

Projections and clusterings

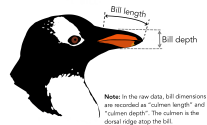
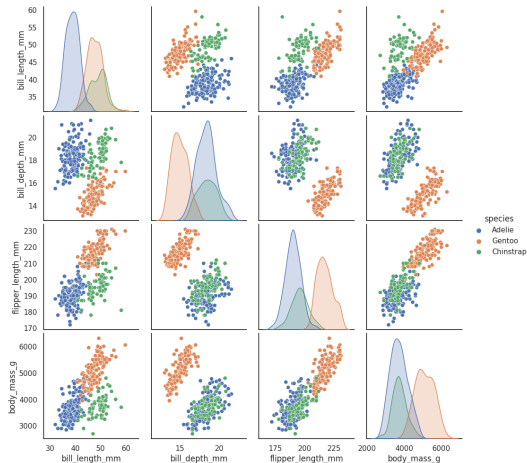
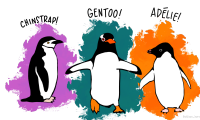
AI for ecologists

Paul Tresson

21/05/25

Introduction

Visualize what is happening in higher dimensions

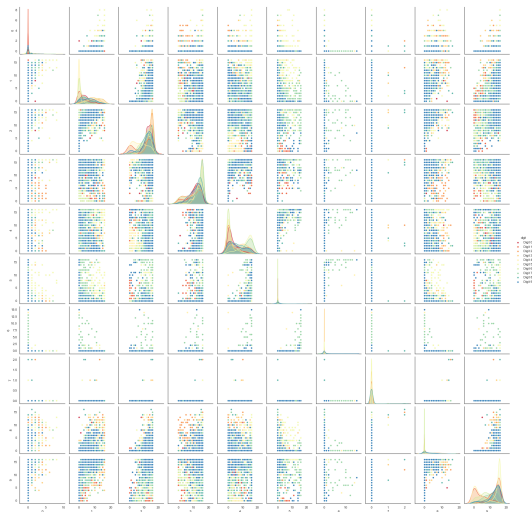


Note: In the raw data, bill dimensions are recorded as "culmen length" and "culmen depth". The culmen is the dorsal ridge atop the bill.

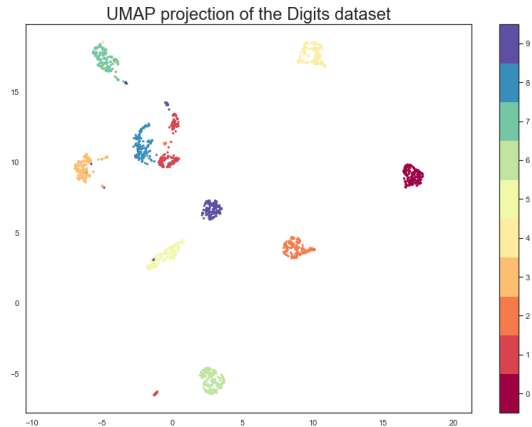
Visualize what is happening in higher dimensions

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2 2 1 3 6 5 8 2 7 0 7 8 6 5 3 6 6 7 6 0
3 3 7 3 3 3 8 3 5 8 9 6 2 7 7 1 6 4 8
4 4 7 4 2 6 4 4 6 2 5 8 2 8 8 0 4 6 7 9
5 5 3 6 1 9 9 5 0 4 8 7 9 9 0 9 3 5 3
6 6 5 6 7 6 0 6 0 1 2 3 5 0 2 1 4 4 0
7 7 1 6 4 1 7 7 9 2 2 4 4 3 2 5 3 4 1
8 8 0 4 6 7 9 8 6 0 4 8 2 5 7 0 9 7 2
9 9 0 9 3 5 8 9 3 3 0 8 3 5 8 9 1 2 3
0 0 2 1 1 4 0 0 2 3 1 7 7 4 6 2 5 7 8 4
1 1 2 5 3 9 7 2 2 1 3 6 6 0 4 8 8 2 6
2 5 9 0 9 7 2 3 3 7 3 3 9 8 7 9 2 4 5 7
3 5 8 3 1 2 3 7 3 3 3 9 8 7 9 2 2 4 5 7
4 6 2 5 7 8 4 4 7 4 2 6 9 8 8 6 0 3 7 8
5 5 0 2 6 2 5 5 3 6 4 4 8 9 9 3 0 1 9 9
6 0 1 8 8 2 6 6 5 6 7 4 7 0 8 3 1 4 5 0
7 5 2 2 4 5 7 7 1 6 3 5 4 4 4 7 7 0 4 1
8 8 6 0 3 7 8 8 0 4 1 4 2 2 1 3 6 5 8 2
9 9 3 0 4 9 9 9 9 3 9 9 9 9 9 9 9 9 9 9

Visualize what is happening in higher dimensions



Visualize what is happening in higher dimensions

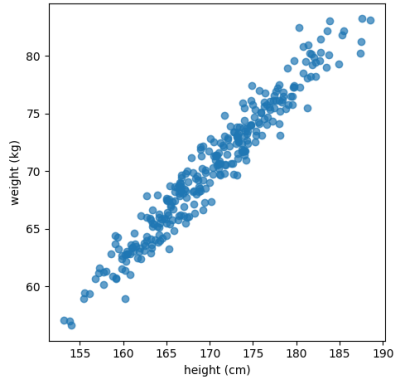


Projections

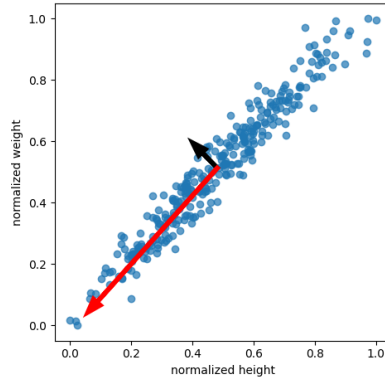
Projections

Principa Component Analysis

PCA



PCA



PCA calculation

$$X = \begin{bmatrix} x_1 & y_1 \\ x_2 & y_2 \\ x_3 & y_3 \\ \dots & \dots \end{bmatrix}$$

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$$C = \frac{1}{n-1} X^T X$$

$$C = \begin{bmatrix} \sigma_x^2 & \sigma_{xy} \\ \sigma_{yx} & \sigma_y^2 \end{bmatrix}$$

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$$Cv = \lambda v$$

$$\begin{bmatrix} \sigma_x^2 & \sigma_{xy} \\ \sigma_{yx} & \sigma_y^2 \end{bmatrix} \begin{bmatrix} v_x \\ v_y \end{bmatrix} = \lambda \begin{bmatrix} v_x \\ v_y \end{bmatrix}$$

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$$P = \begin{bmatrix} v_x & v_y \end{bmatrix}$$

PCA calculation

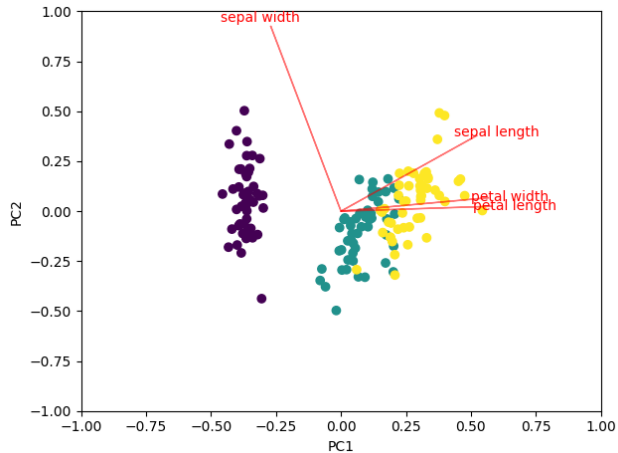
```
# normalize
normalized_data = (points - np.min(points, axis=0)) / (
    np.max(points, axis=0) - np.min(points, axis=0)
)

# get covariance
cov = np.cov(normalized_data, rowvar=False)

# calculate eigenvalues and eigenvectors of the covariance matrix
eigvals, eigvecs = np.linalg.eig(cov)

# scale eigenvectors
scaled_eigvecs = eigvecs * np.sqrt(eigvals)
```

PCA interpretability



PCA advantages and drawbacks

Advantages

- fast

Drawbacks

PCA advantages and drawbacks

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- scales well

Drawbacks

PCA advantages and drawbacks

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- fast
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- explanatory

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PCA advantages and drawbacks

Advantages

- fast
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Drawbacks

- not suited for non-linear data

Non linear data

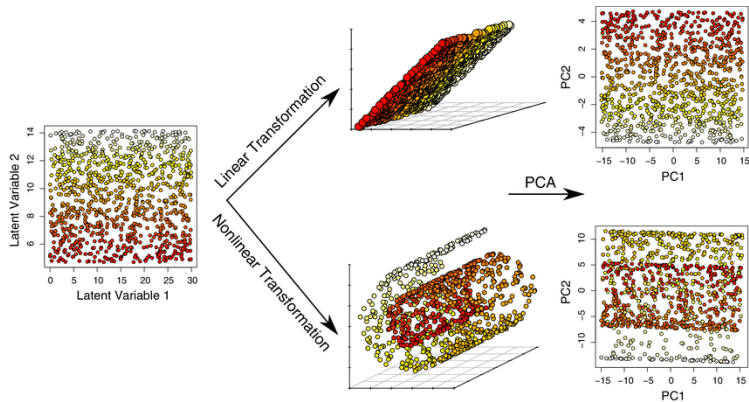


Figure from Du, 2019

Projections

UMAP

How to work with non linear data

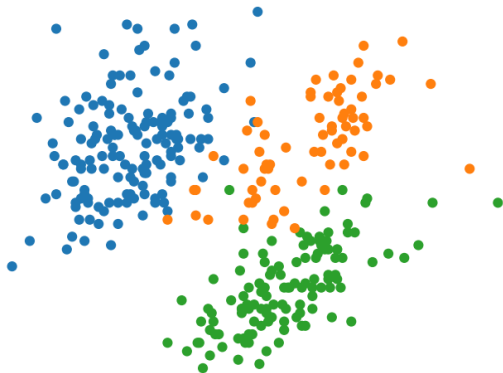
1. Find a good representation of the data in high dimension
2. Fit a good representation of in low dimension

- **SNE** (Stochastic Neighbor Embedding) Hinton and Roweis, 2002

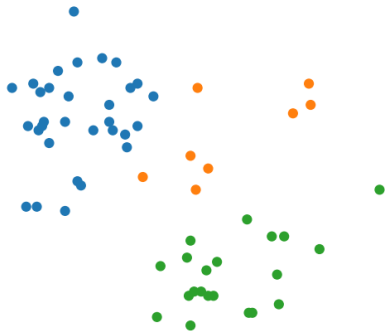
- **SNE** (Stochastic Neighbor Embedding) Hinton and Roweis, 2002
- **T-SNE** (T-distributed SNE) Van der Maaten and Hinton, 2008

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- **UMAP** (Uniform Manifold Approximation and Projection) McInnes et al., 2018

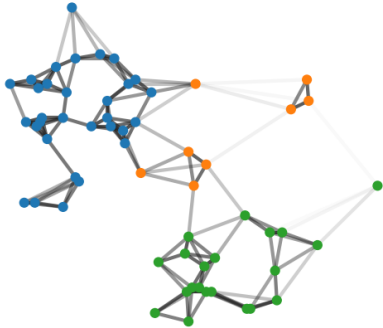
UMAP : Finding high dimension graph



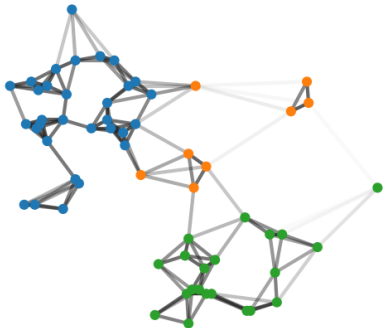
UMAP : Finding high dimension graph



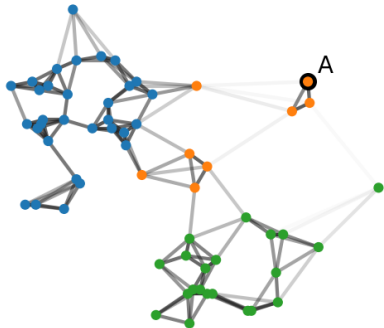
UMAP : Finding high dimension graph



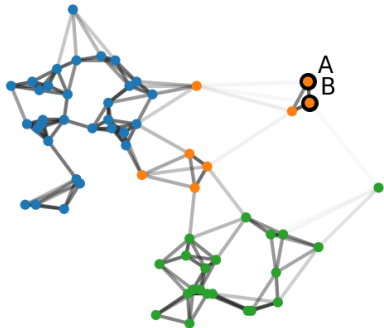
UMAP : Fitting low dimensional representation



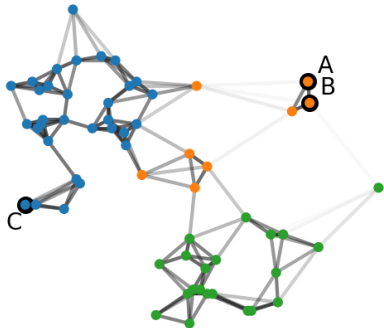
UMAP : Fitting low dimensional representation



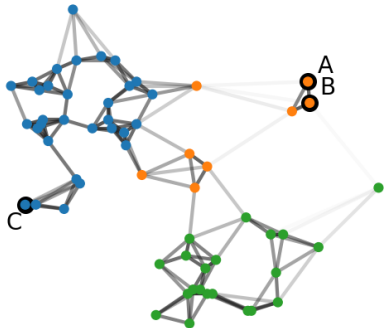
UMAP : Fitting low dimensional representation



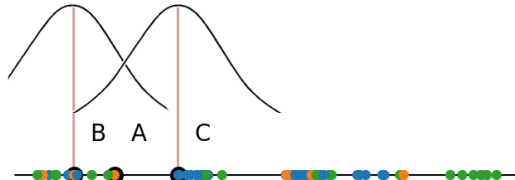
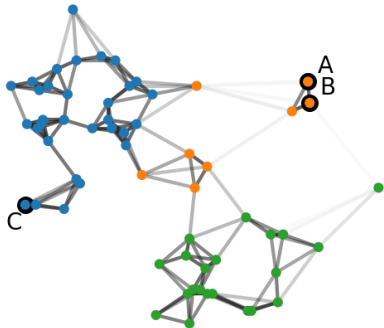
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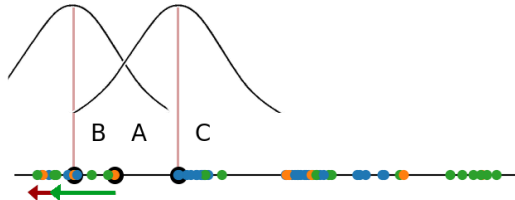
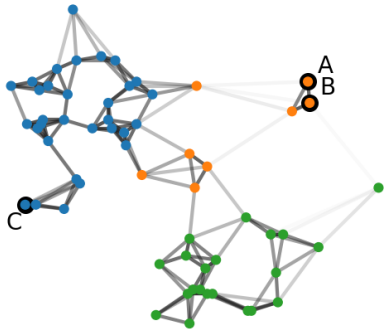
UMAP : Fitting low dimensional representation



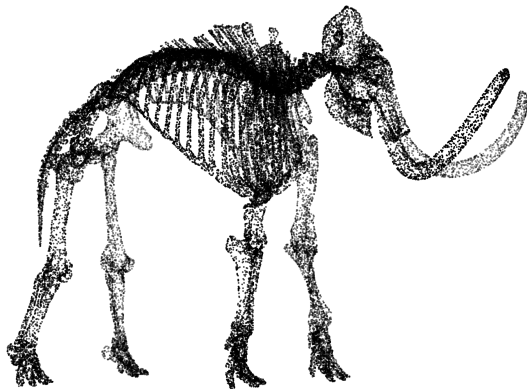
UMAP : Fitting low dimensional representation



UMAP : Fitting low dimensional representation

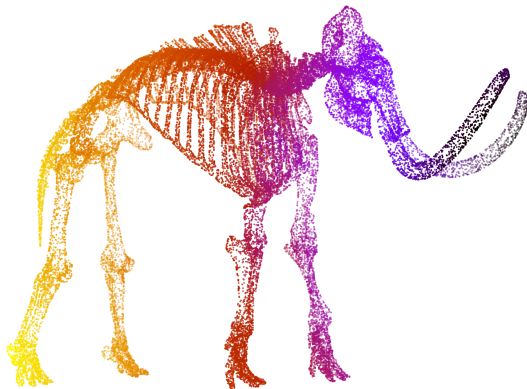


Mammoth example



Mammoth dataset by the Smithsonian, adapted from deepia

Mammoth example

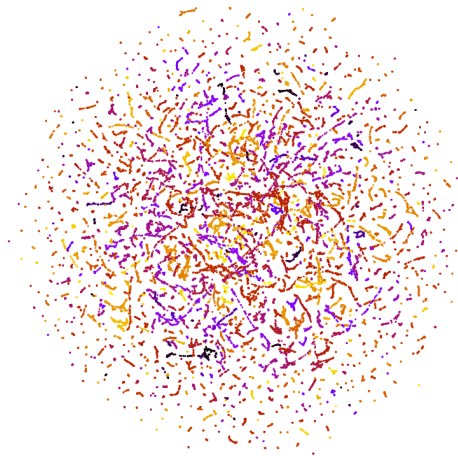


Mammoth dataset by the Smithsonian, adapted from deepia

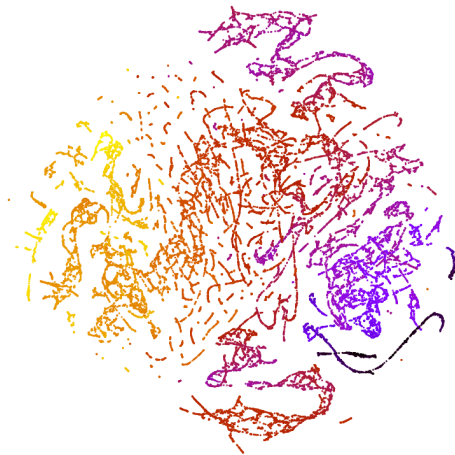
Mammoth example - PCA



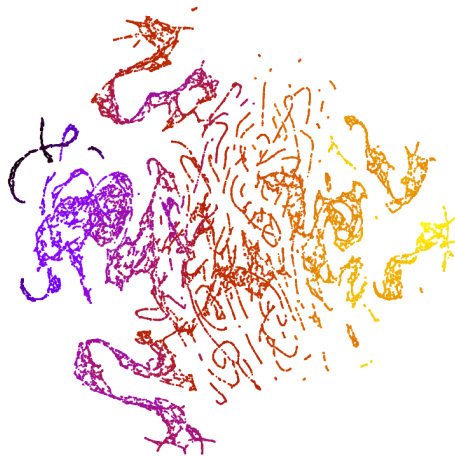
Mammoth example - UMAP



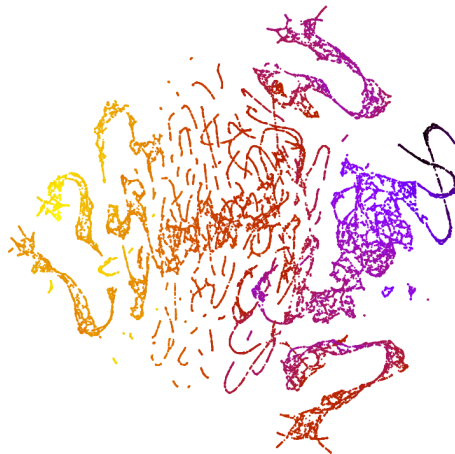
Mammoth example - UMAP



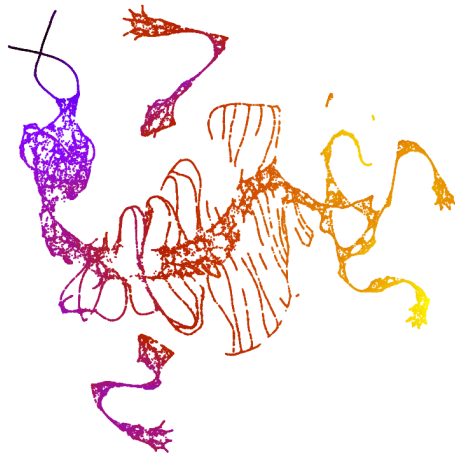
Mammoth example - UMAP



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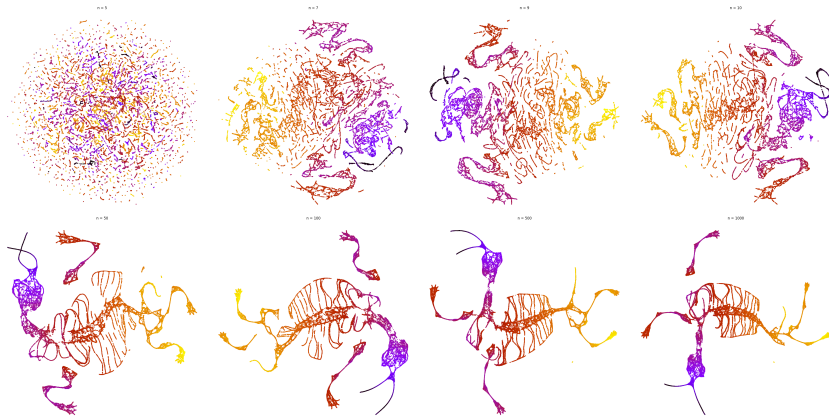
Mammoth example - UMAP



Mammoth example - UMAP



Mammoth example - Number of neighbors



UMAP vs. T-SNE

UMAP

- graph theory, fuzzy logic

T-SNE

- probabilities

UMAP vs. T-SNE

UMAP

- graph theory, fuzzy logic
- determinist initialization

T-SNE

- probabilities
- random initialization

UMAP vs. T-SNE

UMAP

- graph theory, fuzzy logic
- determinist initialization
- $\log_2$ similarity scores

T-SNE

- probabilities
- random initialization
- gaussian distribution similarity

UMAP vs. T-SNE

UMAP

- graph theory, fuzzy logic
 - determinist initialization
 - $\log_2$ similarity scores
 - update by pairs
- scales well for large datasets

T-SNE

- probabilities
 - random initialization
 - gaussian distribution similarity
 - update all points
- scales less

Scaling

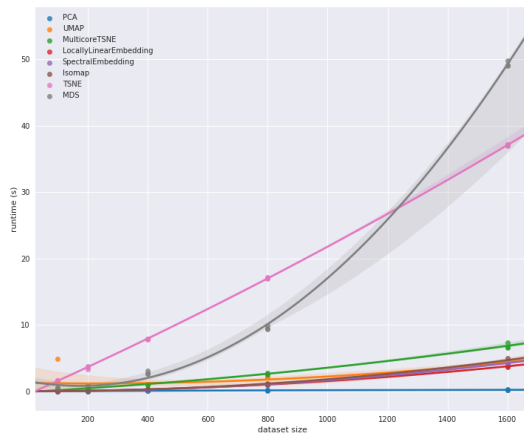


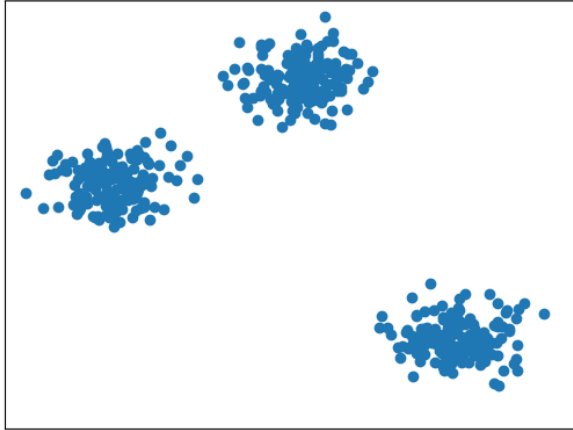
Figure from umap-learn documentation

Clustering

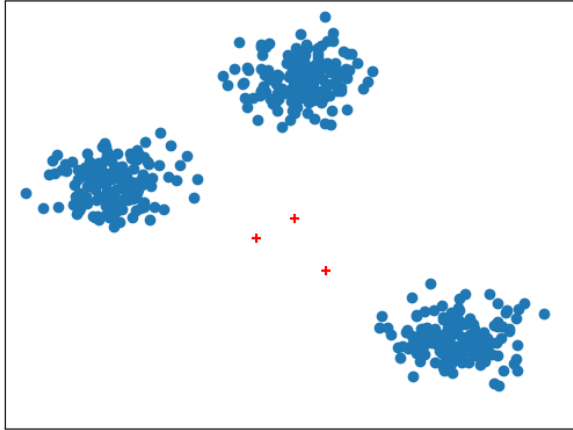
Clustering

K-means

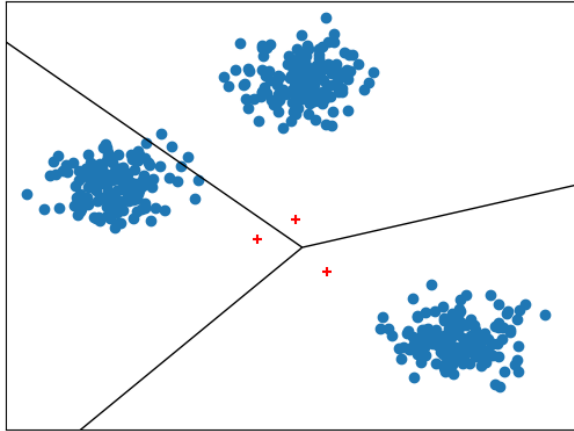
K-means



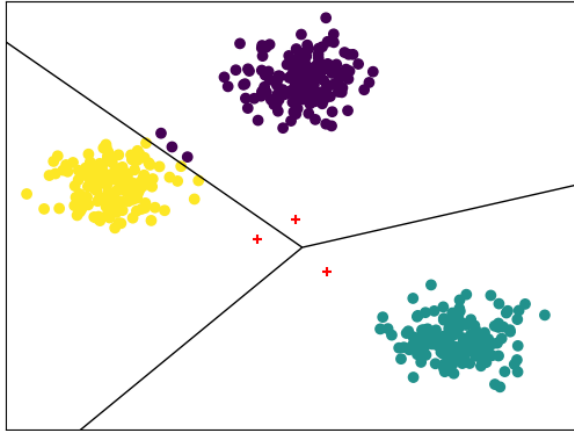
K-means



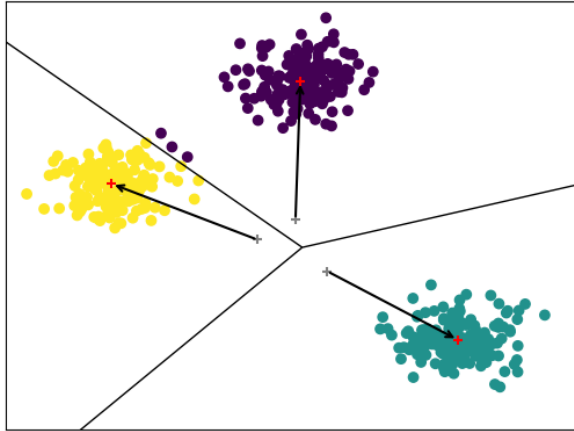
K-means



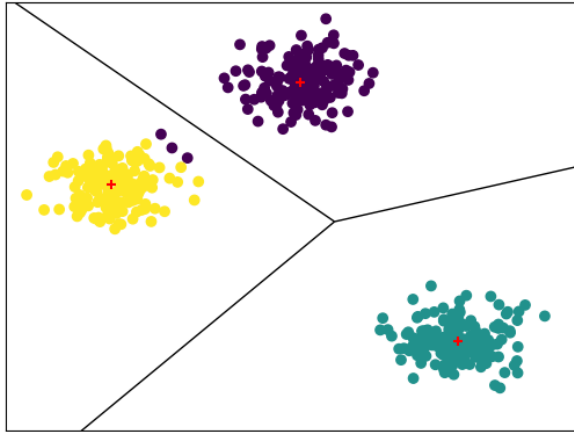
K-means



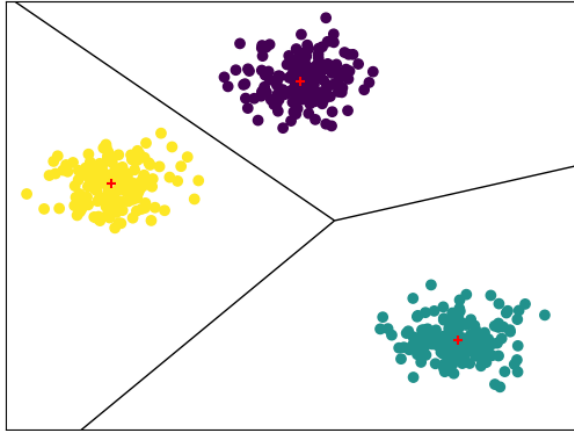
K-means



K-means



K-means



Determine the good K ? Elbow method

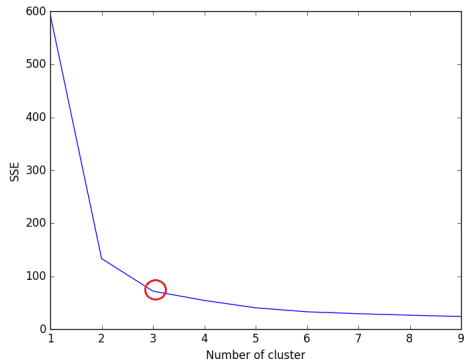
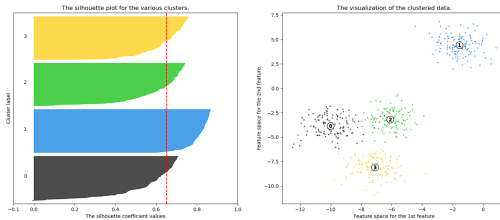


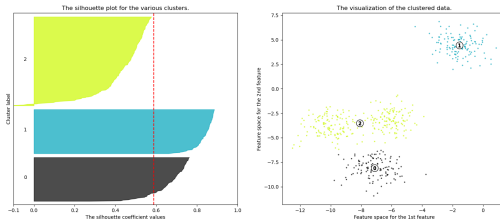
Figure from SO

Determine the good K ? Silhouette

Silhouette analysis for KMeans clustering on sample data with $n_clusters = 4$



Silhouette analysis for KMeans clustering on sample data with $n_clusters = 3$



Figures from scikit-learn documentation

K-means advantages and drawbacks

Advantages

- fast

Drawbacks

K-means advantages and drawbacks

Advantages

- fast
- scales well

Drawbacks

K-means advantages and drawbacks

Advantages

- fast
- scales well
- converges well

Drawbacks

K-means advantages and drawbacks

Advantages

- fast
- scales well
- converges well
- robust

Drawbacks

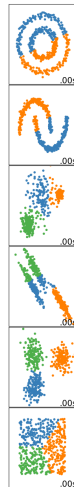
K-means advantages and drawbacks

Advantages

- fast
- scales well
- converges well
- robust

Drawbacks

- not suited for non-linear data



K-means advantages and drawbacks

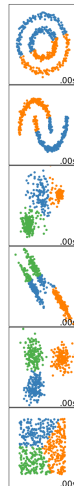
Advantages

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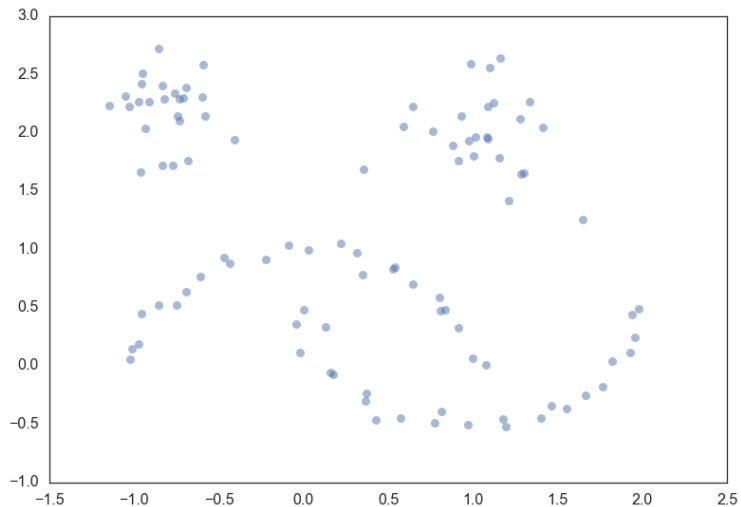
→ Density based clustering



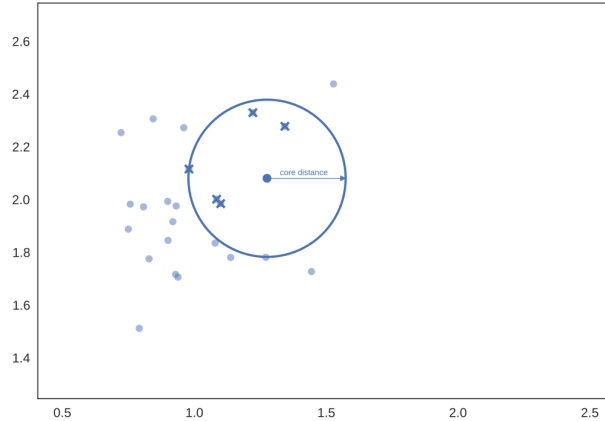
Clustering

HDBSCAN

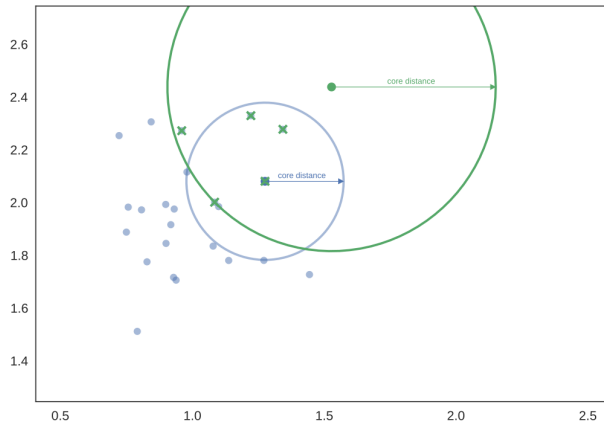
HDBSCAN



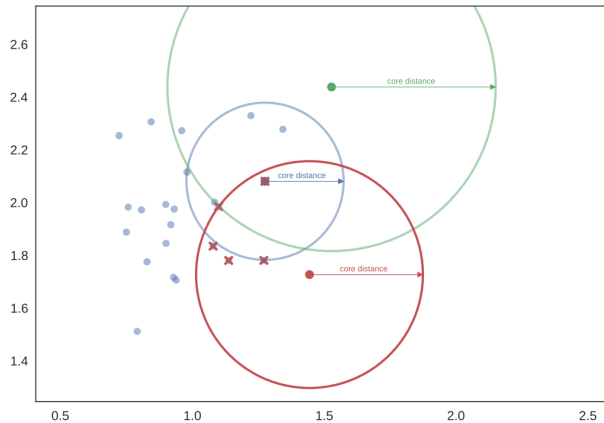
HDBSCAN



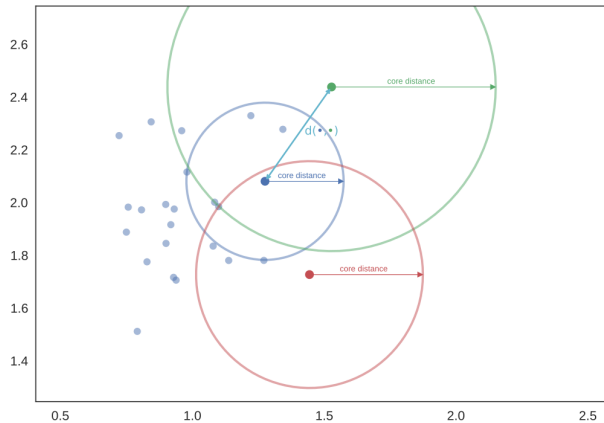
HDBSCAN



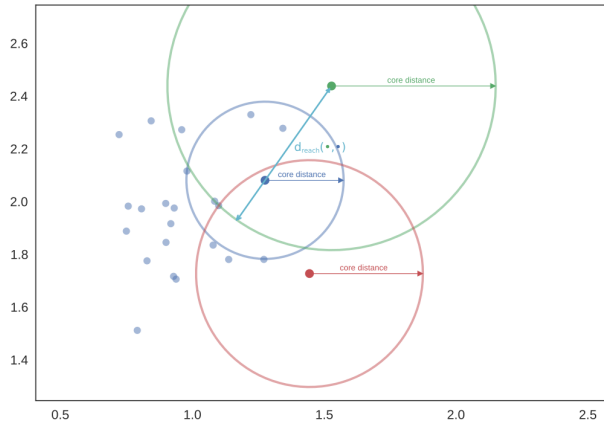
HDBSCAN



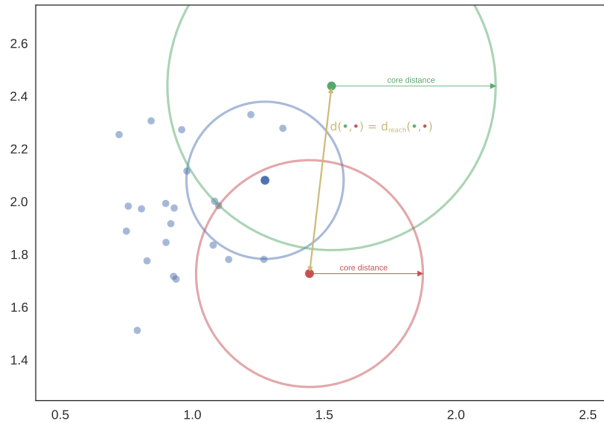
HDBSCAN



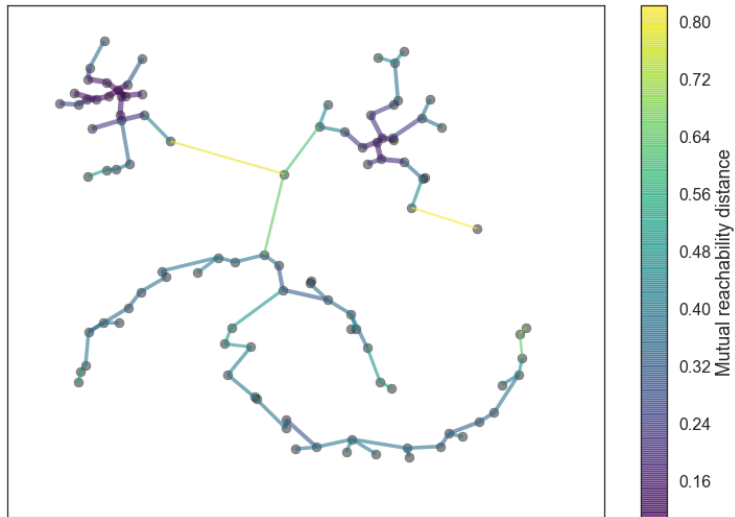
HDBSCAN



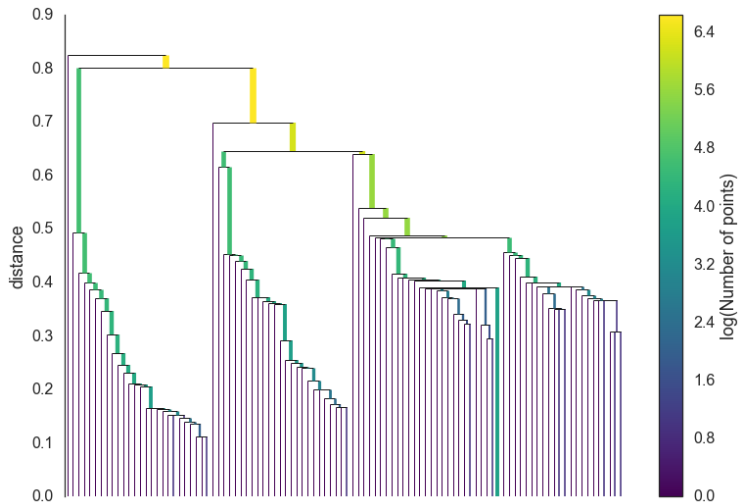
HDBSCAN



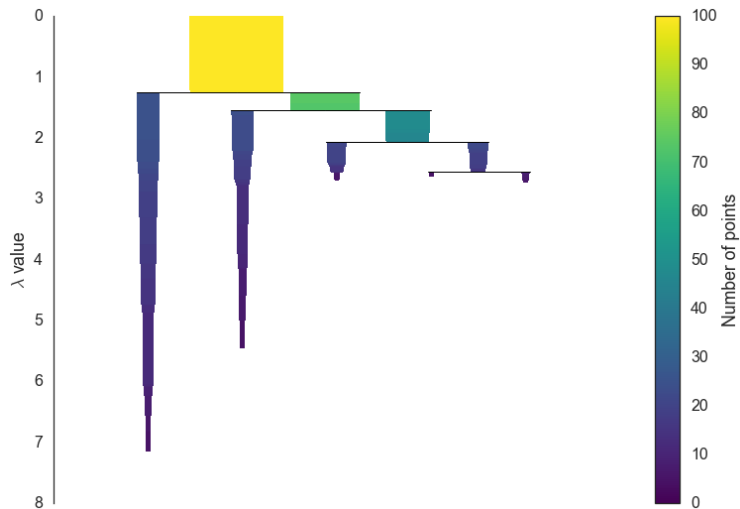
HDBSCAN



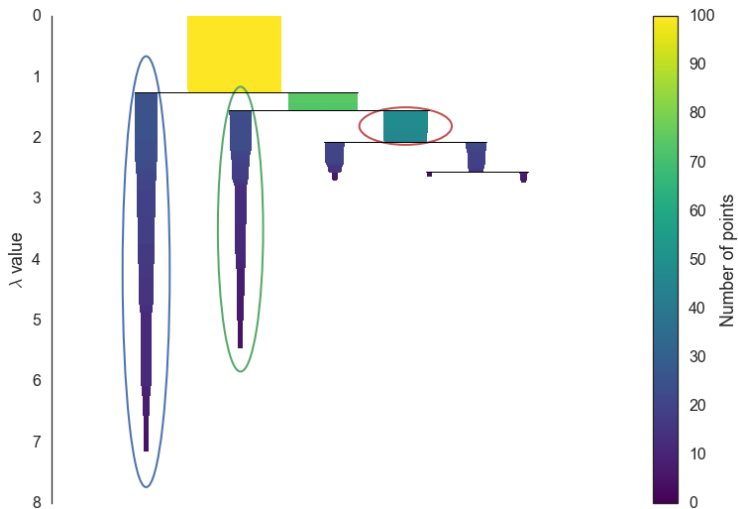
HDBSCAN



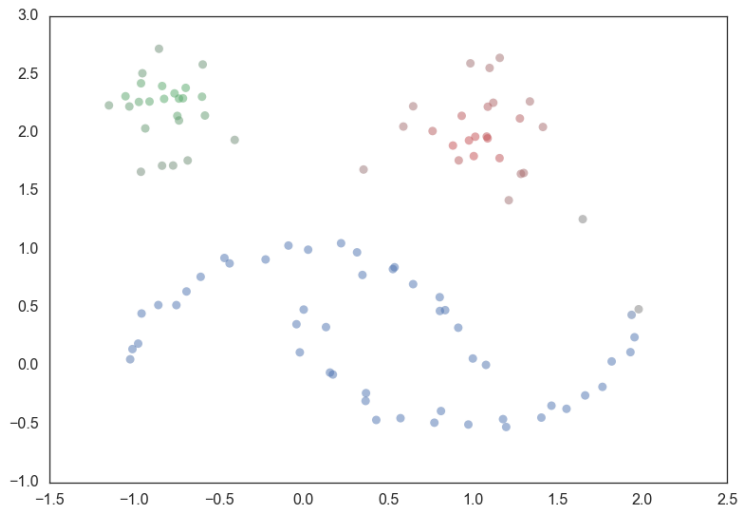
HDBSCAN



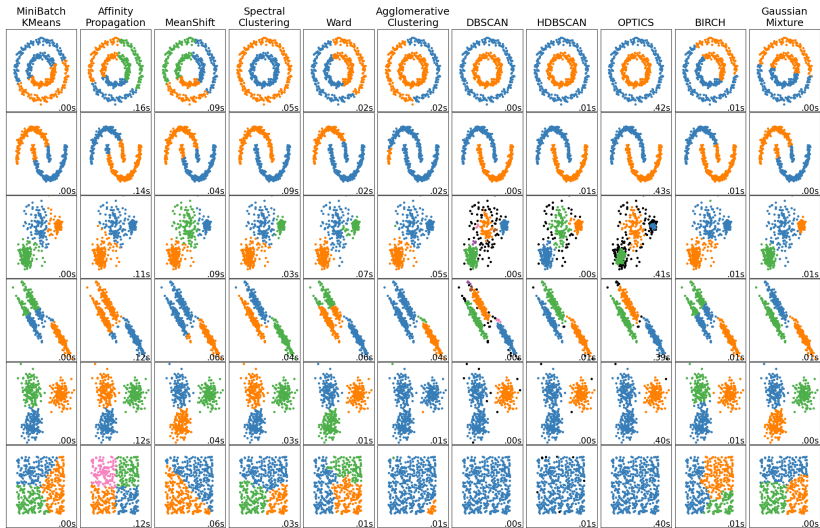
HDBSCAN



HDBSCAN



A lot of options !



Useful ressources

- `scikit-learn docs` !
- `deepia`
- `StatQuest`

Thanks for you attention !

Let's practice !

References i

- Du, Trina Y (2019). “**Dimensionality reduction techniques for visualizing morphometric data: Comparing principal component analysis to nonlinear methods**”. In: *Evolutionary Biology* 46.1, pp. 106–121.
- Hinton, Geoffrey E and Sam Roweis (2002). “**Stochastic neighbor embedding**”. In: *Advances in neural information processing systems* 15.
- McInnes, Leland, John Healy, and James Melville (2018). “**Umap: Uniform manifold approximation and projection for dimension reduction**”. In: *arXiv preprint arXiv:1802.03426*.
- Van der Maaten, Laurens and Geoffrey Hinton (2008). “**Visualizing data using t-SNE.**”. In: *Journal of machine learning research* 9.11.