

CORRECTION

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Correction: Single-cell multi-omics integration for unpaired data by a siamese network with graph-based contrastive loss

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The original article can be found online at <https://doi.org/10.1186/s12859-022-05126-7>.

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Following publication of the original article [1], the authors identified an error in Fig. 2. The correct figure is given below.

The original article [1] has been corrected.



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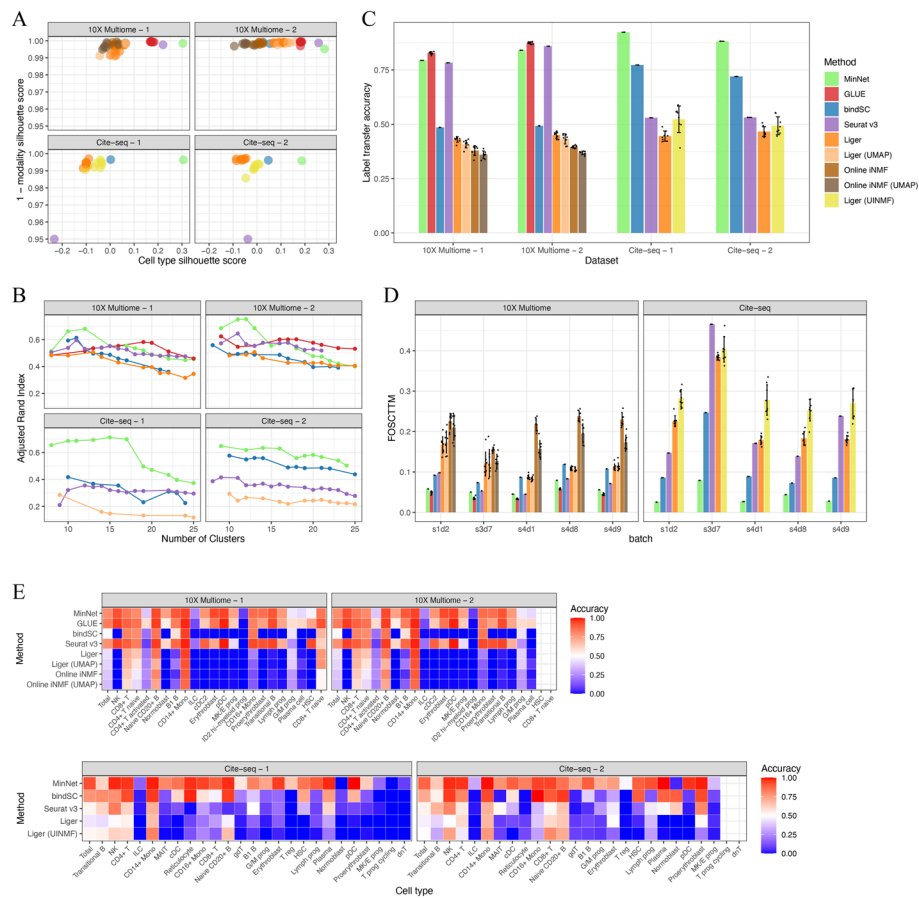


Fig. 2 Performance benchmarks on gold-standard datasets. To test our model and compare it to existing algorithms, we benchmarked the transcriptome and chromatin accessibility data integration model and the transcriptome and cell-surface protein data integration model on datasets from the NeurIPS 2021 competition data. **A** Silhouette scores on the embedding space generated by all algorithms. Cell type silhouette score indicates how well cell types separate from each other, and 1 - modality silhouette score indicates how well modalities mix with each other. **B** Adjusted Rand index along with the number of clusters comparing all algorithms. **C** Average label transfer accuracy bar plot. **D** FOSCTTM (Fraction of samples closer than the true match) score indicates the single-cell level alignment error of all algorithms. **E** Label transfer accuracy heatmap from transcriptome data to chromatin accessibility data (top); or from epitope data to transcriptome data (bottom)

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Reference

1. Liu, et al. Single-cell multi-omics integration for unpaired data by a siamese network with graph-based contrastive loss. BMC Bioinformatics. 2023;24:5. <https://doi.org/10.1186/s12859-022-05126-7>.

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