



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



Schedule



- (45 min) Part 1: Overview: Introduction to single-cell multi-omics and spatial transcriptomics and corresponding challenges. (Dr. Qin Ma: P1a,9-9:25AM and Dr. Dong Xu: P1b,9:25-9:45AM)
- (60 min) Part 2: Introduction to biological analyzing methods: (**hands-on exercises**) (Yi Jiang: P2a,9:45-10:15AM and Mauminah Raina: P2b, 10:15-10:45AM)
- (15 min) *10:45-11:00 am Coffee Break*
- (40 min) Part 3: Clustering-based single-cell analysis and scGNN on AI-ready platform. (Lei Jiang: P3,11:00-11:40AM)
- (80 min) Part 4: Applications #1: Single-cell RNA-seq dataset acquisition, model training, and analysis (**hands-on exercises**). (Dr. Juexin Wang and Yi Jiang: P4,11:40AM-1:00PM)
- (60 min) *Lunch Break 1:00 pm - 2:00 pm*
- (30 min) Part 5: Network analysis on single-cell multi-omics and DeepMAPS. (Dr. Qin Ma: P5,2-2:30PM)
- (90 min) Part 6: Applications #2: Single-cell multi-omics dataset acquisition, model training, and analysis (**hands-on exercises**). (Yi Jiang: P6, 2:30-4:00PM)
- (15 min) *Coffee Break at 4:00 - 4:15 pm*
- (30 min) Part 7: Marker analysis on spatial transcriptomics and BSP. (Dr. Juexin Wang: P7, 4:15-4:45PM)
- (35 min) Part 8: Applications #3: Spatial transcriptomics dataset acquisition, model fitting, and analysis (**hands-on exercises**). (Mauminah Raina: P8, 4:45-5:20PM)
- (35 min) Part 9: Application #4: Around the Block: Neighborhoods in Kidney Health and Disease (Dr. Michael Eadon: P9, 5:20-5:55PM)