# Similarity Search - PQ

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### Outline

- Nearest Neighbour Search (NNS) Problems
- Local Sensitive Hashing (LSH) Random Projection
- Product Quantization (PQ)
- Inverted File Index (non-examinable!!)

### **Product Quantization (PQ)**

- Product Quantization (PQ)
  - A clustering based method
  - Compress the data
  - Speed up searching by using precomputed distances

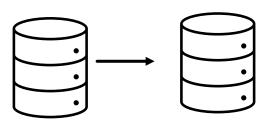
Most materials are from

https://www.pinecone.io/learn/product-quantization/

Paper: Product quantization for nearest neighbor search, 2011

### Overview of PQ for similarity search

Step1: convert the database into compressed vectors (offline step)

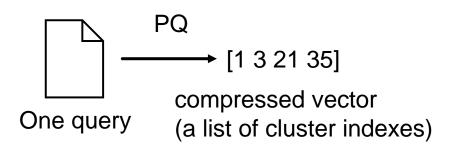


Compressed vectors

When using symmetric distance: Precompute the centroid distances tables for each subspace

Step 2: process query requests
Use efficient approximate distance
(symmetric or asymmetric)
calculation to get top-k retrieved results

When using symmetric distance:
For each query, we need to
convert the query to a compressed vector



# The process of PQ for compression

### **Pre-processing:**

- 1. Define the number of subspaces (subvectors).
- 2. For each subspace, generate k cluster centroids using the samples in the database.

### Generating compressed vectors using PQ

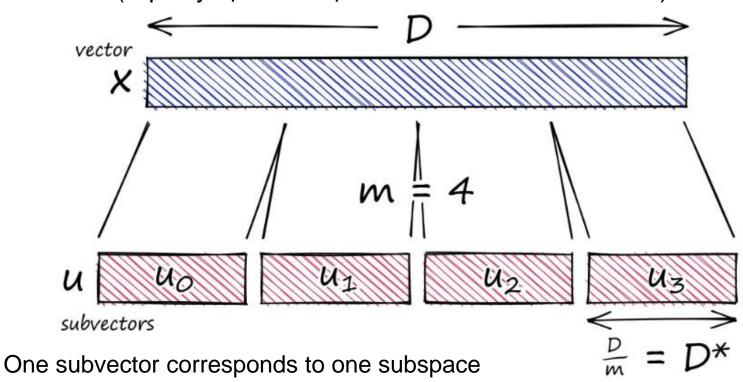
Input: the input feature vector (high-dimensional)

#### Steps:

- 1. Equally split the input into M sub-vectors. Each sub-vector corresponds to one subspace.
- 2. Assigning each of these sub-vectors to its nearest cluster centroid (also called reproduction/reconstruction values)
- 3. Use the assigned cluster IDs (indexes) of all sub-vectors to construct the compressed vector (or called quantized vector).

We define M=4 subspaces.

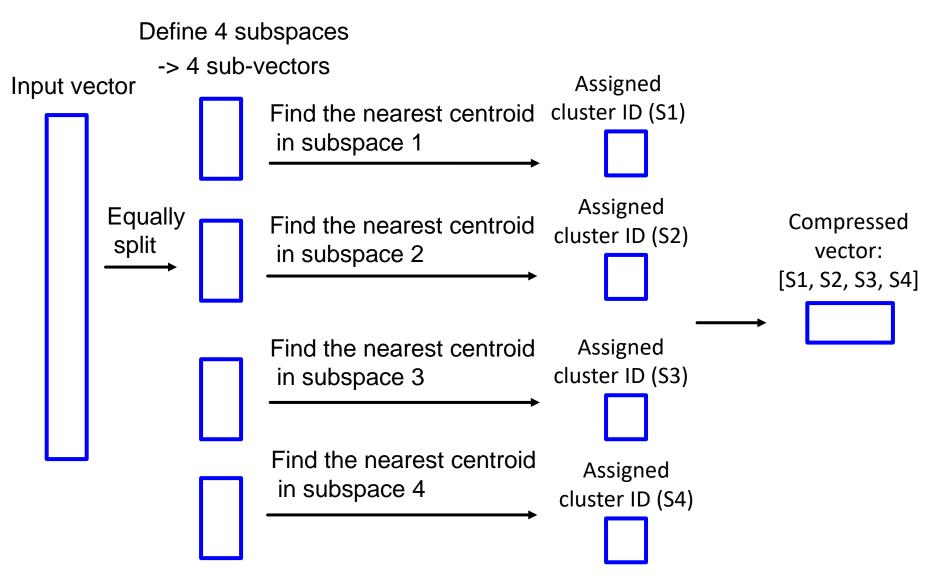
-> We generate 4 sub-vectors for each input. (equally split the input vector into M sub-vectors)



E.g., if the input vector dimension D=100, the length of each sub-vector is 100/4 = 25

Sub-vector generation example

# Compressed vector



Product Quantization example

Define 2 Subspaces
Each subspace has 4 centroids.

Input vectors:

A: [1.82, 5.08, 2.21, 4.21]

B: [4.96, 4.46, 4.1, 1.3]

### **Subspace 1**, We have 4 centroids: C1 to C4.

A1, B1: the sub-vectors for datapoint A and B, respectively

$$A1 = (1.82, 5.08)$$

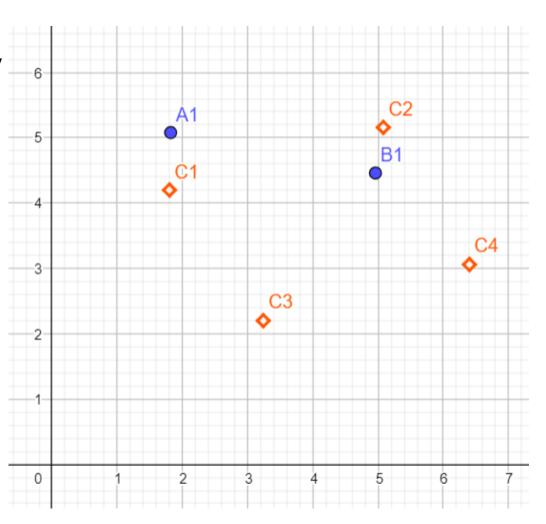
$$B1 = (4.96, 4.46)$$

$$C1 = (1.8, 4.2)$$

$$C2 = (5.08, 5.16)$$

$$C3 = (3.24, 2.2)$$

$$C4 = (6.4, 3.06)$$



### Subspace 2, We have 4 centroids: C1 to C4.

A2, B2: the sub-vectors for datapoint A and B, respectively

$$A2 = (2.01, 4.21)$$

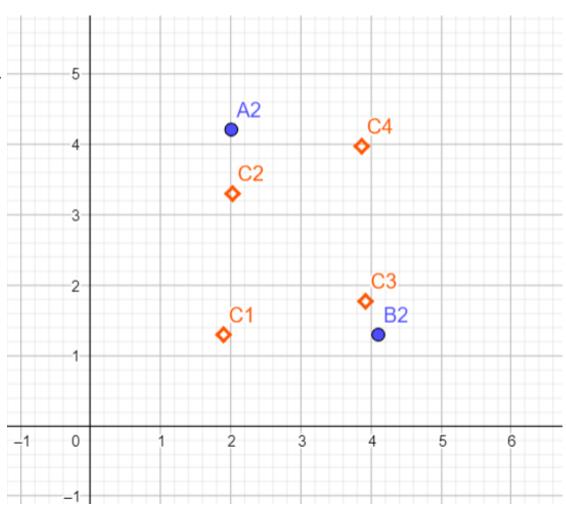
$$B2 = (4.1, 1.3)$$

$$C1 = (1.9, 1.3)$$

$$C2 = (2.02, 3.3)$$

$$C3 = (3.92, 1.77)$$

$$C4 = (3.87, 3.98)$$



Q: generate the compressed vector for datapoint A and B:

#### Answer:

In subspace 1, A is assigned to the centroid C1 (1st dimension of the compressed vector)

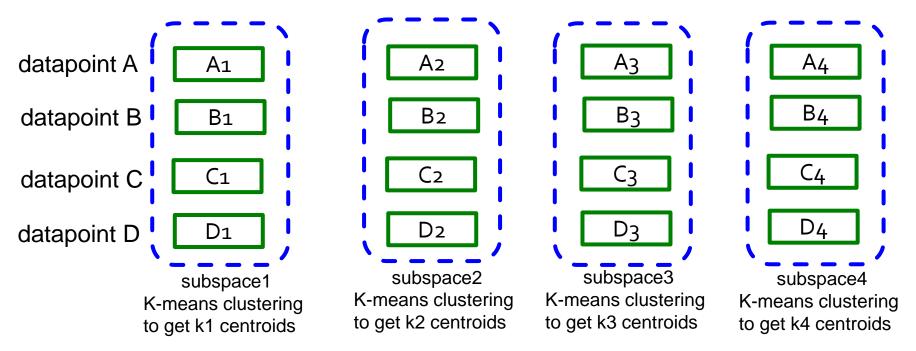
In subspace 2, A is assigned to the centroid C2 (2nd dimension of the compressed vector)

-> A: [1, 2]

In subspace 1, B is assigned to the centroid C2 In subspace 2, B is assigned to the centroid C3
-> B: [2, 3]

- How to generate cluster centroids?
  - Generate sub-vectors for all data examples in the database
    - Define M subspaces -> Generate M sub-vectors for one input.
  - Perform K-means in each subspace to generate k centroids.
    - For example, we can generate k=256 centroids for each sub space

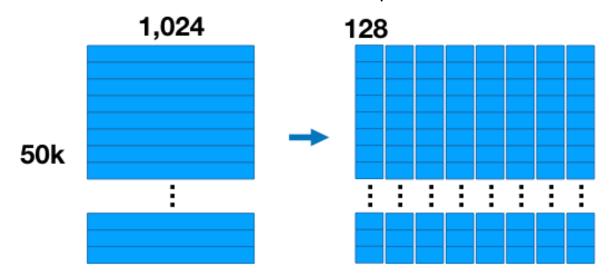
Use datapoints in the database to generate centroids for each subspace



# Example: Subspace clustering

Database: 50K samples, each has 1024 dimensions:

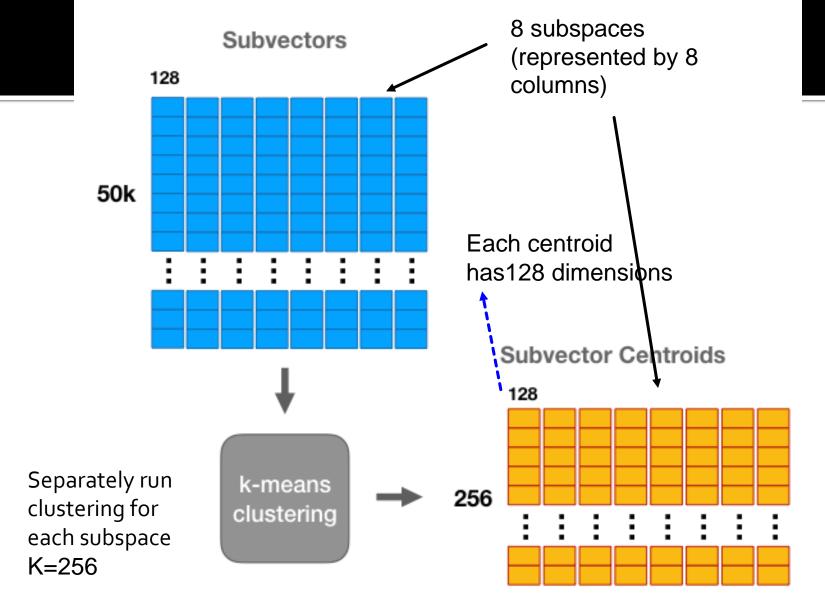
8 sub-vectors for each sample: (each sub-vector's dimension: 128)



Each row indicates one data sample.

Define 8 subspaces. Each vector is spitted into 8 sub-vectors, each of length 128 (8 sub vectors x 128 dimensions = 1,024 dimensions).

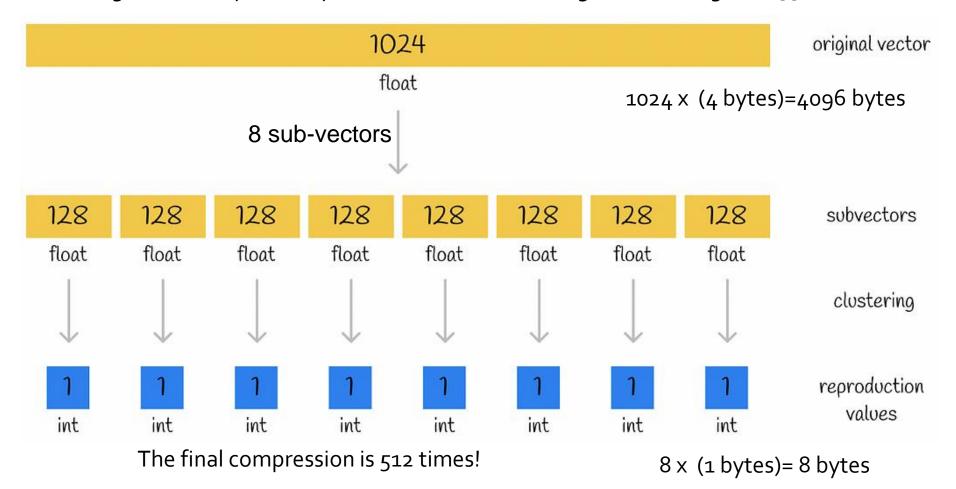
https://mccormickml.com/2017/10/13/product-quantizer-tutorial-part-1/#nearest-neighbor-search



Each subspace has 256 centroid

### Compression analysis

- 1 float value requires 4 bytes (4\*8=32 bits);
- 1 integer value requires 1 byte (here we use 8-bit integer, value range: 0-255)



One centroid ID is an integer value. In this example, we only have 256 centroids, so we can use one 8-bit integer ( $2^{8=256}$ ) to store one cluster ID.

### **Product Quantization**

- Codebook based compression
  - the codebook is the centroids
  - Separate codebook (centroids) for each subspace
- Compress high-dimensional vector to a tiny vector of IDs that only requires very little memory/storage space.

### **Product Quantization**

- Product Quantization (PQ)
  - A data dependent method
    - Need to use the data in the database to determine the parameters (cluster centres) of the algorithm.
  - LSH is a data independent method
    - The hash functions are randomly generated, not using the data in the database.

## PQ for similarity search

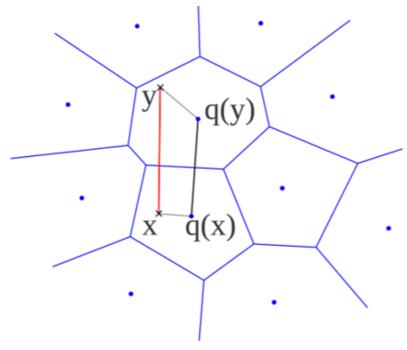
- PQ for Similarity Search
  - Use liner search (exhaustive search )
    - Use approximate distance to speed up distance calculation

- Calculating approximate distance
  - Symmetric distance
    - Use pre-computed distance look-up table to speed up the calculation.
  - Asymmetric distance

# Symmetric distance

Approximate distance: Symmetric distance

$$\hat{d}(x,y) = d(q(x), q(y)) = \sqrt{\sum_{j} d(q_j(x), q_j(y))^2},$$



a(y) and a(y)

q(x) and q(y) are the assigned cluster centroids

x, y are two input vectors

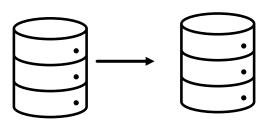
The distance of (x, y) is approximated by the distance of cluster centroids

symmetric case

## Recap

### Overview of PQ for similarity search

Step1: convert the database into compressed vectors (offline step)

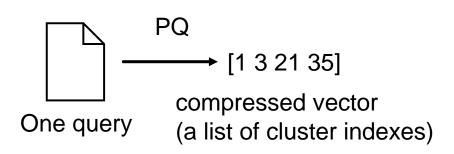


Compressed vectors

When using symmetric distance: Precompute the centroid distances tables for each subspace

Step 2: process query requests
Use efficient approximate distance
(symmetric or asymmetric)
calculation to get top-k retrieved results

When using symmetric distance: For each query, we need to convert the query to a compressed vector



**Subspace 1**, We have 4 centroids: C1 to C4.

A1, B1: the sub-vectors for datapoint A and B, respectively

$$A1 = (1.82, 5.08)$$

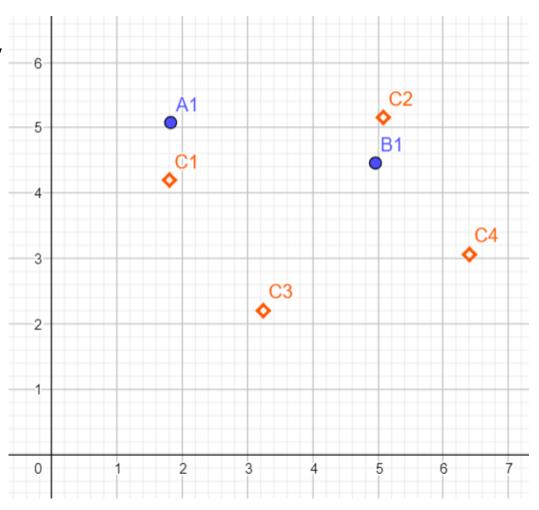
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$$C4 = (6.4, 3.06)$$



#### Subspace 2, We have 4 centroids: C1 to C4.

A2, B2: the sub-vectors for datapoint A and B, respectively

$$A2 = (2.01, 4.21)$$

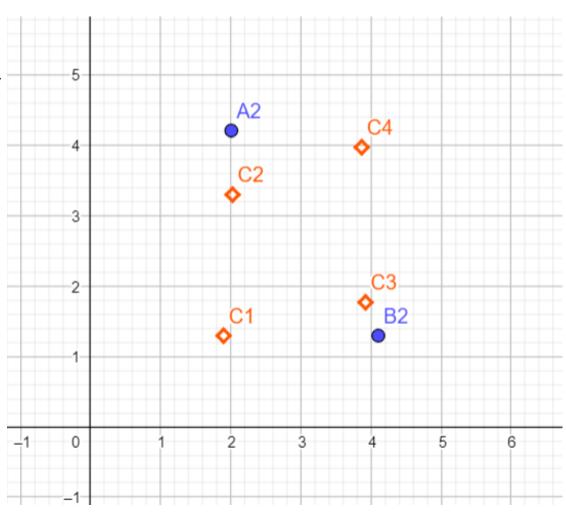
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$$C1 = (1.9, 1.3)$$

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Define 2 subspaces. The centroids and datapoints are given in the above slides.

### **Question:**

- 1. Construct centroid distance look up tables and
- 2. compute the approximate Squared L2 distance (symmetric case) between A and B.

### Solution to Q1:

### Subspace 1

	Centroid 1	Centroid 2	Centroid 3	Centroid 4
Centroid 1	0	11.68	6.07	22.46
Centroid 2	11.68	0	12.15	6.15
Centroid 3	6.07	12.15	0	10.73
Centroid 4	22.46	6.15	10.73	0

Table 1: squared L2 distance table for Subspace 1 (D1)

Distance calculation example:

C1=[1.8, 4.2], C2=[5.08, 5.16],  
D1(C1, C2) = 
$$(1.8-5.08)^2 + (4.2-5.16)^2 = 10.76 + 0.92 = 11.68$$

### Subspace 1, We have 4 centroids: C1 to C4.

A1, B1: the sub-vectors for datapoint A and B, respectively

$$A1 = (1.82, 5.08)$$

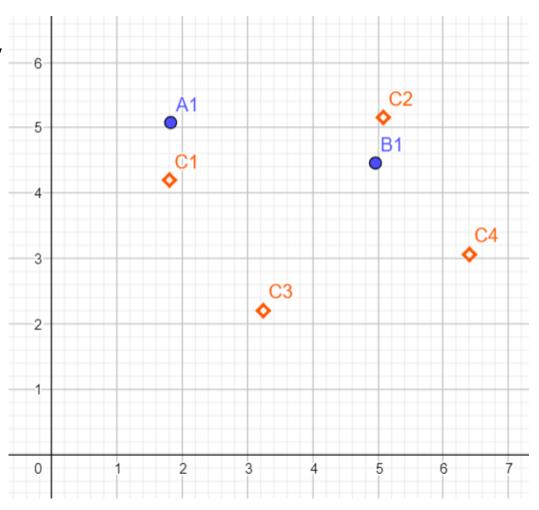
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$$C3 = (3.24, 2.2)$$

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### Subspace 2

	Centroid 1	Centroid 2	Centroid 3	Centroid 4
Centroid 1	0	4.01	4.30	11.06
Centroid 2	4.01	0	5-95	3.88
Centroid 3	4.3	5.95	О	4.89
Centroid 4	11.06	3.88	4.89	0

Table 2: squared L2 distance table for Subspace 2 (D2)

### Subspace 2, We have 4 centroids: C1 to C4.

A2, B2: the sub-vectors for datapoint A and B, respectively

$$A2 = (2.01, 4.21)$$

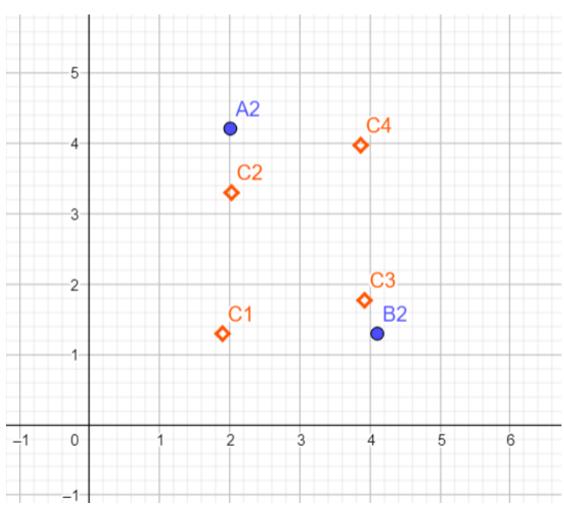
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$$C1 = (1.9, 1.3)$$

$$C2 = (2.02, 3.3)$$

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$$C4 = (3.87, 3.98)$$



#### **Question:**

2. compute the approximate Squared L2 distance (symmetric case) between A and B.

### Solution to Q2:

Compressed vectors: A: [1, 2]; B: [2, 3]

Look up the distance values in table D1 and D2 using the cluster IDs:

$$D (A1, B1) = D1(Centroid 1, Centroid 2) = 11.68$$

$$D(A2, B2) = D2(Centroid 2, Centroid 3) = 5.95$$

$$D(A, B) \sim D(A1, B1) + D(A2, B2) + = 11.68 + 5.95 = 17.63$$

### Subspace 1

	Centroid 1	Centroid 2	Centroid 3	Centroid 4
Centroid 1	0	11.68	6.07	22.46
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### Subspace 2

	Centroid 1	Centroid 2	Centroid 3	Centroid 4
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### Compressed vectors: A: [1, 2]; B: [2, 3]

D (A1, B1) = D1(Centroid 1, Centroid 2) = 11.68

D(A2, B2) = D2(Centroid 2, Centroid 3) = 5.95

 $D(A, B) \sim D(A1, B1) + D(A2, B2) + = 11.68 + 5.95 = 17.63$ 

# Symmetric distance

- Approximate distance calculation
  - we can calculate the distances much more efficiently using just table look-ups and some addition.
  - Using centroid pre-computed distances. Pre-compute and the distances between centroids for each subspace, stored the distances in a matrix or lookup table, use the centroid index pair to retrieve the partial distances for each subspace.
  - Sum-up the partial distances from all subspaces as the final distance output

# Asymmetric distance

### **Asymmetric distance**

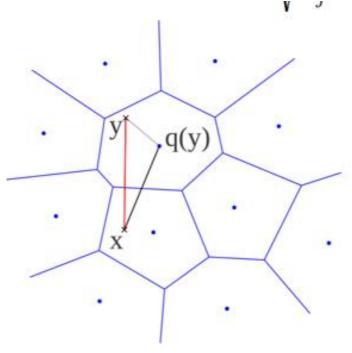
More accurate for distance calculation, as we only quantize one input. (compared to symmetric distance)

$$\tilde{d}(x,y) = d(x,q(y))$$

x: a query example,

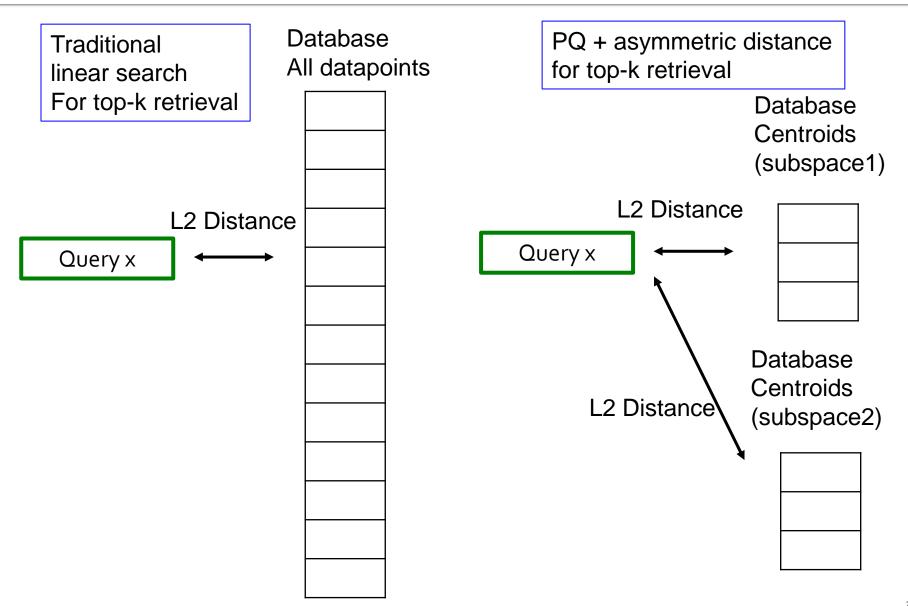
y: an example in the database.

Use q(y) to replace y for distance calculation



asymmetric case

# Example for asymmetric distance



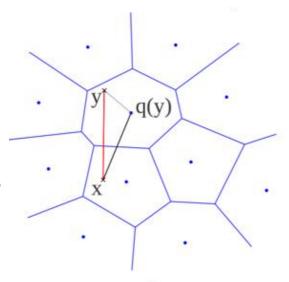
# Asymmetric distance

 Given a query in a top-k retrieval task, we don't need to compute the distance between the query and all the samples in the database.

We only need to calculate the distance between the query and all the centroids in each subspace.

- 2. The number of centroids are much less than the number of samples in the database, so we can speed up the retrieval process.
- 3. We don't need to quantize x, which reduces computation compared to the symmetric case.

$$\tilde{d}(x,y) = d(x,q(y))$$



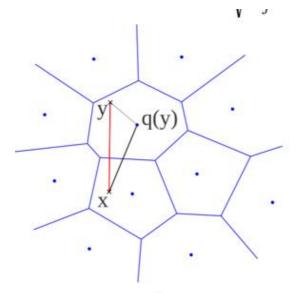
asymmetric case

# Asymmetric distance

- 4. For each subspace, we compute the squared L2 distances between the x and all centroids.
  - This bring extra computation compared to the symmetric case.
- 5. The above extra computation cost is similar with the quantization cost for x. (cluster assignment requires distance calculation between x and all centroids)

That means symmetric and asymmetric distance have the same computation complexity.

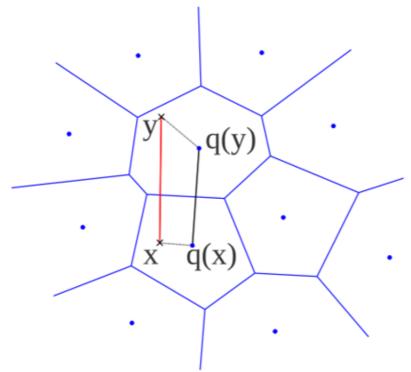
$$\tilde{d}(x,y) = d(x,q(y))$$



asymmetric case

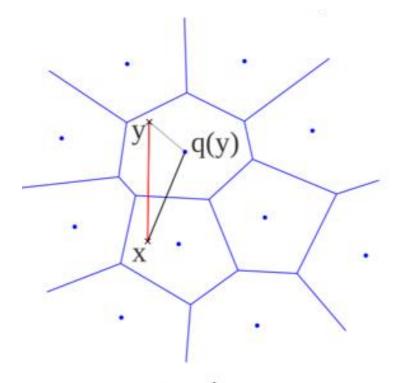
# Comparison

$$\hat{d}(x,y) = d(q(x), q(y)) = \sqrt{\sum_{j} d(q_j(x), q_j(y))^2},$$



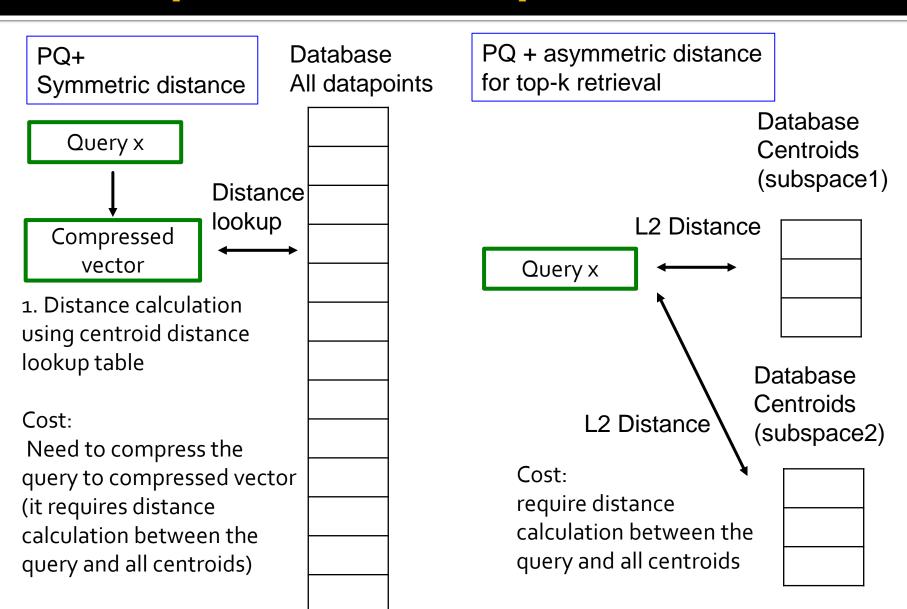
symmetric case

$$\tilde{d}(x,y) = d(x,q(y))$$



asymmetric case

# Comparison for top-k search



## Outline

- Nearest Neighbour Search (NNS) Problems
- Local Sensitive Hashing (LSH) Random Projection
- Product Quantization (PQ)
- Inverted File Index (non-examinable!!)

## **Inverted File Index**



- Inverted File Index
  - Clustering based method
  - Data dependent
  - Reduce the search scope

Non-\_ examinable!

- Inverted File Index (IVT)
  - An inverted index here means a mapping (a lookup table) from cluster centroids (words) to the cluster members.

#### Steps:

- 1. Clustering of the samples in the database, generate the centroids and cells
- 2. Given a query vector, identify the cells for search scope
- 3. Use linear search (exhaustive search) to retrieve results within the selected cells

search scope

nprobe = 1

xq: the query vector

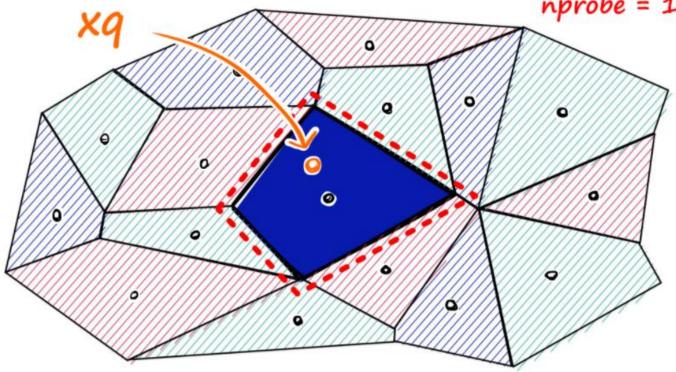
Perform k-means clustering to group the data points in the database (cluster centroids and assignments)

Cluster centroid in one cell.

One cell represents one cluster

xq: the query vector

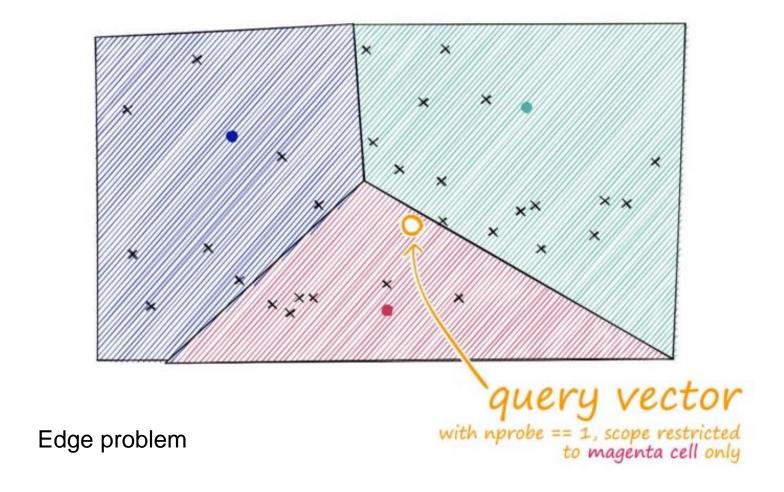




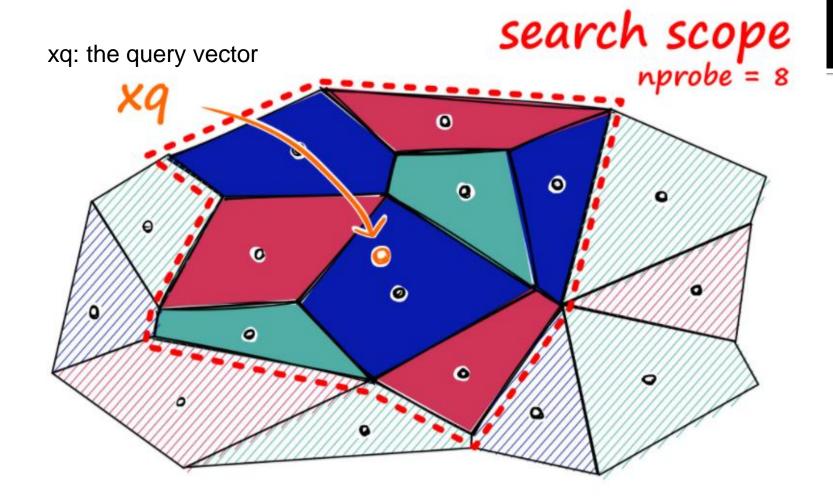
nprobe: select the top k nearest clusters (cells) as the search scope nprobe=1: only select 1 cell for searching

There are 2 parameters in IVT:

- 1. nprobe: the number of cells to search
- 2. The number of cells (clusters) to create.



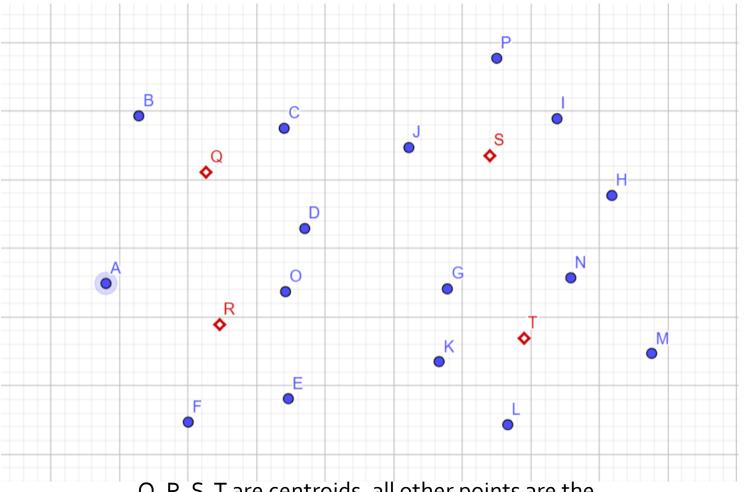
Our query vector  $\mathbf{xq}$  lands on the edge of the magenta cell. Despite being closer to datapoints in the teal cell, we will not compare these if  $\mathbf{nprobe} == \mathbf{1}$  — as this means we would restrict search scope to the magenta cell only.



Increasing **nprobe** increases our search scope.

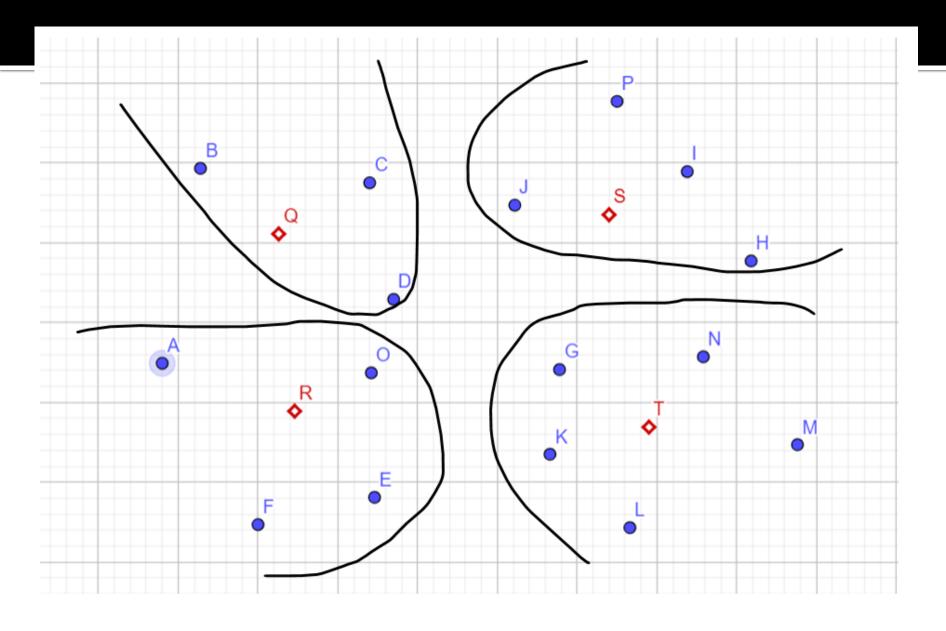
nprobe=8: select the top 8 nearby cells for searching. (ranked by the distance between the query and the centroids)

#### Inverted File Index Example

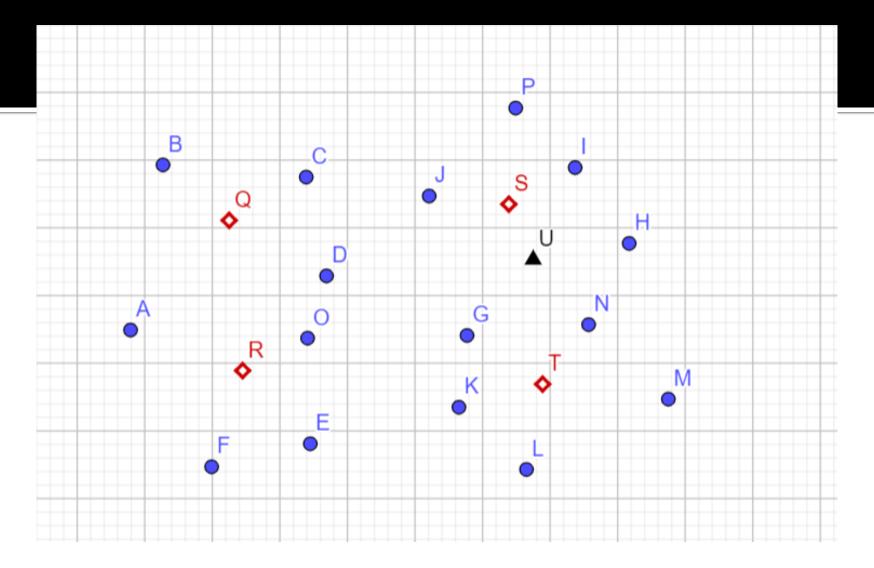


Q, R, S, T are centroids, all other points are the data samples in the database.

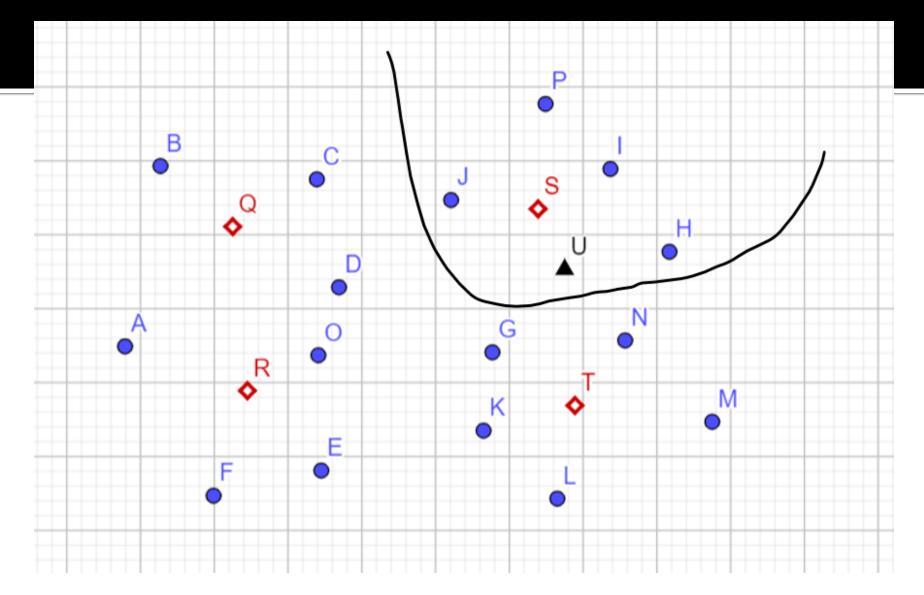
 Q(a): assign the samples to the cells defined by the centroids.



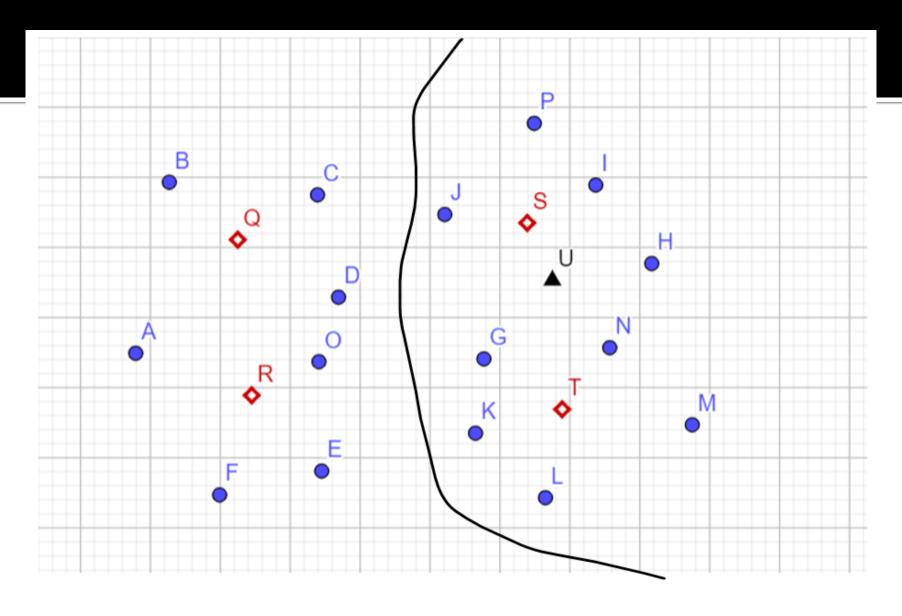
one data point is assigned to its nearest centroid based on L2 distance



Q(b) Given the query sample U, list the candidate samples in the database for similar search when nProbe=1 and nProbe=2, respectively



nProbe=1: only search in 1 cell

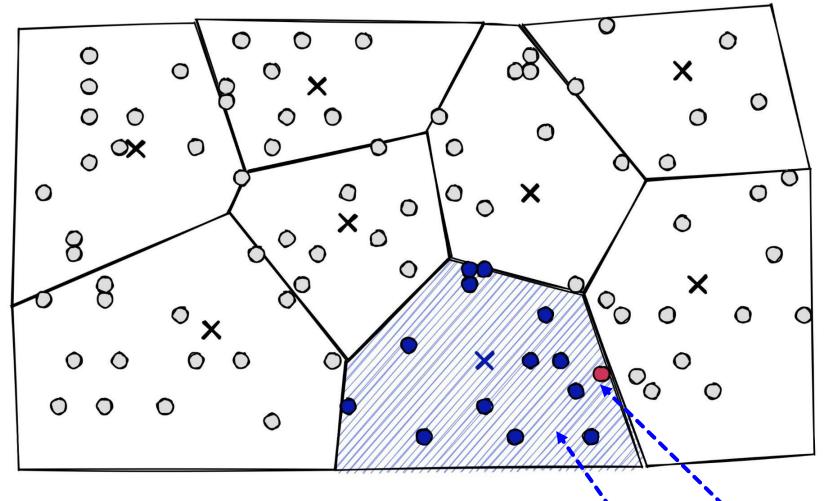


nProbe=2: search in 2 cells (the top 2 closest cells)

### PQ+IVF



- PQ+IVF
  - Product Quantization + Inverted File Index
  - A hierarchical solution
  - Much better performance in searching
  - Reduce search scope by using IVF



Step1: use IVF to identify search scope (cells). Target cell IVF allows us to restrict our search in the target cells only.

Step2: perform PQ based linear search in the target cells. PQ generates compresses vectors and uses fast distance calculation

query

# Experiment: Sift1M dataset, 2048 centroids for each subspace

L2 distance base linear search

	FlatL2	PQ	IVFPQ	
Recall (%)	100	50	52	
Speed (ms)	8.26	1.49	0.09	
Memory (MB)	256	6.5	9.2	

https://www.pinecone.io/learn/product-quantization/

#### Online resources

- FAISS
  - Faiss is a library for efficient similarity search and clustering of dense vectors.
  - https://github.com/facebookresearch/faiss/wiki