Scedar: a scalable Python package for single-cell RNA-seq exploratory data analysis

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Abstract

In single-cell RNA-seq (scRNA-seq) experiments, the number of individual cells has increased exponentially, and the sequencing depth of each cell has decreased significantly. As a result, analyzing scRNA-seq data requires extensive considerations of program efficiency and method selection. In order to reduce the complexity of scRNA-seq data analysis, we present `scedar`, a scalable Python package for scRNA-seq exploratory data analysis. The package provides a convenient and reliable interface for performing visualization, imputation of gene dropouts, detection of rare transcriptomic profiles, and clustering on large-scale scRNA-seq datasets. The analytical methods are efficient, and they also do not assume that the data follow certain statistical distributions. The package is extensible and modular, which would facilitate further development of functionalities for future requirements. The open source package is distributed under the terms of MIT license at https://pypi.org/project/scedar.

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1 Introduction

Cost-effective large-scale transcriptomic profiling of individual cells is enabled by the development of microfluidic, nanodroplet, and massively parallel sequencing technologies. Using these technologies, single-cell RNA-seq (scRNA-seq) experiments usually generate transcriptomic profiles of thousands to millions of individual cells (Svensson *et al.*, 2018). Therefore, scRNA-seq has become more commonly used to either study specific biological questions or comprehensively profile certain tissues or organisms (Filbin *et al.*, 2018; Cao *et al.*, 2017; Regev *et al.*, 2017).

Therefore, analyzing scRNA-seq datasets requires efficient computational programs and sophisticated statistical methods. The programs should be able to manage memory efficiently, exploit multiple cores of the processing units, and handle errors and exceptions gracefully. The statistical methods need to deal with high dimensionality, low signal-to-noise ratio, and different characteristics of data generated from different technologies and protocols (Kiselev *et al.*, 2019; Dueck *et al.*, 2016; Ziegenhain *et al.*, 2017). Such requirements have become a barrier between experiments and biological interpretations of the results.

Several computational tools have been developed to provide programming interfaces to analyze large-scale scRNA-seq datasets, such as `Seurat v3.0` (Butler *et al.*, 2018) and `SCANPY` (Wolf *et al.*, 2018). Seurat is an R package providing visualization and robust statistical methods to explore and interpret the heterogeneity of the dataset. SCANPY is a Python package providing efficient reimplementations of preexisting statistical methods and analytical workflows, which can be used to perform general exploratory data analysis and special inferences. In order to be scalable, previous methods are designed to minimize the usage of hardware resources, so that a large-scale dataset can be analyzed using a desktop computer.

Here, we attempt to achieve the scalability of scRNA-seq data analysis through an alternative approach, which is to enable the analytical methods to exploit modern high-performance computing architectures (Dean and Ghemawat, 2008; Zaharia *et al.*, 2010; Abadi *et al.*, 2016), such as servers and clusters with large amount of memory, multiple central and graphical processing unit cores, and solid-state drives (SSD) with higher read and write speed than traditional hard disk drive (HDD). Such computational resources have been made easily accessible by cloud computing services like Amazon Web Services and Microsoft Azure. Applying this approach, we designed the analytical

methods to be able to run in parallel processes with minimized memory overhead.

Additionally, we also aim to develop robust exploratory data analysis (EDA) methods, so that they could be applied to various datasets generated by different experimental designs, technologies, and protocols. Single-cell RNA-seq datasets have distinct statistical characteristics if generated from different scRNA-seq technologies and platforms (Zappia *et al.*, 2017; Dueck *et al.*, 2016; Ziegenhain *et al.*, 2017), such as SMARTer (Pollen *et al.*, 2014), Drop-seq (Macosko *et al.*, 2015) and 10x Genomics GemCode (Zheng *et al.*, 2017). In order to avoid assumptions on the statistical distributions of the datasets, we incorporated efficient implementations of machine learning methods into the data exploration process. Through extensive exploration, the statistical properties of the data could be observed and used to guide the selection of appropriate methods for biological interpretation (Zappia *et al.*, 2018).

Therefore, we developed a scalable and reliable Python package, single-cell exploratory data analysis for RNA-seq (`scedar`), to facilitate the exploration of large-scale scRNA-seq datasets. `Scedar` provides analytical routines for visualization, gene dropout imputation, rare transcriptomic profile detection, clustering, and identification of cluster separating genes. The visualization methods are integrated with the efficient scRNA-seq data structures to provide intuitive, convenient, and flexible plotting interfaces. We implemented methods to impute gene dropouts (Supplementary Algorithm S1) and detect rare transcriptomic profiles (Supplementary Algorithm S2) based on the k-nearest neighbor (KNN) algorithm. The detected rare transcriptomic profiles could be compared with their nearest neighbors in details to identify rare cell states or types. For clustering analysis, we provide a novel cell clustering algorithm named MIRAC (Algorithm 1), minimum description length (MDL) iteratively regularized agglomerative clustering. In order to identify genes that are able to distinguish the clusters, we provide a method using a sparsity-aware gradient boosted tree system, XGBoost (Chen and Guestrin, 2016).

2 Methods

2.1 `scedar` package design

We designed `scedar` in an object-oriented manner for quickly exploring large-scale scRNA-seq transcription level matrices on a remote server utilizing parallel computing techniques, in order to pro-

vide a robust and extensible platform for EDA, rather than surpassing the analytical performance of any of ≥ 275 existing scRNA-seq data analysis methods (Zappia *et al.*, 2018). The application programming interface (API) is designed to be intuitive to users familiar with the R programming language. The standard analysis workflow is to explore the dataset, cluster cells, and identify cluster separating genes (Figure 1), which is implemented as four main modules: data structure, KNN, clustering and visualization.

The core data structure stores each transcription level matrix as a standalone instance, and it can easily be extended to support customized analytical procedures. The built-in extensions include common procedures like pairwise distance computation, Principal Component Analysis (PCA) (Pearson, 1901), t-Distributed Stochastic Neighbor Embedding (t-SNE) (van der Maaten and Hinton, 2008), UMAP (McInnes and Healy, 2018), and k-nearest neighbor graph (Jacomy *et al.*, 2014). We optimized time and memory efficiency with the following design patterns: parallel computing, lazy loading, caching and copy-on-write.

The KNN and clustering modules utilize the data structure and parallel computing to efficiently perform analytical procedures, and the results are stored in the data structure for further reference.

The visualization module contains plotting methods optimized for large datasets, especially for plotting heatmaps. For example, it takes less than two minutes to generate a heatmap image from a $50,000 \times 20,000$ matrix containing random standard normal entries.

Preprocessing is implemented as selection and transformation routines of the core data structure, which is not a focus of `scedar`. The package is designed to identify the necessity of certain preprocessing procedures by extensively exploring the original state of the data. Although preprocessing, such as batch effect correction and normalization, could facilitate the detection of biological variances between cells, applying preprocessing methods correctly requires careful validation of their assumptions, otherwise they may introduce unwanted bias or variability (Hicks and Irizarry, 2015).

2.2 Minimum description length iteratively regulated agglomerative clustering

Minimum description length (MDL) iteratively regulated agglomerative clustering (MIRAC) extends hierarchical agglomerative clustering (HAC) (Müllner, 2011) in a divide and conquer manner for scRNA-seq data. Input with raw or dimensionality reduced scRNA-seq data, MIRAC starts with one round of bottom-up HAC to build a tree with optimal linear leaf ordering (Bar-Joseph *et al.*,

2001), and the tree is then divided into small sub-clusters, which are further merged iteratively into clusters. Because each individual cluster becomes more homogenous with higher number of clusters, the iterative merging process is regularized with the MDL principle (Hansen and Yu, 2001). The time complexity of MIRAC is $O(n^4 + mn^2)$, where n is the number of samples, and m is the number of features. The space complexity is $O(n^2 + mn)$. Relevant mathematical theories and notations of MDL are briefly described in Supplementary Method section 1.2. The pseudo-code of MIRAC is shown in Algorithm 1.

Comparing to HAC, MIRAC is not designed to be faster but rather to improve the cluster robustness. The asymptotic time complexity of MIRAC is the same as HAC with optimal leaf ordering. However, the use of MDL rather than deterministic similarity metrics, such as silhouette methods, improves the noise tolerance by estimating similarity with probabilistic models to give more weight on signal and less weight on noise (Supplementary Method section 1.2), assuming that signal is stronger than noise.

2.2.1 Rationale

The rationale behind MIRAC is to reduce the number of cell partitions that need to be evaluated and find a good one among them.

The number of all possible partitions of a set with n elements is the Bell number, which could be computed with the following recurrence $B_n = \sum_{k=0}^{n-1} B_k \binom{n-1}{k}$, where $n \geq 1$ and $B_0 = 1$ (Wilf, 1999, chap. 1). It is computationally intractable to compute the code lengths of B_n partitions, so we reduced the number of cell partitions to evaluate with the following steps:

1. We only evaluate the partitions of n cells that consecutively divide the optimal HAC tree T leaf ordering. The HAC tree with optimal leaf ordering maximizes the sum of similarity measurements between adjacent items in the leaf ordering (Bar-Joseph *et al.*, 2001), which could be computed with an algorithm developed by Bar-Joseph *et al.* (2001) that runs in time $O(n^4)$. The number of partitions that consecutively divide an ordering is the same as the number of compositions of n, which is $C_n = 2^{n-1}$. Because this number still grows exponentially with regard to n, it is necessary to further reduce the set of partitions for evaluation.

2. Within step 1 partitions, we only evaluate those with all clusters having $\geq t$ cells. The number of such partitions is the same as the compositions of n with all summands $\geq t$, which is

$$C_n^{\{t,t+1,\ldots,n\}} = \sum_{k=1}^{\lfloor n/t \rfloor} \binom{n-k(t-1)-1}{k-1}$$

given by Abramson (1976). The growth rate of $C_n^{\{t,t+1,\ldots,n\}}$ with regard to n is smaller, but we still need to reduce it further. For example, $C_n^{\{20,21,\ldots,n\}}$ for n in $\langle$ 20, 40, 60, 80, 100, 120, 140, 160, 180, 200 $\rangle$ are $\langle$ 1, 2, 23, 274, 2695, 24941, 232016, 2184520, 20628613, 194570810 $\rangle$, and the values of 2^n are $\langle$ 1048576, 1099511627776, ..., 1.607×10^{60} $\rangle$.

3. Within step 2 partitions, we only evaluate the ones that could be generated by merging adjacent clusters of a specific step 1 partition $P^s = \{P_1^s, P_2^s, ..., P_k^s\}$. We generate P^s by recursively divide the root HAC tree T until the partitioned subtree has $\leq t-1$ leaves. Thus, $\lceil n/(t-1) \rceil \leq k \leq n$. Let $M(P^s)$ denote the number of step 2 partitions that could be generated by merging adjacent clusters of P^s. The upper bound of $M(P^s)$ is the same as the number of step 2 partitions, which could be reached when $k = n$. The lower bound of $M(P^s)$ is not straightforward, since the merged partitions should have all clusters with $\geq t$ cells.

In order to find a good cell partition P^g in the subset of all possible ones, we iteratively inspect each cluster of P^s and merge it with either its left or right adjacent cluster according to the similarity determined by the two-stage MDL scheme described in Supplementary section 1.2. The procedure has the following steps:

1. Merge P^s clusters in the beginning of the optimal ordering until the merged set contains $\geq t$ cells (line 9 Algorithm 1).

2. Similarly, merge P^s clusters in the end of the optimal ordering until the merged set contains $\geq t$ cells (line 11 Algorithm 1).

3. For every cluster P_i^s in the middle, determine the similarity between P_i^s and the cluster on the left and right, and merge P_i^s with the more similar cluster (line 20 - 26 Algorithm 1). Although the cluster on the left P_{i-1}^s always has $\geq n_{\text{min}}^{\text{cluster}}$ cells, the cluster on the right P_{i+1}^s may have a minimum of one cell, so that the determined similarity between P_i^s and P_{i+1}^s

is sensitive to noise. In order to improve the robustness of similarity comparison, instead of determining the similarity between P_i^s and P_{i+1}^s, we determine the similarity between P_i^s and $P_{\text{rmm}}^s = P_{i+1}^s \cup P_{i+2}^s \cup ... \cup P_{i+m}^s$ (line 20 Algorithm 1), where $|P_{\text{rmm}}^s| \geq n_{\text{min}}^{\text{cluster}}$, $|P_{\text{rmm}}^s| - P_{i+m}^s < n_{\text{min}}^{\text{cluster}}$, and rmm is the shorthand for right minimax.

4. Once $|P_i^s| \geq n_{\text{min}}^{\text{cluster}}$, determine the similarity between P_{i-1}^s and P_i^s, and merge them if their similarity is above certain threshold, otherwise split them (line 32 - 36 Algorithm 1). The code length of merged $X_{\text{list}(P_{i-1}^s \cup P_i^s)}$ is

$$L_m = L(X_{\text{list}(P_{i-1}^s \cup P_i^s)}) \ .$$

The code length of divided $X_{\text{list}(P_{i-1}^s \cup P_i^s)}$ is

$$L_d = L(X_{\text{list}(P_{i-1}^s \cup P_i^s)}, \{P_{i-1}^s, P_i^s\}) \ .$$

If $L_d - L_m \geq -r_{\text{min}}^{\text{mdl}} \text{abs}(L_m)$, merge P_{i-1}^s and P_i^s, otherwise split them. This conditional statement generalizes the situations where L_m is either non-negative or negative.

5. Continue inspecting the next cluster in P^s.

6. After inspecting all middle clusters, P^g is the final updated P^s.

We use a standard HAC tree to perform MIRAC when the number of samples is larger than ten thousand, which usually results in decreased but still acceptable performances (Figure S2 and Figure S3). Although the optimal leaf ordering of the HAC tree is an important assumption, its computation takes too long when the number of samples is large. For example, it takes more than a week to compute the optimal leaf ordering of a dataset with about 68,000 samples. However, the time complexity of computing a good HAC linear ordering could be significantly reduced by implementing other ordering techniques (Aydin *et al.*, 2016).

2.2.2 Analysis of complexity

The time complexity of MIRAC is $O(n^4 + mn^2)$, where $n, m \geq 1$. The time complexity of computing the HAC tree with optimal leaf ordering is $O(n^4)$ (Bar-Joseph *et al.*, 2001). The time complexity

of finding P^g is $O(mn^2)$, which is briefly analyzed as following.

The time complexity is $O(nm)$ for computing the code length $L(X_{n\times m}, P)$. In computing $L(X_{n\times m}, P)$, we compute the code lengths of each cluster and their labels. Since it takes $O(n)$ time to compute the code length of n observations with a single feature, computing the code length of all clusters and features individually takes $O(nm)$ time, and computing the code length of n labels take $O(n)$ time.

Similarly, the time complexity is $O(n_1m+n_2m)$ for computing the code length of $X_{n_1\times m}$ encoded by a model fitted with $X_{n_2\times m}$. Fitting a model on $X_{n_2\times m}$ takes $O(n_2m)$ amount of time. Using the model to encode $X_{n_1\times m}$ takes $O(n_1m)$ amount of time.

The time complexity of searching for P^g is $O(mn^2)$. In the worst case scenario, $|P^s| = n$, and the inspecting cluster is always merged with the left hand side cluster in step 4. However, the impact of $n_{\text{min}}^{\text{cluster}}$ and step 3 on the time complexity is not straight forward, so we divide step 3 code length computation into three parts and analyze the upper bound of them individually. The divided three parts are the left cluster, inspecting cluster, and right minimax cluster. Because we keep increasing the size of the left cluster, the upper bound of computing the left cluster code length throughout the execution is $O(mn^2)$. The maximum size of the inspecting cluster is $n_{\text{min}}^{\text{cluster}} - 1$, so the upper bound of computing the inspecting cluster code length is also $O(mn^2)$, when every middle singleton is evaluated $n_{\text{min}}^{\text{cluster}} - 1$ times before merging with the left. The maximum size of the right minimax cluster is $2n_{\text{min}}^{\text{cluster}} - 1$,so the upper bound of evaluating right minimax cluster is also $O(mn^2)$, when every increment of the left cluster takes $n_{\text{min}}^{\text{cluster}}$ times of evaluating right minimax cluster. Summarizing these three parts, the overall upper bound is $O(mn^2)$.

The space complexity of MIRAC is $O(nm + n^2)$, which could be decomposed into the following three parts. The space complexity of storing the $n \times m$ data matrix X is $O(nm)$. The space complexity of storing the HAC tree with optimal leaf ordering is $O(n)$. The space complexity of storing the pairwise distance matrix is $O(n^2)$.

2.3 Cluster separating genes identification

We use XGBoost (Chen and Guestrin, 2016), a scalable and sparsity-aware boosted tree system, to identify genes that are able to separate a specific set of clusters. This method is designed for data exploration after applying any one of a number of various statistical approaches that have been

developed to identify differentially expressed genes (Vallejos *et al.*, 2016, 2015; Kharchenko *et al.*, 2014; Qiu *et al.*, 2017; Korthauer *et al.*, 2016; Soneson and Robinson, 2018), in order to quickly identify genes or sets of genes that are able to separate an arbitrary set of clusters for further inspection.

Rather than providing a meticulous p-value for each gene among the compared clusters, we rank the genes by their importances on separating the clusters under comparison. The importance of a gene in the trained classifier is the number of times it has been used as a inner node of the decision trees. We use cross validation to train an XGBoost classifier on the compared clusters, and the classifier is essentially a bag of decision trees (Chen and Guestrin, 2016). In order to alleviate the influences of stochasticity on interpretation, we use bootstrap with feature shuffling to better estimate the importances of genes in separating the compared clusters. The obtained list of important genes could be further explored by inspecting transcription level fold changes and decision tree structures.

Comparing to NSForest (Aevermann *et al.*, 2018), a method based on random forest (Breiman, 2001; Pedregosa *et al.*, 2011) to identify a parsimonious set of cluster separating genes from scRNA-seq data, our method identifies all possible cluster separating genes using gradient boosting. Practically, NSForest version 1.3 is distributed on GitHub as a Python script without encapsulation or testing (checked on Oct 11, 2018), but our method is distributed through the Python Package Index, comprehensively tested, and easy to use through the user friendly API. With regard to scalability, our method uses a scalable implementation of gradient boosting algorithm (Chen and Guestrin, 2016), whereas NSForest uses the implementation of random forest in scikit-learn (Pedregosa *et al.*, 2011).

2.4 K-nearest neighbor methods

We developed two methods based on the KNN algorithm to facilitate the exploration of scRNA-seq datasets. With relative large number of cells profiled in each scRNA-seq experiment, we assume that each one of the non-rare cells is similar to at least k other cells in their transcriptomic profiles. With this assumption, we detect rare transcriptomic profiles and impute gene dropouts.

2.4.1 Detect rare transcriptomic profiles

We mark transcriptomic profiles as rare if they are distinct from their k-nearest neighbors, according to the pairwise similarity between cells (Algorithm S2). The algorithm could take multiple iterations, so that the most distinct transcriptomic profiles could be marked at first and less distinct ones in the following iterations.

This method is provided mainly to facilitate detailed inspection of rare transcriptomic profiles rather than removing outliers from the data. Because rare transcriptomic profiles may have various biological and technical causes, samples and features in a dataset should only be removed after extensive exploratory data analysis and rigorous reasoning with domain specific knowledge. Closely comparing rare transcriptomic profiles with their nearest neighbors may also yield insights into their biological differences, which may further facilitate the identification of rare cell types and states.

2.4.2 Impute gene dropouts

In an scRNA-seq experiment, if a truly expressed gene is not detected in a cell, the gene is considered a 'dropout', and such events are called gene dropouts (Kharchenko *et al.*, 2014). Gene dropouts may be caused by biological and technical reasons (Kharchenko *et al.*, 2014; Risso *et al.*, 2018; Pierson and Yau, 2015; Zappia *et al.*, 2017). The rationale behind the possible causes of biological dropouts mainly involves transcriptional bursting (Suter *et al.*, 2011; Tantale *et al.*, 2016) and RNA degradation. With regard to technical dropouts, the main concerns are the relatively small number of RNA transcripts of a gene, amplification efficiency, and batch effect (Zappia *et al.*, 2017).

We exploit the transcriptomic profiles of the k-nearest neighbors of a cell to impute the gene dropouts in the cell (Algorithm S1). The algorithm could take multiple iterations, so that the dropped-out genes that are expressed in all k-nearest neighbors could be imputed at first, and the ones that are expressed in most but not all of k-nearest neighbors could be imputed in the following iterations.

2.5 Benchmark

We benchmarked the clustering and KNN performances of `scedar` on simulated and experimental scRNA-seq datasets. We obtained previously published experimental scRNA-seq datasets (Table 1).

We also generated 50 simulated scRNA-seq read count datasets with Splatter (Zappia *et al.*, 2017). The simulation parameters are estimated by Splatter according to a Drop-seq dataset (Macosko *et al.*, 2015) and a 10x Genomics GemCode dataset (Zheng *et al.*, 2017). Within each simulated dataset, the cells have 8 clusters taking approximately the following proportions: $\langle$ 0.3, 0.2, 0.15, 0.15, 0.05, 0.05, 0.05, 0.05 $\rangle$, with a gene dropout rate around 5%.

We performed all benchmark analyses on a high-performance computing cluster, of which the computing resources are strictly managed by Univa Grid Engine. The cluster nodes have CPUs of Intel Xeon E5-2680 v3 or Intel Xeon E7-8880 v3. The memory sizes are either 128GB, 256GB, or 1TB. When scheduling analytical jobs for benchmarking, we make sure that the number of cores and allocated memory are enough for the program.

2.5.1 Clustering

The clustering accuracy and stability of MIRAC were benchmarked together with several other clustering methods on experimental scRNA-seq datasets listed in Table 1.

The following clustering methods are directly applied on the original data without preprocessing.

- MIRAC on 2D t-SNE projection.
- Single-cell consensus clustering (SC3) version 1.7.7 (Kiselev *et al.*, 2017). SC3 is selected for comparison because it was extensively compared with other methods on different experimental datasets.
- K-means clustering on 2D t-SNE projection.
- Hierarchical agglomerative clustering on 2D t-SNE projection.
- Density-based spatial clustering of applications with noise (DBSCAN) (Ester *et al.*, 1996) on 2D t-SNE projection.

Although MIRAC could be directly applied on the expression matrix, dimensionality reduction is able to improve the performance of similarity and density based clustering methods when the number of features is high (Aggarwal *et al.*, 2001). The mathematical influences of the high number of features are briefly described in Supplementary section 1.3.

Among many dimensionality reduction methods, we chose t-SNE for demonstration in this report in order to visualize the clustering results more clearly. Although t-SNE projections are stochastic and influenced by the perplexity parameter, t-SNE has been extensively used as dimensionality reduction method for scRNA-seq data (Macosko *et al.*, 2015; Cao *et al.*, 2017; Manno *et al.*, 2018). `Scedar` also supports the use of PCA and UMAP for MIRAC clustering, which can be applied just as easily as the t-SNE method.

When benchmarking for accuracy, we cluster the cells in each experimental dataset using the compared clustering methods with a grid of parameters. The maximum similarities between the clustering results and the cell types from the publications are used to compare the accuracy of different clustering methods. Although taking the maximum increases the chance of overfitting, it resembles the procedure of clustering analysis in practice.

Similarly, when benchmarking for stability, we cluster the cells in each experimental dataset using the compared methods with the same parameters but ten different random states. The similarity of clustering results between different random states are used to compare the stability of different clustering methods.

2.5.2 Cluster similarity metrics

We use two cluster similarity metrics, cluster consistent ratio (CCR) and adjusted Rand index (ARI) (Hubert and Arabie, 1985) for measuring the accuracy and stability of clustering methods respectively. When we have a coarse reference partition P_r and a finer clustering partition P_c, the CCR is computed as the ratio of pairs within each cluster of P_c that are also in the same cluster of P_r, with the number of clusters kept the same across compared methods. The ARI is computed with the Python package `scikit-learn` (Pedregosa *et al.*, 2011) using the mathematical formula given by Hubert and Arabie (1985).

The reference partitions P_r of real datasets are obtained from their original publications (Supplementary Table S1). The clusters in Deng *et al.* (2014) is experimentally determined by manual single cell isolation. The clusters in Pollen *et al.* (2014) is experimentally determined by the cell line or tissue type of the isolated single cells. The clusters in Kolodziejczyk *et al.* (2015) are determined by the embryonic stem cell culturing conditions and batches. The clusters in Zeisel *et al.* (2015) are determined by the BackSPIN clustering method (Zeisel *et al.*, 2015) and further inspected with

domain specific knowledge.

We choose CCR to measure clustering accuracy rather than ARI, because ARI greatly penalizes the split of a large cluster in P_r into multiple smaller ones in P_c. This behavior of ARI could prevent the evaluation of transcriptomic variabilities within a large group of cells in clustering analysis, which is an important goal of scRNA-seq experiments that cannot be easily achieved by bulk RNA-seq experiments. In addition, we also provide a method in `scedar` to easily merge multiple clusters together, in case the users found the sub-types of a cell type are very similar to each other.

However, we used ARI to measure clustering stability rather than CCR, because the differences between P_r and P_c are completely caused by different random states, hence splitting a cluster in P_r should be penalized.

MDL is not used as a cluster similarity metric, even though MDL is used in MIRAC to guide the process of finding good partitions. MDL is only used to guide and regularize the merging process of local adjacent sub-clusters by evaluating their similarity, but it is not used as an objective to be optimized globally. Using MDL as a benchmarking metric would introduce a bias as among the various methods, MIRAC is the only method using MDL. Moreover, interpreting relative global MDL differences is not straightforward as it is not only affected by cluster labels, but also transcription levels.

2.5.3 Detection of rare transcriptomic profiles

We visualize real datasets before and after removing rare transcriptomic profiles in t-SNE projection and pairwise distance heatmaps, without quantitative evaluations like receiver operating characteristic (ROC) curve, since rare transcriptomic profiles are not well defined with a large number of genes (Aggarwal and Yu, 2001; Aggarwal *et al.*, 2001). Approaches to identify rare data points in low-dimensional spaces (≤ 3) do not scale well to higher dimensions due to the exponentially decreased density of data points in the space and increased instability of distances, which is elaborated in Supplementary section 1.3.

It is important to note that rare transcriptomic profiles are detected to facilitate detailed inspection rather than the removal of them from the data. The visualizations are only used to illustrate the capability of the KNN method for detecting rare transcriptomic profiles.

2.5.4 Gene dropout imputation

We simulate gene dropouts using Splatter (Zappia *et al.*, 2017) to obtain a dropout rate around 5%. Then, we benchmark the performance of imputing gene dropout as two parts, detection and smoothing. On simulated data, because the true gene dropouts are known, we use ROC curve and mean squared errors (MSEs) to characterize the performance of gene dropout detection and smoothing respectively. On real data, we visualize the cells in 2D t-SNE space before and after imputation. The compared methods are KNN gene dropout imputation (KNNGDI) version 0.1.5, SAVER version 1.0.0 (Huang *et al.*, 2018), MAGIC version 1.1.0 (van Dijk *et al.*, 2018), and scImpute version 0.0.6 (Li and Li, 2018).

2.6 Data availability

The real datasets can be obtained from `https://hemberg-lab.github.io/scRNA.seq.datasets/` and `https://support.10xgenomics.com/single-cell-gene-expression/datasets`. The simulated datasets can be generated using scripts at `https://github.com/logstar/scedar/tree/master/docs/r_scripts`.

3 Results

3.1 Basic workflow of `scedar`

We illustrate the basic workflow of using `scedar` for scRNA-seq exploratory data analysis with the dataset published by Zeisel *et al.* (2015) (Figure 1). The dataset contains the RNA unique molecule identifier (UMI) counts of 19,972 genes in 3005 cells from mouse brain. We selected this dataset for demonstration because it could be clearly visualized in small graphs, although our package is capable of analyzing much larger datasets (Figure S2 and S3).

In Figure 1, each box represents a data analysis step, and they are consecutively executed according to the arrow. The purpose and runtime are listed in the upper ribbon. The code that are essential to the step is listed in the box, and their results are also shown.

The preparation step imports required packages and loads the data. The class SampleDistanceMatrix is one of the core data structures in the package that is used to store the read counts and

pairwise distances of an scRNA-seq dataset. Because the pairwise distance computation is delayed until necessary, i.e. lazily loaded, this step only takes 12 seconds. We use cosine distance rather than correlation distance to greatly speed up the computation, since we implemented the computation procedure of pairwise cosine distances completely with numpy linear algebra operations implemented with OpenBLAS in the C programming language.

The t-SNE scatter plot and KNN graph are used to explore the dataset. The cell type labels published by Zeisel *et al.* (2015) are truncated to fit in the space. We also provide methods to visualize arbitrary statistics, e.g. number of expressed genes, of individual cells as color gradient. The layouts of cells in t-SNE and KNN graph are similar to each other. Although KNN graph is faster than t-SNE, the runtime for t-SNE could be greatly reduced by optimizing its parameter or computation procedure (Linderman *et al.*, 2017).

The MIRAC step clusters the cells and visualizes them with t-SNE scatter plot and pairwise distance matrix heatmap. The heatmap generation procedure in `scedar` is optimized for large-scale datasets, which is able to generate a heatmap with tens of thousands of columns and rows in a few minutes. Users could also generate heatmaps for the read count matrix to directly inspect the sparsity of datasets (Figure S2B and S3B).

The last step identifies cluster separating genes with XGBoost (Chen and Guestrin, 2016). Users could choose an arbitrary set of clusters to compare, and the genes are each ranked by their importance in separating the clusters. Then, the read counts of a gene across clustered labels could easily be visualized by t-SNE scatter plot.

3.2 Performance of MIRAC clustering

We benchmarked several clustering methods on the datasets listed in Table 1 (Figure 2). Each dataset is clustered multiple times with each clustering method to obtain different numbers of clusters (Table S1).

The t-SNE based clustering methods are faster than SC3 (Figure 2A). Also, the t-SNE based clustering methods have similar runtimes with their lines overlapping in the Figure 2A, since the time limiting step is the computation of t-SNE projection.

The CCRs of t-SNE based clustering methods are comparable to SC3. The CCRs of Zheng *et al.* (2017) and Macosko *et al.* (2015) datasets are not included in Figure 2B, since the SC3 cluster

labels are `NA`s in all 10 runs with different number of clusters. However, the representative MIRAC clustering results of Zheng *et al.* (2017) and Macosko *et al.* (2015) datasets are visualized with t-SNE scatter plot and pairwise distance matrix heatmap (Figure S2 and S3). For smaller datasets, the representative MIRAC results are shown in Figure S4. Although t-SNE projections obtained with different random states are distinct from each other, the consistency of clustering results is comparable to SC3 (Figure S1).

3.3 Performance of imputing gene dropouts

We benchmarked several gene dropout imputation methods on the simulated 10x Genomics (Figure 3) and Drop-seq (Figure S5) datasets. KNNGDI is faster than other compared methods (Figure 3A).

The performance of KNNGDI on detecting gene dropouts is comparable to SAVER and better than scImpute and MAGIC. The ROC curve of scImpute sharply turns around TPR = 0.25 (Figure 3B and S5B) because its threshold parameters, determining whether a zero entry is a dropout or not, are not sensitive enough to achieve any higher TPRs. Although the AUCs of KNNGDI and SAVER are higher than scImpute and MAGIC, they all have comparable performances when FPRs are lower than 0.05 (Figure 3B), except that MAGIC has worse performance on the simulated Drop-seq datasets that have higher sparsity than the Zeisel *et al.* (2015) dataset (Figure S5B).

The MSEs of KNNGDI on correcting gene dropouts are comparable to SAVER and smaller than scImpute and MAGIC (Figure S5C and S5D). However, these methods all have MSEs many times higher than the MSEs of the observed counts to the true counts, which implies that these methods all introduced many times more reads than the true dropout reads.

None of the compared gene dropout imputation methods greatly improved the separation of different cell types (Figure 3C, S2E, and S3E) in the t-SNE projection of the large, shallow and high dropout rate experimental datasets. On the other hand, the small datasets with higher depth and relatively lower dropout rate do not need gene dropout imputations for cell type separation (Figure S4). Notably, MAGIC incorrectly mixed mural and endothelial cells in the Zeisel *et al.* (2015) dataset (Figure 3C).

3.4 Performance of detecting rare transcriptomic profiles

We detected rare transcriptomic profiles in datasets listed in Table 1 with the KNN method (Figure 4, S4, S2, and S3). Although the detection method has many limitations, rare transcriptomic profiles tend to be points on the t-SNE scatter plots either far away from the majority of their same types or along the edges of a group of agglomerated points. On the pairwise distance matrix heatmap, rare transcriptomic profiles tend to be small chunks that are distinct from their neighbors, and the heatmap becomes smoother after removing the rare transcriptomic profiles. The detected rare transcriptomic profiles could be further inspected as potential rare cell types and states by comparing with their nearest neighbors.

3.5 Identification of cluster separating genes

We used `scedar` to identify the genes distinguishing the MIRAC cluster 1, 15, and 22 of the Zeisel *et al.* (2015) dataset (Figure 5 and Table S2). In the original publication, the upper to lower MIRAC clusters 22, 1, and 15 in the t-SNE scatter plot are assigned to microglia, endothelial cells, and astrocytes respectively (Figure 3C). We choose these three clusters to inspect one of the discrepancies between cell types and MIRAC clustering results, where the small isolated upper part of the MIRAC cluster 15 is assigned to microglia instead of endothelial cells in the original publication.

The smaller upper isolated part of MIRAC cluster 15 might be a distinct cell sub-type of microglia. Although it expresses a microglia marker gene C1qb (Figure 5B) (Beutner *et al.*, 2013), it does not express Mrc1 or Apoe in the same pattern as the MIRAC cluster 22 (Figure 5B and 5C). According the transcription levels of the cluster separating genes (Figure 5C), the smaller upper isolated part of MIRAC cluster 15, which is located at the top of the cluster 15 rows, has some genes expressed in the same pattern as the microglia, but it also has some other genes expressed distinctly from the microglia.

4 Discussion

Comprehensive profiling of the transcriptomes of individual cells within an organism or tissue by scRNA-seq is able to facilitate the systematic study of physiological or pathological states (Regev

et al., 2017; Baslan and Hicks, 2017; Cao *et al.*, 2017). Previous scRNA-seq experiments identified novel cell types or states (Villani *et al.*, 2017), obtained insights into the regulation of differentiation process (Cao *et al.*, 2017; Rizvi *et al.*, 2017), and inferred molecular mechanisms of tissue functions (Zeisel *et al.*, 2015; Haber *et al.*, 2017; Lake *et al.*, 2018).

The biological results of scRNA-seq experiments are obtained from extensive data analyses, which could take more time than doing the experiments. As the size of scRNA-seq datasets increases rapidly (Svensson *et al.*, 2018; Rozenblatt-Rosen *et al.*, 2017), computational methods also need to be scalable by exploiting hardware and software techniques for big data analytics, in order to complete an analysis within a reasonable amount of time.

`Scedar` is able to facilitate gene dropout imputation, rare transcriptomic profile detection, clustering, and identification of cluster separating genes for scRNA-seq data by exploiting scalable system design patterns and high-performance computing architectures. We parallelized time-consuming computational procedures by multi-processing without excessive copies of shared data in memory. We also decompose the whole analytical procedure into multiple steps, so that certain steps could be specifically optimized without repeating others. In addition, intermediate results, such as pairwise distances and t-SNE projections, are lazy loaded and cached in a unified data structure to speed up analytical routines, prevent repeated computations, and alleviate the burden on users to keep track of all intermediate results.

Comparing to other computational tools that were developed or updated for large scale scRNA-seq data analysis, like `PAGODA2` (Fan *et al.*, 2016), `Seurat v2.0` (Butler *et al.*, 2018), and `SCANPY` (Wolf *et al.*, 2018), `scedar` distinguishes itself with an additional research focus on developing new analytical methods based on machine learning. In `scedar`, we adapted KNN, a typical machine learning algorithm, to impute gene dropouts and detect rare transcriptomic profiles. MDL principle, an important concept in computational learning, is applied to cluster single cells (Hansen and Yu, 2001). A scalable and sparsity-aware gradient boosted tree system XGBoost (Chen and Guestrin, 2016), which implements a typical machine learning algorithm, is used to identify genes that are able to distinguish different clusters. In addition, these machine learning methods are able to exploit modern high-performance computing architecture, which improves the scalability of the package.

In `scedar`, we developed a clustering algorithm, MIRAC, for scRNA-seq data. MIRAC clusters observations in three steps: 1) build a tree by hierarchical clustering, 2) divide the tree into sub-

trees, and 3) merge similar sub-trees into individual clusters. This clustering strategy adapts the basic ideas of BIRCH (Zhang *et al.*, 1996) and BackSPIN (Zeisel *et al.*, 2015). Instead of building a balanced tree structure, like the clustering feature tree in BIRCH for further partitioning, MIRAC divides the tree structure built by hierarchical clustering optionally in a balanced manner (Figure S6 and Supplementary Method section 1.4), which simplifies the clustering procedure. In BackSPIN, a sorted pairwise correlation matrix is recursively bi-partitioned into clusters according a criteria based on the normalized sums of correlation coefficients. In contrast, MIRAC iteratively merges the relatively small sub-clusters according a criteria based on the MDL principle, which increases the robustness for determining whether two groups of observations should be put in the same cluster or not. Especially, when the number of observations is large within a group, finding an optimal bi-partition is not straightforward, since there may be multiple distinct sub-groups. Although the performance of MIRAC under certain metrics is comparable to other clustering algorithms, it is able to provide distinct clusters that are sensitive to local structures, which could be used as alternative perspectives to interpret the source of heterogeneity within the dataset.

There are still many possible improvements on `scedar`. To improve the scalability of MIRAC, we could provide more efficient methods to obtain the optimal leaf ordering using linear embedding techniques (Aydin *et al.*, 2016). To improve the scalability of the backend data structure, we could extend it with distributed analytic systems such as Apache Spark (Zaharia *et al.*, 2016). To improve the scalability of KNN methods, we could also provide implementations with approximate nearest neighbor methods (Andoni and Indyk, 2006; Kushilevitz *et al.*, 2000). To visualize the differences between different clusters, we could plot the fold changes of gene transcription levels on the pathway maps in the KEGG (Kyoto Encyclopedia of Genes and Genomes) database (Kanehisa and Goto, 2000).

5 Conclusion

`Scedar` is an efficient and extensible Python-based platform for large-scale scRNA-seq exploratory data analysis, which will facilitate biological interpretations in specific domains. The package provides a straightforward user interface to perform gene dropout imputation, rare transcriptomic profile detection, clustering analysis, and visualization. In addition, the modular design and compre-

hensive tests of `scedar` facilitate customization for specific use cases, extensibility for incorporating analytical procedures, and for future refactoring to further improve scalability.

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8 Algorithms

input : X, a numeric data matrix of size $n \times m$
$n_{\text{min}}^{\text{cluster}}$, minimum number of rows for a cluster
$r_{\text{min}}^{\text{mdl}}$, minimum ratio of MDL reduction for increasing the number of cluster
output: Clusters of n rows a list of n $\langle$row index, cluster index$\rangle$ pairs

```
// Phase 1:  divide n rows into sub-clusters
// build HAC tree with linear optimal leaf ordering
hacTree ← HAClinearOptLeafOrd(X)
// divide the tree leaves into sub-clusters with less than n_min^cluster rows
subClusters ← DivideHACTree (hacTree, n_min^cluster)
// Phase 2:  iteratively merge sub-clusters into clusters
// Merge beginning and end sub-clusters to form two minimum sub-clusters
// with more than n_min^cluster rows
MergeSubCls (subClusters, start = 1, minSize =n_min^cluster)
n_sub-clusters ← Length (subClusters)
MergeSubCls (subClusters, start =n_sub-clusters, step = −1, minSize =n_min^cluster)
i ← 2
while i ≤ n_sub-clusters do
    left ← subClusters [i − 1]
    this ← subClusters [i]
    // merge this with left or right until this has ≥ n_min^cluster rows
    while Length (this) < n_min^cluster and i + 1 ≤ n_sub-clusters do
        right ← subClusters [i + 1]
        // minimum merged sub-cluster with ≥ n_min^cluster rows starting from i + 1
        rightMM ← MergeSubCls (subClusters, start = i + 1, minSize =n_min^cluster, inPlace =false)
        if EncodeMDL (left, this) < EncodeMDL (rightMM, this) then // merge left and this
            left ← MergeSubCls (subClusters, selected = [i − 1, i])
            this ← right
        else // merge this and right
            this ← MergeSubCls (subClusters, selected = [i, i + 1])
        end
    end
    // decide whether merge left and this or not
    merged ← Concatenate (left, this)
    mergedMDL ← MDL (merged)
    splitMDL ← MDL (left) + MDL (this) + SplitOverheadMDL (left, this)
    if splitMDL < MaxSplitMDL (mergedMDL, r_min^mdl) then // split
        i ← i + 1
    else // merge
        MergeSubCls (subClusters, selected = [i − 1, i])
    end
end
return subClusters
```

Algorithm 1: Minimum description length iteratively regulated agglomerative clustering

9 Figures

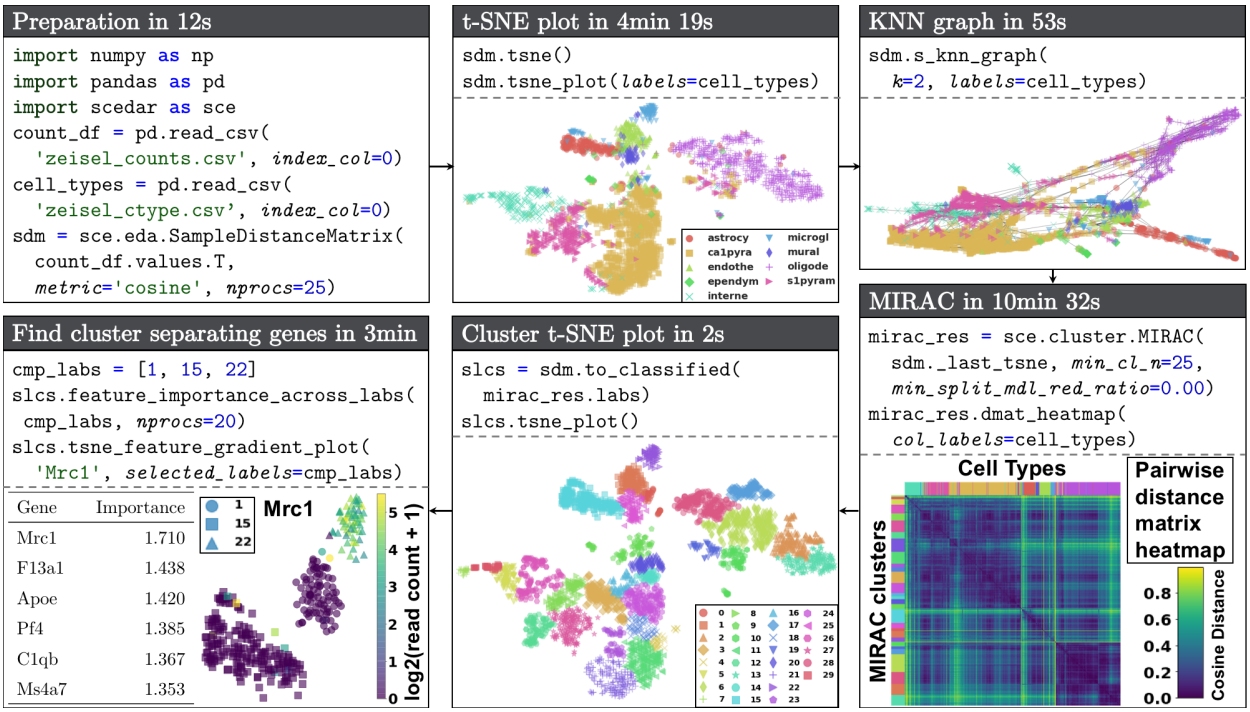

Figure 1: Demo of `scedar`. Workflow of using `scedar` to analyze an scRNA-seq dataset with 3005 mouse brain cells and 19,972 genes generated using the STRT-Seq UMI protocol by Zeisel *et al.* (2015). Procedures and parameters that are not directly related to data analysis are omitted. The full version of the demo is available at `https://github.com/logstar/scedar/tree/master/docs/notebooks`.

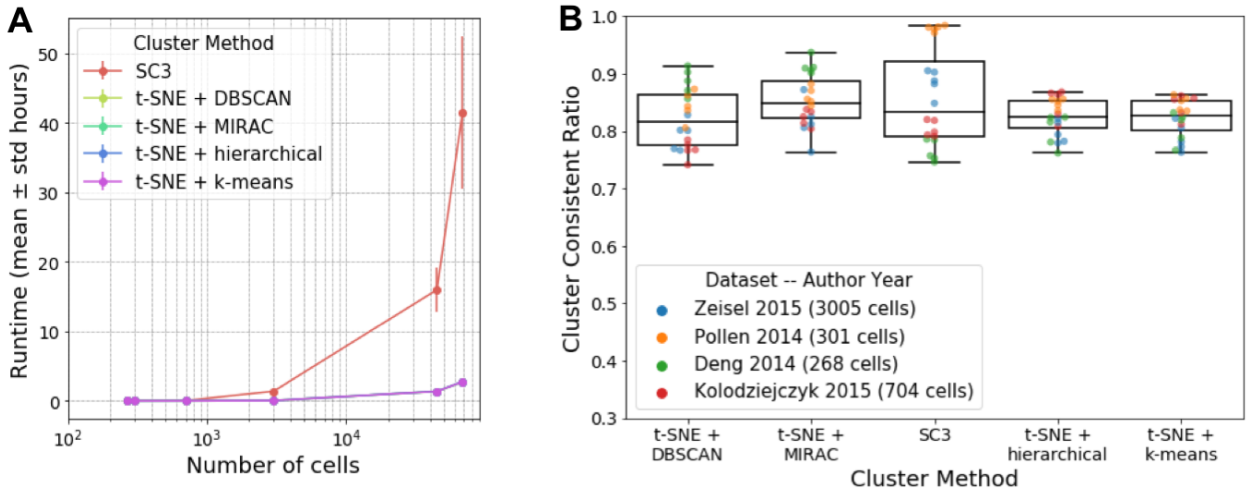

Figure 2: Clustering method benchmarks on experimental datasets. A) Runtimes. B) CCRs on different datasets, with different points of each dataset representing different numbers of clusters. For each dataset, the numbers of clusters are the same across all compared clustering methods.

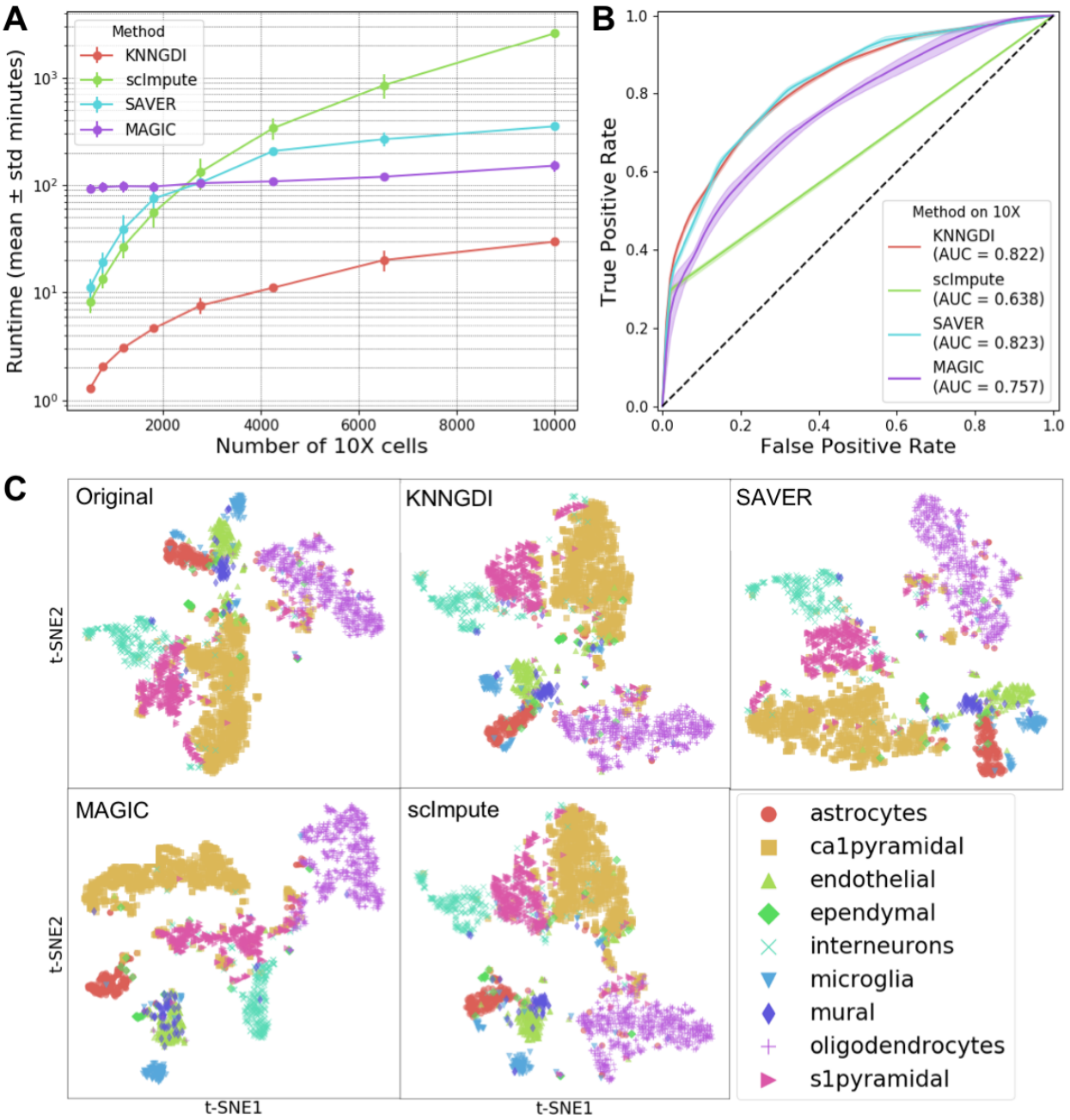

Figure 3: Gene dropout imputation method benchmarks. A) Runtimes on 40 simulated 10x Genomics datasets. B) ROC curves (± standard deviation) of dropout detection on the simulated 10x Genomics datasets. C) t-SNE scatter plots of the Zeisel *et al.* (2015) dataset after gene dropout imputations.

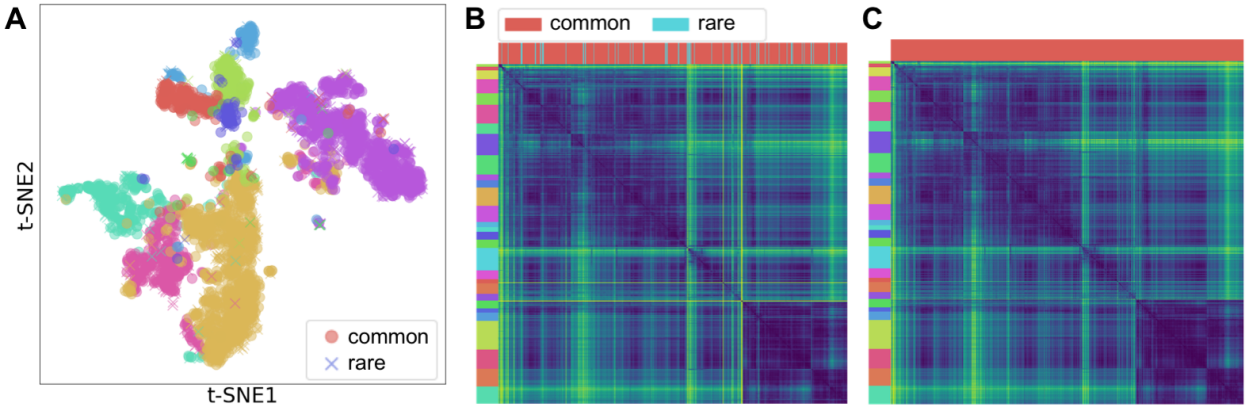

Figure 4: KNN rare transcriptomic profile detection on the Zeisel *et al.* (2015) dataset. A) t-SNE scatter plot with colors labeling cell types and markers labeling common or rare transcriptomic profiles. 9.3% cells are marked as rare. B) Pairwise cosine distance heatmap with left strip as MIRAC labels and upper strip as common or rare transcriptomic profiles labels. C) Pairwise cosine distance heatmap with rare transcriptomic profiles removed.

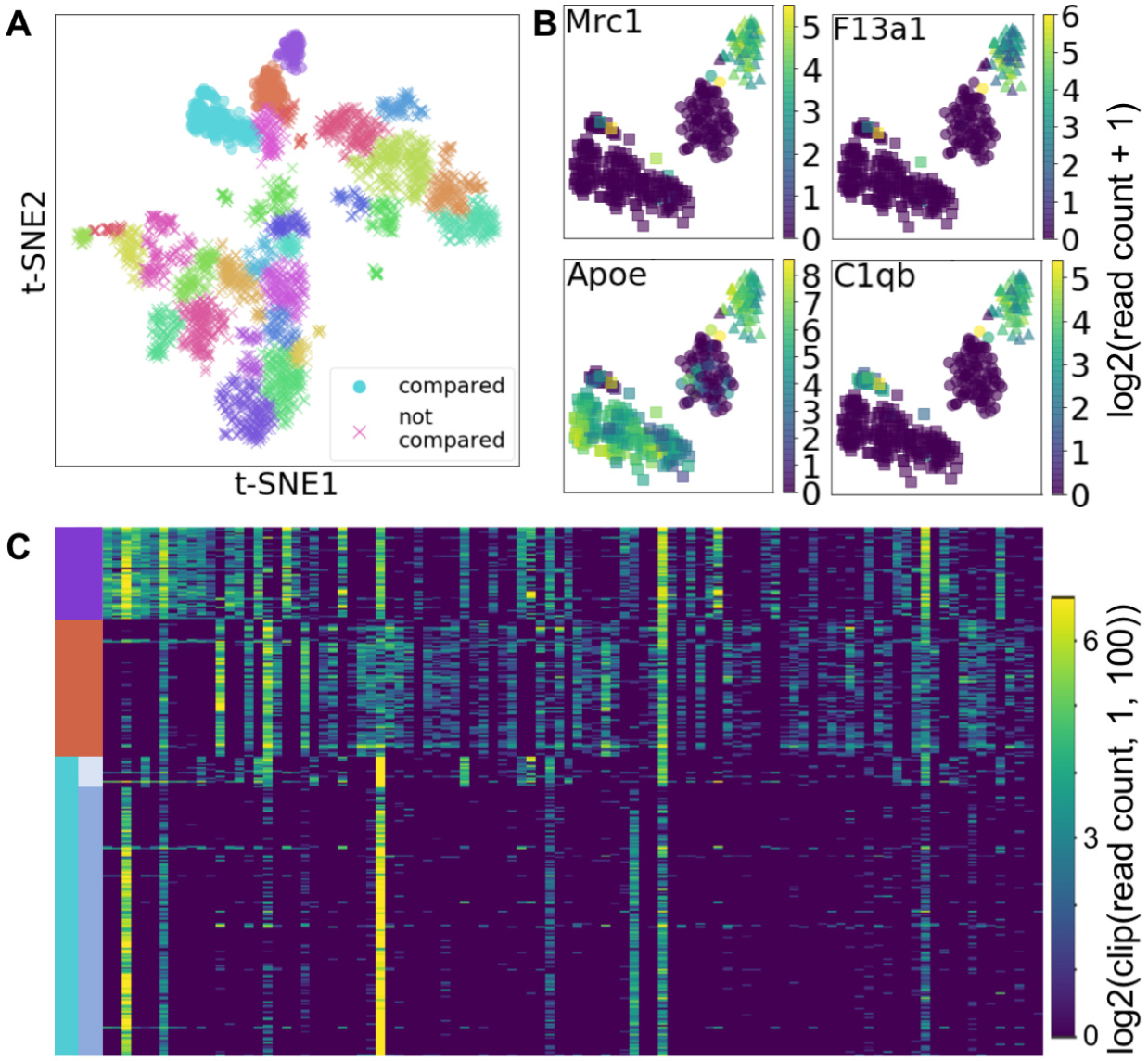

Figure 5: Identified genes separating the MIRAC clusters 1, 15, and 22 of the Zeisel *et al.* (2015) dataset. A) t-SNE scatter plot with color as MIRAC cluster labels and marker shape as compared or not compared. B) t-SNE scatter plots of the compared clusters with color as $\log_2(\text{read count} + 1)$ of the corresponding gene and marker shape as MIRAC clusters. C) Transcription level heatmap of the top 100 important cluster separating genes in the compared cells, with rows as cells ordered by cluster labels and columns as genes ordered by importances. The color gradient is $\log_2(\text{clip}(\text{read count}, 1, 100))$, where the $\text{clip}(\text{read count}, 1, 100)$ function changes any read count below 1 to 1 and above 100 to 100, in order to better compare genes at different transcription levels.

Table 1: Real scRNA-seq datasets for benchmark

Publication	# cells	# genes	Organism	Tissue	Protocol	Raw Data Type
Deng *et al.* (2014)	268	22,431	Mus musculus	embryo	Smart-Seq / Smart-Seq2	read count
Pollen *et al.* (2014)	301	23,730	Homo sapiens	dermal, blood, pluripotent, and neural	SMARTer	TPM
Kolodziejczyk *et al.* (2015)	704	38,653	Mus musculus	Embryonic stem cell	SMARTer	read count
Zeisel *et al.* (2015)	3005	19,972	Mus musculus	brain	STRT-Seq UMI	read count
Macosko *et al.* (2015)	44,808	23,288	Mus musculus	retina	Drop-seq	read count
Zheng *et al.* (2017)	68,579	33,694	Homo sapiens	peripheral blood mononuclear cell	GemCode	read count

Source: `https://hemberg-lab.github.io/scRNA.seq.datasets/`. TPM represents Transcripts Per Million in the raw data type column.

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