15-440
Distributed Systems
Kmeans

October 13, 2022

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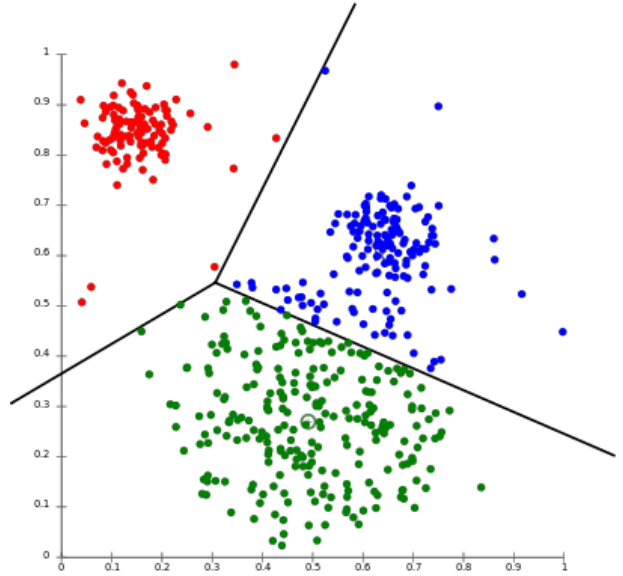
(Slides by Laila Elbeheiry)



K-Means at a High Level

- Clustering Algorithm

> **Cluster analysis** or **clustering** is the task of grouping a set of objects in such a way that objects in the same group (called a **cluster**) are more similar (in some sense) to each other than to those in other groups (clusters).
> - Wikipedia

- Applications:
  - Data mining
  - Statistical data analysis: machine learning, pattern recognition, image analysis, information retrieval, and bioinformatics
  - Visualization
  - Detecting anomalies or outliers

What is “k”?

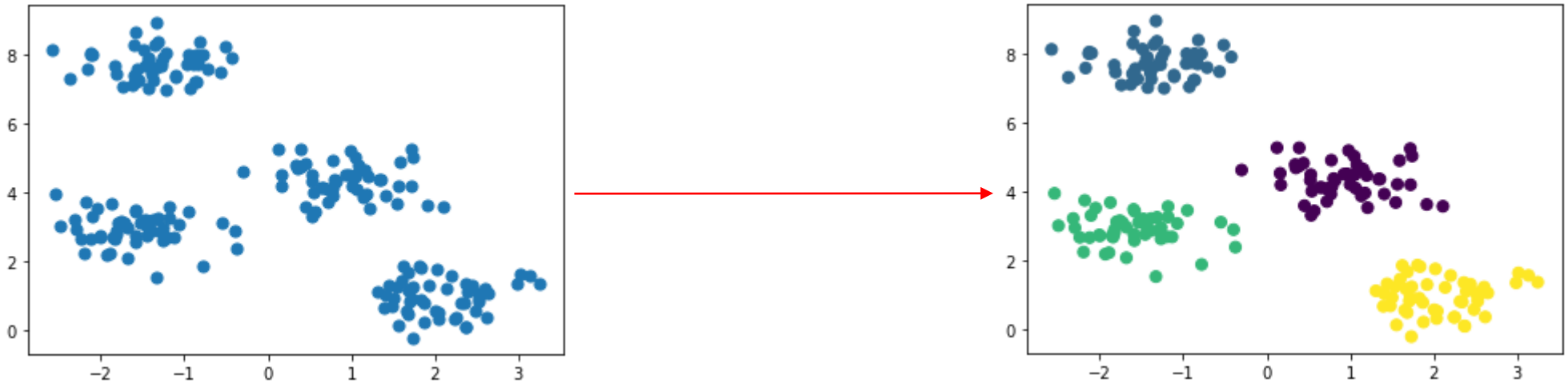


Image source:
https://towardsdatascience.com/k-means-clustering-explained-4528df86a120

K-Means Explained

K-means is an iterative process that works by executing the following steps:

1. Select centroids (center of cluster) for each of the k clusters. The list of centroids can be selected by any method (e.g., randomly from the set of data points). It is usually better to pick centroids that are far apart.
2. Calculate the distance of all data points to the centroids.
3. Assign data points to the closest cluster.
4. Find the new centroids of each cluster by taking the mean of all data points in the cluster.
5. Repeat steps 2,3 and 4 until all points converge and cluster centers stop moving.

Let's see how it works!

K-Means in Project 3

You need to define a distance function and a mean function.

- How to calculate the distance between points in a 2D plane?
- How to calculate the distance between DNA strands?
- How to find the mean of points in a 2D plane?
- How to find the mean of DNA strands?

Sequential Kmeans

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

Initial centroids/means

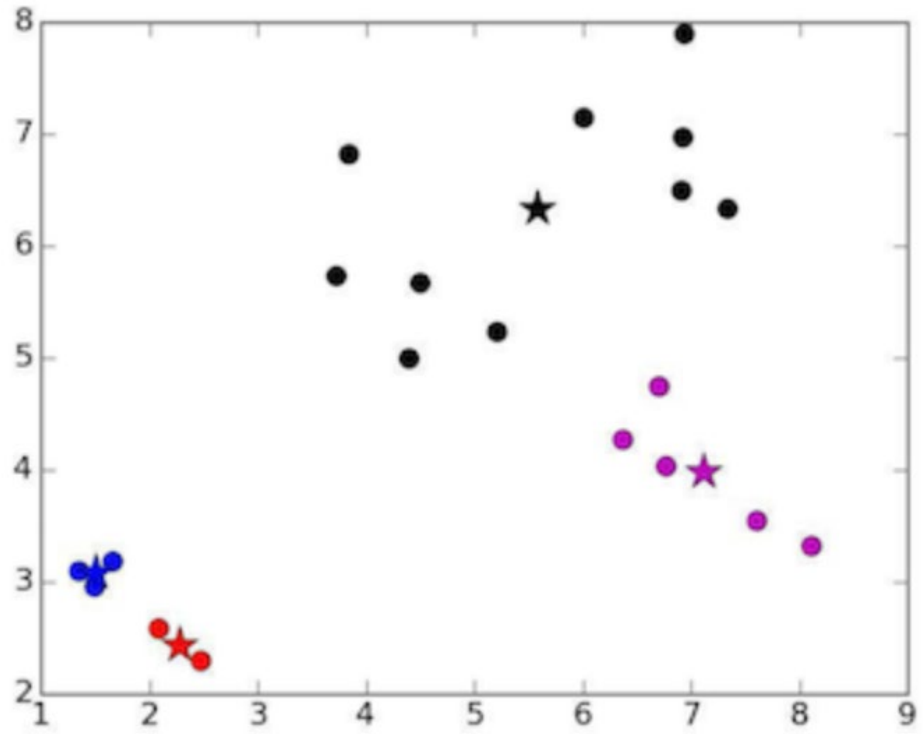
P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

Initial centroids/means

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9



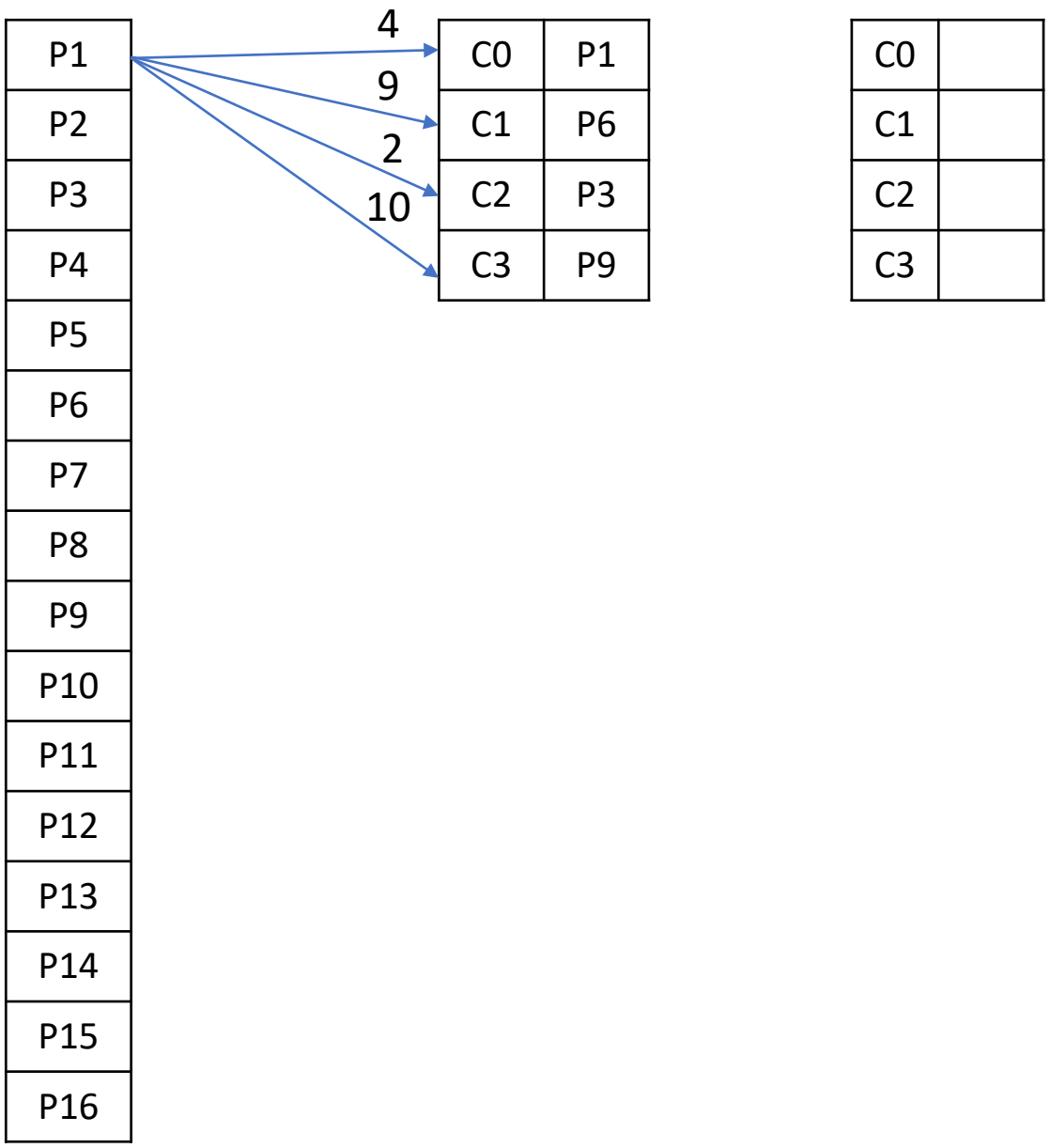
The blue and red starts are called unlucky centroids (*)
A poor choice of the initial centroids will take longer to converge or may result in bad clustering. You can handle this in:
- Try different sets of random centroids, and choose the best set.

Initial centroids/means

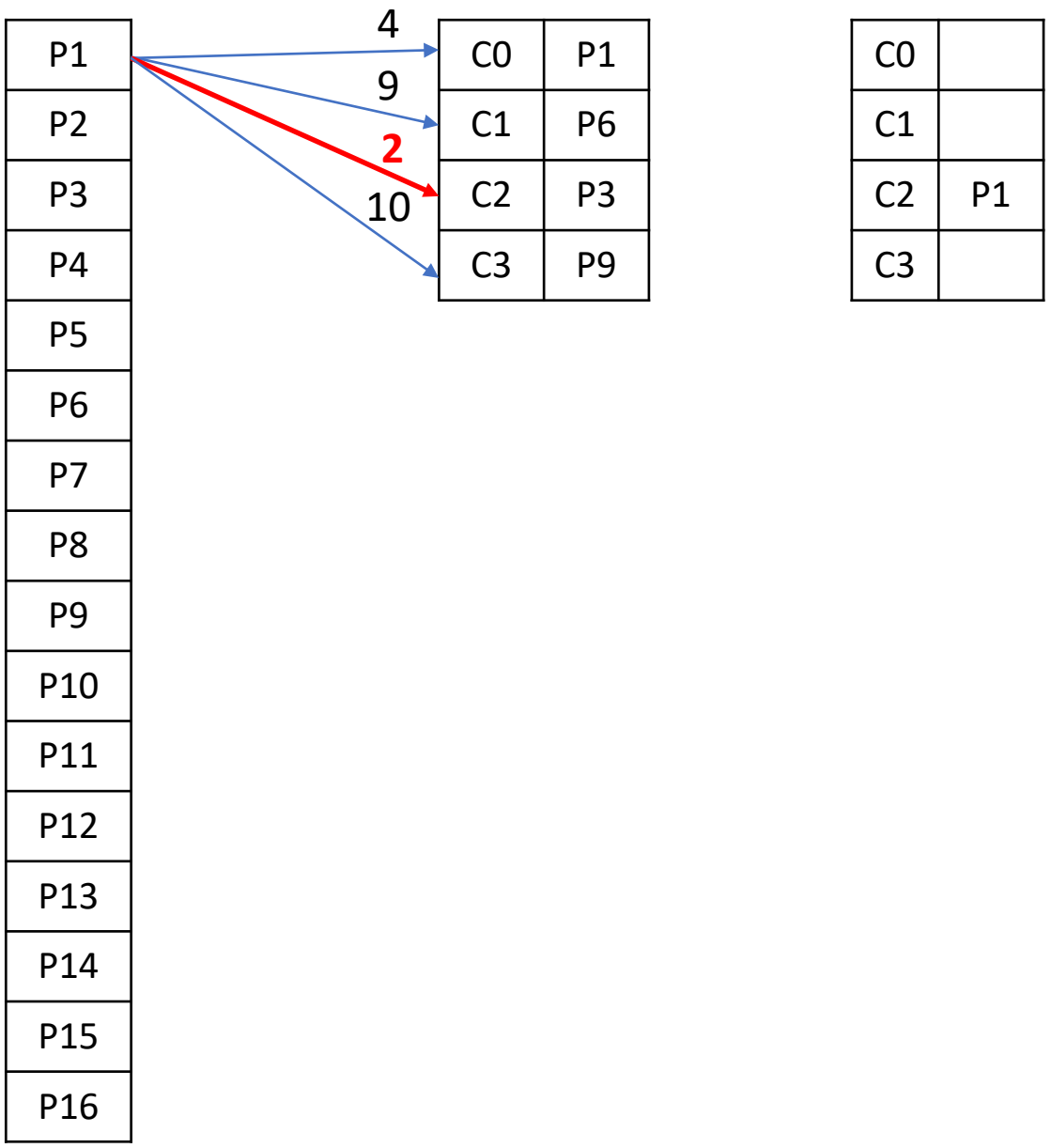
P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

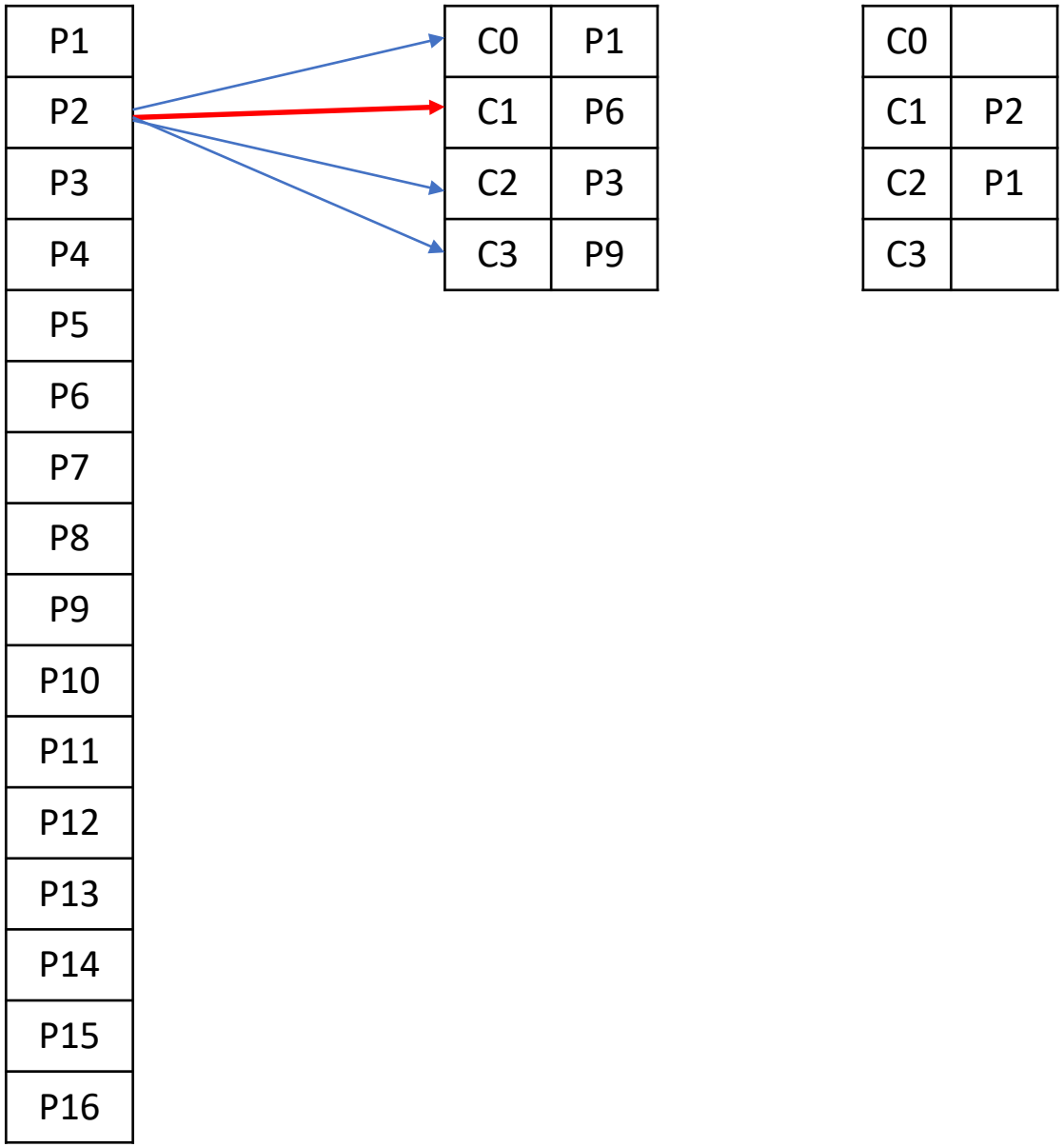
Initial centroids/means



Initial centroids/means

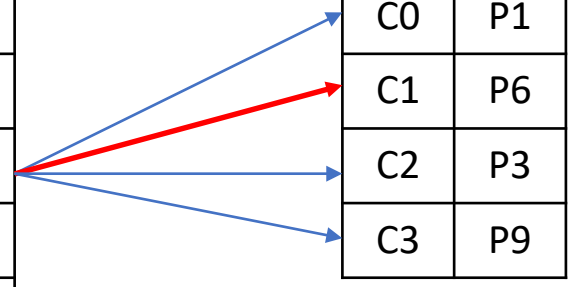


Initial centroids/means



Initial centroids/means

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16



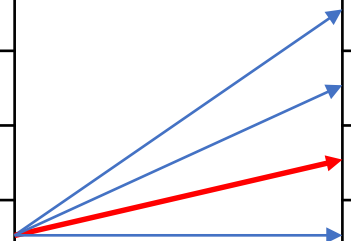
C0	P1
C1	P6
C2	P3
C3	P9

C0	
C1	P2 + P3
C2	P1
C3	

** P1 + P2 = (x1,y1) + (x2,y2) = (x1+x2, y1+y2)*

Initial centroids/means

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

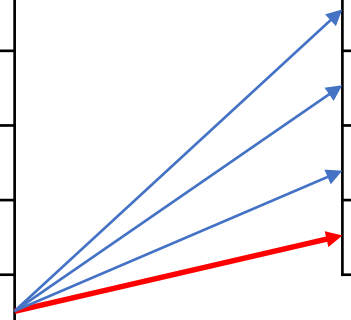


C0	P1
C1	P6
C2	P3
C3	P9

C0	
C1	P2 + P3
C2	P1 + P4
C3	

Initial centroids/means

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16



C0	P1
C1	P6
C2	P3
C3	P9

C0	
C1	P2 + P3
C2	P1 + P4
C3	P5

Initial centroids/means

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

C0	P6 + P8 + P10 + P13
C1	P2 + P3 + P7 + P11
C2	P1 + P4 + P12 + P15 + P16
C3	P5 + P9 + P14

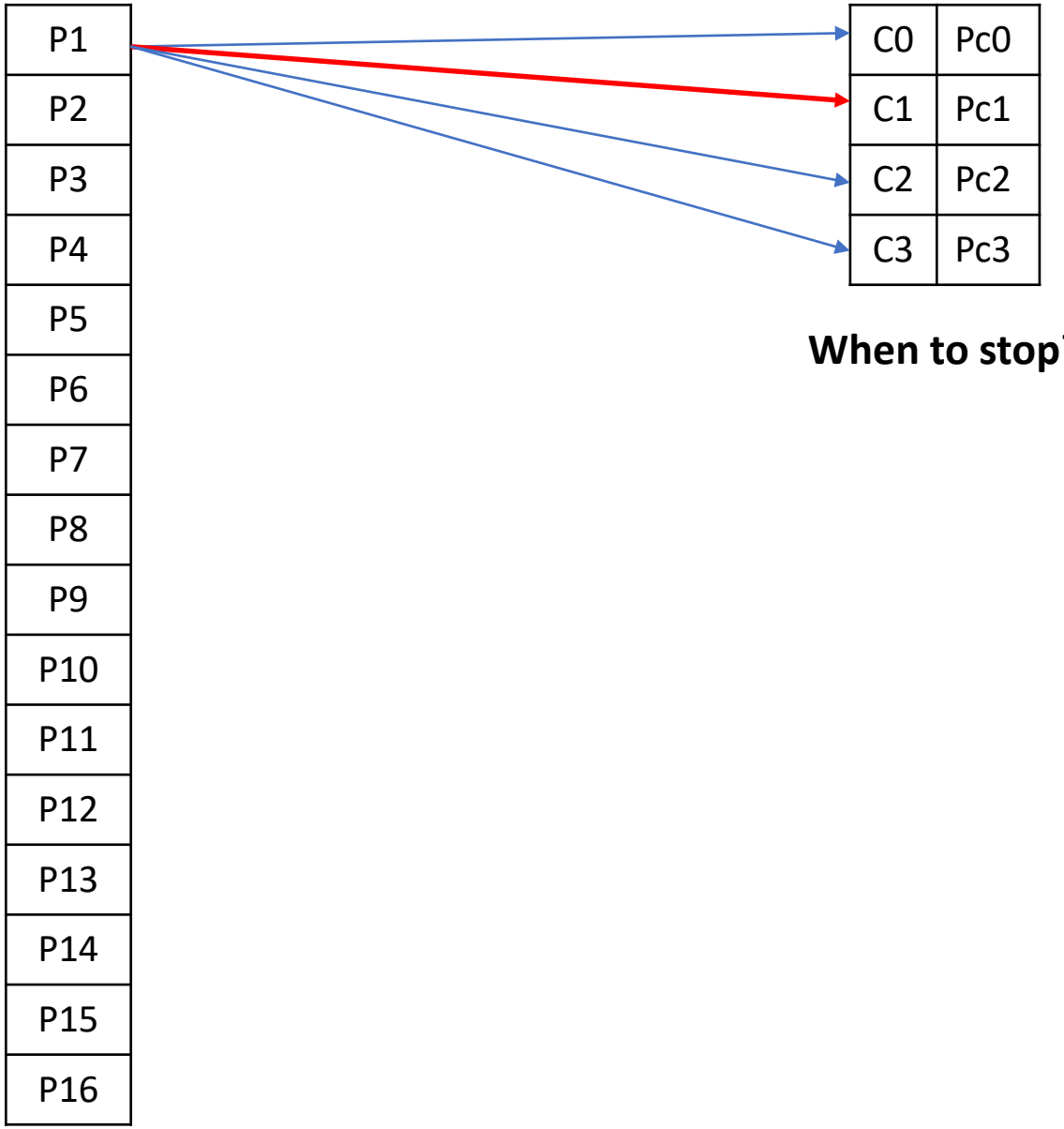
Centroids after iteration 1

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

C0	(P6 + P8 + P10 + P13)/4
C1	(P2 + P3 + P7 + P11)/4
C2	(P1 + P4 + P12 + P15 + P16)/5
C3	(P5 + P9 + P14)/3

** P/N = (x/N,y/N)*


P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16
C0
Pc0
C1
Pc1
C2
Pc2
C3
Pc3

When to stop?

Parallel K-Means

How can we parallelize?

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

How can we parallelize?

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

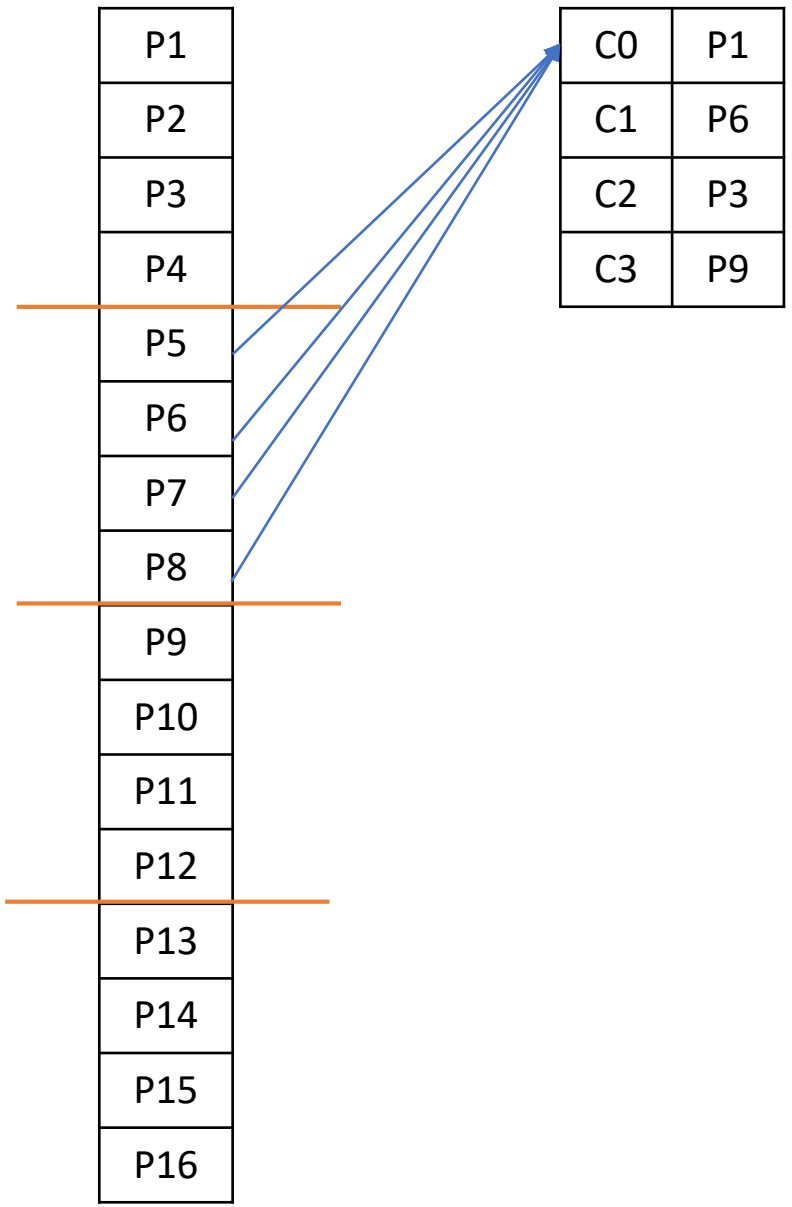
C0	P1
C1	P6
C2	P3
C3	P9

How can we parallelize?

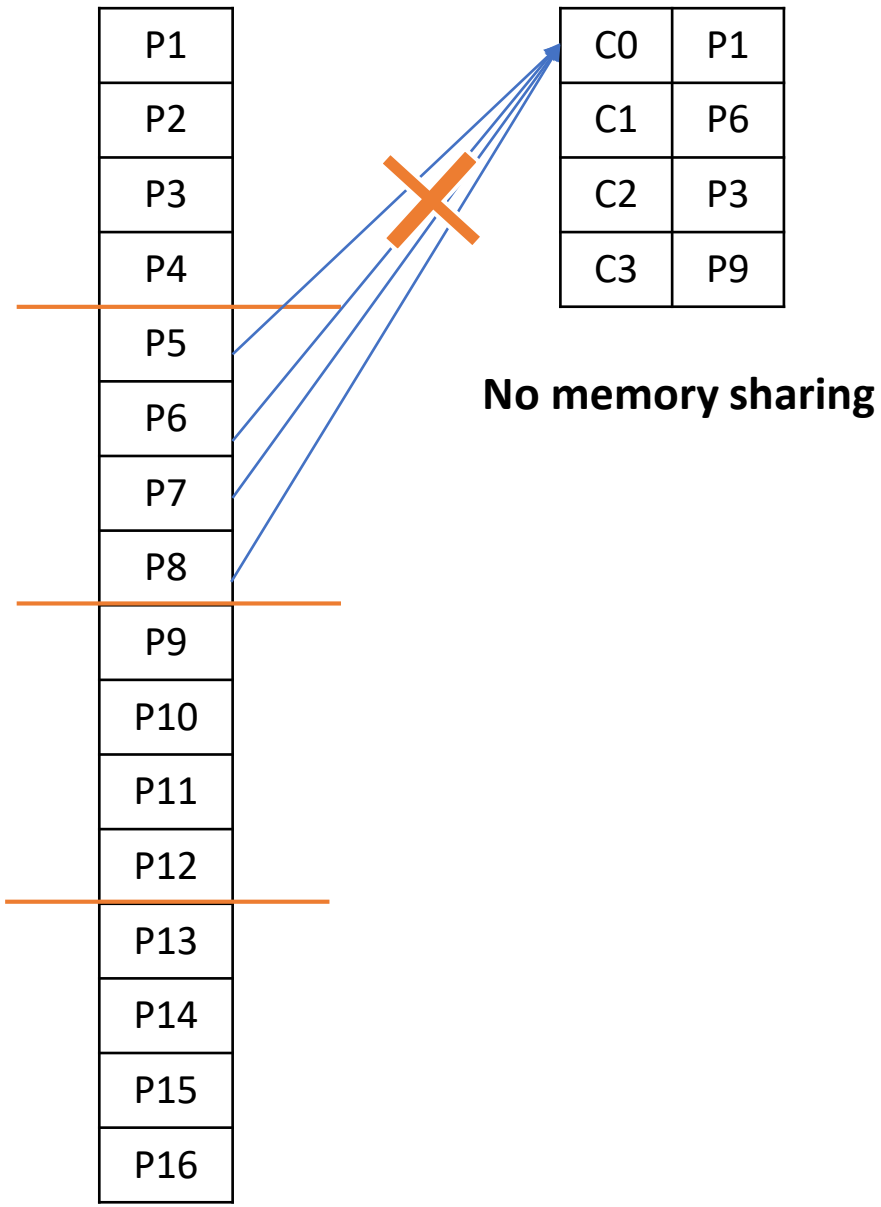
P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

How can we parallelize?

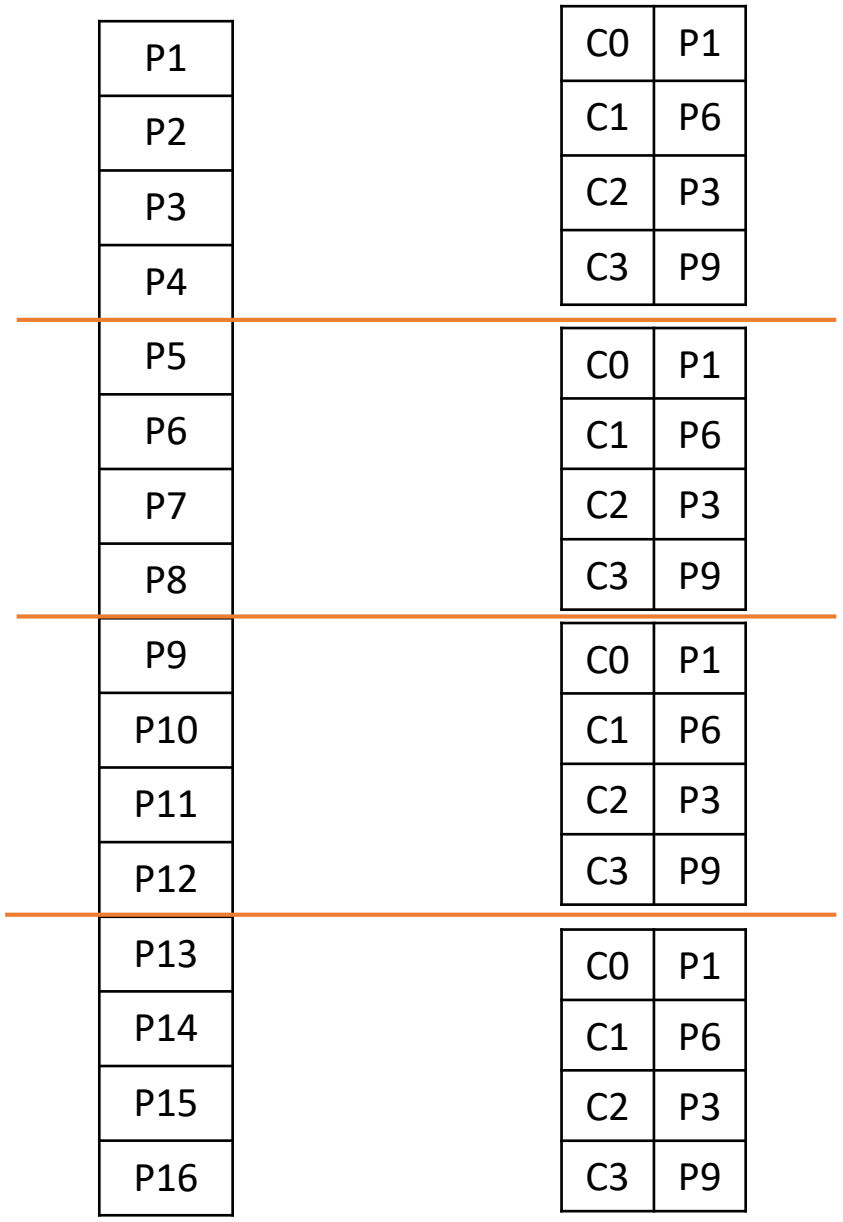


How can we parallelize?

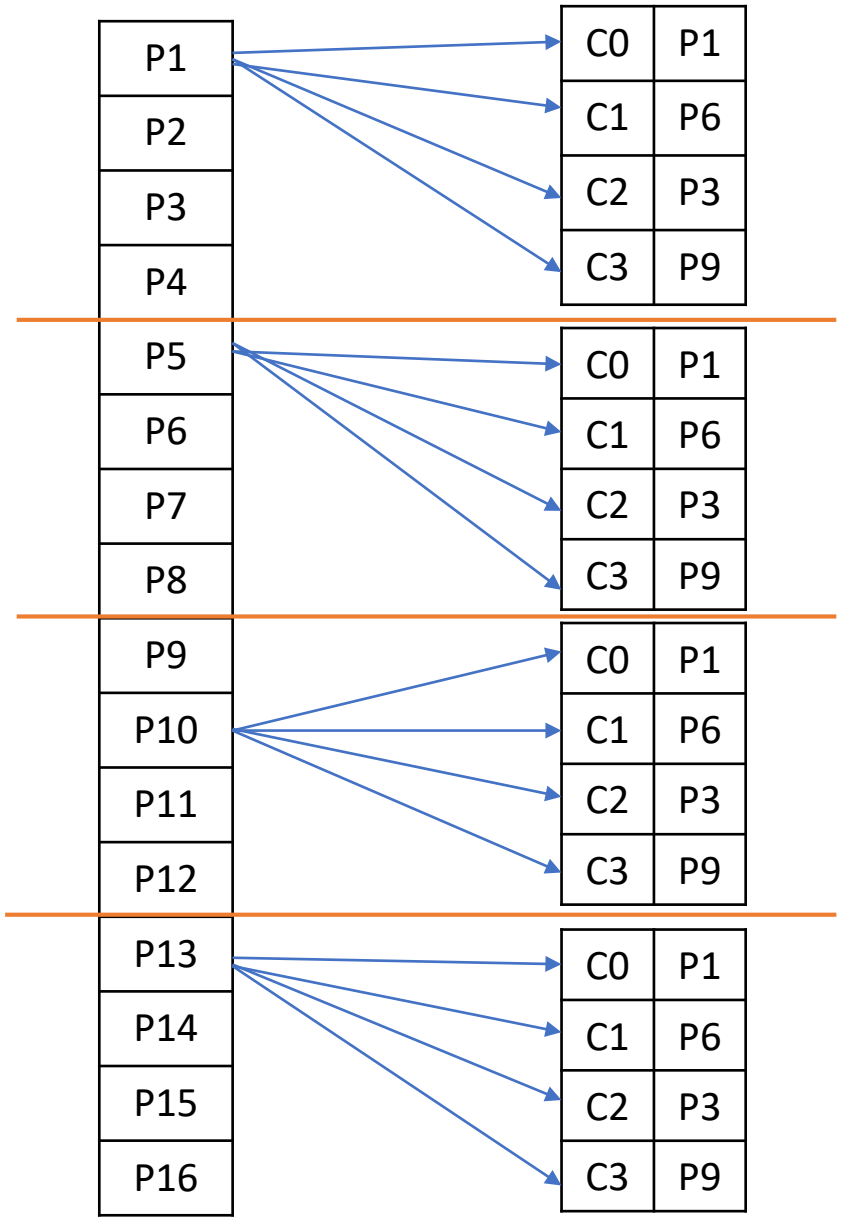


No memory sharing

How can we parallelize?



How can we parallelize?



How can we parallelize?

P1
P2
P3
P4

C0	P1
C1	P6
C2	P3
C3	P9

C0	P2 + P3
C1	0
C2	P1
C3	P4

P5
P6
P7
P8

C0	P1
C1	P6
C2	P3
C3	P9

C0	P5
C1	P7
C2	P8
C3	P6

P9
P10
P11
P12

C0	P1
C1	P6
C2	P3
C3	P9

C0	0
C1	P12
C2	P10 + P11
C3	P9

P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

C0	P13 + P14 + P16
C1	0
C2	0
C3	P15

How can we parallelize?

P1
P2
P3
P4

C0	P1
C1	P6
C2	P3
C3	P9

C0	P2 + P3 /2
C1	0
C2	P1 /1
C3	P4 /1

P5
P6
P7
P8

C0	P1
C1	P6
C2	P3
C3	P9

C0	P5
C1	P7
C2	P8
C3	P6

P9
P10
P11
P12

C0	P1
C1	P6
C2	P3
C3	P9

C0	0
C1	P12
C2	P10 + P11
C3	P9

P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

C0	P13 + P14 + P16
C1	0
C2	0
C3	P15

How can we parallelize?

P1
P2
P3
P4

C0	P1
C1	P6
C2	P3
C3	P9

C0	P2 + P3
C1	0
C2	P1
C3	P4

P5
P6
P7
P8

C0	P1
C1	P6
C2	P3
C3	P9

C0	P5
C1	P7
C2	P8
C3	P6

P9
P10
P11
P12

C0	P1
C1	P6
C2	P3
C3	P9

C0	0
C1	P12
C2	P10 + P11
C3	P9

P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

C0	P13 + P14 + P16
C1	0
C2	0
C3	P15

How can we parallelize?

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

C0	P1
C1	P6
C2	P3
C3	P9

C0	P1
C1	P6
C2	P3
C3	P9

C0	P1
C1	P6
C2	P3
C3	P9

C0	P2 + P3
C1	0
C2	P1
C3	P4

C0	P5
C1	P7
C2	P8
C3	P6

C0	0
C1	P12
C2	P10 + P11
C3	P9

C0	P13 + P14 + P16
C1	0
C2	0
C3	P15

How can we parallelize?

P1
P2
P3
P4

C0	P1
C1	P6
C2	P3
C3	P9

C0	P2 + P3 + P5 + P13 + P14 + P16	/6
C1	P7 + P12	/2
C2	P8 + P10 + P11	/3
C3	P6 + P9 + P15	/3

P5
P6
P7
P8

C0	P1
C1	P6
C2	P3
C3	P9

P9
P10
P11
P12

C0	P1
C1	P6
C2	P3
C3	P9

P13
P14
P15
P16

C0	P1
C1	P6
C2	P3
C3	P9

How can we parallelize?

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

C0	Pc0
C1	Pc1
C2	Pc2
C3	Pc3

How can we parallelize?

P1
P2
P3
P4
P5
P6
P7
P8
P9
P10
P11
P12
P13
P14
P15
P16

C0	Pc0
C1	Pc1
C2	Pc2
C3	Pc3
C0	Pc0
C1	Pc1
C2	Pc2
C3	Pc3
C0	Pc0
C1	Pc1
C2	Pc2
C3	Pc3
C0	Pc0
C1	Pc1
C2	Pc2
C3	Pc3

DNA stranding

ACTG
GTCA
SGGT
TAAA
ATAT

ACTG
GTCA
SGGT
TAAA
ATAT

How to get the centroid of these DNA strands?

How many repetitions of A in index 0 of all strands

A				
C				
G				
T				
Output strand				

ACTG
GTCA
SGGT
TAAA
ATAT

A	2			
C				
G				
T				
Output strand				

ACTG
GTCA
SGGT
TAAA
ATAT

A	2	1	2	1
C	0	1	1	0
G	1	1	1	1
T	1	2	1	2
Output strand				

ACTG
GTCA
SGGT
TAAA
ATAT

A	2	1	2	1
C	0	1	1	0
G	1	1	1	1
T	1	2	1	2
Output strand				

Get the mean or the median (sort the values and select the middle one)

ACTG
GTCA
SGGT
TAAA
ATAT

A	2	1	2	1
C	0	1	1	0
G	1	1	1	1
T	1	2	1	2
Output strand	**T**	**G**	**C**	**A**

ACTG
GTCA
SGGT
TAAA
ATAT

A	2	1	2	1
C	0	1	1	0
G	1	1	1	1
T	1	2	1	2
Output strand	**T**	**G**	**C**	**A**