



(A) csMAHN performed well on weighted-F1 score compared to Seurat, SAMap and came on 8 tissues of HCL and MCA. human as reference and mouse as query (left panel). mouse as reference and human as query (left panel). (B) The UMAP plot of embeddings outputted by brain, applied with Seurat, SAMap, CAME and csMAHN, mouse as reference and colored with species and cell type (C) Weighted-F1 score of csMAHN is improved after appending the homology information of one2many and many2many to the model on three pairs of cross-species scRNA-seq data sets about the retina with zebrafish as the reference and with chick, mouse, and human as the queries. (D) The performance of csMAHN under different hyperparameters is stable and robust. exchange hyperparameters, n_hvgs and ndegs (left panel), n_feats and hidden (right panel).