

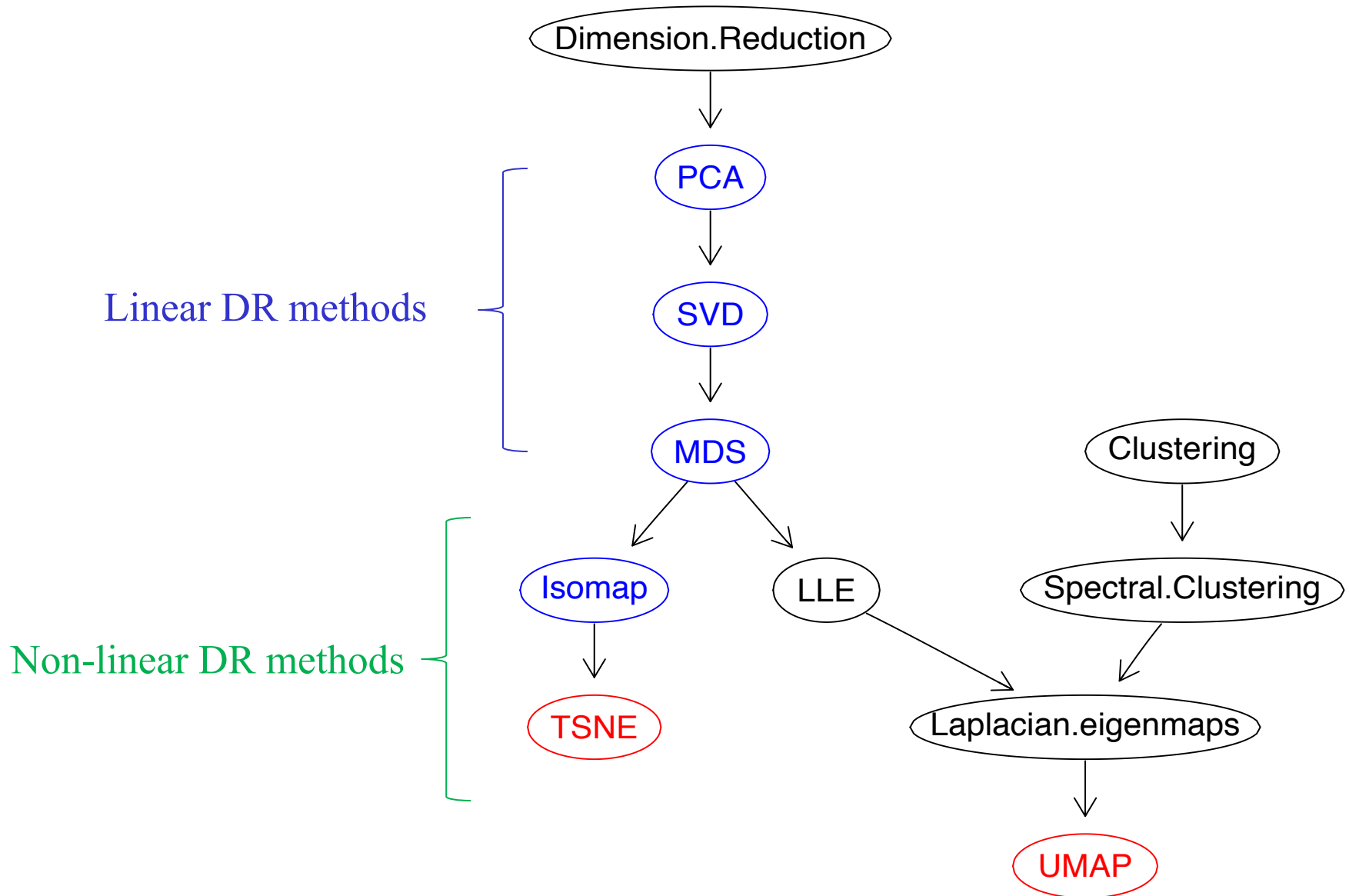
Dimension Reduction Methods: From PCA to TSNE and UMAP

Maxwell Lee

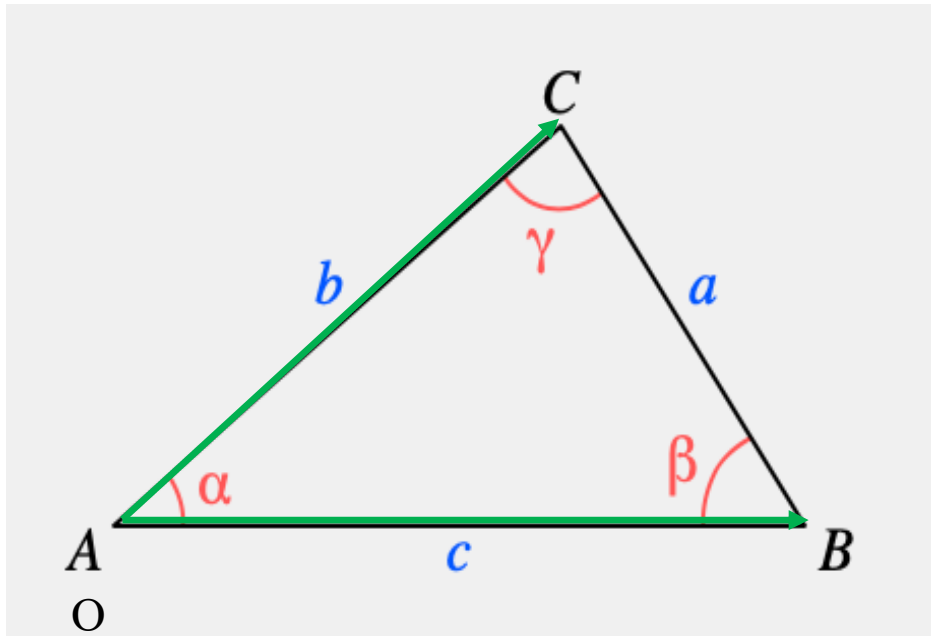
High-dimension Data Analysis Group
Laboratory of Cancer Biology and Genetics
Center for Cancer Research
National Cancer Institute

May 7, 2020

Road Map for Dimension Reduction Methods



The Dot Product of Two Vectors is the Difference Between the Squared Distances (Law of Cosines)



$$a^2 = b^2 + c^2 - 2bc \cos(\alpha)$$

$$bc \cos(\alpha) = -\frac{1}{2}(a^2 - b^2 - c^2)$$

$$\mathbf{b} \cdot \mathbf{c} = -\frac{1}{2}(a^2 - b^2 - c^2)$$

Warren Torgerson in 1958

Eigen Decomposition of Gram Matrix (Similarity Matrix)

$$G = \begin{bmatrix} g_{11} & g_{12} & \cdots & g_{1n} \\ g_{21} & g_{22} & \cdots & g_{2n} \\ \cdot & & & \cdot \\ \cdot & & & \cdot \\ g_{n1} & g_{n2} & \cdots & g_{nn} \end{bmatrix}$$

g_{ij} is dot product between element i and j
which captures similarity or relatedness

$$G = U\Lambda U^T$$

$$Z = U\Lambda^{1/2}$$

G: Gram matrix or kernel matrix

U: Eigen vector

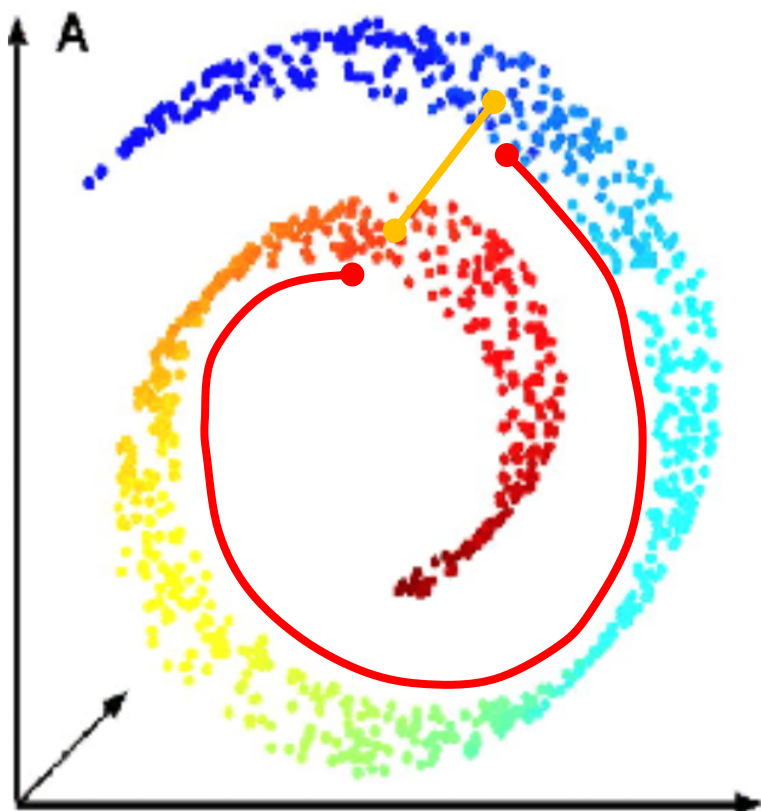
Λ : Eigen value

Z: principal component

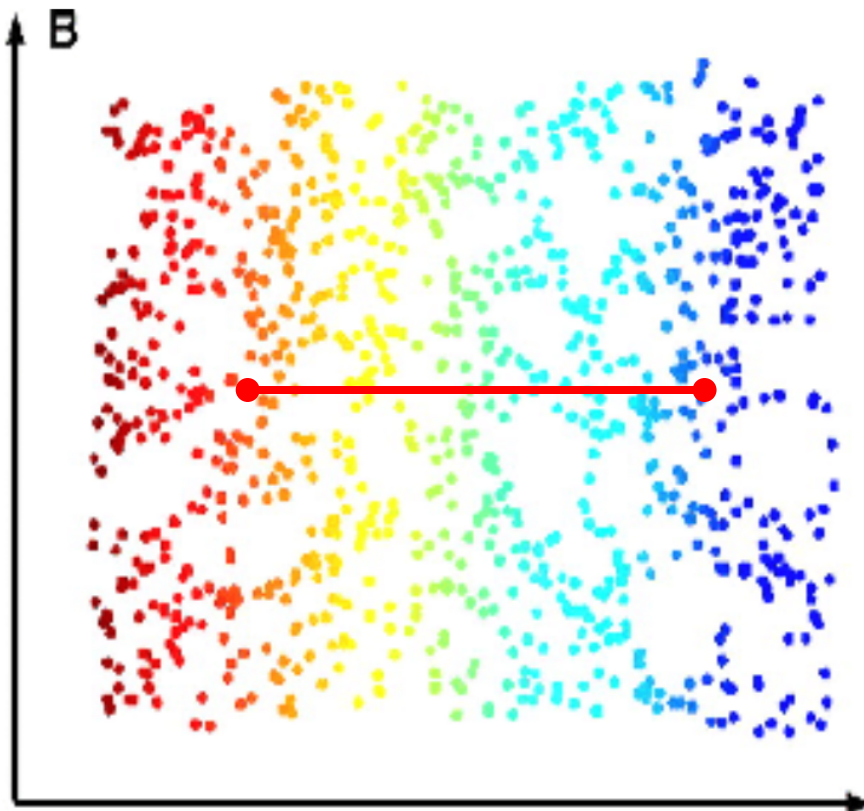
Nonlinear Dimension Reduction of Swiss Roll Dataset

Swiss roll manifold in 3D $\xrightarrow{\text{unfolding}}$ 2D sheet

—●— Euclidean distance —●— Geodesic distance



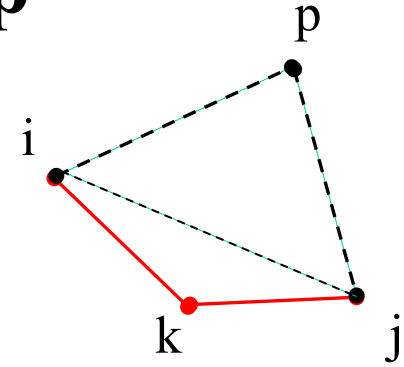
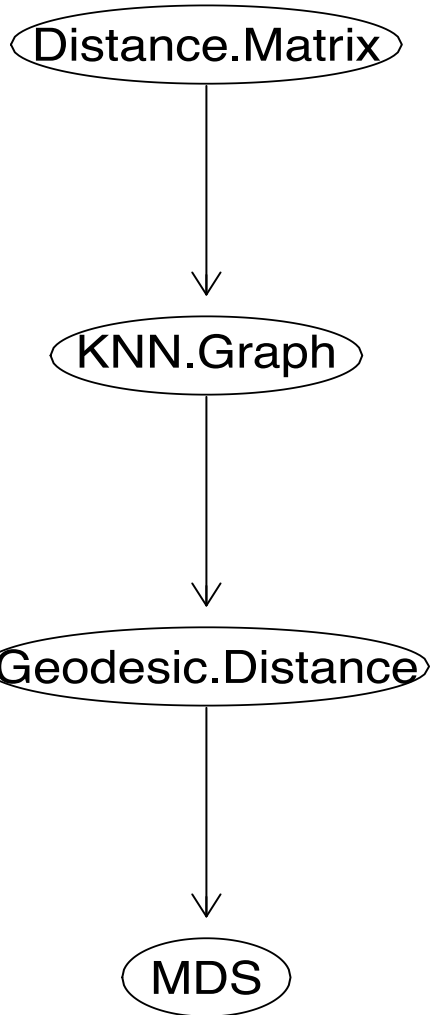
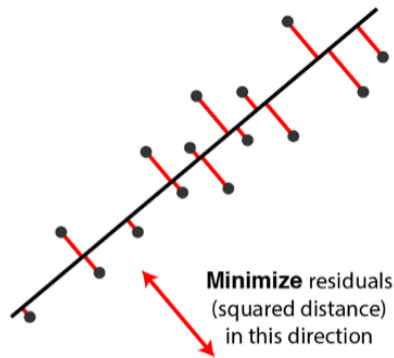
3-dimension



2-dimension

Algorithm of Isomap

KNN: k nearest neighbor



d_{ij} through k is the shortest path.

$$E = \|\tau(D_G) - \tau(D_Y)\|_{L^2}$$

$$\tau(D) = -1/2(HDH)$$

$$H = I - 1/n(ee^T)$$

E : cost function

D_G : distance matrix in high dim

D_Y : distance matrix in low dim

τ : transform D to Gram matrix

H : centering matrix

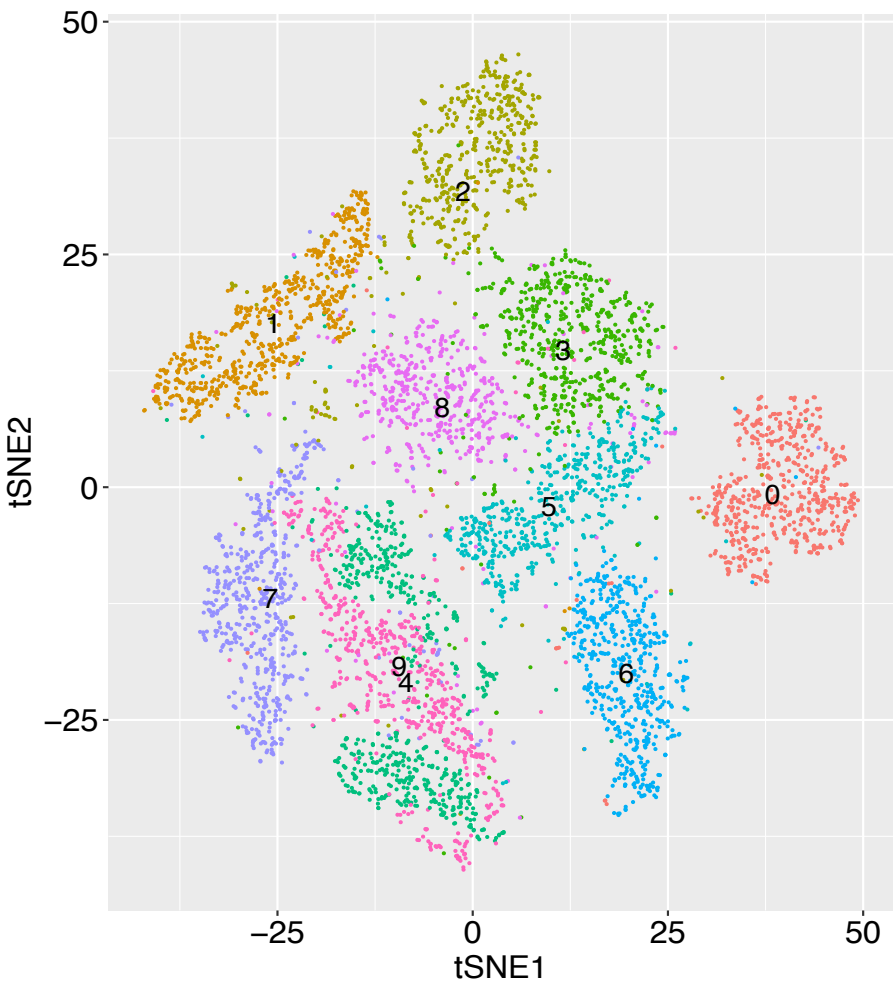
I : identity matrix

e : vector of 1

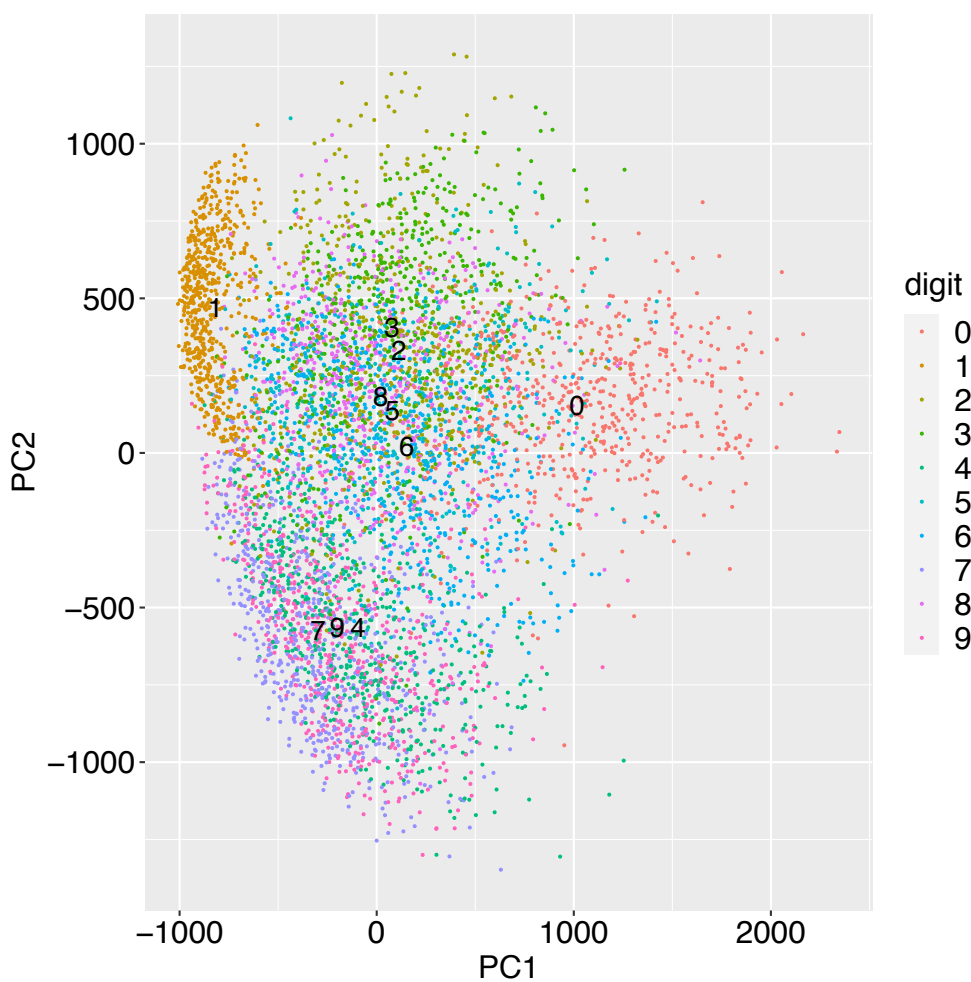
TSNE Versus PCA of the Same MNIST Dataset

sample size n=6000

TSNE



PCA

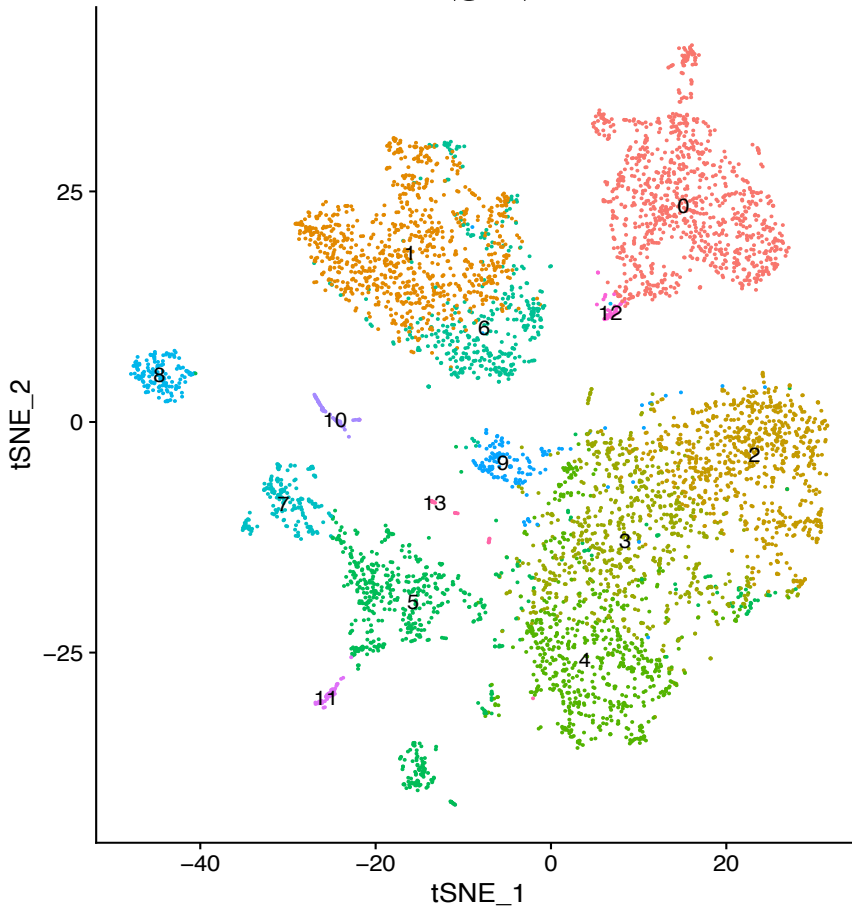


TSNE vs. PCA of a Single Cell RNAseq Data

cell number n~6000

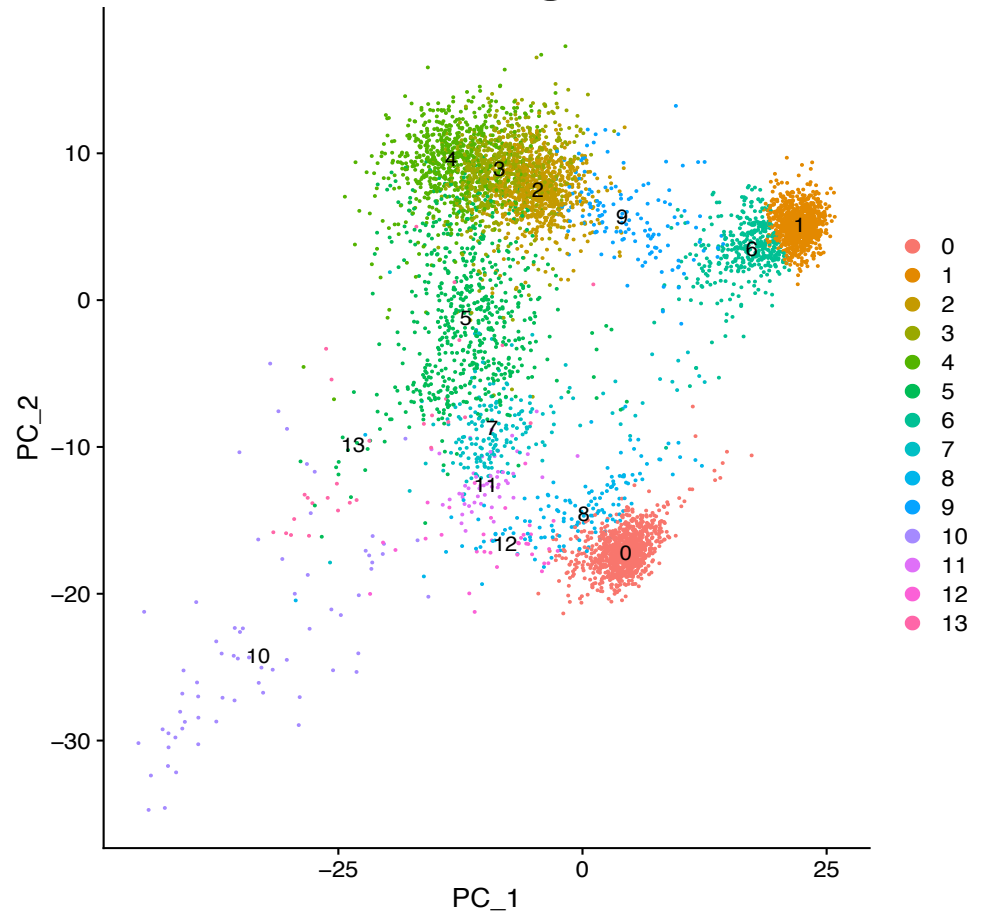
Clusters were identified before TSNE and PCA analysis

TSNE



Cells in cluster are more spread out.

PCA

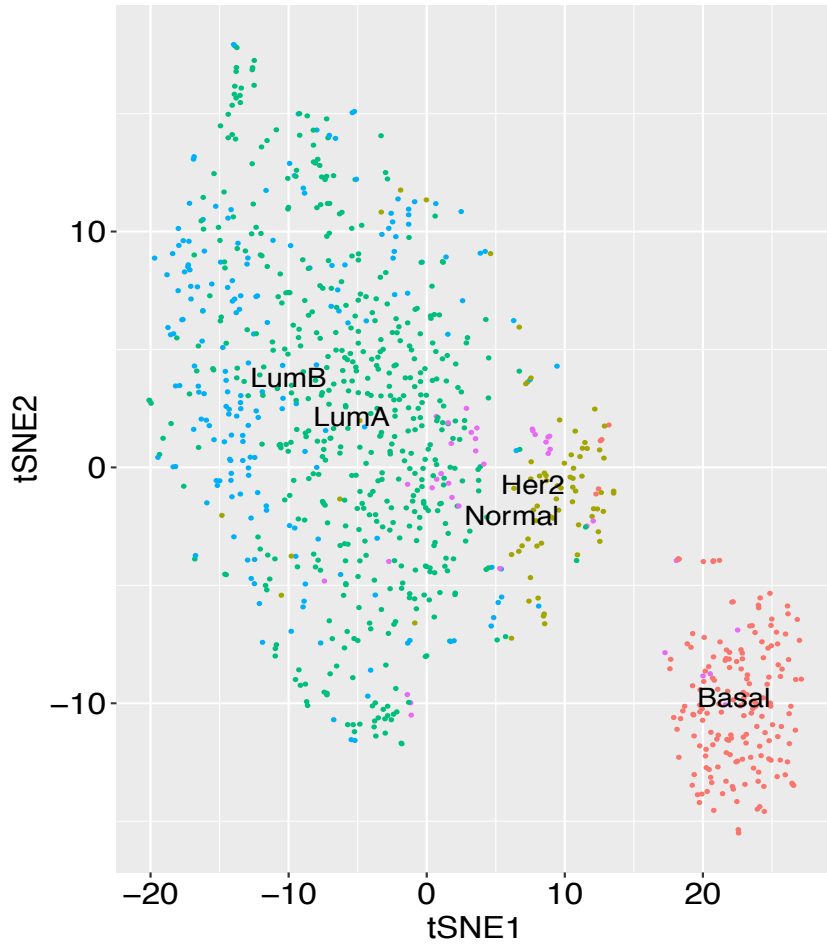


Variance of PC is driven by outliers.

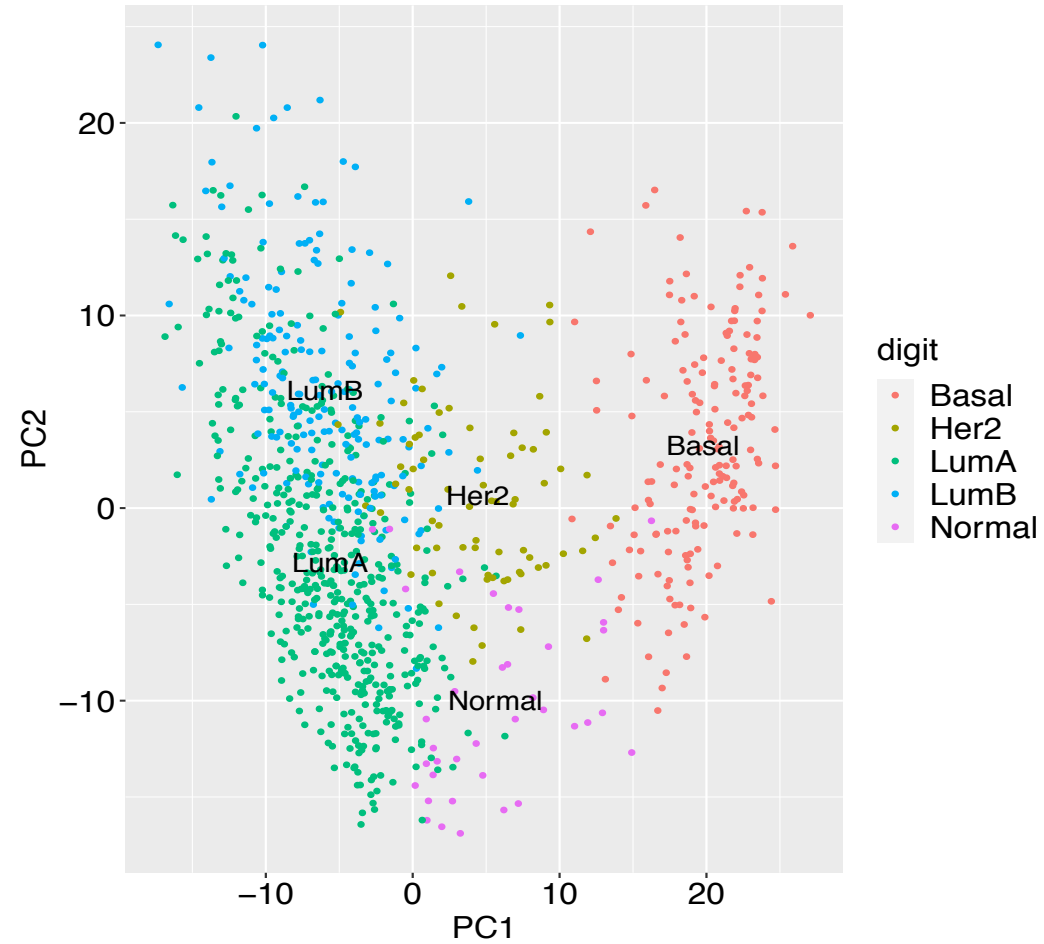
TSNE vs. PCA of TCGA Breast Cancer Data

sample size n=977

TSNE

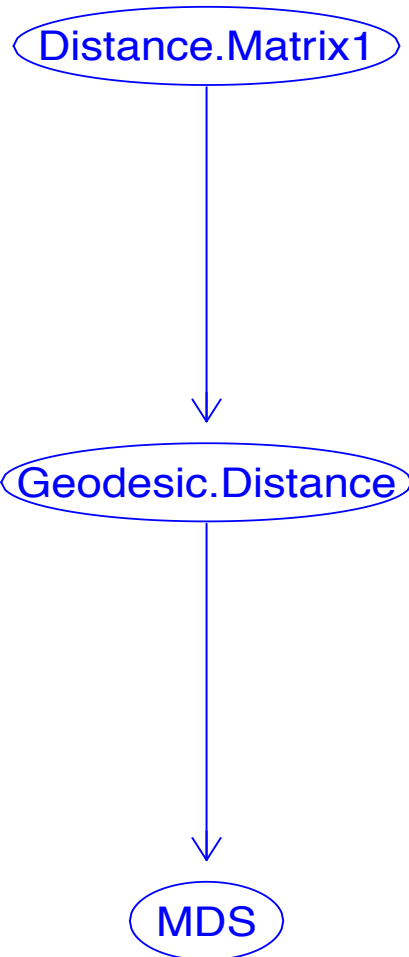


PCA

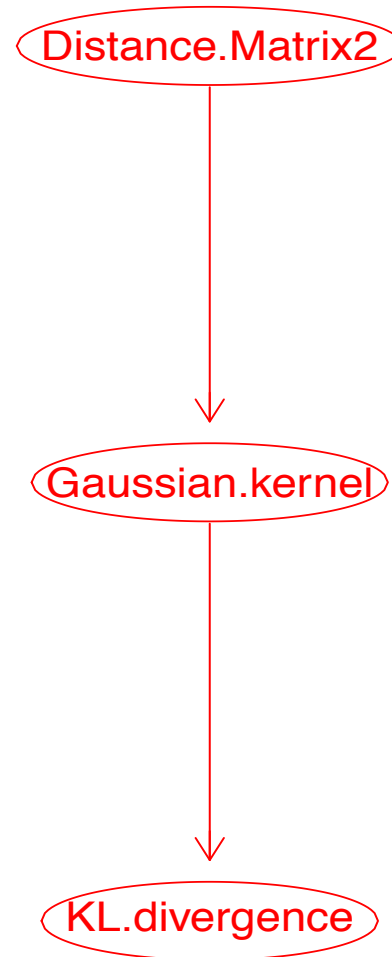


Isomap vs. TSNE

Isomap

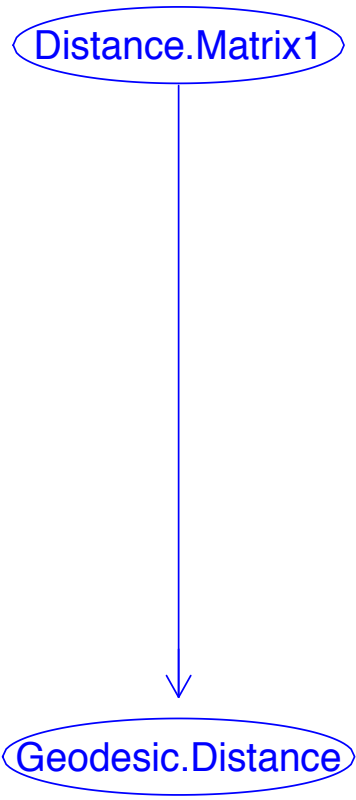


TSNE

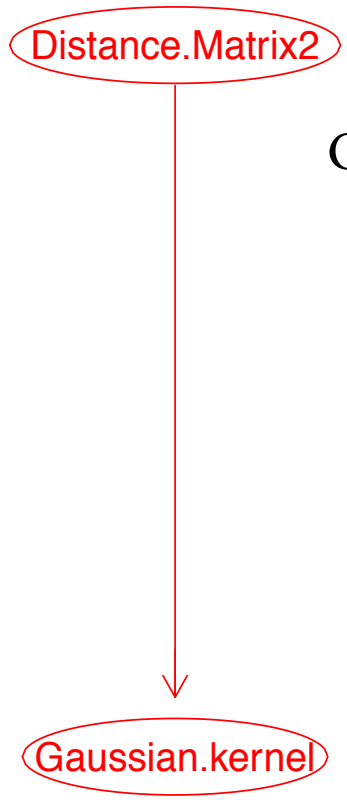


Isomap vs. TSNE

Isomap



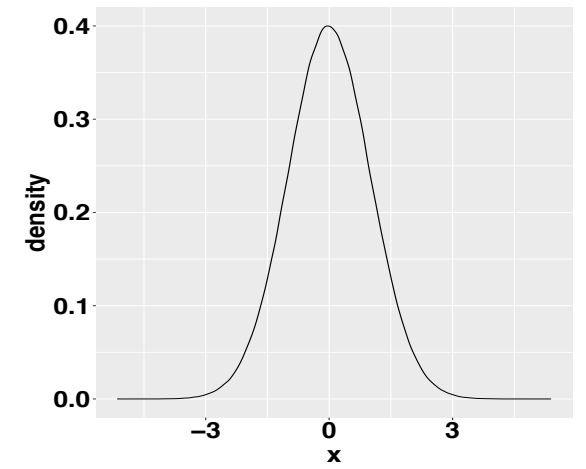
TSNE



Gaussian density function

$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2}$$

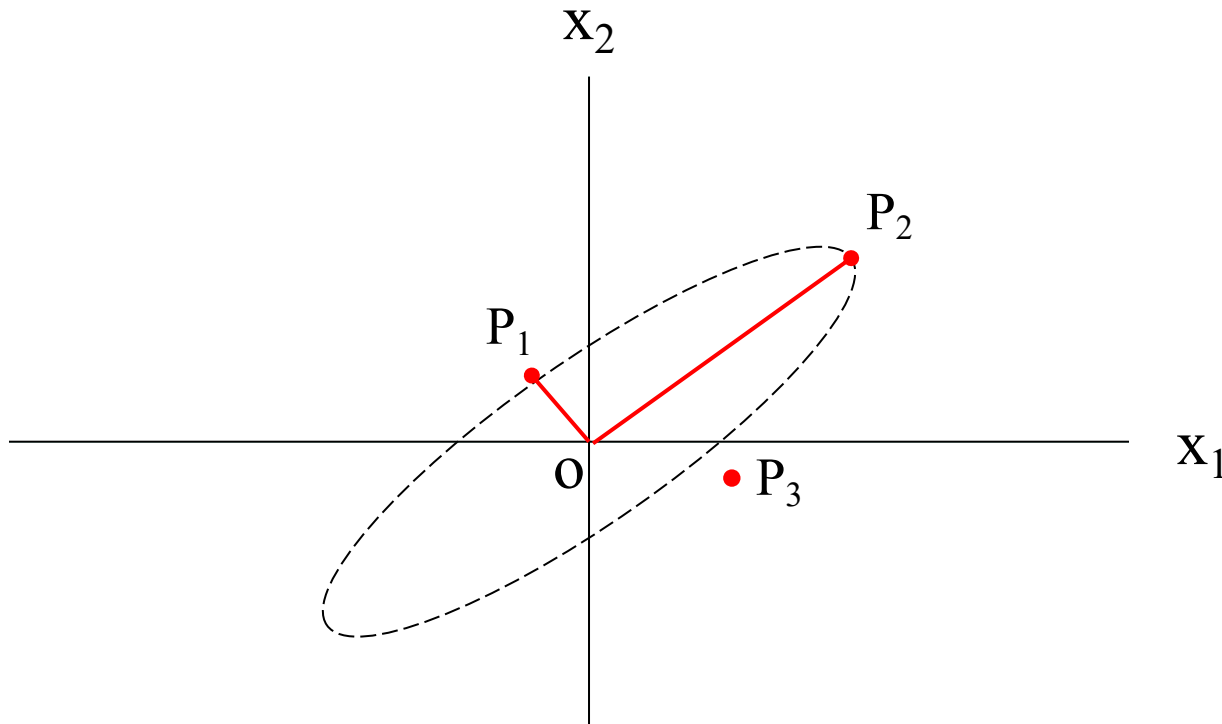
$$z^2 = (x - \mu)^2/\sigma^2$$



D: distance matrix
G: Gram matrix

$$D \longrightarrow G$$

Euclidean Distance vs Mahalanobis Distance

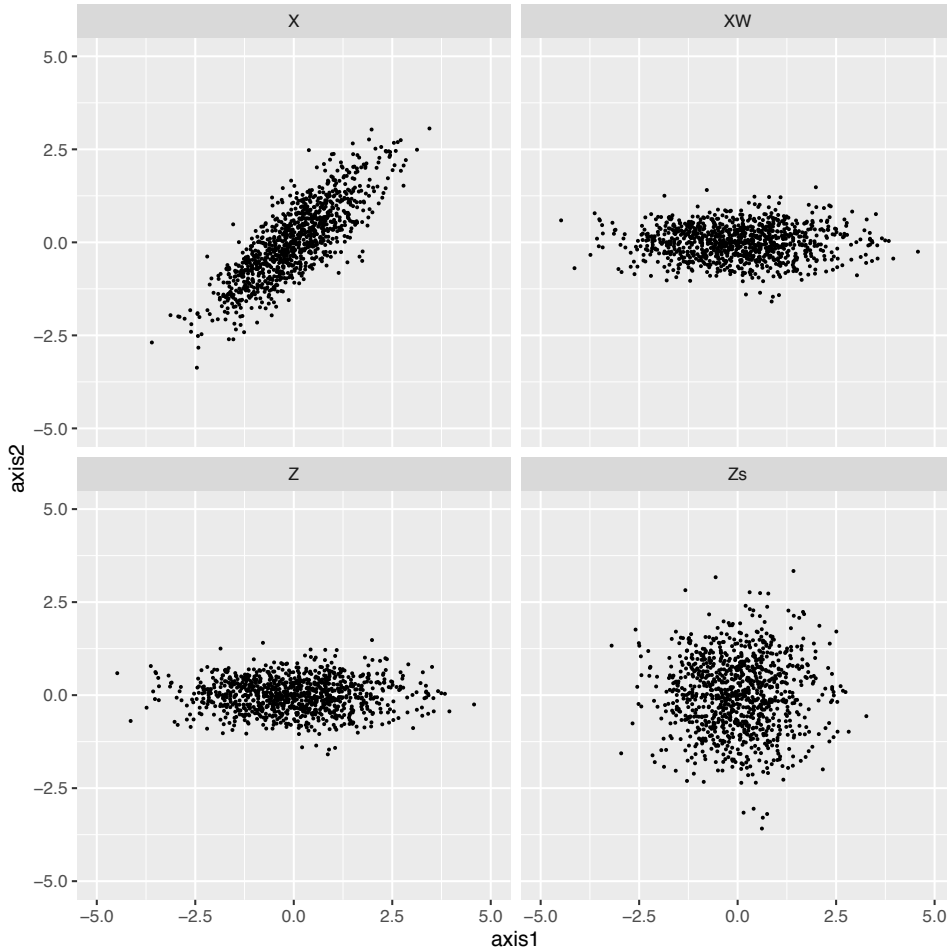


Euclidean distance: $P_1 < P_3 < P_2$

Probability: $p_1 = p_2 > p_3$

Mahalanobis distance is a statistical distance related to probability

Multivariate Gaussian Distribution



Σ : covariance matrix

Σ^{-1} : inverse of Σ

Λ : Diagonal matrix with Eigen values

W : Eigen vectors

Z : Principal Components

Z_s : Standardized Z

z : a sample from Z_s

T : Transposition

μ : mean vector

$$Z = XW$$

$$Z_s = XW\Lambda^{-1/2}$$

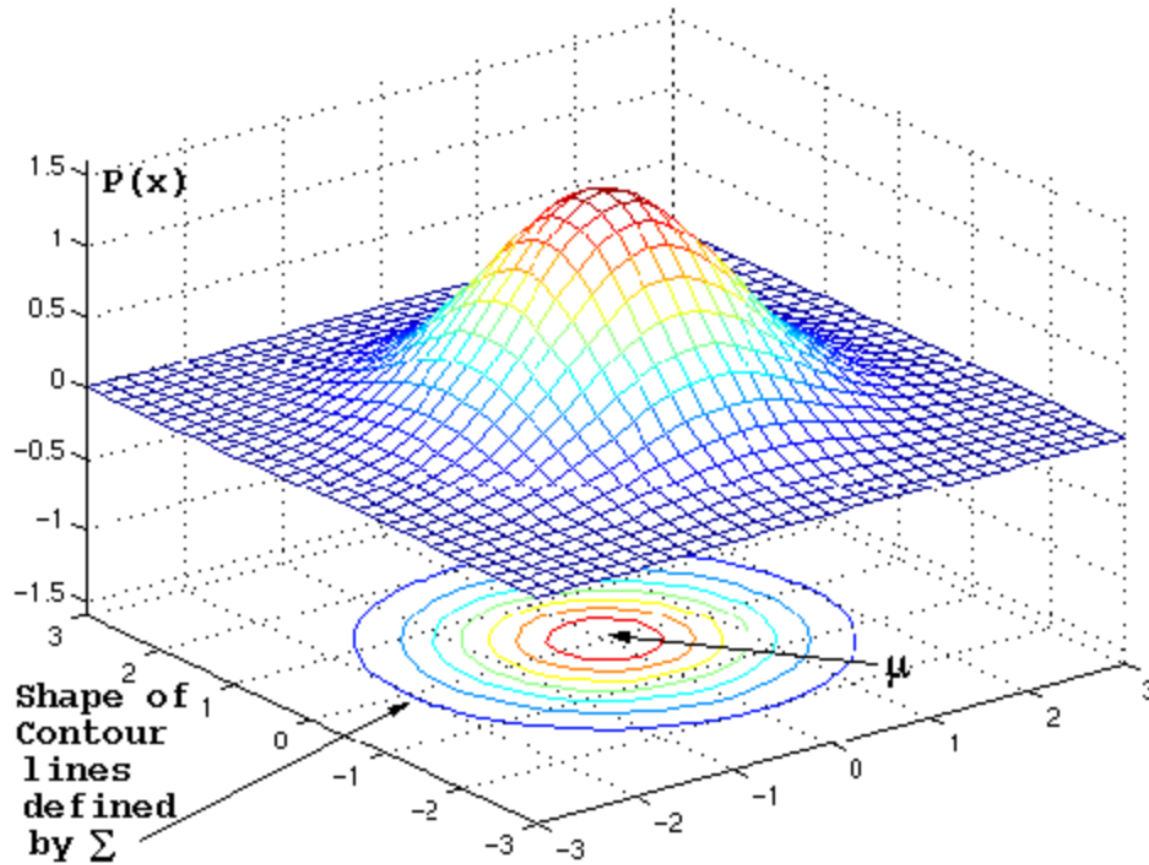
$$z = \Lambda^{-1/2}W^T X$$

$$Z^T Z = X^T W \Lambda^{-1/2} \Lambda^{-1/2} W^T X$$

$$Z^T Z = X^T \Sigma^{-1} X$$

$$p(x; \mu, \Sigma) = \frac{1}{(2\pi)^{\frac{n}{2}} |\Sigma|^{\frac{1}{2}}} \exp\left(-\frac{1}{2}(x - \mu)^T \Sigma^{-1}(x - \mu)\right)$$

Multivariate Gaussian Distribution



T-distributed Stochastic Neighbor Embedding (TSNE)

Isomap

Geodesic.Distance



MDS

$$G = U\Lambda U^T$$

$$Z = U\Lambda^{1/2}$$

TSNE

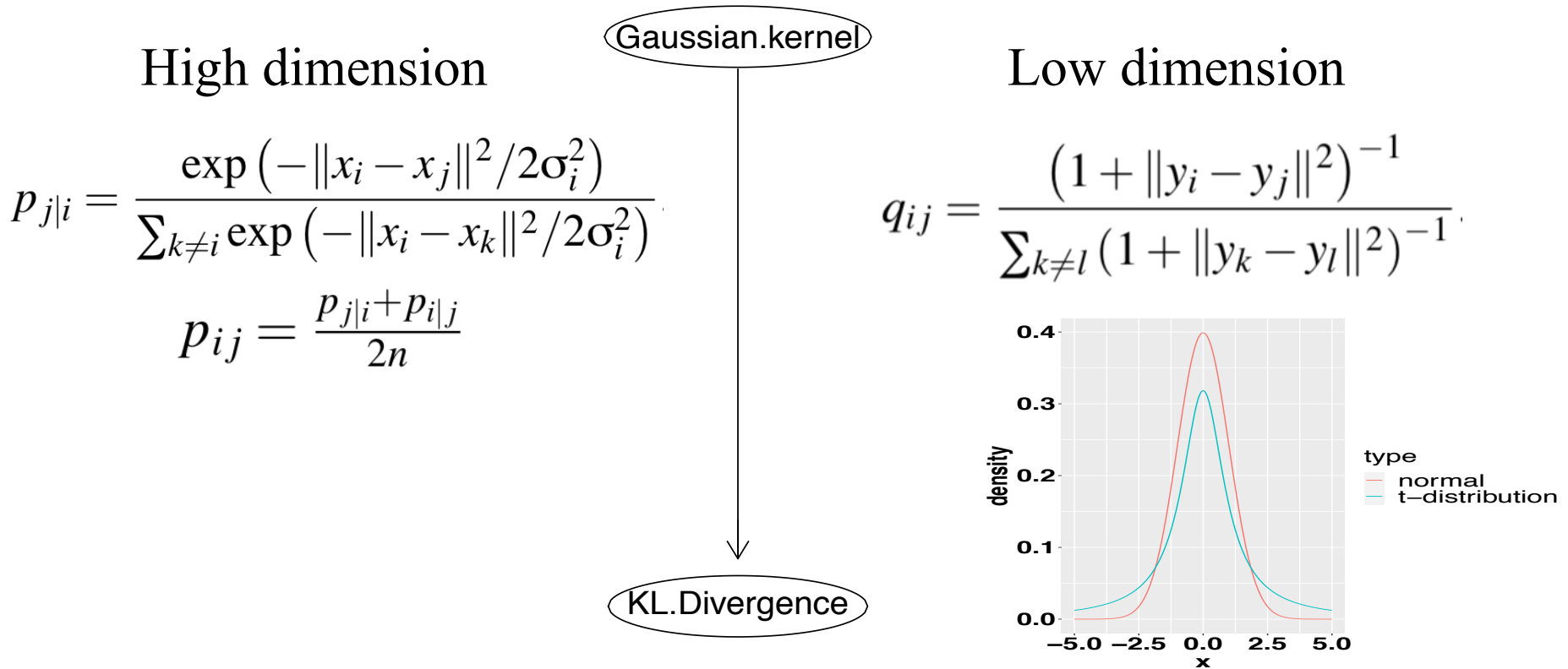
Gaussian.kernel



KL.divergence

$$C = KL(P||Q) = \sum_i \sum_j p_{ij} \log \frac{p_{ij}}{q_{ij}}$$

T-distributed Stochastic Neighbor Embedding (TSNE)



$$C = KL(P||Q) = \sum_i \sum_j p_{ij} \log \frac{p_{ij}}{q_{ij}}$$

$$\frac{\delta C}{\delta y_i} = 4 \sum_j (p_{ij} - q_{ij})(y_i - y_j) (1 + \|y_i - y_j\|^2)^{-1}$$

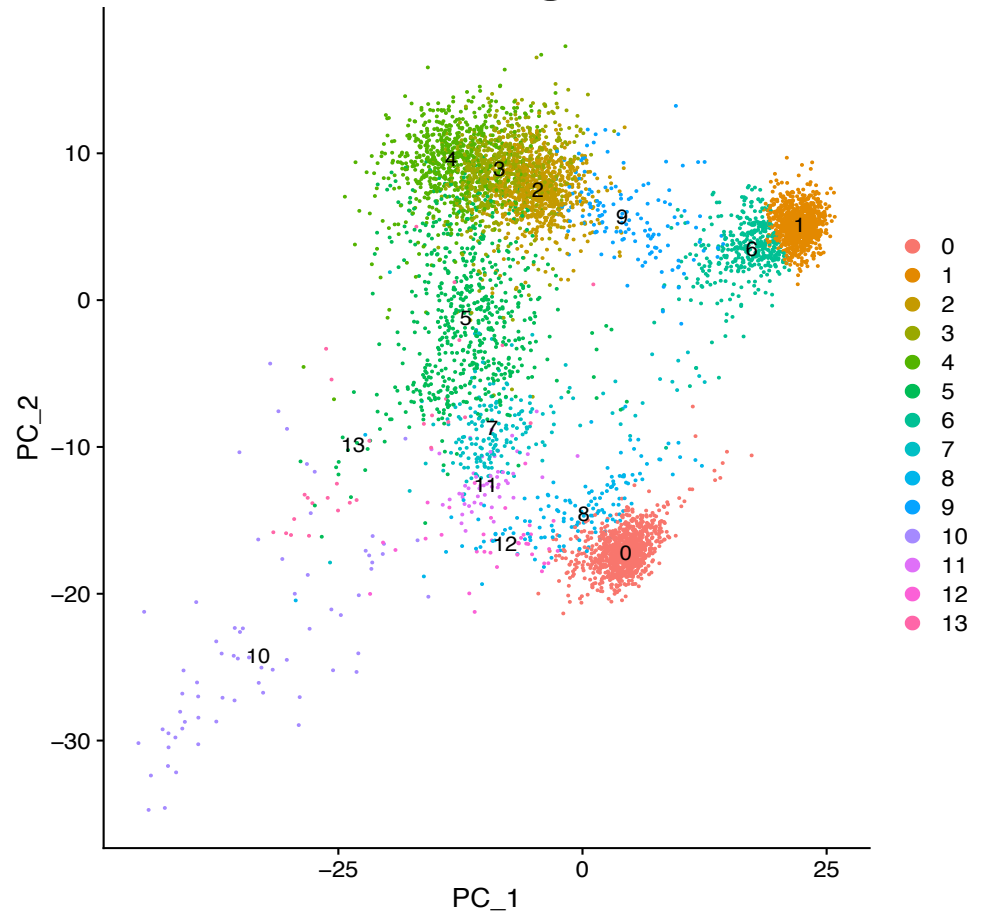
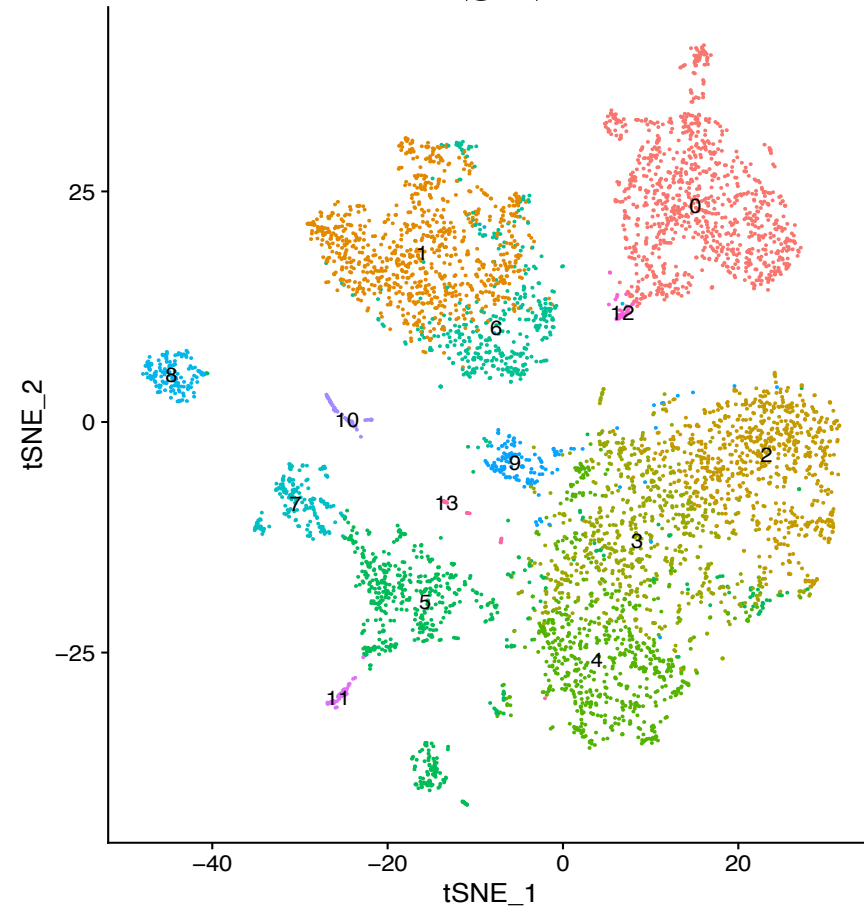
TSNE vs. PCA of a Single Cell RNAseq Data

cell number n~6000

Clusters were identified before TSNE and PCA analysis

TSNE

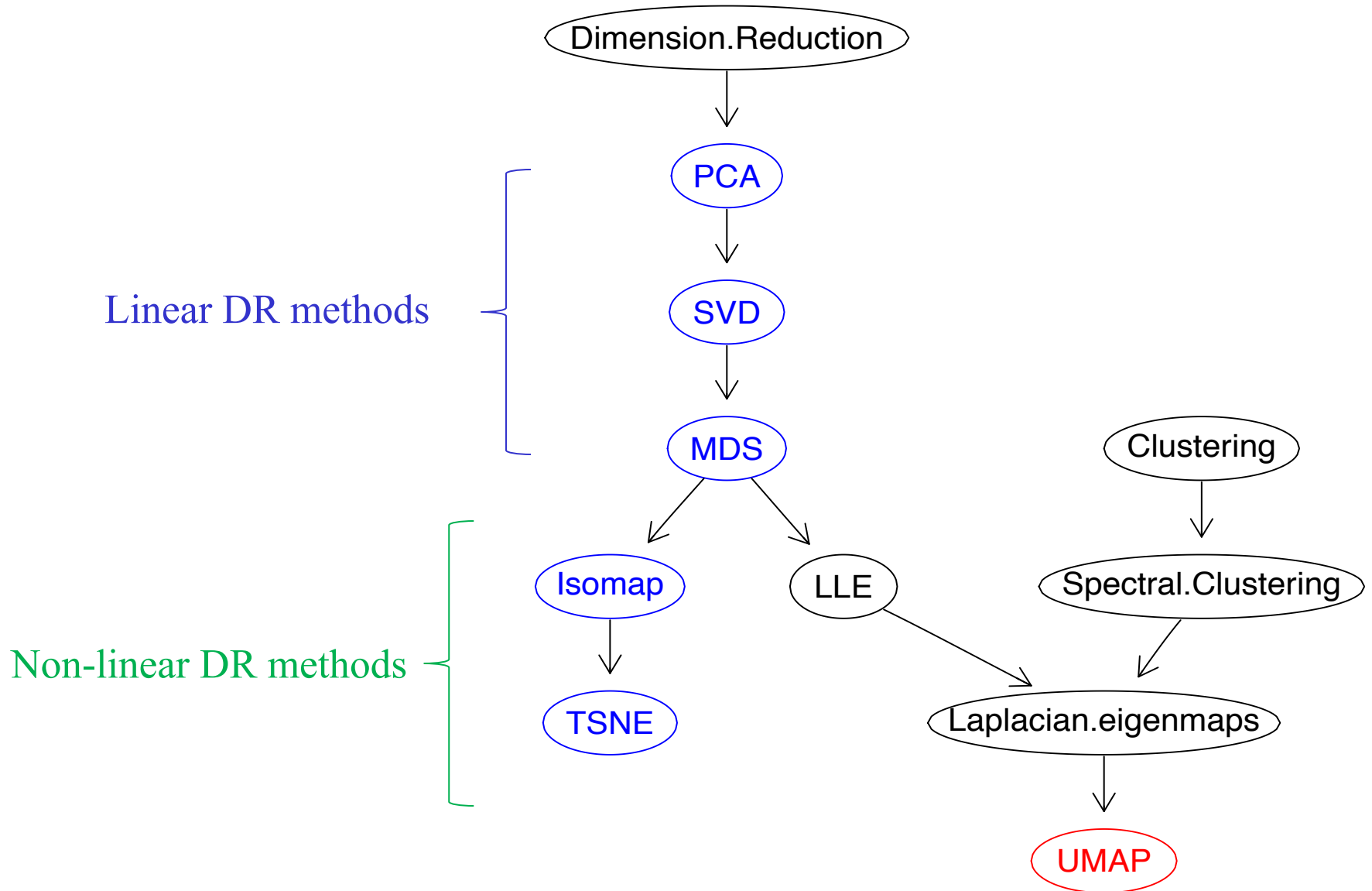
PCA



Cells in cluster are more spread out.

Variance of PC is driven by outliers.

Road Map for Dimension Reduction Methods



Uniform Manifold Approximation and Projection (UMAP)

TSNE is pretty good.

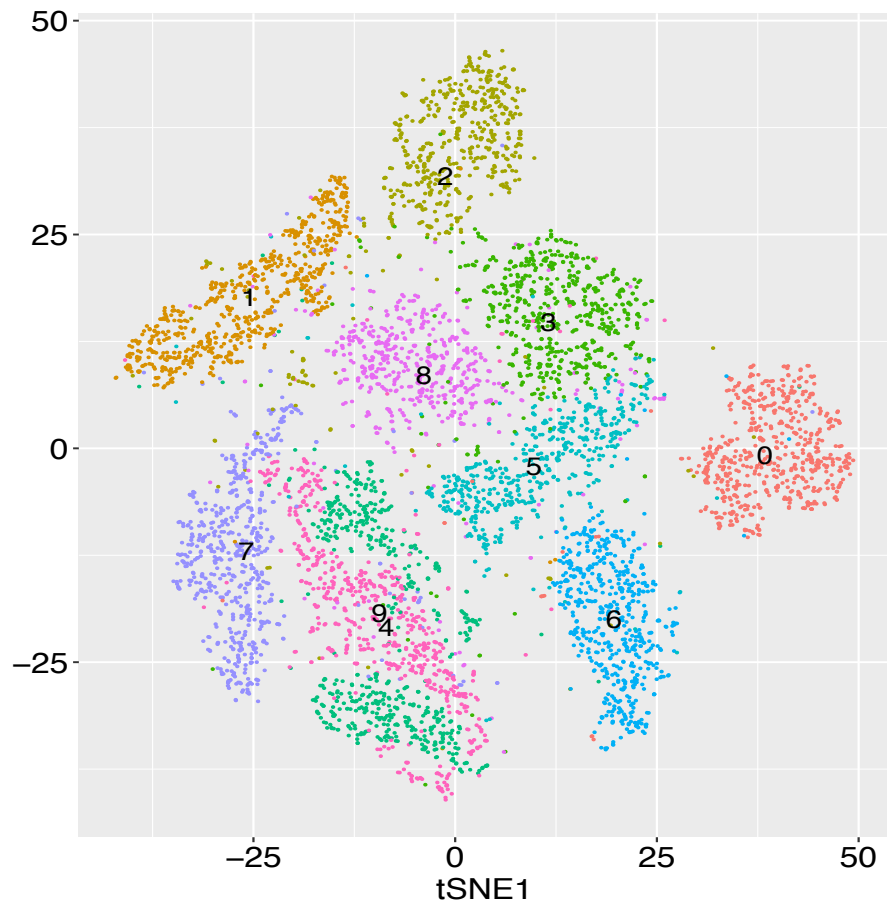
Why do we need UMAP?

	TSNE	UMAP
speed	moderate	fast
Structure preserved	local and global	local and global
Number of components	2	2 or more

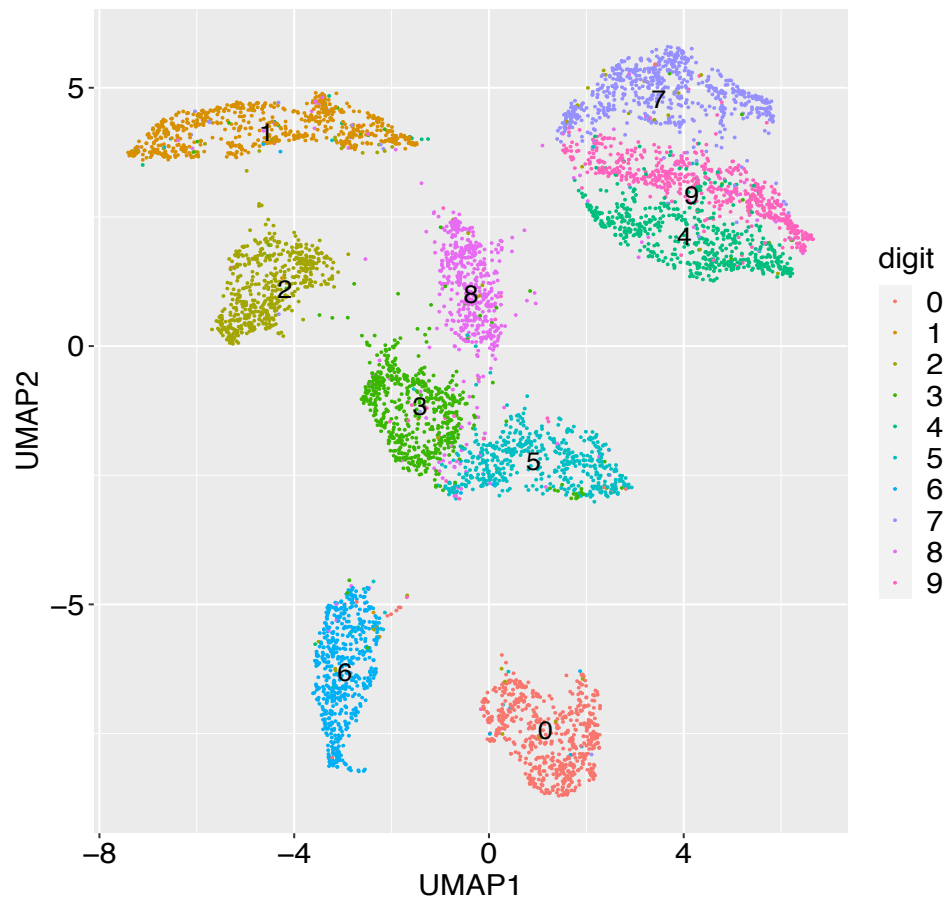
TSNE Versus UMAP of the MNIST Dataset

sample size n=6000

TSNE



UMAP

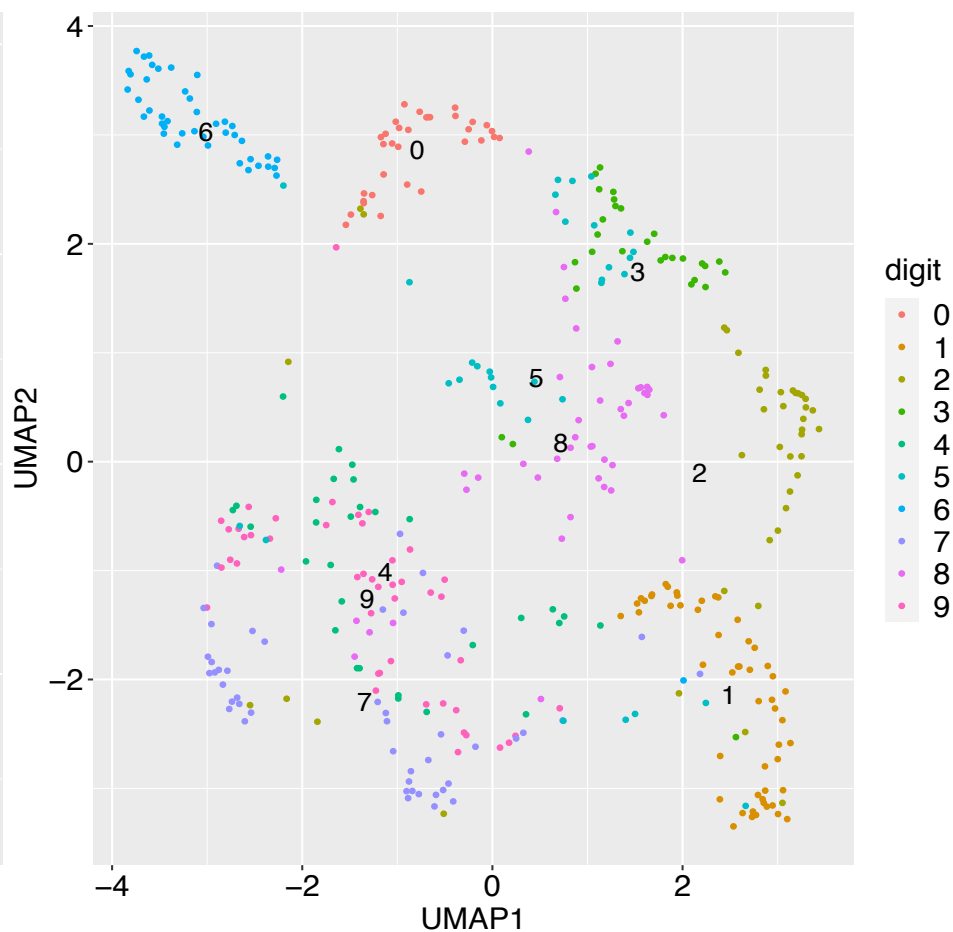
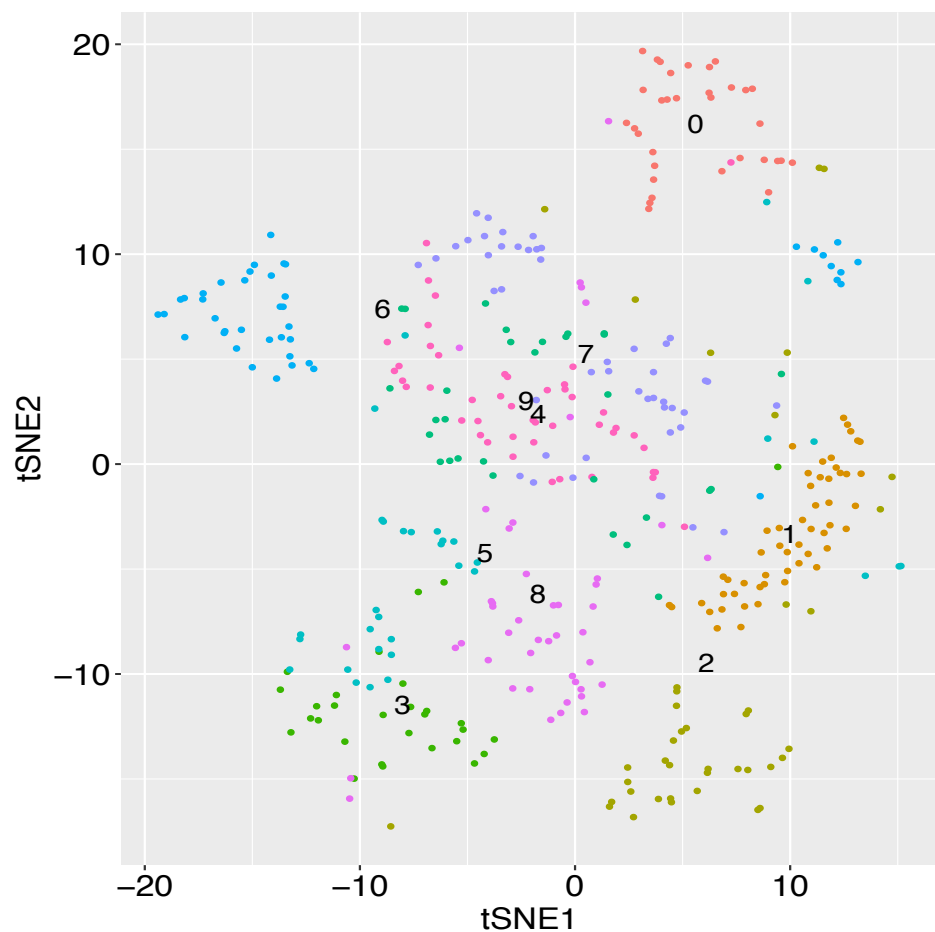


TSNE Versus UMAP of the Same MNIST Dataset

sample size n=400

TSNE

UMAP

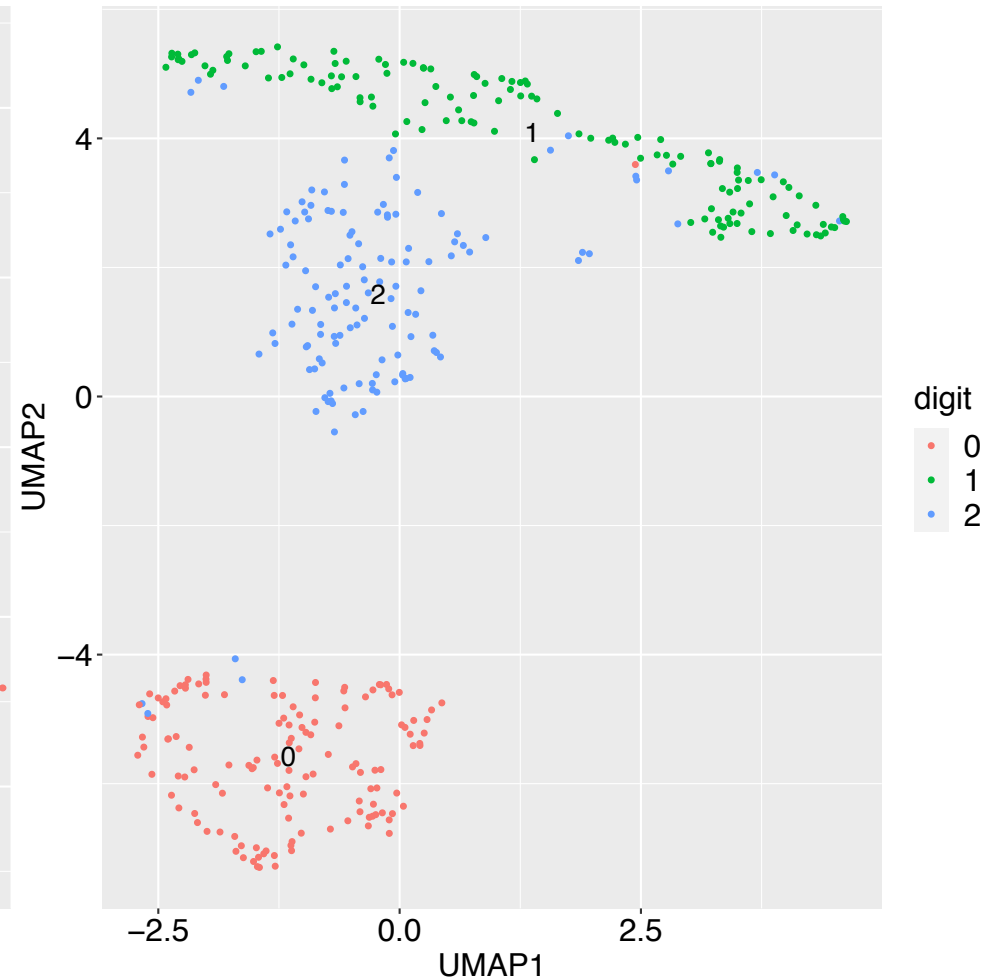


TSNE Versus UMAP of the Same MNIST Dataset

sample size n=400 and digits of 0, 1, and 2

TSNE

UMAP

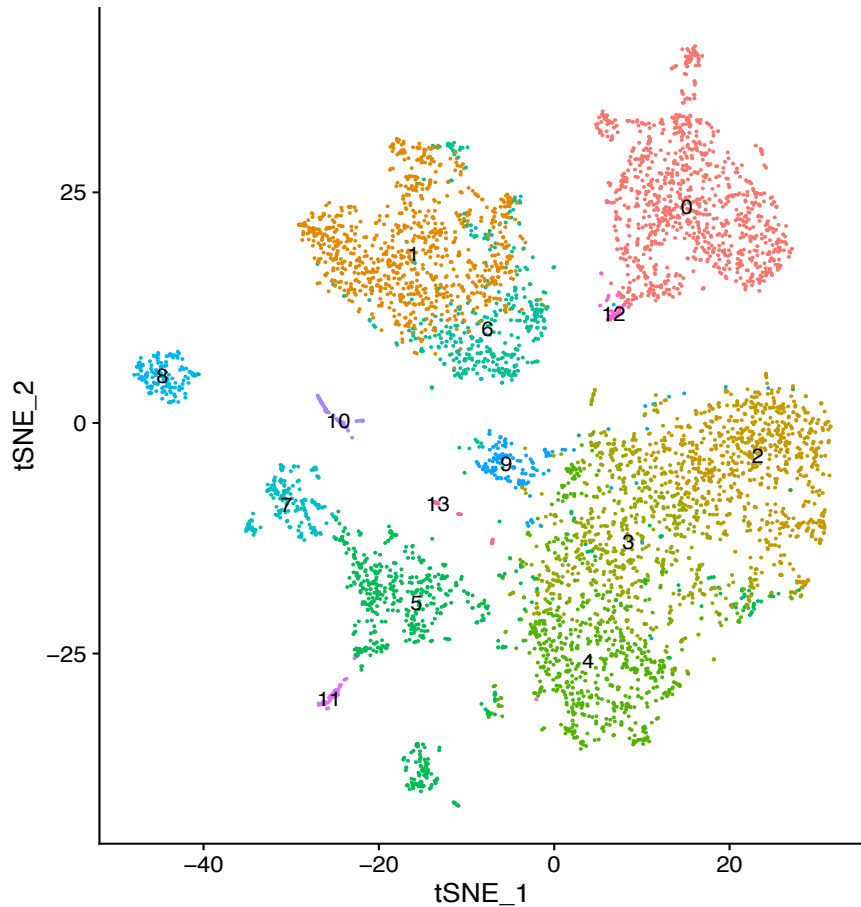


TSNE vs. UMAP of a Same Single Cell RNAseq Data

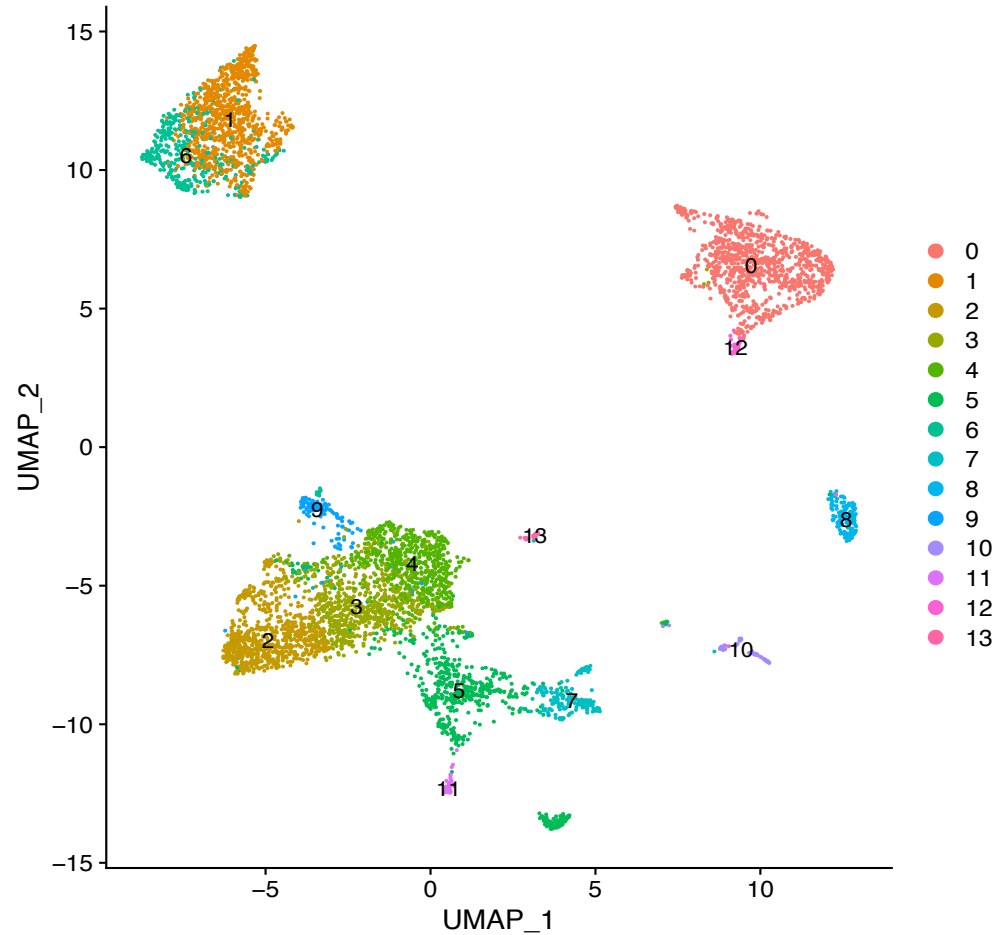
cell number n~6000

Clusters were identified before TSNE and UMAP analysis

TSNE

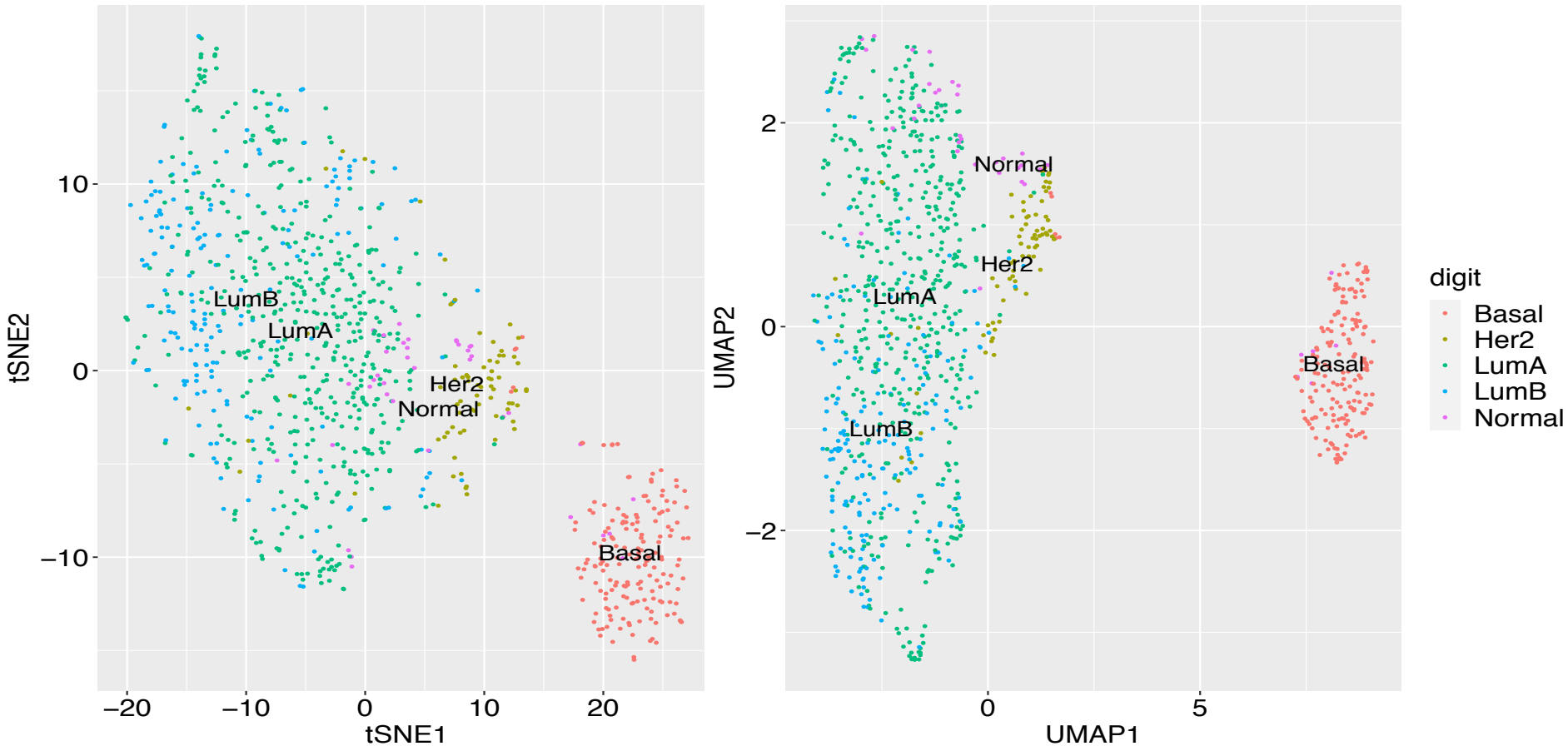


UMAP



TSNE vs. UMAP of TCGA Breast Cancer Data

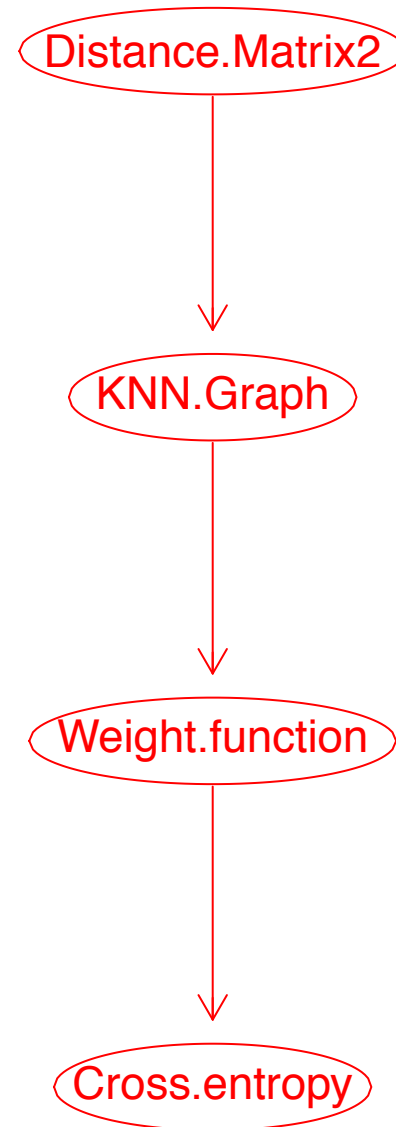
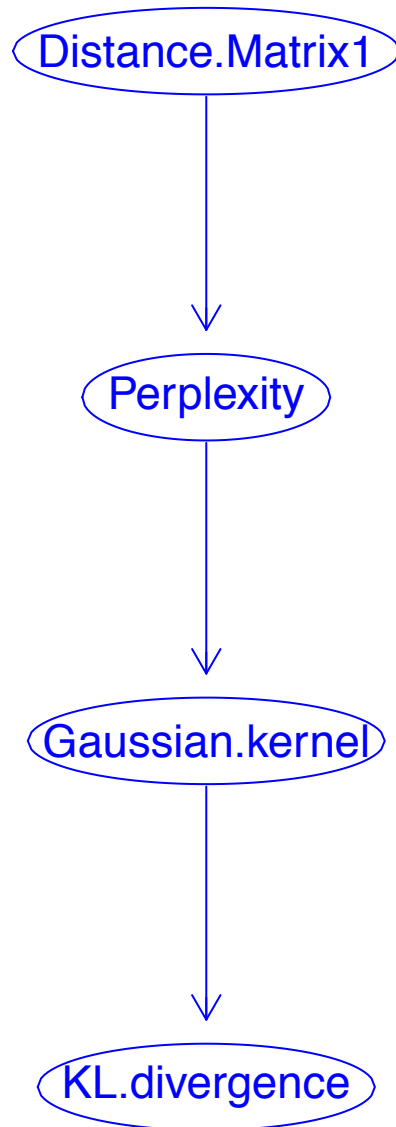
sample size n=977



Comparison of PCA, TSNE, and UMAP

	Data type	Sample size	complexity	Performance
MNIST	image	6000	High	UMAP > TSNE > PCA
ScRNAseq	ScRNAseq	~6000	High?	UMAP ~ TSNE > PCA
TCGA	Bulk RNAseq	~1000	moderate	UMAP ~ TSNE ~ PCA

TSNE vs. UMAP



TSNE vs. UMAP

Distance.Matrix1



Perplexity



Gaussian.kernel

$$p(x; \mu, \Sigma) = \frac{1}{(2\pi)^{\frac{n}{2}} |\Sigma|^{\frac{1}{2}}} \exp\left(-\frac{1}{2}(x - \mu)^T \Sigma^{-1}(x - \mu)\right)$$

Distance.Matrix2



KNN.Graph

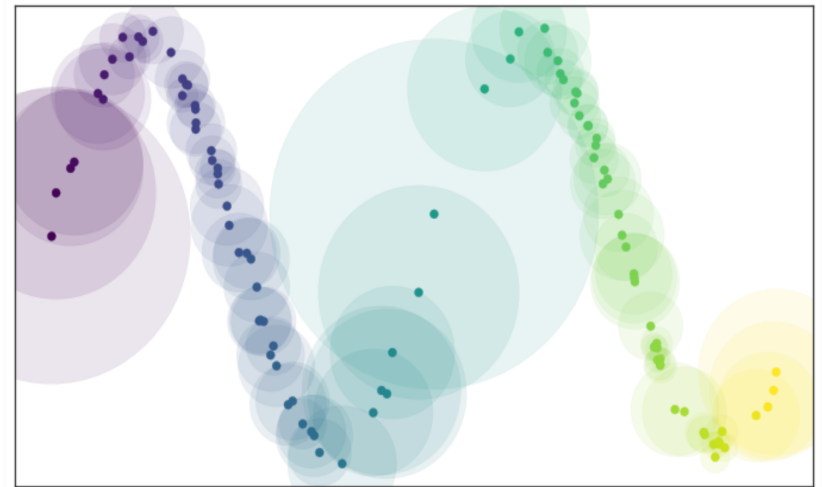


Weight.function

$$w((x_i, x_{i_j})) = \exp\left(\frac{-\max(0, d(x_i, x_{i_j}) - \rho_i)}{\sigma_i}\right)$$

$$B = A + A^T - A \circ A^T$$

$$\sum_{j=1}^k \exp\left(\frac{-\max(0, d(x_i, x_{i_j}) - \rho_i)}{\sigma_i}\right) = \log_2(k)$$



ρ_i : shortest distance of x_i neighbors

Uniform Manifold Approximation and Projection (UMAP)

Weight.function

High-dimension

Low-dimension

Laplacian Eigenmaps



$$w((x_i, x_{i_j})) = \exp\left(\frac{-\max(0, d(x_i, x_{i_j}) - \rho_i)}{\sigma_i}\right)$$

$$B = A + A^T - A \circ A^T$$

$$\Phi(\mathbf{x}, \mathbf{y}) = (1 + a(\|\mathbf{x} - \mathbf{y}\|_2^2)^b)^{-1}$$

Cross.entropy

TSNE cost function

UMAP cost function

$$C = KL(P||Q) = \sum_i \sum_j p_{ij} \log \frac{p_{ij}}{q_{ij}}$$

$$C((A, \mu), (A, \nu)) = \sum_{a \in A} \mu(a) \log \left(\frac{\mu(a)}{\nu(a)}\right) + (1 - \mu(a)) \log \left(\frac{1 - \mu(a)}{1 - \nu(a)}\right)$$

Road Map for Dimension Reduction Methods

