

Fig. 1 | Integration of single-cell multiome with spatial transcriptome using ISON. a. ISON takes spatial transcriptome and paired single-cell multiome data as input. It captures the spatial gene expression and scRNA-seq in a shared low-dimensional representation and captures chromatin accessibility pattern of scATAC-seq into a lower dimensional embedding. The patterns of the two modalities are then mapped and aligned at a single-cell level. Then, spatial chromatin accessibility data is obtained by transferring from single-cell data to spatial transcriptome using shared representations. b. Spatial chromatin accessibility obtained from ISON preserves cis- and trans- regulatory signal. Spatial chromatin accessibility can be used to obtain spatially resolved gene-regulatory networks which can help in identifying disease-associated gene regulatory modules.