Multimodal integration data and methods Unpaired diagonal integration Unpaired mosaic integration Paired integration Mod1 Mod1 Cells Mod2 Gene Peak Spatial Protein Mod2 Cells Cells Cells 18 paired scRNA+scATAC methods, 14 paired scRNA+ADT methods, 8 mosaic scRNA+ADT methods, 14 unpaired scRNA+scATAC 3 spatial Multiomics methods 8 mosaic scRNA+scATAC methods diagonal methods Integration output Joint embedding Aligned embeddings for Modality imputations from paired datasets unpaired datasets Cells Protein Peak Performance evaluation Usability Scalability Quality of software Quality of document 3PU Quality of paper System restrictions Dataset size Dataset size Dataset size Accuracy Cell alignment accuracy Modality imputation Embedding accuracy accuracy Batch effect Biological structure conservation Alignment accuracy removal 100% Source of Single batch Multiple batches batch ٥% Fraction of Fraction of Mod1 Mod2 True Match False Match Global Impute Cell type1 accuracy 100% Local Cell type2 Cell match Cell type match Sites Donors accuracy Rare cell 0% Mod1 Mod2 accuracy Robustness Robustness to dropout Robustness in multiple runs Total reads per cell Embeddina accuracy Accuracy 100% 0.50 AUC=0.883 품 _{0.25}

75 50 RNA Down %

Accuracy after dropout

Algor1

0%

Modality dropout simulation