



# Summary of tutorial

## Advanced machine learning methods for modeling, analyzing, and interpreting single-cell omics and spatial transcriptomics data

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07/12/2024



[https://github.com/juexinwang/Tutorial\\_ISMB2024](https://github.com/juexinwang/Tutorial_ISMB2024)

# Learning outcomes

- To understand the basic principles of deep learning, graph representation learning, and model interpretation.
- To understand the specifics of computational tools such as scGNN, DeepMAPS, and BSP, and become aware of the appropriate tools to use in different applications in single-cell multi-omics and spatial transcriptomics studies.
- To gain hands-on experience in applying tools and interpreting results using standalone python-based software scGNN, R-based BSP, webserver-based DeepMAPS, and integrated AI-ready platform.

# Feedback survey



- <https://docs.google.com/forms/d/e/1FAIpQLSfrjbxGdE45OFPQgM58JDt59B--gonwjuKw1HkHrR4FLvhhw/viewform?pli=1>
- Acknowledgement:

