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 and Dr. Dong Xu)

- (60 min) Part 2: Introduction to biological analyzing methods: (**hands-on exercises**) (Yi Jiang and Mauminah Raina)

- (15 min) *10:45-11:00 am Coffee Break*

- (60 min) Part 3: Clustering-based single-cell analysis and scGNN. (Yi Jiang and Dr. Juexin Wang)

- (60 min) Part 4: Applications #1: Single-cell RNA-seq dataset acquisition, model training, and analysis (**hands-on exercises**). (Dr. Juexin Wang and Yi Jiang)

- (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 and Yi Jiang)

- (90 min) Part 6: Applications #2: Single-cell multi-omics dataset acquisition, model training, and analysis (**hands-on exercises**). (Yi Jiang)

- (15 min) *Coffee Break at 4:00 - 4:15 pm*

- (30 min) Part 7: Marker analysis on spatial transcriptomics and BSP. (Dr. Juexin Wang)

- (35 min) Part 8: Applications #3: Spatial transcriptomics dataset acquisition, model fitting, and analysis (**hands-on exercises**). (Mauminah Raina)

- (40 min) Part 9: Application #4: Around the Block: Neighborhoods in Kidney Health and Disease (Dr. Michael Eadon)