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Multi-modal learning for single-cell multi-omics data integration

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Single-cell data constitute a major breakthrough in life sciences. Their integration will enable us to investigate outstanding biological and medical questions thus far inaccessible. However, still few methods exist to integrate different single-cell modalities, corresponding to omics data (e.g. DNA methylation, proteome, chromatin accessibility), plus spatial positioning and images. Single-cell multi-modal integration requires novel computational developments to overcome the numerous intrinsic challenges of single-cell data and exploit their richness. In this talk, I will give an overview of our ongoing research activity in two main methodological directions: (i) dimensionality reduction methods to cluster cells based on their multi-modal similarity and (ii) graphs to reconstruct regulatory mechanisms based on multi-modal data

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