|  |  |  |  |
| --- | --- | --- | --- |
| Data | LRMC(ADMM 1000 epoch) | WEDGE (MAX 500 epoch) | scIWNN(200 epoch) |
| Adam | 0.29387 | 1.18147 | **0.27838** |
| Alles | 0.23112 | 0.81697 | **0.21627** |
| Baron | 0.17934 | 0.27224 | **0.15476** |
| Muraro | 0.28709 | 0.55984 | **0.25346** |
| Tabula | 0.68503 | 1.03998 | **0.61256** |
| Young | 0.30017 | 1.12739 | **0.29882** |
| Zeisel | 0.13915 | 0.18095 | **0.12181** |

**Supplementary Table 1** Comparison of Restoration Errors with Traditional Matrix Completion Algorithms. LRMC is based on nuclear norm optimization and is solved using the standard ADMM algorithm. Only errors for known non-zero positions are calculated and the dropout rate is 0.6

**Supplementary Table 2** Comparison of Restoration Errors with Traditional Matrix Completion Algorithms. The dropout rate is 0.6 and the position of zero also participates in the error calculation.

|  |  |  |  |
| --- | --- | --- | --- |
| Data | LRMC(ADMM 1000 epoch) | WEDGE (MAX 500 epoch) | scIWNN(200 epoch) |
| Adam | **2.90393** | 3.20221 | 2.91012 |
| Alles | **2.66613** | 2.81722 | 2.66940 |
| Baron | 1.64966 | 1.83934 | **1.60703** |
| Muraro | 0.58455 | 0.81572 | **0.54843** |
| Tabula | 1.85901 | 2.16843 | **1.57391** |
| Young | 4.48239 | **3.87305** | 4.48502 |
| Zeisel | 0.53210 | 0.73423 | **0.50616** |

|  |  |  |  |
| --- | --- | --- | --- |
| Method | Time(second) | Memory(GB) | Video Memory(GB) |
| scIWNN | 758 | 5.8 | 16.8 |
| SAVER | >24 | 18 | - |
| scImpute | NA | NA | NA |
| WEDGE | 3999 | 13 | - |
| MAGIC | 2935 | 9.2 | - |
| DeepImpute | 603 | 8.4 | 1.9 |

**Supplementary Table 3** Use the workstation to run the imputation algorithm on SRP073767, the number of CPU cores is 128, the GPU is RTX3090, and the memory is 128GB.

|  |
| --- |
| mse_rate_0.6leger_shu |
| **Supplementary Figure 1** |
| MSE after logarithmic transformation relative to the Reference data. |
| The MSE when the dropout rate is 0.6 (60% of the elements in the reference data are randomly erased), and a 2-logarithmic transformation is performed. |

|  |  |
| --- | --- |
| ARI_0.2 | C:\Users\zs\Documents\ipython\TsImpute\ARI_0.4.png |
| ARI_0.6  leger_shu | |
| **Supplementary Figure 2** | |
| Comparison of clustering results of different imputation methods | |
| ARI comparison of different imputation methods when the dropout rate is 0.2, 0.4, 0.6. | |

|  |  |
| --- | --- |
| person_cell_rate_0.2 | person_gene_rate_0.2 |
| person_cell_rate_0.4 | person_gene_rate_0.4 |
| person_cell_rate_0.6 | person_gene_rate_0.6 |
| leger_shu | |
| **Supplementary Figure 3** | |
| Pearson correlation with reference data. | |
| Calculate the Pearson correlation of the cell-cell gene-gene between the imputation data and the reference data, with dropout rates of 0.2, 0.4, and 0.6. | |

|  |  |
| --- | --- |
| Prkar2b | Tbr1 |
| Bcap29 | Nrxn3 |
| **Supplementary Figure 4** | |
| Violin plot of some low-expressed genes in Zeisel. | |
| SAVER prefers a conservative imputation strategy in the face of low-expression genes. scIWNN, scImpute, WEDGE and DeepImpute tend to assign a lower value to these underexpressed genes. MAGIC showed a more bimodal distribution. | |

|  |  |
| --- | --- |
| draw_graph_fr_WEDGE_gu | draw_graph_fr_WEDGE_time |
| draw_graph_fr_scImpute_gu | draw_graph_fr_scImpute_time |
| draw_graph_fr_DeeImpute_gu | draw_graph_fr_DeeImpute_time |
| draw_graph_fr_MAGIC_gu | draw_graph_fr_MAGIC_time |
| **Supplementary Figure 5** | |
| Trajectory inference results for different imputation methods. | |
| Most of the methods caused the problem of excessive separation of cell clusters at 0h, which made it impossible to perform pseudo-chronological analysis under the default parameters. DeepImpute has different results from other methods, making it difficult to distinguish between 36h and 72h cells. | |

|  |  |  |
| --- | --- | --- |
| MAGIC_CXCR4 | MAGIC_NANOG | MAGIC_POU5F1 |
| scImpute_CXCR4 | scImpute_NANOG | scImpute_POU5F1 |
| SAVER_CXCR4 | SAVER_NANOG | SAVER_POU5F1 |
| WEDGE_CXCR4 | WEDGE_NANOG | WEDGE_POU5F1 |
| DeeImpute_CXCR4 | DeepImpute_NANOG | DeepImpute_POU5F1 |
| **Supplementary Figure 6** | | |
| Violin plots on CXCR4, NANOG, POU5F1 after imputation by different method. | | |
| MAGIC weakened the expression of NANOG and POU5F1 from 36h to 72h, and WEDGE also showed a similar situation. DeepImpute may overestimate the expression of CXCR4 from 0h to 24h. SAVER retained the original heterogeneity information, but did not reflect the up-regulated expression of CXCR4 at 36h. | | |