AFFINITY PROPAGATION:

- We use a type of clustering algorithm where the complete data is viewed as a network with each data point being a node in the network.
- The entire algorithm is based on finding iteratively how well one point is suited to be a representative of another point (i.e., how suited a particular point is to be an exemplar to another point by gaining information about other prospective representatives in the data).
- Unlike clustering algorithms such as k-means or k-medoids, affinity propagation does not require the number of clusters to be determined or estimated before running the algorithm
- A dataset is described using a small number of exemplars, 'exemplars' are members of the input set that are representative of clusters. The messages sent between pairs represent the suitability for one sample to be the exemplar of the other, which is updated in response to the values from other pairs
- This updating happens iteratively until convergence, at that point the final exemplars are chosen, and hence we obtain the final clustering.

ALGORITHM:

- The first step is to create the similarity matrix based on the given data.
- The similarity matrix is formed using the distance between two points. Similarity is the negative of the sum of squares of distance between the points.
- Then calculate the responsibility matrix using the similarity matrix and availability matrix. Availability matrix however is initialised to zero.
- Once the responsibility matrix is calculated we use it to calculate the availability matrix that was initialized to zero.
- Once we have both availability and responsibility matrix we add them to get the criterion matrix which decides the ultimate clusters.

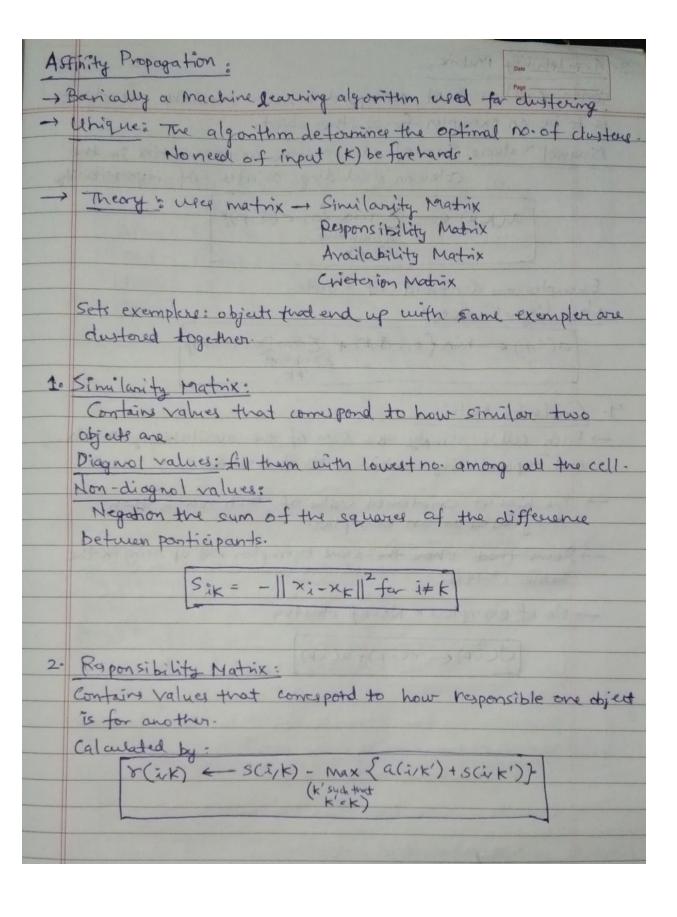
$$r(i,k) \leftarrow s(i,k) - \max_{k' \text{ such that } k' \neq k} \{a(i,k') + s(i,k')\}, \qquad (1)$$

$$a(k,k) \leftarrow \sum_{i' \text{ such that } i' \neq k} \max\{0, r(i',k)\}, \qquad (2)$$

$$a(i,k) \leftarrow \min\left\{0, r(k,k) + \sum_{i' \text{ such that } i' \neq \{i,k\}} \max\{0, r(i',k)\}\right\} \qquad (3)$$

$$c(i,k) \leftarrow r(i,k) + \underline{A}(i,k). \qquad (4)$$

When updating the messages, it is important that they be damped to avoid numerical oscillations that arise in some circumstances. Each message is set to l times its value from the previous iteration plus 1-l times its prescribed updated value, where the damping factor l is between 0 and 1. In all of our experiments (3), we used a default damping factor of l=0.5



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contains values that correspond to how	- available one object
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Exempler => Centroid of cluster	Tilde revisionerya ala
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Non-diagnol values. a(irk) = min (or (k/k) + Emaxs i'such that i'k	or serviced
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4. Chieforion Matrix	of poday wisting
-> Each cellie simply the sam of the	re availability matrix
and Responsibility matrix at that I	ocation.
	each mus + Hou
- The highest crietarion value of designated as an exemplar.	Total 1000 is then
Roug that share the some exem	plen end up being in the
same cluster.	32
- No. of exempters = No. of clusters	
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Example

Preformed of five participants:

Participant	Tax Pate	Fee	Interest Page	Quantity limit	Price
Alice	3	4	3	2	1
Bob	4	13	5	1	1
Cary	3	5	3	3	3
Doug	1 2	1 1	3	3	2
Edna	1 1	1	3	2	3

In an experimental exercise participants are asked to indicate on a 5-point scale their preferences with tax rate fee, interest rate, quantity limit and price limit.

Cal austing off-diagnol dements in Similarity Matix:

Similarity bis alice A Bob:

Similarity (Alice, Bob) = (-7)

Similarly calculate Similarity for all other non-digned elements.

Similarity bow Edna and bob comes out to be the lost.

[S(E,B)=-22] - least.

The heart non-diagnol element is placed in the diagnol positions (A11).

		-	1	Novie	Edha
Participant	Alice	Bob	cary	Doug	
Alice	(-22)	-7	-6	-12	-17
Bob	1-7	(-22)	100	-17	
Cary	-6	- A	(22)	(-22)	-21
Doug	-12	-17	-18	-2	1-2-2
Edna	1 -17	-22	1-21	-3	(-22)

Reason for placing (-22) in diagnol values:

The algorithm will converge around a small no. of stuplers if a smaller value is chosen there (22) is the smallest off-diagnol value, sophich this value in every one of the diagnol elements diagnol the algorithm to converge onto a small no of duto

Responsibility Matrix:

Responsibility of Bob (coloumn) to Alice (row) is Similarity of Bob to Alice (=-+) runus the movin of the hemaining similarities of Alice's now (6).

S(i/k) - max {a (i/k')+5(i/k)} = r(i/k)

Initially all the elements of availability matrix as set to zero.

a (i,R') = 0. (A11).

RCBA) = S(B,A) - max (or row similarities of)

R(B,A)= (+1) - (-6) = (-1)

RCAMA) = (-16) = (-16)

Similarly others,

R(A, B) = S(A,B) - max (o, remaining similarities

R(AB) = (7) - (14) = 10 - (Bob 10 W)

Responsibility Matrix.

Participant	Alice	Bob	Cary	Daug	Edma
Alice	-16	-1	1	-6	-11
Вор	10	-15	-10	-10	-15
Cary	11	-11	-16	-12	-15
Doug	-9	-14	-15	-19	9
Edna	-14	-19	-18	14	-19

Availability Matrix

Following Egics) are used to update availability matrix.

a(k/k) & 5 max {0,2(i/k)} Diagnol elements:

(i/such that) excluding self-rapon sibility

a(ix) < min So. r(k) + E max (o, r(i/k)) |
isun that > Non-diagnal elements.

Self-availability of Alices is Sum of positive responsibility
ties of Alice coloumn excluding Alice's self-responsibility
10 + 11 = 211. (Diagnol Value).

Availability of Bob (voloumn) to Alice (row) is bob's self responsibility plus the sum of the remaining positive responsibilities of bob's coloumn excluding the responsibility of bob to Alice

(-15 + 0 + 0 + 0) = (-15).

Participant 1	Alice	Bob	Carry	Doug	Edia
Alice	21	-15	-16	-5	10
Bob	-5	0	-15	-5	-10
Cary	-6	-15	1	-5	-10
Doug	0.	-15	, -15	14	9
Bdra	0	45	-15	-191	
21-	lal-	101-			
1 21-			110	P	
Crieterion Ex used t	Matrix:	21-	N.T.	10.2	

hence, crictorion value of Bob (coloumn) to Alice crow) is the sum of the responsibility and availability of bob to Alice.

(-1)+(-15)=(-16).

Chietorion matrix:

Participant	Alice	bob	Carry	Doug	Edna	
Adice	(3)	-16	-15	1-11	-21	
bob	(5)	F3	-25	-15	- 25	1
carry	(5)	-26	-15	-17	-25	1
Doug	-9	-29	-30	(3)	-10	1
Edna	14	-34	-33	(-3)	1-10	1

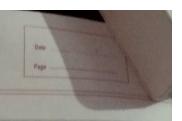
The coloumn with highest existed on value for each row identifies the exemplar for that item of that row.

Rome that share the same exemplar arein same

heme, two dustous appear.

cluster 1: {Alicer bob, cary }

cluster 2: { Doug, Edra],



the solution iso here the first sell is the sell.

I this was one iteration, we went through all 4 agr, Initially.

Now in second iteration, we keep the value of a (i/k) obtained from first iteration and calculate second crieticis matrix.

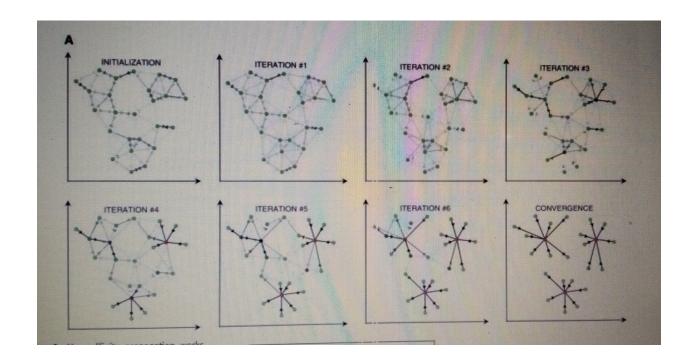
To assure convergence a tiny bit of random noise is added to the similarity matrix.

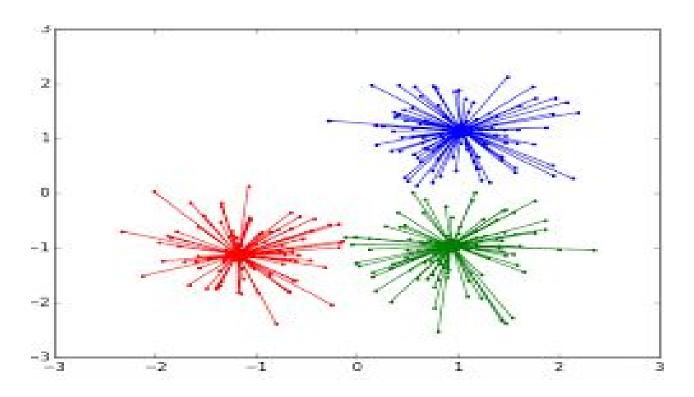
Domping updates of the availability and raponsibility matrices by 50%.

{\mathbf{r}_x', \mathbf{q}_x'} \tau \text{Undamped updates of responsibility and availability matrices at iteration \text{t'}.

Then damped updates are

 $\gamma_{t} = 0.5\gamma_{t-1} + 0.5\gamma_{t}'$ $q_{t} = 0.5q_{t-1} + 0.5q_{t}'$





implementation:

https://colab.research.google.com/drive/1CfVKsR1MJkr x85f7SA62X9JryH4e5-Xa?usp=sharing

https://colab.research.google.com/drive/1KUBixlLWRc A6R75gSMd-FXKIaDG4v291?usp=sharing

References:

http://utstat.toronto.edu/reid/sta414/frey-affinity.pdf http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1 .1.490.7628&rep=rep1&type=pdf