

Dataset	scFP	scBFP	scCR (ours)
Baron Mouse	0.517 $\pm$ 0.000	0.465 $\pm$ 0.000	0.304 $\pm$ 0.000
Pancreas	0.537 $\pm$ 0.001	0.506 $\pm$ 0.001	0.352 $\pm$ 0.000
Mouse Bladder	0.374 $\pm$ 0.000	0.374 $\pm$ 0.001	0.170 $\pm$ 0.000
Zeisel	0.580 $\pm$ 0.001	0.538 $\pm$ 0.000	0.489 $\pm$ 0.000
Worm Neuron	0.330 $\pm$ 0.000	0.190 $\pm$ 0.000	0.049 $\pm$ 0.000
Baron Human	0.493 $\pm$ 0.000	0.475 $\pm$ 0.000	0.328 $\pm$ 0.000

Table 1: Performance on dropout recovery under Missing Not At Random (MNAR) settings, measured by RMSE. Dropout is applied only to the genes with the lowest 1000 expression levels. The number of dropouts is set to 20% of the total number of values in the cell-gene matrix.

PRE	COM	DEN	Baron Mouse	Zeisel	Baron Human
✓	✓	✗	0.437 $\pm$ 0.061	0.682 $\pm$ 0.024	0.580 $\pm$ 0.036
✓	✗	✗	0.409 $\pm$ 0.008	0.732 $\pm$ 0.001	0.571 $\pm$ 0.007
✓	✗	✓	0.584 $\pm$ 0.000	0.822 $\pm$ 0.000	0.681 $\pm$ 0.000
✓	✓	✓	0.827 $\pm$ 0.093	0.902 $\pm$ 0.000	0.823 $\pm$ 0.000

Table 2: Further ablation study of scCR on cell clustering measured by ARI. PRE, COM, and DEN denote the pre-imputation stage, the complete relation stage, and the denoising stage, respectively.

Method	Macro-F1	Micro-F1
scGPT	0.637 $\pm$ 0.018	0.823 $\pm$ 0.005
scCR + scGPT	0.650 $\pm$ 0.019	0.832 $\pm$ 0.006

Table 3: Performance on cell type annotation in the Multiple Sclerosis dataset, measured by Macro F1 score and Micro F1 score. Performance on cell type annotation in the Multiple Sclerosis dataset. Unlike cell clustering, cell type annotation is a classification task that belongs to supervised learning.

α	Baron Mouse	Zeisel	Baron Human
0.01	0.627 $\pm$ 0.000	0.903 $\pm$ 0.000	0.823 $\pm$ 0.000
0.05 (used)	0.827 $\pm$ 0.093	0.902 $\pm$ 0.000	0.823 $\pm$ 0.000
0.1	0.727 $\pm$ 0.141	0.904 $\pm$ 0.000	0.824 $\pm$ 0.000
0.5	0.701 $\pm$ 0.000	0.901 $\pm$ 0.000	0.681 $\pm$ 0.000
0.9	0.448 $\pm$ 0.001	0.825 $\pm$ 0.000	0.683 $\pm$ 0.001

Table 4: Performance of scCR on cell clustering measured by ARI for different values of α .

β	Baron Mouse	Zeisel	Baron Human
0.1	0.440 $\pm$ 0.046	0.659 $\pm$ 0.058	0.553 $\pm$ 0.040
0.5	0.476 $\pm$ 0.049	0.724 $\pm$ 0.000	0.560 $\pm$ 0.001
0.9	0.509 $\pm$ 0.004	0.740 $\pm$ 0.000	0.657 $\pm$ 0.000
0.95	0.498 $\pm$ 0.002	0.910 $\pm$ 0.000	0.666 $\pm$ 0.011
0.99 (used)	0.827 $\pm$ 0.093	0.902 $\pm$ 0.000	0.823 $\pm$ 0.000
0.999	0.925 $\pm$ 0.000	0.900 $\pm$ 0.000	0.819 $\pm$ 0.000

Table 5: Performance of scCR on cell clustering measured by ARI for different values of β .

γ	Baron Mouse	Zeisel	Baron Human
0.001	0.927 $\pm$ 0.001	0.902 $\pm$ 0.000	0.824 $\pm$ 0.000
0.01 (used)	0.827 $\pm$ 0.093	0.902 $\pm$ 0.000	0.823 $\pm$ 0.000
0.05	0.635 $\pm$ 0.000	0.903 $\pm$ 0.000	0.822 $\pm$ 0.000
0.1	0.595 $\pm$ 0.000	0.903 $\pm$ 0.000	0.667 $\pm$ 0.001
0.5	0.469 $\pm$ 0.003	0.740 $\pm$ 0.000	0.627 $\pm$ 0.011
0.9	0.409 $\pm$ 0.009	0.749 $\pm$ 0.000	0.586 $\pm$ 0.006

Table 6: Performance of scCR on cell clustering measured by ARI for different values of γ .

k	Baron Mouse	Zeisel	Baron Human
1	0.628 $\pm$ 0.000	0.905 $\pm$ 0.000	0.827 $\pm$ 0.000
2 (used)	0.827 $\pm$ 0.093	0.902 $\pm$ 0.000	0.823 $\pm$ 0.000
3	0.631 $\pm$ 0.000	0.903 $\pm$ 0.000	0.819 $\pm$ 0.000
5	0.625 $\pm$ 0.002	0.902 $\pm$ 0.001	0.818 $\pm$ 0.000
10	0.621 $\pm$ 0.000	0.903 $\pm$ 0.000	0.818 $\pm$ 0.000
15	0.630 $\pm$ 0.000	0.902 $\pm$ 0.000	0.817 $\pm$ 0.000

Table 7: Performance of scCR on cell clustering measured by ARI for different values of k .

Method	Input	Big-O
scTAG	$\mathbf{X}, \mathbf{A}^{cell}, \theta$	$O(GC) + O(\mathcal{E}_{cell}) + O(\theta)$
DCA	$\mathbf{X}, \theta$	$O(GC) + O(\theta)$
AutoClass	$\mathbf{X}, \theta$	$O(GC) + O(\theta)$
scGNN 2.0	$\mathbf{X}, \theta$	$O(GC) + O(\mathcal{E}_{cell}) + O(\theta)$
scGCL	$\mathbf{X}, \mathbf{A}^{cell}, \theta$	$O(GC) + O(\mathcal{E}_{cell}) + O(\theta)$
MAGIC	$\mathbf{X}, \mathbf{A}^{cell}$	$O(GC) + O(\mathcal{E}_{cell})$
scFP	$\mathbf{X}, \mathbf{A}^{cell}$	$O(BC) + O(\mathcal{E}_{cell})$
scBFP	$\mathbf{X}, \mathbf{A}^{cell}, \mathbf{A}^{gene}$	$O(BC) + O(\mathcal{E}_{gene}) + O(BG) + O(\mathcal{E}_{cell})$
scCR (Ours)	$\mathbf{X}, \mathbf{A}^{cell}, \mathbf{A}^{gene}$	$O(BC) + O(\mathcal{E}_{gene}) + O(BG) + O(\mathcal{E}_{cell})$

Table 8: Comparison of Inputs and memory complexity. $\mathbf{X} \in \mathbb{R}^{G \times C}$ denote a cell-gene matrix, where C and G represent the number of cells and genes, respectively. $\mathbf{A}^{cell} \in \mathbb{R}^{C \times C}$ and $\mathbf{A}^{gene} \in \mathbb{R}^{G \times G}$ denote cell-cell and gene-gene adjacency matrices, respectively. θ denotes trainable parameters. B represents the batch size for batch-wise k -NN graph construction.

Dataset	Memory usage (GB)
Baron Mouse	1.811
Pancreas	1.837
Mouse Bladder	1.957
Zeisel	2.037
Worm Neuron	1.927
Baron Human	3.861

Table 9: Memory usage of scCR for different datasets, measured by gigabytes (GB).