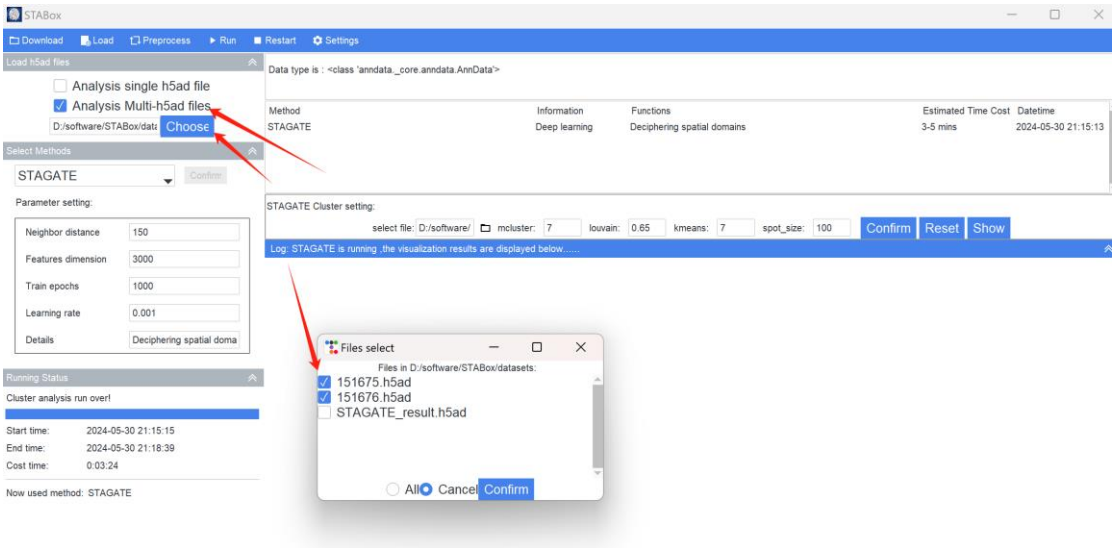

We can also display the tissue structure of the slice in 3D space by setting a port number.



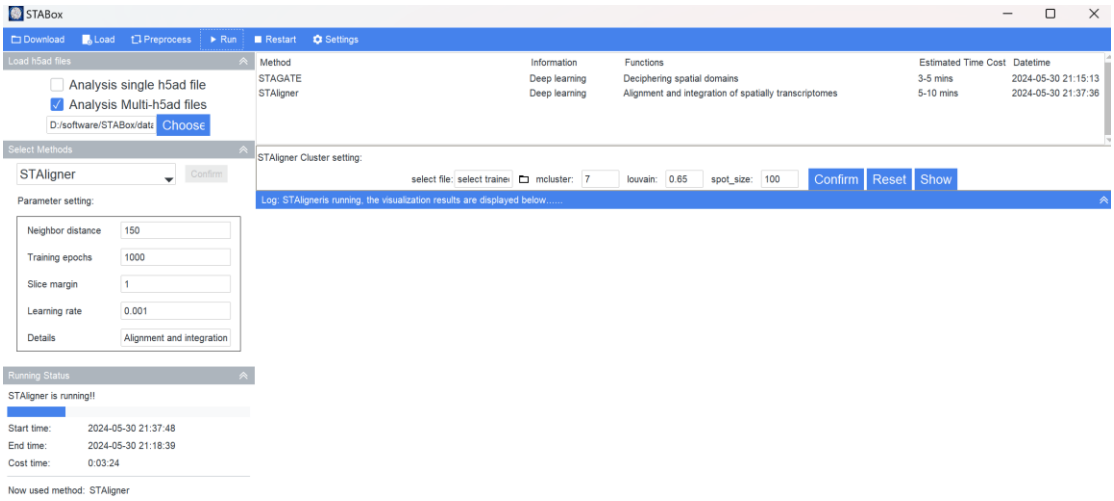



# Running STAligner

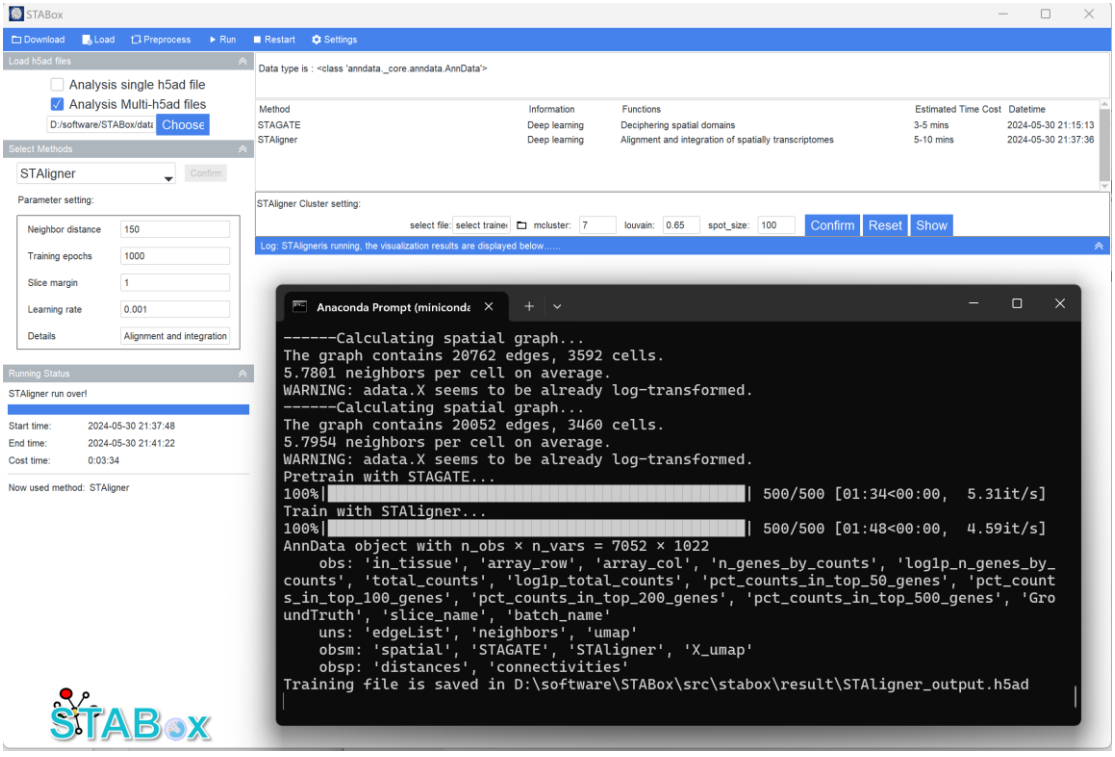
Firstly, we need to switch to multi-slice running mode, then set the directory path storing h5ad files, and select the h5ad files to be integrated.



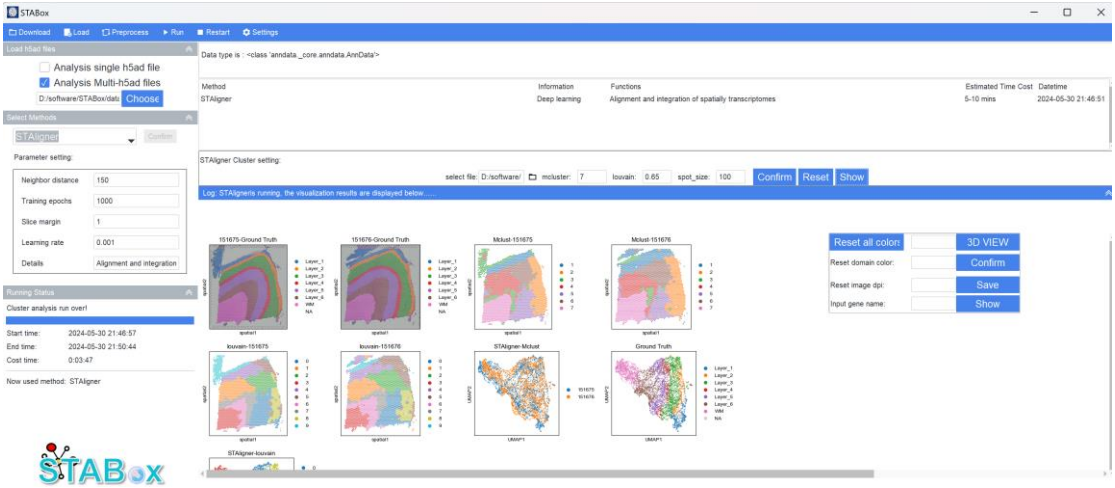

Next, we need to set the training parameters of the STAligner model, and then click “Run” to start the training process.




During the model training process, we can monitor the training progress by checking the command line window. The results are stored at D:\software\STABox\src\stabox\result\ STAligner_output.h5ad, and we can find this path from the print history from the command window.




Next, we import the h5ad file with running results, and run the three clustering methods: mclust, Louvain, and kmeans. Then, click “Confirm” to start the clustering process.


STABox
Download
Load
Preprocess
Run
Restart
Settings
Load h5ad files
Analysis single h5ad file
Analysis Multi-h5ad files
D:/software/STABox/data
Choose
Select Methods
STAligner
Confirm
Parameter setting:
Neighbor distance
150
Training epochs
1000
Slice margin
1
Learning rate
0.001
Details
Alignment and integration
Running Status
Cluster analysis run over!
Start time:
2024-05-30 21:46:57
End time:
2024-05-30 21:50:44
Cost time:
0:03:47
Now used method: STAligner
Data type is : <class 'anndata._core.anndata.AnnData'>
Method
Information
Functions
Estimated Time Cost
Datetime
STAligner
Deep learning
Alignment and integration of spatially transcriptomes
5-10 mins
2024-05-30 21:46:51
STAligner Cluster setting:
select file:
D:/software/
mcluster:
7
louvain:
0.65
spot_size:
100
Confirm
Reset
Show
Log: STAligner is running, the visualization results are displayed below.....
151675-Ground Truth
151676-Ground Truth
Mclust-151675
Mclust-151676
louvain-151675
louvain-151676
STAligner-Mclust
Ground Truth
STAligner-louvain
Reset all colors:
3D VIEW
Reset domain color:
Confirm
Reset image dpi:
Save
Input gene name:
Show