

Visualising How Non-linear Dimension Reduction Warps Your Data

Jayani P.G. Lakshika

Econometrics & Business Statistics, Monash University
and

Dianne Cook

Econometrics & Business Statistics, Monash University
and

Paul Harrison

MGBP, BDInstitute, Monash University
and

Michael Lydeamore

Econometrics & Business Statistics, Monash University
and

Thiyanga S. Talagala

Statistics, University of Sri Jayewardenepura

January 23, 2024

Abstract

Non-Linear Dimension Reduction (NLDR) techniques have emerged as powerful tools to visualize high-dimensional data. However, their complexity and parameter choices may lead to distrustful or misleading results. To address this challenge, we propose a novel approach that combines the tour technique with a low-dimensional manifold generated using NLDR techniques, hexagonal binning, and triangulation. This integration enables a clear examination of the low-dimensional representation in the original high-dimensional space. Our approach not only preserves the advantages of both tours and NLDR but also offers a more intuitive perception of complex data structures and facilitates accurate data transformation assessments. The method and example data sets are available in the **quollr** R package.

Keywords: high-dimensional data, dimension reduction, triangulation, hexagonal binning, low-dimensional manifold, manifold learning, tour, data vizualization

1 Introduction

High-dimensional (high-D) data is prevalent across various fields, such as ecology and bioinformatics (Guo et al. 2023), due to advancements in data collection technologies (Johnstone & Titterton 2009, Ayesha et al. 2020). However, visualization of high-D data introduces significant challenges, because the complexity of visualizing data beyond two dimensions (Jia et al. 2022). In recent years, interactive and dynamic graphics systems like **liminal** (Lee et al. 2020) —which employs interactive tools like brushing and linking (Wickham et al. 2015)—and software tools such as **XGobi**, **GGobi** (Swayne et al. 1998), **tourr** (Wickham et al. 2011), **detourr** (Hart & Wang 2022), and **langevitour** (Paul Harrison 2022), involving dynamic methods like tours (Asimov 1985), have played a key role in visualizing high-D data (data-vis).

To create low-dimensional representations (typically in 2D) (m-vis) (Buja et al. 1996) of high-D data, it is common to apply dimension reduction (DR) techniques. Approaches for DR involve linear methods such as principal component analysis (PCA) (F.R.S. 1901), non-linear methods such as multi-dimensional scaling (MDS) (Torgerson 1967). In the past decade, many new non-linear dimension reduction (NLDR) techniques have emerged, such as t-distributed stochastic neighbor embedding (tSNE) (van der Maaten & Hinton 2008) and uniform manifold approximation and projection (UMAP) (McInnes & Healy 2018), designed to capture the complex and non-linear relationships present within high-D data (Johnstone & Titterton 2009). NLDR techniques are the 2D models of high-D data in our context.

It is important to visualize various Non-Linear Dimensionality Reduction (NLDR) techniques for the same high-D data in order to understand and find the best representation. After doing so, the 2D models may differ considerably from each other and may also deviate from the original data structure in high-dimensional space. Therefore, visualizing the 2D model in high-D space (m-in-ds) is more useful to answer different types of questions:

- Is there a best 2D representation of high-D data or are they all providing equivalent information? Is there a best parameter choice to fit the 2D model? How does the model change when its parameters change?
- How well does the 2D model capture the data structure? Is the model fitting able to capture different data structure like non-linear, clustering?

If we cannot easily ask and answer these questions, our ability to understand the models is limited. To find the best 2D model and parameter choices, a better understanding of the underlying science is important.

Also, the importance of m-vis along with data-vis has been recognized and incorporated into interactive software, **liminal** (Lee et al. 2020). But the 2D model and high-D visualize side by side and interactive like brushing and linking connect the data in the two panels. To address this challenge, we propose a novel approach by combining the tour technique with a low-dimensional manifold. This manifold is created through the synergistic use of NLDR techniques, hexagonal binning, and triangulation. This integration facilitates a more understanding of the data structure, how well (or how poorly) NLDR techniques perform.

The outline of this paper is as follows. The Section 2 provides an detailed overview of dimension reduction methods, and tours. Building upon this foundation, the Section 3 delves into the proposed algorithm, its implementation details, how to tune the model, model summaries, and a synthetic example to illustrate the functionality of the algorithm. Subsequently, Section 4 showcases applications of the algorithm on different data sets, particularly in single-cell RNA-seq data. These applications reveal insights into the performance and trustworthiness of NLDR algorithms. We analyze the results to identify situations where NLDR techniques may lead to misleading interpretations. Finally, **conclusions** concludes by summarizing the findings and emphasizing the significance of the proposed approach in tackling the challenges of high-dimensional data visualization.

2 Background

2.1 Dimension Reduction

Consider the high-dimensional data a rectangular matrix $X_{n \times p}$, where $X_{n \times p} = [\mathbf{x}_1 \ \mathbf{x}_2 \ \cdots \ \mathbf{x}_n]^\top$, with n observations in p dimensions. The objective is to discover a low-dimensional projection $Y_{n \times d} = [\mathbf{y}_1 \ \mathbf{y}_2 \ \cdots \ \mathbf{y}_n]^\top$, represented as an $n \times d$ matrix, where $d \ll p$. The reduction process seeks to remove noise from the original data set while retaining essential information.

There are two main categories of dimension reduction techniques: linear and non-linear methods. Linear techniques involve a linear transformation of the data, with one popular example being PCA. PCA performs an eigen-decomposition of the sample covariance matrix to obtain orthogonal principal components that capture the variance of the data (F.R.S. 1901). However, linear methods may not fully capture complex non-linear relationships present in the data.

In contrast, NLDR techniques generate the low-dimensional representation Y from the high-dimensional data X , often using pre-processing techniques like k -nearest neighbors graph or kernel transformations. Multidimensional Scaling (MDS) is a class of NLDR methods that aims to construct an embedding Y in a low-dimensional space, approximating the pair-wise distances in X (Torgerson 1967). Variants of MDS include non-metric scaling (Kruskal 1964) and Isomap, which estimate geodesic distances to create the low-dimensional representation (Silva & Tenenbaum 2002). Other approaches based on diffusion processes, like diffusion maps (Coifman et al. 2005) and the PHATE algorithm (Moon et al. 2019), also fall under NLDR methods.

A challenge with NLDR methods is selecting and tuning appropriate parameters. One specific technique we focus on is Pairwise Controlled Manifold Approximation (PaCMAP). Similar considerations apply to related methods like tSNE (van der Maaten & Hinton 2008), UMAP (McInnes & Healy 2018), and TrMAP (Amid & Warmuth 2022).

It is important to note that methods like PCA and auto-encoders (Rumelhart et al. 1986) provide a reverse mapping from the low-dimensional space back to the high-dimensional space, enabling data reconstruction. However, many non-linear methods, including tSNE, prioritize visualization and exploration over reconstruction. Their focus is on capturing

complex structures that may not be easily represented in the original space, making a straightforward reverse mapping challenging.

2.1.1 Non-linear dimension reduction techniques

Non-linear dimension reduction techniques play a crucial role in the analysis and visualization of high-dimensional data, where the complexities of relationships among variables may not be adequately captured by linear methods. Among these techniques, tSNE stands out for its emphasis on preserving pairwise distances. By minimizing the divergence between probability distributions in both the high and low-dimensional spaces, t-SNE effectively reveals intricate structures and patterns within the data. Its application is widespread in tasks requiring the visualization of clusters and local relationships, though it does require careful consideration of the perplexity parameter for optimal results.

UMAP is another powerful non-linear technique that strikes a balance between preserving local and global structures. Constructing a fuzzy topological representation using a weighted k-nearest neighbors graph, UMAP optimizes the low-dimensional embedding to resemble this representation. Known for its efficiency and scalability, UMAP is versatile across various scales of relationships in the data, although parameter sensitivity, particularly concerning the choice of neighbors, must be taken into account.

For trajectory data, PHATE provides specialized capabilities. It models the affinity between data points, simulating a heat diffusion process to capture developmental processes, particularly in single-cell genomics. While PHATE excels in revealing trajectory structures and offering insights into cellular development, it necessitates careful parameter tuning due to its specialized nature.

TriMAP adopts a unique approach by approximating the data manifold through the construction of a triangulated graph representation. This technique efficiently captures both global and local structures by representing the data as a network of triangles. TriMAP’s strength lies in its ability to efficiently capture complex structures, albeit with sensitivity to parameter choices, including the number of neighbors.

In contrast, PaCMAP introduces supervised learning to create a low-dimensional representation while preserving pair-wise relationships. Constructing a graph based on pair-wise distances, PaCMAP optimizes an embedding using a customizable loss function. Particularly notable is PaCMAP’s flexibility in incorporating class labels or additional information to guide the embedding process, offering users a means to customize its behavior and performance.

2.2 Linear overviews using tours

A tour is a powerful visualization technique used to explore the shape and global structure of high-dimensional data by generating a sequence of projections, typically into two dimensions. There are two main types of tours: the grand tour ([Asimov 1985](#)) and the guided tour ([Cook et al. 1995](#)). A grand tour involves randomly selecting new orthonormal bases, enabling users to understand the structure by exploring the subspace of d-dimensional projections ([Asimov 1985](#)). In contrast, a guided tour can be employed to generate a sequence



Figure 1: 2D layouts from different NLDR techniques applied the same data: (a) tSNE (perplexity = 27), (b) UMAP (n_neighbors = 50), (c) PHATE (knn = 5), (d) TriMAP (n_inliers = 5, n_outliers = 4, n_random = 3), and (e) PaCMAP (n_neighbors = 10, init = random, MN_ratio = 0.9, FP_ratio = 2). Is there a best representation of the original data or are they all providing equivalent information?

of ‘interesting’ projections based on an index function (Cook et al. 1995).

The process begins with the data matrix X . It generates a sequence of $p \times d$ orthonormal projection matrices (bases) P_t , usually d is one or two dimensions. For each pair of orthonormal bases P_t and P_{t+1} , a geodesic path is interpolated to create smooth animation between projections. The resulting tour continuously visualizes the projected data $Y_t = XP_t$ as it interpolates between successive bases.

Furthermore, software like **langevitour** can visualize both types of tours, providing flexibility for exploring high-dimensional data with various objectives. In our context, use grand tour along with the model to observe how effectively the model captures the underlying structure of the data.

3 Methodology

In this paper, we present a novel method that aims to determine the most effective way to represent high-D data by selecting the best method and hyperparameter choice. Our approach involves dividing the data set into two parts: a training set to construct the model and a test set to generate predictive values and residuals. To implement our approach, we first use a 2D embedding data set as the initial point. The output of our algorithm is a tour that displays the model and original data in the high-dimensional space. A flow chart of the proposed algorithm is shown in Figure 2. Our algorithm comprises two main phases: (1) generate the model in the 2D space, and (2) generate the model in the high-D space. These two phases are described in detail in this section using UMAP 2D embedding of the S-curve data set, which has seven dimensions, including four noise dimensions.

3.1 Preprocessing steps

In order to reduce the computational complexity associated with performing NLDR techniques to high-D data, and as a initial step of noise reduction of high-D data, PCA (Jolliffe & Cadima 2016, Howley et al. (2005), Indhumathi & Sathiyabama (2010)) is applied as a preprocessing step. Subsequently, the identified principal components, representing directions of maximum variance, are used to construct the model.

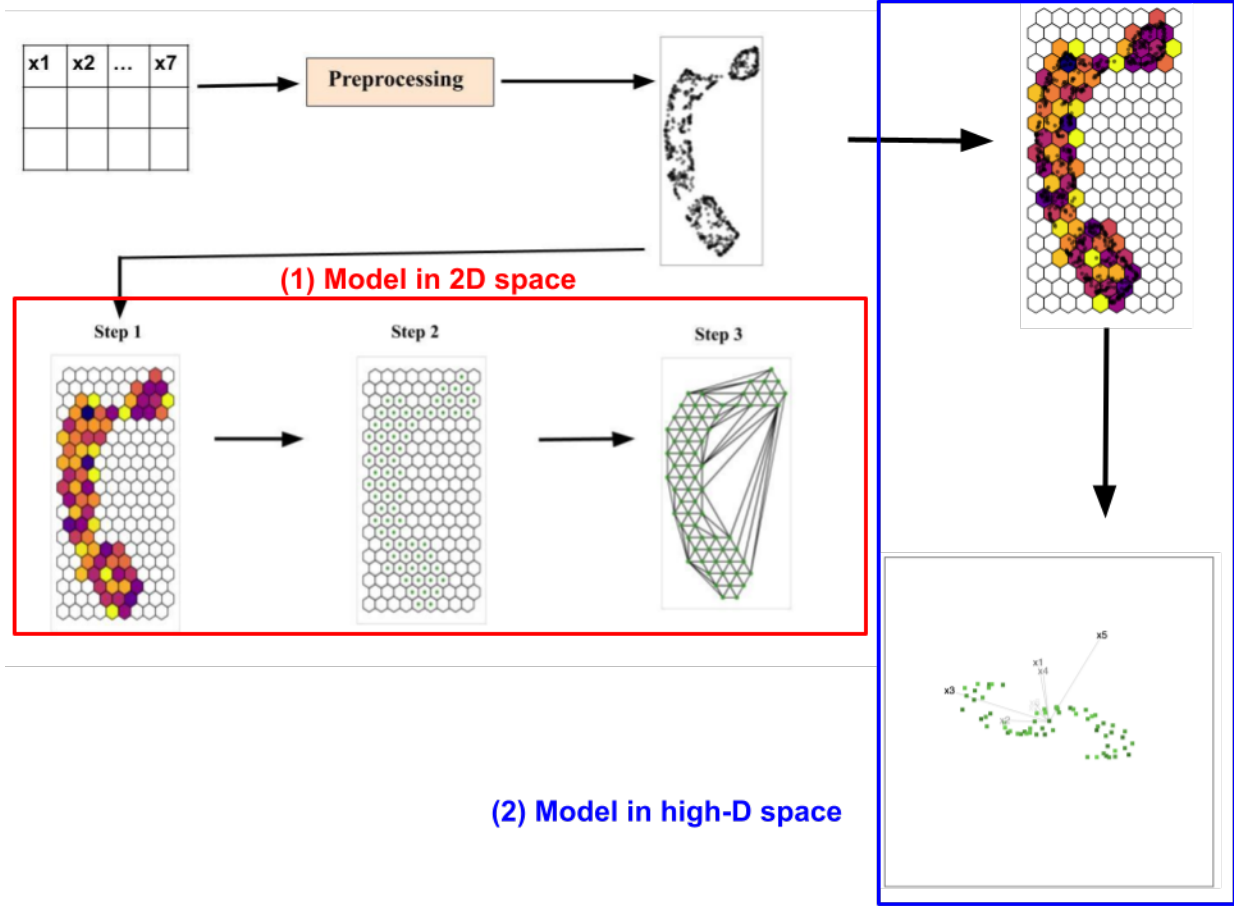


Figure 2: A flow diagram detailing the steps taken to create the low-dimensional manifold in the high dimensional space. There are two basic phases, one to generate the model in the 2D space, and other to generate the model in the high-D space.

3.2 Constructing the 2D model

Step 1: Computing the hexagonal grid configuration

The hexagonal grid, formed through hexagonal binning (Carr et al. 1987, Carr (1992)), serves as a type of bivariate histogram employed to visualize the structure of high-D data. Hexagons, being one of only three regular polygons capable of tessellating a plane (Carr et al. 2013), possess both symmetry of nearest neighbors and the maximum number of sides for a regular tessellation of the plane. This unique combination makes hexagons more efficient in covering the plane compared to other regular tessellations. Additionally, hexagons exhibit lower visual bias when displaying densities, setting them apart from other regular tessellations (Carr et al. 2023). In our algorithm, hexagonal binning is used as the initial step of constructing the 2D model and the total number of bins (b) is the crucial parameter that defines the granularity of the hexagonal grid.

(a) Determine the number of bins along the x-axis (b_1)

First, the number of bins along the x-axis (b_1) is computed using the relationship between the diameter (h) and the area (A) of regular hexagons (see Equation 1).

$$A = \frac{\sqrt{3}}{2}h^2 \quad (1)$$

To construct regular hexagons, $A = 1$ (see Figure 4) use as the default setting. Then, the diameter (h) of the regular hexagons is calculated (see Equation 2).

$$h = \sqrt{\frac{2}{\sqrt{3}}A} \quad (2)$$

Carr et al. (2013) mentioned about the relationship between the diameter (h) of regular hexagons and the height (y) of the plotting region. According to our algorithm, the height (y) of the plotting region is the the range of 2D embedding component 1 (r_1) (see Equation 3).

$$h = \frac{r_1}{b_1} \quad (3)$$

After rearranging the Equation 3 as Equation 4, b_1 is computed. The b_1 value is rounded up to the nearest whole number to have an integer value.

$$b_1 = \frac{r_1}{h} \quad (4)$$

(b) Determine the shape parameter (s)

In this step, we determine the shape parameter (s) for the hexagonal bins, which significantly influences their shape and arrangement within the grid. The s in the hexagonal

binning algorithm is defined as the ratio of the height (y) to the width (x) of the plotting region as defined in Equation 5.

$$s = \frac{y}{x} \quad (5)$$

The shape parameter (s) of our algorithm is calculated as the ratio of the ranges of 2D embedding components, where r_1 and r_2 represent the ranges of 2D embedding components 1 and component 2, respectively (see Equation 6).

$$s = \frac{r_2}{r_1} \quad (6)$$

(c) Determine the number of bins along the y-axis (b_2)

Next, the number of bins along the y-axis is computed based on the number of bins along the x-axis (b_1) and the shape parameter (s) (see Equation 7) (Carr et al. 2013).

$$b_2 = 2 * \left(\frac{(b_1 \times s)}{\sqrt{3}} + 1.5001 \right) \quad (7)$$

(d) Determine the total number of bins (b)

The total number of bins is determined by multiplying the number of bins along the x-axis (b_1) with the number of bins along the y-axis (b_2) (see Equation 8).

$$b = b_1 \times b_2 \quad (8)$$

Step 2: Obtain bin centroids

As a result of hexagonal binning for high-D data, all the high-D data are clustered into hexagons. In this step, the bin centroids ($C_k^{(2)} \equiv (C_{ky_1}, C_{ky_2})$) (see Figure 2 Step 2) are obtained (Carr et al. 2013).

Step 3: Triangulate bin centroids

In this step, the algorithm proceeds to triangulate the hexagonal bin centroids (see Figure 2 Step 3). Triangulation is a fundamental process in computational geometry and computer graphics that involves dividing a set of points in a given space into interconnected triangles (Lloyd 1977). One common algorithm used for triangulation is Delaunay triangulation (Lee & Schachter 1980, Renka (1996)), where points are connected in a way that maximizes the minimum angles of the resulting triangles, leading to a more regular and well-conditioned triangulation.

Since we are working with the centroids of regular hexagonal bins, the resulting mesh will predominantly comprise equal-sized regular triangles. However, the triangulation also helps span any gaps that may exist between clusters of points, allowing for a more complete and interconnected representation of the data.

3.3 Lifting the model into high dimensions

3.3.1 Lifting the triangular mesh points into high dimensions

Step1: Cluster 2D points to hexagons

Expanding upon the information regarding hexagonal binning discussed in Step 1 of Section 3.2, the primary objective in this step is to determine the 2D embedding points associated with each hexagon. As the initial process of hexagonal binning, the 2D points are clustered into their respective hexagonal bins. By mapping this information with the hexagonal bin centroids ($C_k^{(2)} \equiv (C_{ky_1}, C_{ky_2})$) that obtained in Step 2 of the 2D model building (see Section 3.2), we can find which 2D points are assigned to which data set (see Figure 3 (a)).

Step2: Cluster high dimensional points to hexagons

Following the step 1, the main focus in this step to determine the corresponding high dimensional points for each hexagon. Every 2D embedding point serves as a projection of a data point belonging to high dimensional space. By using this mapping between the high dimensional data and their corresponding projections, the high dimensional points allocated to each hexagons are determined (see video linked in Figure 3).

Step3: Compute the mean within hexagon

Having identified the high-dimensional points associated with hexagons, the final step involves computing the mean within each hexagonal bin. This implies calculating the average of the high-dimensional data points located within each hex bin. These averaged high-dimensional data points, denoted as $C_k^{(p)} \equiv (C_{kx_1}, \dots, C_{kx_p})$, serve as the representative coordinates for the hex bin centroids within the expansive high-dimensional space (see video linked in Figure 3).

3.3.2 Lifting the 2D triangular mesh into high dimensions

Based on the insights gained in Step 3 of Section 3.2, where connected edges in the 2D triangular mesh were identified, this step involves lifting these connections into the high dimensions. Having the mappings of all 2D triangular mesh points into high dimensions, the points connected in 2D are also connected in high dimensional space (see video linked in Figure 3).

3.4 Tuning the model

The performance and robustness of our model depend on three key parameters: (i) the total number of bins (b), (ii) a benchmark value used to remove low-density hexagons, and (iii) a benchmark value used to remove long edges. However, there is no analytical formula to calculate an appropriate value for these parameters (see Appendix for details on how default values are calculated). The selection of these parameter values depends on the model performance computed by Mean Squared Error (MSE) (see Section 3.5.2).



Figure 3: How the 2D model lift into high dimensions? (a) visualize the points and the hexagonal bin centroids related 2nd and 15th hexagons, (b) visualization of the edge connected the 2nd and 15th hexagons (colored in red) in the triangular mesh. A video of tour animation is available at <https://youtu.be/ffWFK1UTlc>.

3.4.1 Total number of bins

The number of hexagonal bins in the hexagonal grid has a considerable impact on the construction of the 2D model. This is because it is the initial step in building the 2D model. The hexagonal grid with the chosen total number of bins must be able to capture the structure of the NLDR data. If the number of bins is too low, the model may not be able to capture the structure of the NLDR data effectively (see Figure 4 (a)), while if there are too many bins, it may result in over-fitting the individual points of the NLDR data (see Figure 4 (c)). Therefore, it is important to determine an appropriate number of bins to build an effective model.

Furthermore, the total number of bins is determined by the number of bins along the x-axis and y-axis (see Equation 8). To calculate the effective total number of bins, the minimum and approximate maximum number of bins along the x-axis are used as candidate values. The minimum number of bins along the x-axis is 1. The maximum number of bins along the x-axis can be estimated by taking the square root of the number of NLDR data points. To investigate the impact of the number of bins on MSE, the analysis is focused on the MSE for different total numbers of bins. This range encompasses the total number of bins calculated for the minimum and maximum values of the number of bins along the x-axis.

Typically, the MSE plot will have a steep slope at the beginning, indicating that a smaller number of bins causes a larger amount of error. Then, the slope will gradually decline or level off, indicating that a higher number of bins generates a smaller error. This MSE plot is useful in determining the effective number of bins required to construct the 2D model. Figure 5 (b) has created a graph that shows how the Mean Squared Error (MSE) changes depending on the number of bins assigned in the hexagonal grid for various NLDR techniques applied to the S-curve data set. As per the rule of thumb mentioned earlier,

the effective number of bins for each NLDR method is shown in the `?@tbl-msebinsnlldr`. Furthermore, Figure 12 shows the 2D models constructed for each NLDR technique with the selected total number of bins and how the models look in high-D with original data.

	NLDR technique	total number of bins	AIC
1	tSNE	72	-21882.46
2	UMAP	98	-20013.27
3	PHATE	90	-15036.91
4	TriMAP	154	-23001.90
5	PaCMAP	132	-21330.06

Table 1: Total number of bins suggested by rule of thumb and AIC values for each NLDR technique applied to S-curve dataset.

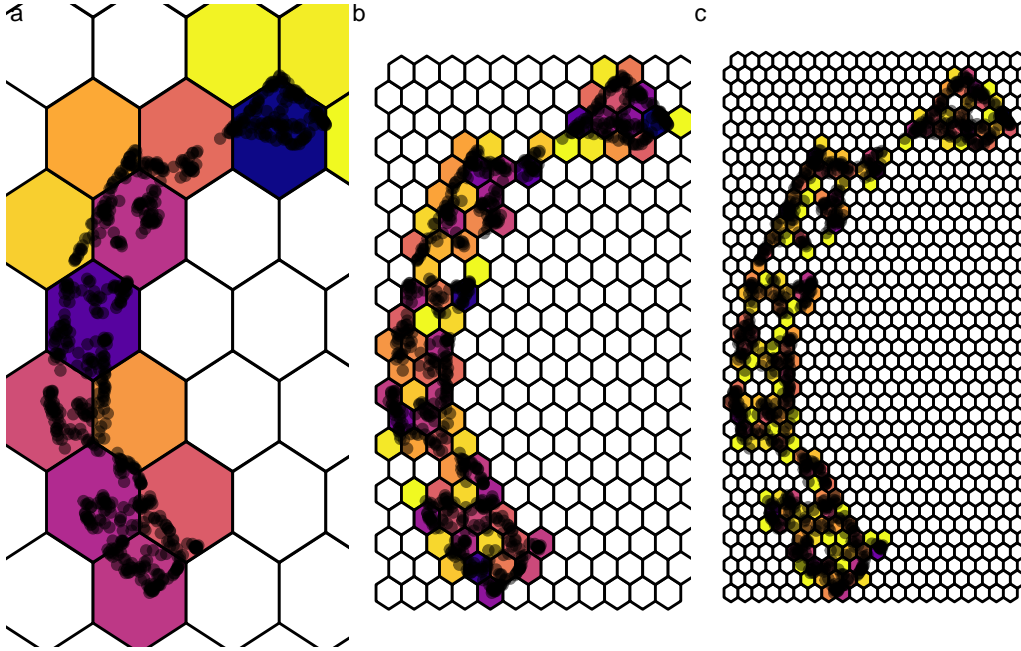


Figure 4: Hexbin plots from different number of bins for the **UMAP** projections of **S-curve** data: (a) $b = 32$ (4, 8), $s = 1.643542$, (b) $b = 264$ (12, 22), $s = 1.643542$, and (c) $b = 840$ (21, 40), $s = 1.643542$. The hexbins are colored based on the density of points, with darker colors indicating higher point density and yellow color representing lower point density within each bin. What is the number of bins that would be effective in representing low-dimensional data?

3.4.2 Benchmark value to remove low-density hexagons

After setting up the hexagonal grid with an appropriate number of bins, it is possible that some hexagonal bins may have very few or no data points within them. To ensure comprehensive coverage of the NLDR data, it is necessary to select hexagonal bins that have a considerable number of data points within their hexagons. To achieve this, the

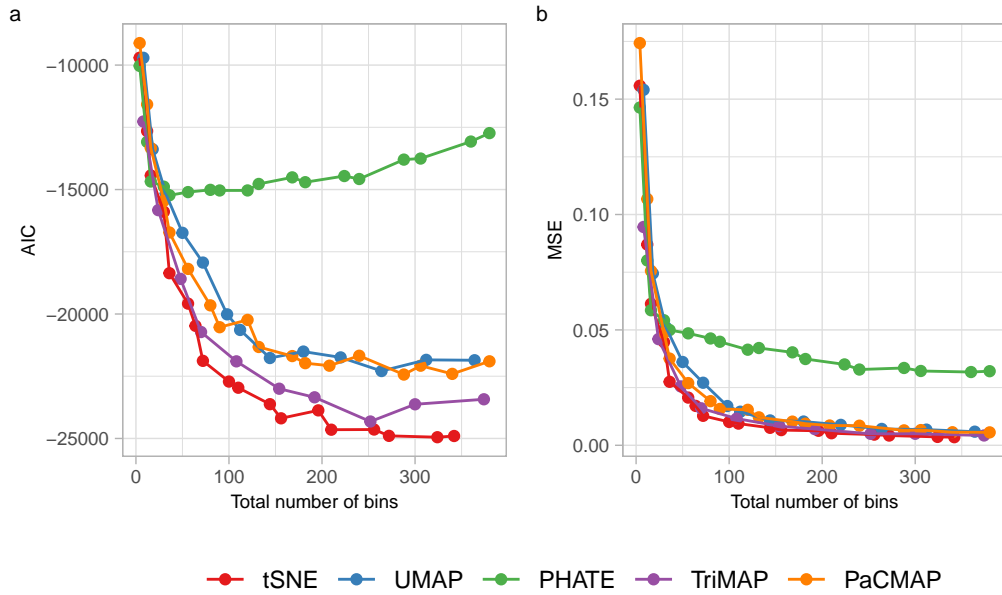


Figure 5: Goodness of fit statistics from different NLDR techniques applied to training S-curve dataset. What is the most effective NLDR technique to represent the original data in a 2D space? What is the effective number of bins in each NLDR technique to create a 2D model?

standard number of points within each hexagon is first calculated. This standard count is obtained by dividing the number of points within each hexagon by the maximum number of points in the grid (see Equation 9). Next, the bins that have a standard number of points less than a certain benchmark value are removed. After removing the hexagons that have insufficient data density, the hexagons with more substantial data representation are used to construct the 2D model.

$$\text{standard count} = \frac{\text{count}}{\text{max count}} \quad (9)$$

Furthermore, it is crucial to choose the benchmark value to remove low-density hexagons carefully. If we remove unnecessary bins, then it may result in long edges and an uneven 2D model. Therefore, instead of removing hexagons only identified by the benchmark value, we examine the standard number of points in the neighboring hexagons of the identified low-density hexagons. If the neighboring bins also have low counts, then only those bins will be removed. The other identified bins will be kept and used for constructing the 2D model along with the high-density bins (see Appendix for more details).

The benchmark value for removing low-density hexagons has a range of 0 and 1. When analyzing how these benchmark values affect model performance, it's important to observe the change in Mean Squared Error (MSE) as the benchmark value increases. The MSE exhibits a gradual increase as the benchmark value progresses from 0 to 1. Assessing this rate of increase is crucial. If the increment is not substantial, the decision might lean towards retaining low-density hexagons. According to Figure 7, the change in MSE for NLDR techniques is relatively small across different benchmark values, except for the PHATE method.

Consequently, it is not necessary to remove low-density hexagons when constructing the 2D model for the S-curve dataset in NLDR techniques, except for PHATE. While there may be some fluctuations in MSE between benchmark values of 0 to 1, the absence of significant changes suggests that maintaining low-density hexagons is preferable. However, to choose the best selection, it's recommended to examine the benchmark values around the first local minimum in the MSE curve. However, the MSE for PHATE fluctuates when benchmark values range between 0 and 1. Therefore, it is necessary to explore the benchmark values surrounding the first local minimum to determine an effective benchmark value. There is no universal rule for selecting a process. As shown in Figure 7, the MSE values for PHATE fluctuate, and the first local minimum is at 0. Therefore, nearby benchmark values such as 0.01, 0.04, and 0.06 were explored to identify the best value for preserving the data structure. In this case, a benchmark value of 0.06 was chosen. The resulting 2D model is shown in Figure 12 (c), while the video link provides a visual representation of how the model appears in high-D.

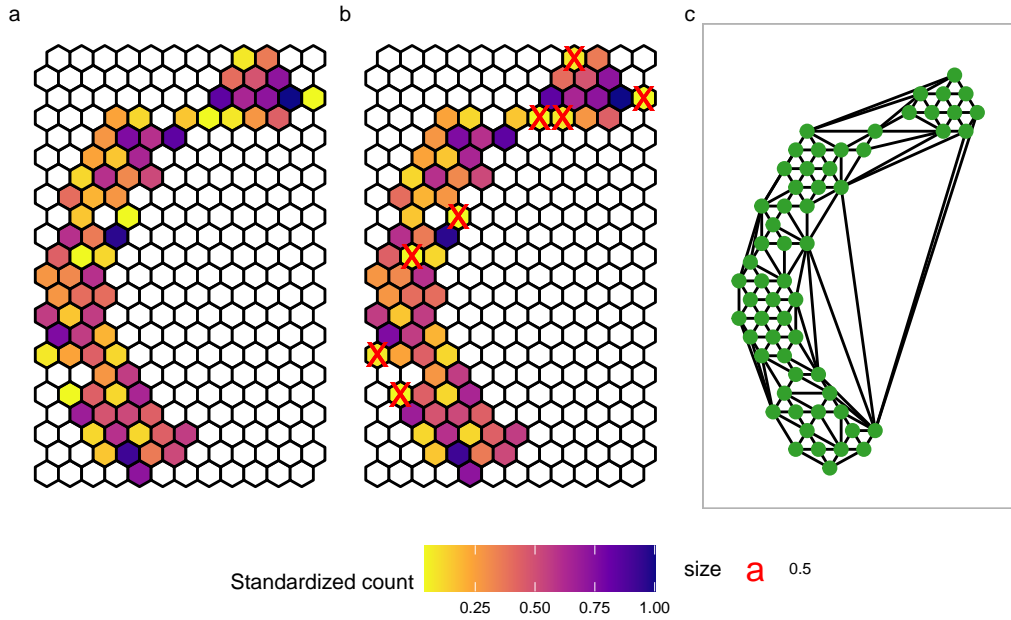


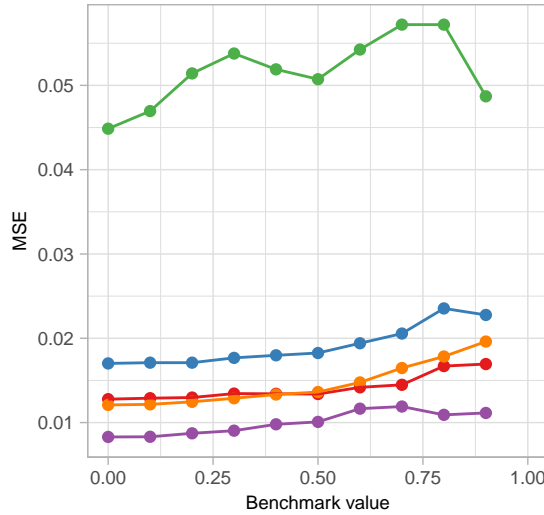
Figure 6: Goodness of fit

3.4.3 Benchmark value to remove long edges

Achieving a smooth representation in 2D space is crucial, and one factor influencing this smoothness is the presence of long edges (see Figure 8). These long edges occur when a line connects points that are distant in the triangular mesh, impacting the overall smoothness of the mesh.

To investigate the effect of removing long edges on the MSE, we analyzed the MSE for various benchmark values. Surprisingly, the results indicated that the MSE remained consistent across different benchmark values, as shown in Figure 9. It's important to note that edges are defined only in the 2D model and do not extend to higher dimensions. Consequently, removing edges does not affect the model in higher dimensions.

There is no definitive rule for determining the benchmark value to remove long edges.



— tSNE — UMAP — PHATE — TriMAP — PaCMAP

Figure 7: Goodness of fit statistics from different NLDR techniques applied to training S-curve dataset with different benchmark values to remove the low-density heaxgons. What is the effective benchmark value to remove the low-density heaxgons?

However, we have a method to find a default value (see Appendix). Adjusting values around this default can help to find benchmark value to remove long edges, contributing to the construction of a smoother 2D representation (see Figure 9).

3.5 Model summaries

3.5.1 Predicted values and residuals

The approach involves employing the K-nearest neighbors (KNN) algorithm to identify the nearest hexagonal bin centroid in the 2D space. Subsequently, the coordinates of this centroid are assigned as the low-dimensional predicted values for the test data in 2D space. It is noteworthy that traditional NLDR methods, such as tSNE, often lack a direct predict function, making our approach valuable for generating predicted values in the absence of such functionalities.

The concept of “residuals” is pivotal in evaluating the accuracy of representing bin centroids in high dimensions. To quantify this accuracy, we introduce an error metric, which measures the sum of squared differences between the high-dimensional data (x_{ij}) and the predicted bin centroid data in high-dimensional space ($C_{x_{ij}}$) across all bins and dimensions. Mathematically, this error is expressed as:

$$\text{Error} = \sum_{j=1}^n \sum_{i=1}^p (x_{ij} - C_{x_{ij}})^2 \quad (10)$$

Here, n represents the number of bins, p represents the dimensions, x_{ij} is the actual high-dimensional data, and $C_{x_{ij}}$ is the predicted bin centroid data in high dimensions.

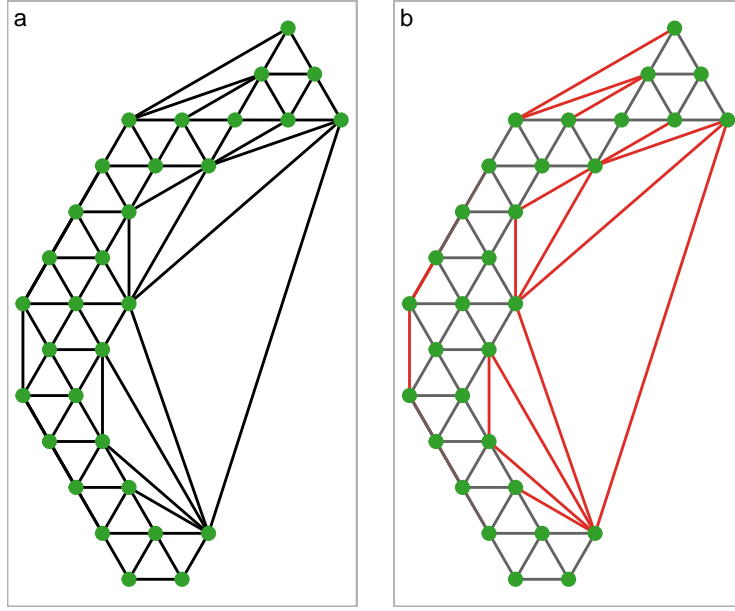


Figure 8: What does the 2D model, constructed using UMAP (applied to the S-curve dataset), look like in high dimensions with long edges? (https://youtu.be/pSL_G_n7-fM) (a) 2D model without removing the long edges, and (b) 2D model with long edges coloured by red. The default benchmark value is used to identify long edges.

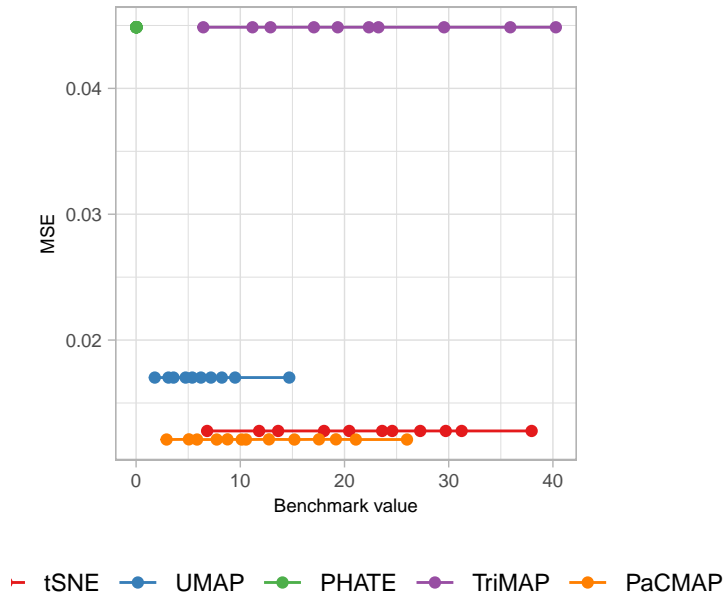


Figure 9: Goodness of fit statistics from different NLDR techniques applied to training S-curve dataset with different benchmark values to remove the long edges. What is the effective benchmark value to remove the long edges?

The error metric outlined above provides valuable insights into the overall accuracy of our predictive model. By quantifying the squared deviations between the actual and predicted values across all bins and dimensions, we gain a comprehensive understanding of how well our method captures and represents the underlying structure of the data in the reduced 2D space. This assessment is crucial for evaluating the efficacy of our NLDR technique in preserving the essential information present in the original high-dimensional data.

3.5.2 Goodness of fit statistics

Moving on to the assessment of prediction accuracy, we calculate the Mean Squared Error (MSE). The MSE helps measure the average squared differences between the actual high-dimensional data (x_{ij}) and the predicted bin centroid data in high-D ($C_{x_{ij}}$) values across all bins. Mathematically, this is expressed as:

$$\text{MSE} = \sum_{j=1}^n \frac{\sum_{i=1}^p (x_{ij} - C_{x_{ij}})^2}{b} \quad (11)$$

Here, b signifies the total number of bins, p denotes the number of dimensions in the high-dimensional data, and n represents the number of observations.

Additionally, we gauge the model's performance using the Akaike Information Criterion (AIC), calculated by the formula:

$$\text{AIC} = 2bp + np * \log(\text{MSE}) \quad (12)$$

These metrics, MSE and AIC, collectively offer valuable insights into the model's predictive performance, considering both accuracy and complexity in the predictions.

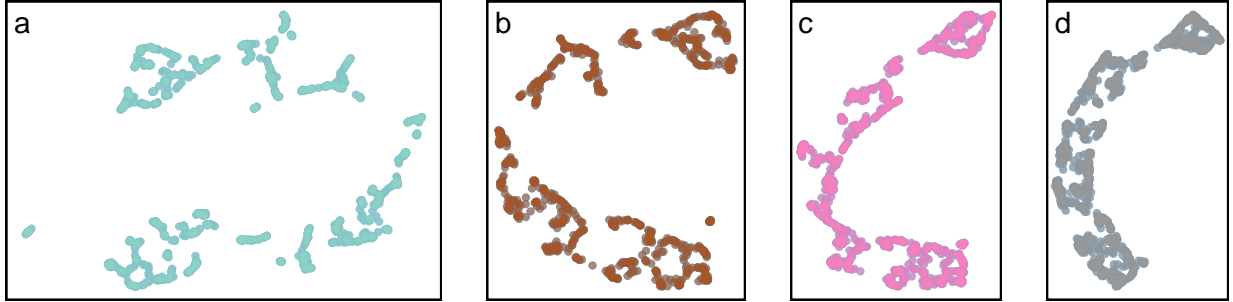


Figure 10: 2D layouts from UMAP applied for the S-curve data: (a) UMAP ($n_neighbors = 7$), (b) UMAP ($n_neighbors = 15$), (c) UMAP ($n_neighbors = 32$), (d) UMAP ($n_neighbors = 50$). Is there a best parameter choice in representing UMAP or are they all providing equivalent information?

3.6 Model interpretation

The visualizations of NLDR techniques for the S-curve dataset shows different representations in 2D, as showcased in Figure Figure 1. The question at hand is determining the

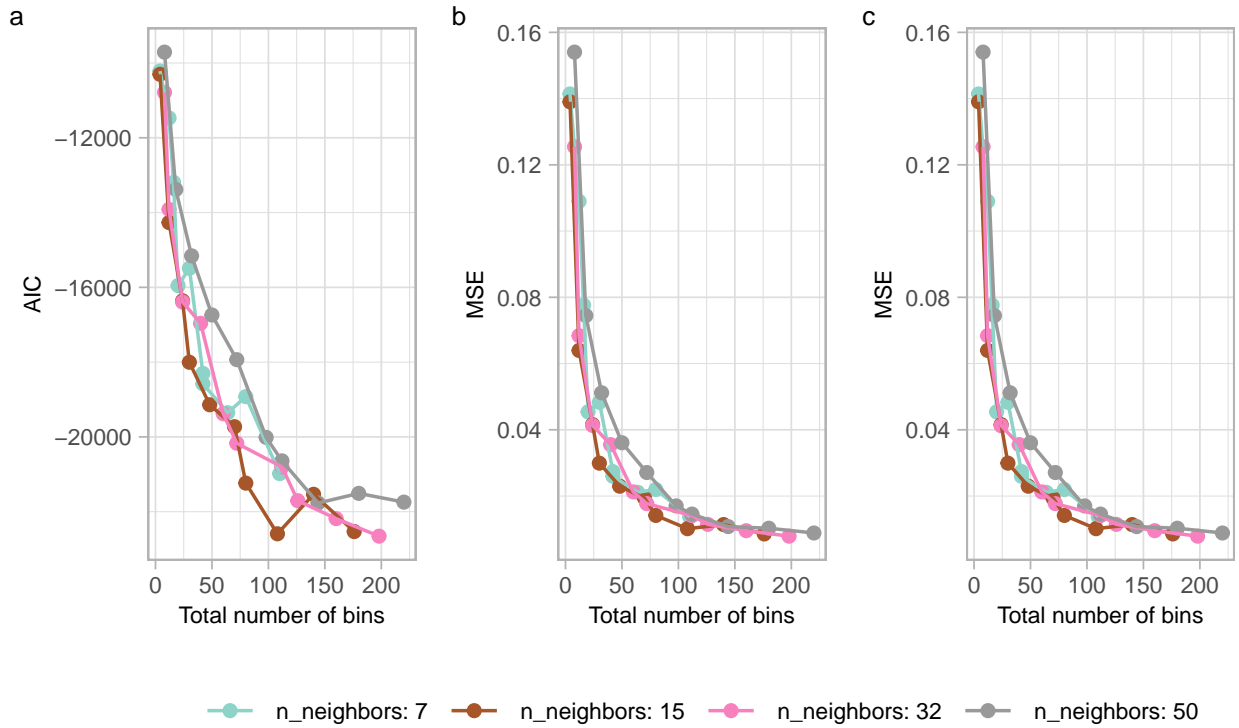


Figure 11: Goodness of fit statistics from different $n_neighbors$ parameter of UMAP applied to training S-curve dataset. What is the best parameter choice in UMAP to represent the original data in 2D?

best NLDR technique to represent the S-curve data. Examining the 2D layouts in Figure 1 suggests that TriMAP or PaCMAP may be best representations. However, the challenge is to decide the best representation with considerable evidence.

After considering the models constructed from the algorithm for each NLDR techniques and visualizing them in high-D space with the original data, shows that all the NLDR techniques capture the non-linearity of the S-curve (see videos of the models linked in Figure 12). But thorough examination of each model in high-D space shows some surprising findings. The model of PHATE is flattened and lack of capturing the width of S-curve (see videos of the model with PHATE linked in Figure 12). This nature of PHATE is also evicted by the considerably higher AIC and MSE values for PHATE as shown in Figure 5. Furthermore, there are two edges that are not connected to any points in the model of TriMAP (see see videos of the model with TriMAP linked in Figure 12). This model shows how the patterns in 2D representation of TriMAP capture by the model (see Figure 1 (d)). As shown in Figure 1 (b), UMAP have four clusters in a curvilinear structure. However, the model reveals that even though UMAP shows a curvilinear in 2D, UMAP actually capture the structure of the S-curve without any disjoint in the model (see see videos of the model with UMAP linked in Figure 12). In the 2D layouts of tSNE and PaCMAP (see Figure 1 (a), (e)), there are some sparse areas that are captured by the models effectively (see see videos of the model with tSNE and PaCMAP linked in Figure 12).

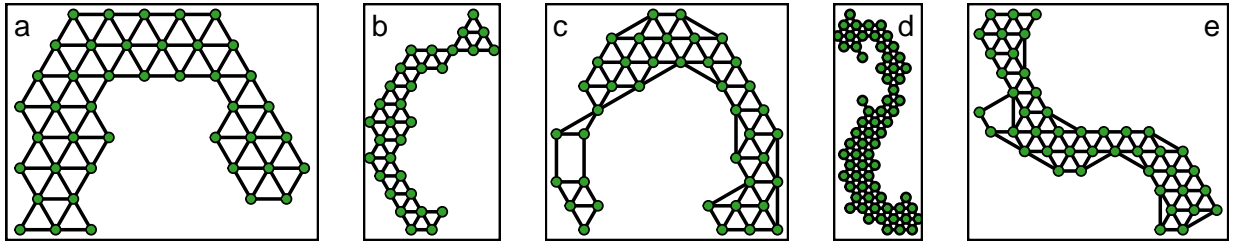


Figure 12: Is there a good model to represent the original data in 2D space or are they all providing equivalent information?, (a) Model in the 2D space with tSNE (<https://youtu.be/uy9SkAo6gAE>), (b) Model in the 2D space with UMAP (https://youtu.be/0MJDhHrh_Ug), (c) Model in the 2D space with PHATE (<https://youtu.be/HbVv0uy0QWk>), (d) Model in the 2D space with TriMAP (<https://youtu.be/2OGwipAjzc8>), and (e) Model in the 2D space with PaCMAP (<https://youtu.be/pkokI8d-cBk>).

3.7 Model selection

In the process of selecting the most suitable NLDR technique to represent high-D data, the Akaike Information Criterion (AIC) stands as a crucial tool for insightful comparisons. Once the effective number of bins has been determined for each method, AIC values can be compared to identify the best NLDR technique with the lowest AIC value. For example, as shown in Figure 5 (a), TriMAP is the most suitable NLDR technique to represent the S-curve data (see table 1).

3.8 Prediction

In this context, “prediction” denotes the 2D embedding generated for the NLDR technique. The methodology encompasses identifying the nearest averaged high-D points in the high-D space for the test data, by computing high-D Euclidean distances. As the averaged high-D point corresponds to the lifting of the 2D model, determining its nearest counterpart allows us to map its hexagonal bin centroid coordinates. Consequently, these centroid coordinates serve as the assigned low-dimensional predicted values for the test data in the 2D space.

Some NLDR techniques, such as tSNE, often lack a direct prediction, making our approach valuable for generating predicted values in the absence of such functionalities.

3.9 Simulated data example

In this section, we showcase the effectiveness of our methodology using simulated data. The dataset comprises five spherical Gaussian clusters in 4- d , with each cluster containing an equal number of points and consistent within variation.

We *strongly* recommend viewing the linked videos for each study while reading. Links to the videos are available in the figures for each example. The videos show the visual appearance of the **langevitour** interface with low-dimensional view and how we can interact with the tour via the controls.

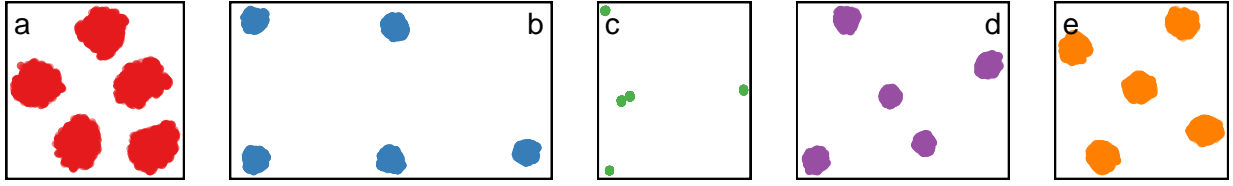


Figure 13: 2D layouts from different NLDR techniques applied the same data: (a) tSNE (perplexity = 61), (b) UMAP (n_neighbors = 15), (c) PHATE (knn = 5), (d) TriMAP (n_inliers = 5, n_outliers = 4, n_random = 3), and (e) PaCMAP (n_neighbors = 10, init = random, MN_ratio = 0.9, FP_ratio = 2). Is there a best representation of the original data or are they all providing equivalent information?

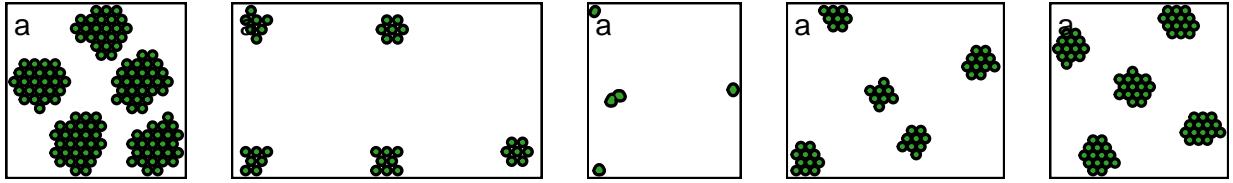


Figure 14: Is there a best model to represent the original data in 2D space or are they all providing equivalent information?, (a) Model in the 2D space with tSNE (<https://youtu.be/x5VPB-wOLm4>), (b) Model in the 2D space with UMAP (<https://youtu.be/Cm1dW6iLyHQ>), (c) Model in the 2D space with PHATE (<https://youtu.be/HB0Y3ilz6sI>), (d) Model in the 2D space with TriMAP (<https://youtu.be/iSVkXIrOrSA>), and (e) Model in the 2D space with PaCMAP (<https://youtu.be/O2QBctsc4uM>).

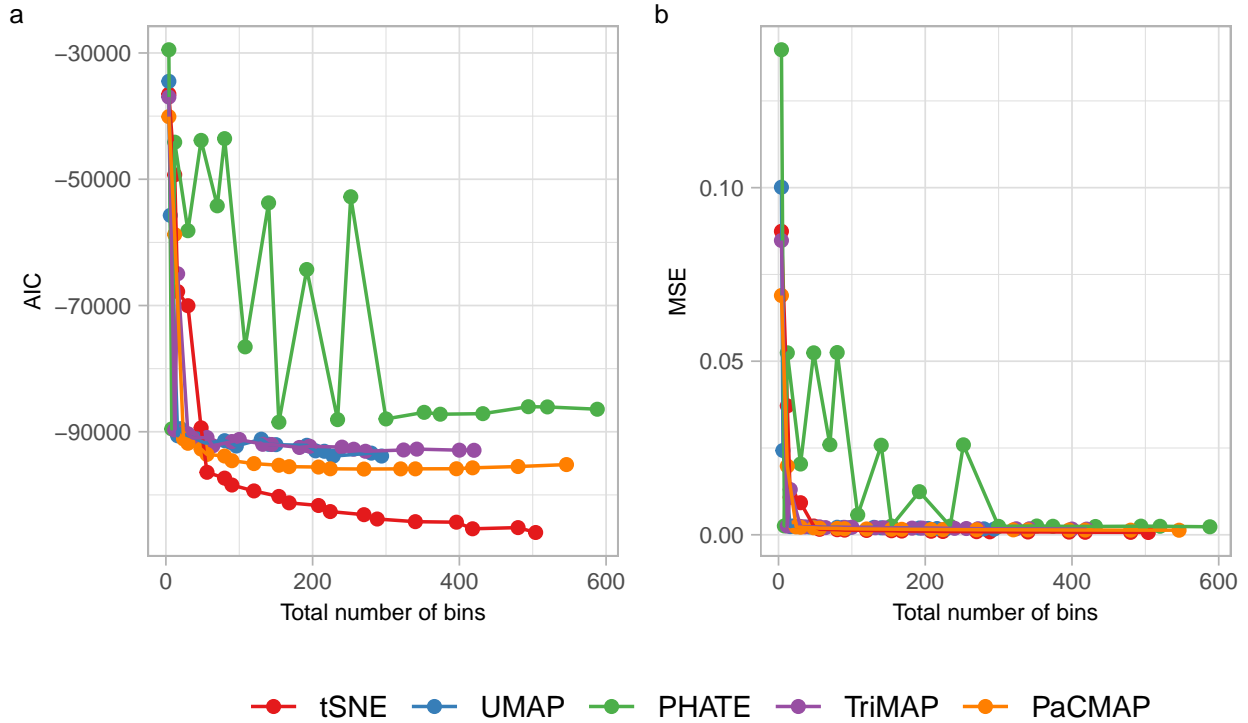


Figure 15: Goodness of fit statistics from different NLDR techniques applied to training five spherical Gaussian cluster dataset. What is the best NLDR technique to represent the original data in 2D?

4 Applications

4.1 Human peripheral blood mononuclear cells (PBMCs) data

- Intro to the data set (This data set contains 13,714 features across 2,700 samples within a single assay. The active assay is RNA, with 13,714 features representing different gene expressions.)
- 2622 cells
- Evaluate Festem on DEG detection (Festem enabled identification of often-missed fine cell types)
- Using the Festem-selected genes, identified 10 clusters in the PBMCsk data and annotated them based on the expression of canonical markers
- The 10 clusters included immune cells such as naive CD4 T cells, memory CD4 T cells, CD8 T cells, CD14 monocytes, FCGR3A monocytes, Natural Killer (NK) cells, B cells and Dendritic Cells (DC).
- In addition to these common cell types, Festem identified a fine cell type, CD27- CD4+ memory T cells, which were often missed by other methods.
- The CD27- CD4+ memory T cells identified by Festem expressed common marker genes (IL7R and S100A4) of memory T cells, but did not express CD27. These cells also had downregulated expression of SELL, CCR7, MAL and LEF1, and upregulated expression of CCL5 (Fig. 4B) and thus were the CD27- CD4+ memory T cells in the literature (36). The CD27- CD4+ memory T cells were known to be at a more differentiated state and have stronger antigen-recall responses than their CD27+ counterparts.
- 15 PCs
- learned from the model: There are 3 well-separated clusters in 2D, but if look at the model in high-D space, the three clusters are much closer. Also, there is some continuity within the clustering structure and it didn't capture well. Therefore UMAP with `n:neighbour 30` is not a good representation for this data set.
- The most important parameter is `n_neighbors` - the number of approximate nearest neighbors used to construct the initial high-dimensional graph. It effectively controls how UMAP balances local versus global structure - low values will push UMAP to focus more on local structure by constraining the number of neighboring points considered when analyzing the data in high dimensions, while high values will push UMAP towards representing the big-picture structure while losing fine detail.
- The second parameter we'll investigate is `min_dist`, or the minimum distance between points in low-dimensional space. This parameter controls how tightly UMAP clumps points together, with low values leading to more tightly packed embeddings. Larger values of `min_dist` will make UMAP pack points together more loosely, focusing instead on the preservation of the broad topological structure.

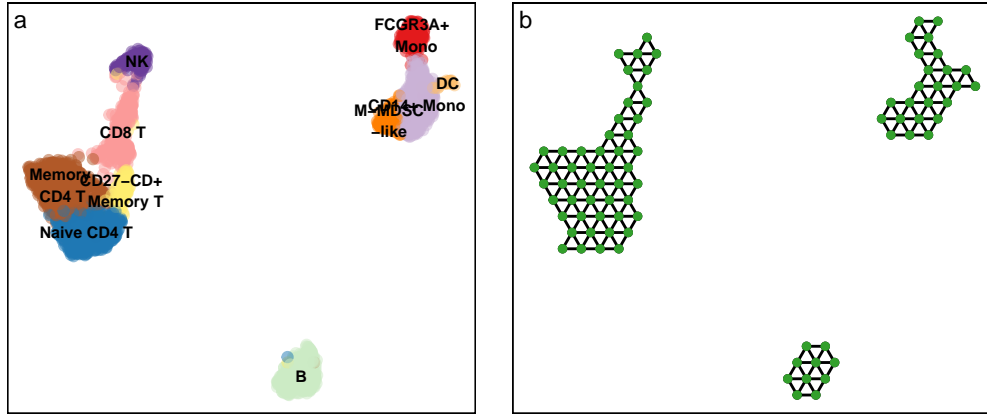


Figure 16: (a) 2D layout from UMAP ($n_neighbors = 30$, $min_dist = 0.3$) applied for the PBMC3k dataset. Is this a best representation of the original data?, (b) Model in the 2D space with UMAP (https://youtu.be/CNXjWZMyh_M)

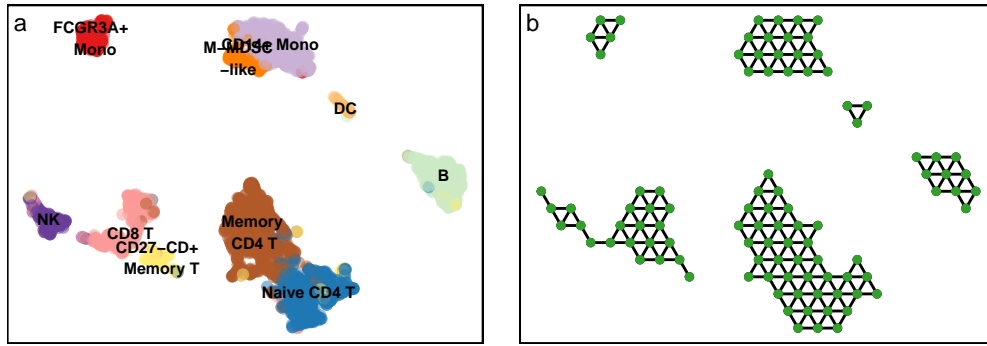


Figure 17: (a) 2D layout from UMAP ($n_neighbors = 5$, $min_dist = 0.1$) applied for the PBMC3k dataset. Is this a best representation of the original data?, (b) Model in the 2D space with UMAP (<https://youtu.be/SO3thJ8PMi8>)

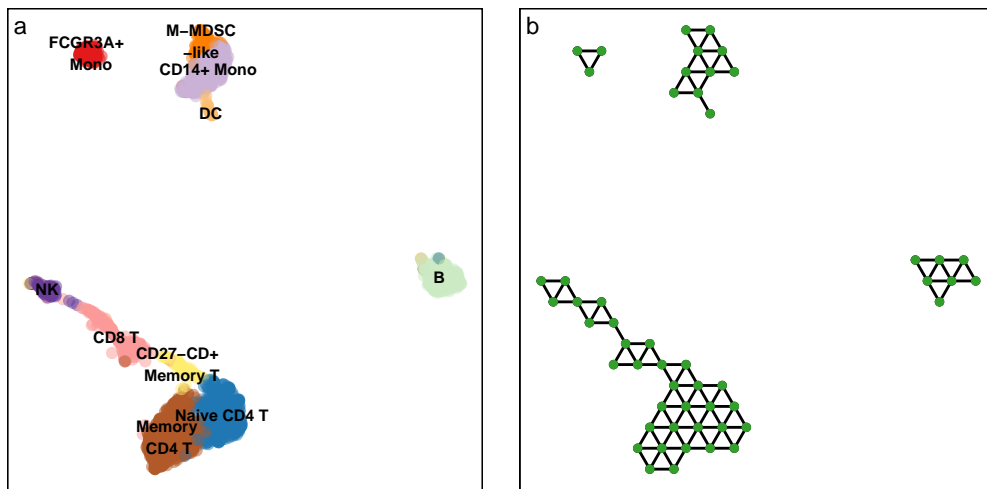


Figure 18: (a) 2D layout from UMAP ($n_neighbors = 30$, $min_dist = 0.01$) applied for the PBMC3k dataset. Is this a best representation of the original data?, (b) Model in the 2D space with UMAP (https://youtu.be/hP8ie_oMXw0)

4.2 HARPS GTO sample dataset

- In 2D, there are two well-separated clusters
- One cluster have a sparse data space within the cluster
- There is a line in right corner of the structure that is not connected any other trimesh points. This line create a long edge in high-D space.
- In high-D view, the clusters having some non-linearity pattenr, which is also not captured in tSNE. Therefore, this is not a good choice.
- The parameter is, in a sense, a guess about the number of close neighbors each point has.

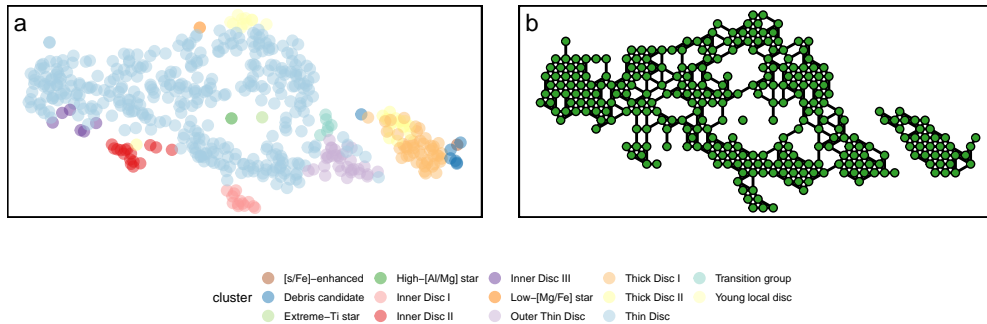


Figure 19: (a) 2D layout from tSNE (perplexity = 40) applied for the HARPS GTO dataset. Is this a best representation of the original data?, (b) Model in the 2D space with tSNE (<https://youtu.be/txTD7Gtxt6Y>)

5 Conclusion

We introduce a new tool to help to determine which method, which parameter choice provide the most useful representation of high-D data.

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