SCPInt: an adversarial disentanglement-based explicit batch correction and integration method for MS-based single-cell proteomics

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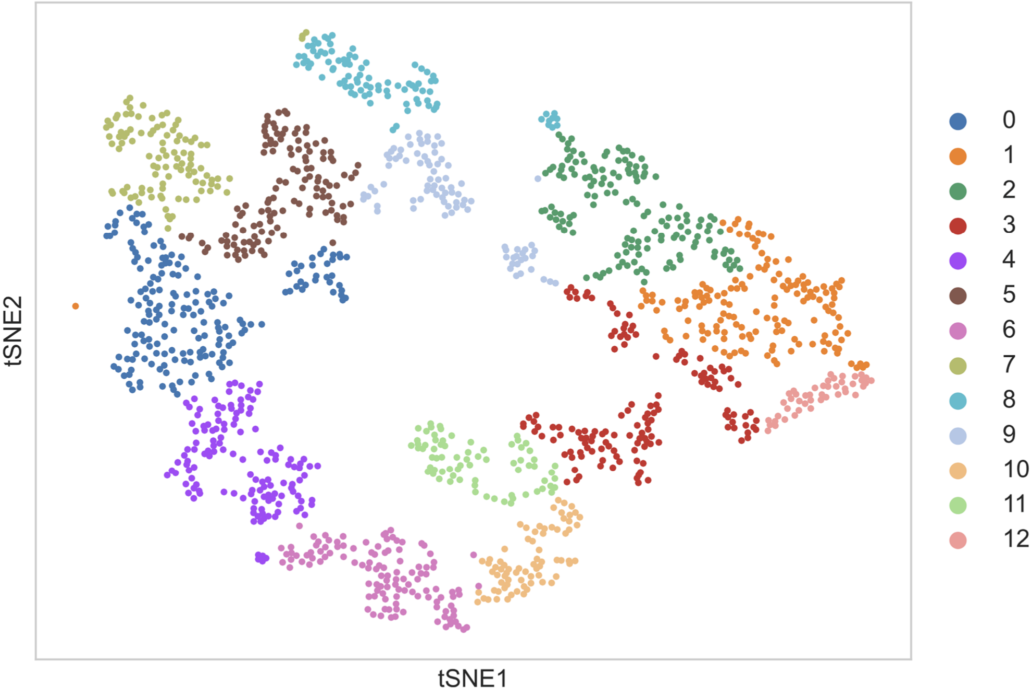
Supplementary Figures



Supplementary Figure 1. Distribution of clusters identified by Leiden clustering after integrating Huffman and Specht datasets with SCPInt.

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a

Method	isolated_labels	nmi	ari	silhouette_label	clisi	ilisi	kbet	graph_conn
	Bio conservation					Batch correction		
SCPInt	0.65	1.00	1.00	0.71	1.00	1.00	1.00	1.00
Liger	1.00	0.74	0.69	0.75	0.58	0.90	0.22	0.65
scVI	0.00	0.17	0.41	0.73	0.16	0.84	0.42	0.71
combat	0.55	0.32	0.43	0.81	0.64	0.54	0.03	0.79
Raw	0.72	0.00	0.08	0.96	0.65	0.55	0.10	0.71
Harmony	0.78	0.34	0.00	1.00	0.69	0.56	0.04	0.36
Scanorama	0.88	0.31	0.11	0.97	0.57	0.00	0.07	0.70
scProtein	0.06	0.02	0.04	0.00	0.00	0.68	0.00	0.00

c

Method	isolated_labels	nmi	ari	silhouette_label	clisi	ilisi	kbet	graph_conn
	Bio conservation					Batch correction		
SCPInt	1.00	0.35	0.86	0.87	0.38	1.00	1.00	1.00
Harmony	0.69	0.35	0.59	0.88	0.55	0.95	0.49	0.42
Scanorama	0.73	0.39	1.00	0.84	0.81	0.75	0.24	0.45
scProtein	0.00	0.00	0.02	0.00	0.00	0.82	0.61	0.01
Liger	0.72	0.45	0.51	0.49	1.00	0.08	0.28	0.26
scVI	0.13	0.09	0.00	0.13	0.37	0.49	0.50	0.00
combat	0.82	0.64	0.52	0.85	0.76	0.09	0.00	0.37
Raw	0.69	1.00	0.30	1.00	0.91	0.00	0.03	0.28

Supplementary Figure 2. a. Quantitative evaluation of biological conservation and batch-correction performance for SCPInt and comparative methods on Khan dataset. **b.** Scatter plots visualizing the integration results of SCPInt and comparison methods on the Leduc2024 dataset. **c.** Quantitative evaluation of biological conservation and batch-correction performance for SCPInt and comparative methods on Leduc2024 dataset.