Course on Introduction to Medical Imaging and Analysis Softwares
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Module 02
Lecture 07: Region Growing and Clustering

So welcome to yet another exiting lecture fine here we will be covering on initial topics of segmentation, so I would be starting with the most basic technique which is called as region growing and eventually we would be walking over to clustering and preliminary lee targeted (()) (0:35)segmentation but I would also be looking onto the classification aspects with clustering as well.

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Now how this lecture is organized is basically I start defining what segmentation is in terms of its mathematical and say theoretic definitions so that you have a very clear understanding about what we meant by segments and what are the characteristics of segment, what are different regions. From there since we are looking into region growing this segmentation and this particular method is basically a semi supervised or user initiated segmentation method and it starts with some initial estimates of what region is and what kind of pixels are going to define region and that is called as a seed.

So what these seeds are as initial estimates for the region growing is what I will be discussing followed by something called as a distance measure that is about look into which pixel is similar to these seeds such that you can include them into your region of interest and immediately start on expanding your whole segment over there in order to do segmentation. From there we have a particular iterative process for region growing with for segmentation purposes so we have a very practical example where I show you how you can write down in terms of coding parlance each of them, or whether you can solve it out your own self on a pen and paper problem as well.

From there we move on to clustering which grows on top of what we had learnt for segmentation expect for the fact that it is no more user initialized in any way. So basically you can start the whole process without giving a user initialization and the algorithm itself learns how to do the initialization and build on top of it as well.

So that we will be learning for segmentations as well as for classification in case you want to basically annotate with single image. So the say feature descriptors which we have learnt in the previous lecture on textures how you can use each of this texture measures or some other kind of a feature measure and combine them for classifying different images itself we have a practical problem which we will be looking and exploring in details.

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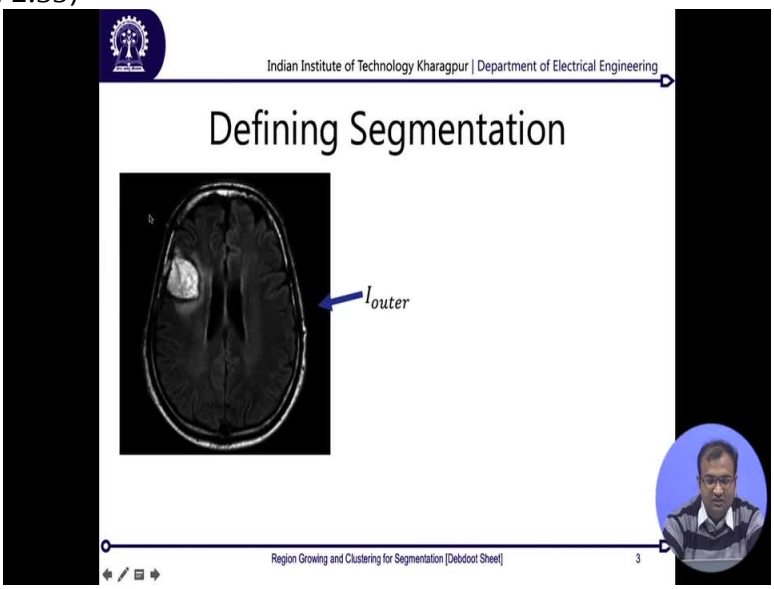

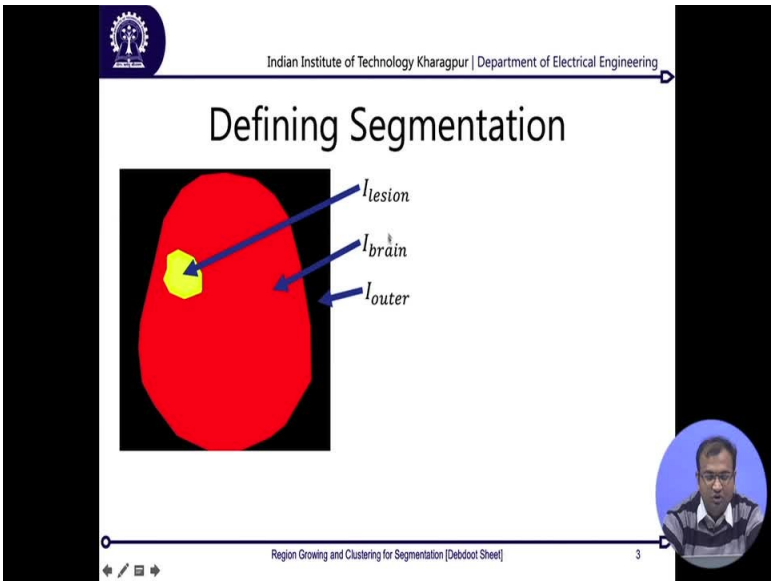

So say I am looking into segmentation and this is a T1 MR of the brain along with lesion which appears in quite bright over here and now the problem is that you need to segment out this lesion from rest of the brain area and together from the this background over here which is called as the outer region. So if that is the situation then this part of everything in black is called as outer, the part marked in red is called as the brain and the part marked in yellow is called as the lesion and three of them typically are called as a three segments of the whole image.

Now although you might have an initial intuition that your lesion is also part of the brain, but what we call as the brain tissue over here or the class of those particular tissues that is something which excludes the lesion in total, so that is the abnormal part of the brain. So we are not taking those abnormal tissues in any way. That is defined as a separate distinct segment which is called as a lesion. Now the first mathematical definition which it has is that the union of all of these three segments is supposed to define the image itself.

Now if I am defining only this part over here so it can have a possibility that there might be some part of it which overlaps with the brain between the lesion and the brain or there can be overlaps between a brain and the outer, but that is not so because the other definition says that if you are intersecting between all the regions it should return you a null set, so basically there is not a single pixel which is shared between two different segments or the three segments in total.

So in fact intersection of lesion and brain will also be a null set, intersection of brain and outer will also be a null set, intersection of lesion and outer will also be a null set by definition. Now from there what we do is that now that we have defined each of them in terms of set theoretic parlance, the next which remains is each of these individual pixels how are they defined as.

Now l of x is basically called as the label assigned to a particular pixel at a location x and we define that by this notion of small omega. Now small omega is a particular element of the entry from a larger set called as the set of all possible labels which is called as capital omega. Now for our problem, all possible classes which you have are basically lesion, brain and outer. So small omega can for any pixel can be either of lesion, brain or outer over there but it cannot be two of them together or any other combination in any way.

So basically for an image if we say that it is some sort of a labeling problem that given that you have an image I and every pixel over there is defined as x then you have another matrix which is called as l or the labels matrix, every element in that labels matrix is called as l of x and that will be given a particular label which is called as this small omega, this is how it is defined technically in terms of a segmentation problem. Now from there since we are looking into region growing and that does make use of seeds as the initial estimate over there, let us look what these seeds are basically.

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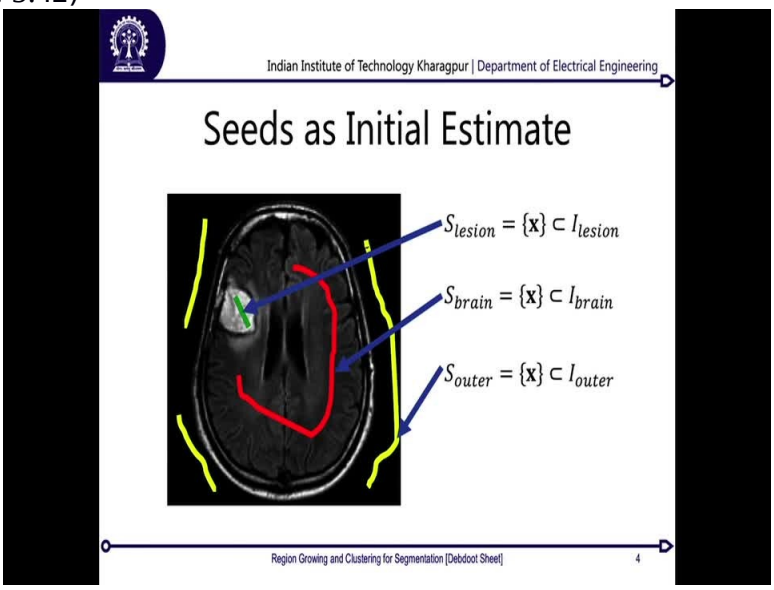

Now, on this image since my whole problem is to segment out this lesion from the brain and from the outer, so what I would initially start with is defining some seeds for lesion itself. So I draw a small straight line in green which will be say some set of pixel which can help me in defining that this this set of pixels at least conservatively represent what a lesion should look like or they belong to definitely a lesion.

So that is how I am going to define so S lesion is a small set of some pixels x which is a subset of I lesion necessarily. Now I can define another set of labels over here which will belong to the brain region, so all of this pixels on this marked in red they will be the what belong to this particular S brain and then I can mark another group of pixels over here in the outer in yellow and they will all belong to this S outer over there.

Now once I have all of these marked over here this is what is called as the seeds for my initialization of the segmentation algorithm. Now the idea for region growing is basically imagine that these seeds are now going to propagate, so everything in the neighborhood is trying to look at what is a closest neighbor to it and then it is trying to expand itself. So this would mean that initially from what we have as small independent pixels over here it would grow into a group of pixels or a cluster and eventually come down to a converges.

Now this converged phenomenon over there at the conversion state which is the steady state you would find out that this whole region should be marked as lesion, this whole region should be marked within your brain and everything in the outer should be marked over there. Now you can achieve the same sort of a conversions by in fact doing a raster scan like mechanism over there, which shall be you take one of these pixels and then keep on counting column wise then shift the row and keep on counting column wise, basically look into a serial way into all the pixels over there and try to find out which is the closest neighbor to each of them and try to assign that label which is similar to a nearest neighbor search.

You will be able to achieve this same sort of a steady state configuration for the segmentation problem as well. Let us look into how it is done.

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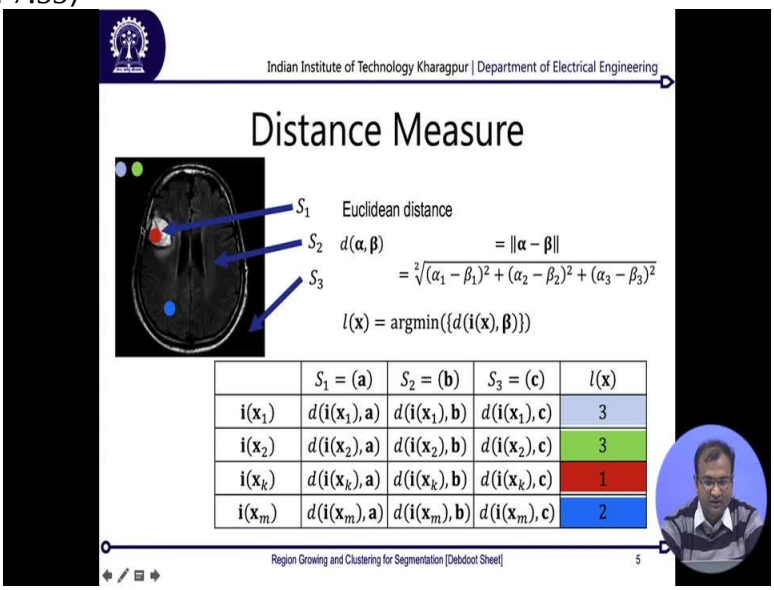

The first thing which you will need is now that you have a seed present say I boil this problem into a much smaller problem instead of taking a group of seeds. now let us look into it such that you have one single seed within each region, say for the lesion region I call it as S1 so there is one particular pixel which is S1, there is another pixel over here which is called as S2 which is within the brain region and say there is another pixel called as S3 which is in this outer region over there.

Now, for any particular pixel which comes down I can have a distance measure, now say alpha is the feature vector which represents this S over here. Or for us if we are just looking into intensities and it is just a intensity value or scalar value at that location x. Now, any pixel over here at any point is what represents this value beta over here, now the distance between them is computed in terms of Euclidean distance and say over here I have a three tuple vector, so say this was a RGB image or you can have some different layers, so it can be the image itself the intensity of the image the second vector over there can be the texture of the image computed in terms of say a local binary pattern.

The third vector can be the texture of the image computed in terms of the say a wavelet transform version over there a laws mask one of the features over there. Now you can take all of these features together, and try to form a feature vector which will represent that particular pixel

and then you can find out the distance between two of those pixels in this particular kind of a way.

Now for our problem, what it will end up is that you can get this kind of a table such that you start at any one of these pixels you will be getting one of these entries, so say we took this first pixel over here which is a x1 so I take the vector at x1 which is my Ix1 and then I can find out the distance to all of these three segments over there S1, S2 and S3. Now based on all of these three segments, it will be closest to one of the segments than all of the others which is what is written through my argmin over here.

So what it is trying to do is whichever is my shortest distance to whatever beta, beta is basically whichever class label I am going to represent over here. So this particular class which has my smallest segment over there so for my S1 which is my segment 1 I have one point which is called as a and the distance between this point and this point is what I find out using my Euclidean distance measure over here. Similarly I repeat for my S2 and my S3 and then find out over all of these three distances which is my minimum and then try to return the argument of that.

Now argument of this is obviously a, b or c nothing else because I am this axis of Ix1 is the same for all that the only variation between them is a, b or c. So over here it returns the argument c which belongs to S3 which is a class level of 3, so this is the label which gets assigned to a particular pixel at x over here. Similarly I repeat for the second pixel over there and also get a class level of three return.

Now for another pixel which is over here which is my kth pixel I see that it returns me a class level of 1, okay. Now for another pixel which is located over here I see that it returns a class level of 2, now using this table completely together what will happen is that you will be able to label each pixel over there in this whole problem.

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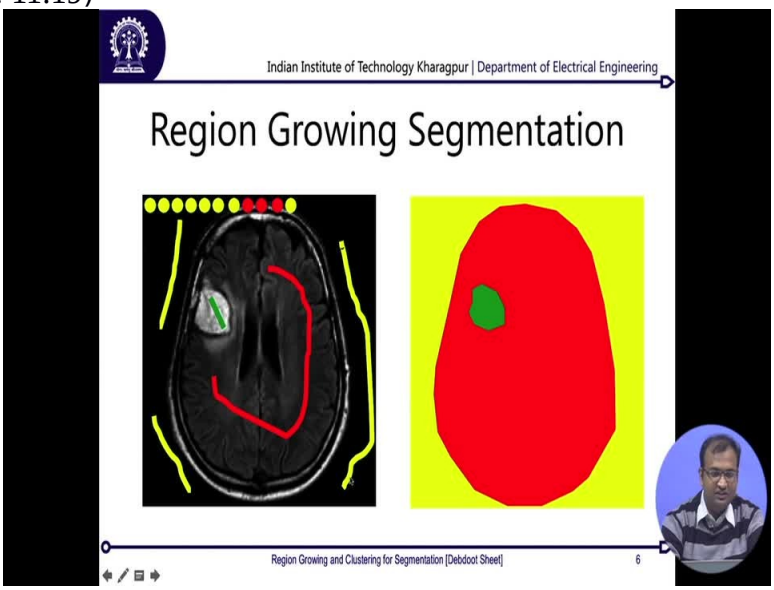

Now that is what will result in your actual algorithm for region growing segmentation in which what you have is you have the whole image, you are going to mark down distinct regions within the image. Now the only difference over here is since you have a group of pixels so all of these distance measure will be found out through these group of pixels and then you find out which particular pixel on the seed or whichever particular element on the seed is the closest to your particular pixel you are looking to.

And whatever the label for that one you are going to assign it over there. Now to start as a problem we start with these particular ones it keeps on going and since it is very close to this yellow label so all of these pixels get assigned the color yellow or that particular class which is my outer. Now for the next one you would see that it is actually close to the brain tissue, not closer to these ones that why they colored in red which is the class label for my brain tissue over there.

Now the next one will again be falling into my outer region and that is how I am going to do this. Now if I repeat this whole thing I will be able to get this kind of a mask which is for my lesion which is represented over here in green, for my brain region which is represented in red and my for my outer region which is represented in yellow and that is where my segmentation problem ends over there in terms of region growing principle.

So obviously this is quite an intuitive and interesting because all you have to do as a user is basically make some sketches and marks over there which will select out my seeds and then using these seeds it can actually grow. So the beauty is it is invariant to your image variations across devices so if you have the same algorithm which you can basically use say across CT, MR, X-rays, ultrasound any of them, so it is not dependent on one particular modality.

Next you can use the same algorithm in order to segment lesions in the brain versus lesions in the liver, because you are just going to manually annotate which particular object you want to segment. Now if you want to make it even finer say you want to find out these ventricles of the brain and segment them out as well. So you can actually define another class of seeds over here which defines a ventricle of the brain and then you can change this three class classification problem into a four class classification problem.

One word of caution is obviously that you cannot define just one single seed label and assume that it is getting segmented, because segmentation problem basically means that you need one region and the compliment of the region to be defined, both of them. So there is nothing called as one class segmentation as such. You basically have two classes so that class and the complimentary of that class. So if you wanted to segment only the lesion from everything else which comes in the image including the outer and this brain tissue to be grouped down together then basically what you will do is you put down one seed over here which is say this green and then you can club this yellow and red seeds into one single class over there, so you will get down a lesion segmentation algorithm over here.

And this is very intuitive, very easier to use and it is a person specific one which we are proving over here. Now this is about region growing for segmentation purposes. Now based on this idea about looking via distance measures into closest neighbors there is another very interesting concept which is called as clustering.

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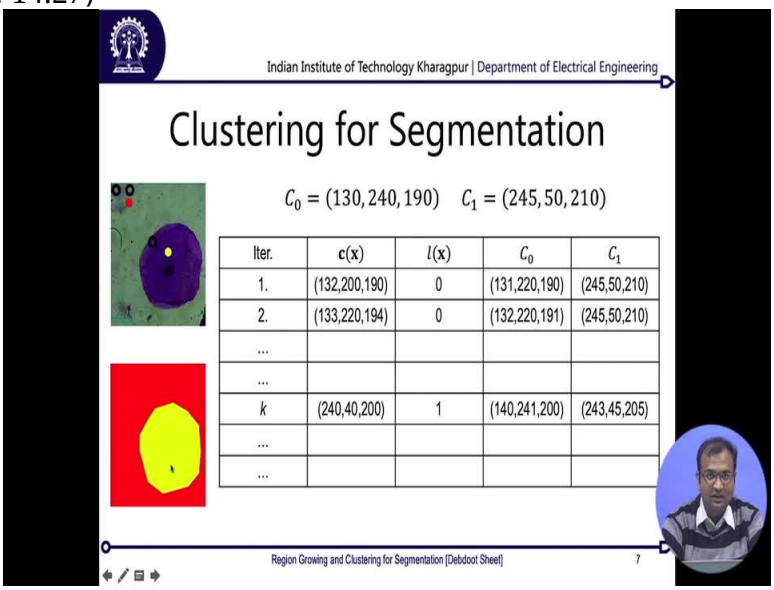

So if you are looking into clustering for segmentation as a problem over there now we are definitely going to borrow certain concept which we have learned in the previous one for being region growing based segmentation. Now say the problem is something like where I want to segment out this particular nucleus from the background, now this a image of basically an epithelial cell of the oral mucosa and how you can get this one is pretty easy. So you can take one your swabs for ear waxing which you use and just rub it around your mouth inside of your mouth and then you put this excision onto a glass slide, you air dry it and then stain this with haemotoxylin and eosin stain and put it into a microscope.

Now all the cells you would be seeing over there are pretty similar to the cell over here, the one which appears in sort of a violet color. Now this is an epithelial cell and the objective over here is that I want to segment this epithelial cell from the background over there. Now as a starting point the major difference is that nobody needs to interactively place the number of seeds over there, you do not need to say that there is a seed inside this cell and there is a seed outside over there.

The only thing you will have to tell a clustering algorithm is a number of clusters you would like to segment out over there. And for that purpose what we say is that we need two different clusters and for that the starting point is that you will need some sort of a seed still but this one of this seeds will be selected in random from anywhere on this image. So say for the first cluster I

am taking a seed which is randomly selected over here and for the second cluster I take a seed which is randomly selected over here.

So under a good likelihood condition they basically got selected in two distinct regions and that will guarantee a much faster conversions, whereas if both of the seed were selected around on the background region itself, it would take much longer to convert but eventually you would find out that the centroids and the cluster conversions is would be guaranteed in either of the cases over there.

Now, if this is a situation what we can do next is that we will have to do a raster scan over a whole image, try looking into each of this pixels and compute out the rest of the table over here. Now for this table what we do is say in the first iteration we take the first pixel on this image over there.

Now this pixel has a RGB value which is represented as 132, 200 and 190 and this is a standard 8-bit RGB representation for the whole image, okay. So we are just going to cluster based on color appearances module over there. Now, if I compare the distance of this particular pixel to both of them, then the distance will be shortest to C0 you can find you can compute your Euclidean distance and you find out that this will be the shortest distance.

Now accordingly, my labeling concept which is my arg minimum of my shortest distance will return me the minimum label as 0 class 0 over here. Now once I have this class 0 created what comes down in the next part is that my cluster of class 0 consists of this pixel and this pixel together and now that I do not have one single pixel but two pixels definitely the centroid of the cluster is going to change over there. The centroid of the cluster will be located somewhere in the arithmetic mean between these two values which create my cluster over there.

So we find out what is the mean value over there and that comes down to be 131, 200 and 190. Now, for my cluster 1 C1 which is the second cluster I basically do not have any change because none of the pixels so there is only one pixel which is my starting pixel and no other pixel from the image came down over there. So the centroid of C1 will remain the same. Now in the second iteration I take the second pixel over here that has a value of 133, 220 and 190.

Now I am going to compare this one with my centroid measure which is over here. So the closest distance is 2 C0 and the furthest is from C1 from your Euclidean distance masure. So this gives you a label of 0 and accordingly you again place this into the cluster C0. Now see your C0 cluster now has this particular pixel, this pixel and this pixel together. So now it is going to be a centroid based on all the three pixels based together over there. So now based on all the three pixels you get down a combined centroid which is at 132, 220 and 191.

You still are not getting any pixel into your C1 cluster, so the centroid remains the same over there you keep on repeating over here now say for the kth pixel somewhere over here, okay. For this particular pixel I have a color intensity value 240, 40 and 200. Now together with this one you can actually compare with whatever is this C0 and C1 value over here and we find out that it is basically closer to C1 than to C0. So this gets labeled as 1 and now you need to modify, so your C0 whatever is the centroid over here will remain the same so that incidentally comes down as 140, 241, 200.

Whereas your C1 now is so till whatever was the value so till here basically we did not get any pixel which was labeled in to C1 itself so C1 centroid was preserved. So this value and this value together and you find out what is the mean value over there and that is your new centroid for C1. And together you can keep on populating this table together such that at the end of the population of this table you would be able to find out this kind of a label for each of these pixels.

So all of these pixels marked in red are what belongs to the background and everything marked in yellow is what belongs to this epithelial cell region over there. So this is to solve out your problem through a clustering approach where you do not need to give down initial estimates of seed, nobody needs to put down except for the fact that number of clusters has to be defined. So well at good we are definitely going a long way in solving segmentation problems over there.

Now this does raise a lot of questions over there, so are we going to learn only segmentations over here or is there some more practical problems which we are doing because at the end of the day your all of your problem is not just to segment out images, there might even be analysis problems which is where can you analyze images and tell whether these images are say benign or malignant whether they belong to a perfectly healthy category or there is a tumor which is benign or there is a tumor which is malignant.

Say if you are looking at cells then can you say that this particular kind of a cell an epithelial cell or a WBC is a healthy WBC or it is not a healthy WBC over there.

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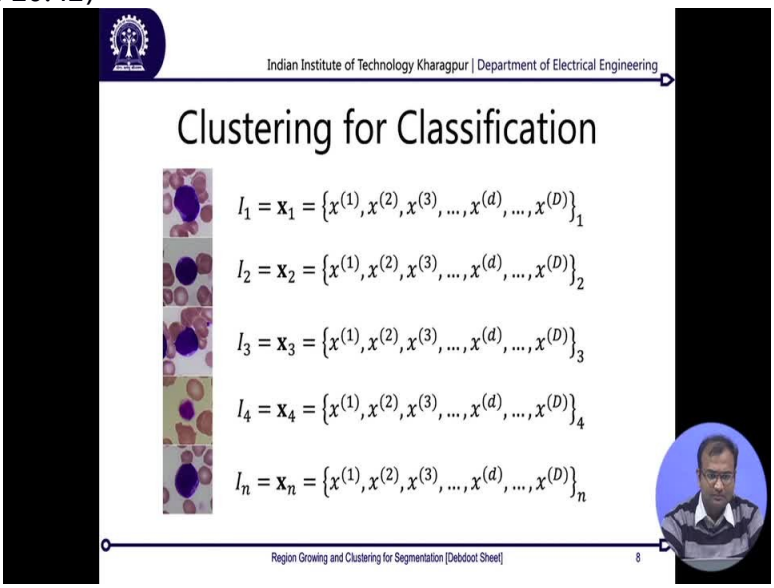

So we take one of those problems over here for classification and what we solve over here is quite interesting. So basically we have these small snapshots of WBC's which are Leishman stain, so now whatever you see these red ones in the background are RBC's red blood corpuscles and the one in violet is a WBC over there. And there are different kinds of WBCs which you would be seeing over here.

Now if you have a very careful look you see that these three almost look very similar, whereas this one looks a bit smaller and unhealthy or something of that sort but interestingly this is actually a healthy WBC, whereas this particular one is something which is very distinctly defined as a malignant case of WBC or something which is close to a lymphoblastic leukemia. And you have similar ones are those over here also.

So if the problem is about classification of each of these WBC's and let us try to say that I have a mixture of WBC's over there I can have healthy WBC's and I have some lymphoblastic leukemia WBC's but I do not know what is defined as what but I want to cluster them, so all the leukemia WBC should be in one cluster and all the healthy WBC's in one cluster, okay.

So if that is the problem what we do is we have multiple of these images each of is an image patch in which one patch you have just one WBC. Now, for I1 you can represent it in terms of a feature vector x1. Now what that has is basically a tuppled arrangement with D such number of features. Now how you would be getting these features is you can use your texture measures which we have learnt in the last lecture. So you can have a whole feature vector of textures you can have the entropy of the histogram of oriented gradient, you can have the local binary pattern histogram over there, you can have entropy of co-occurrence matrix as one of the features, you can have the average color intensity over there as one of the features.

So similarly you can have shape, size anything after segmentation as features, so say that there are D number of features. So this can be even very large numbers, I mean D can D in most general cases would be ranging something more than 20 to 100 or 200 and at times people use something like 3,000 features as well, so it is a very dimensional space on which you operate. Now typically it represented that the subscript 1 denotes the sample number so your subscripts over here are all different samples over there.

The superscript in bracket denotes an ordered position of the feature, so x1 if this denotes say local binary pattern the average LBP value on an image then across all of them it will be denoting the (loc) average LBP value x2 if its denotes the entropy of the co-concurrence matrix, then across all of them x2 is going to denote the occurrence the entropy of co-occurrence matrix and you cannot interchange between any of them at any point of time. In that case, you are basically messing up the whole arrangement of looking into features spaces and the dimensions, okay.

So this tuppled vector this D tuppled vector over there is also has a subscript of 1, 2, 3 which corresponds to the sample subscript over here, this is a classical way in which features are represented for our classification problem and we would be following this in the subsequent lectures as well, so just keep a note of how these are done and what are the common followed conventions for this one. Now once we have this one, so this is about the whole data set and the features which you will be using in order to do your classification of image patches.

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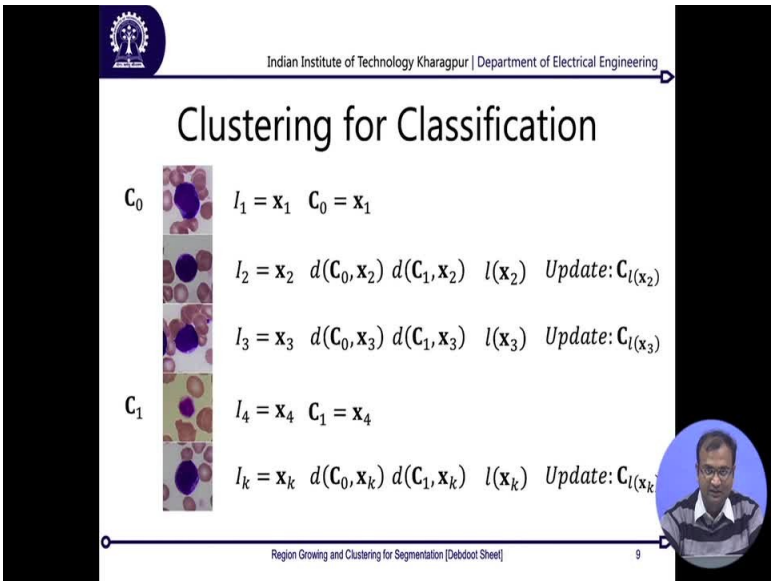

Now, from there if you look into this clustering problem this as solving this as a clustering problem. So say what we said was that basically there are WBC's and there are two kind of WBC's, okay one of them is a healthy, another is a leukemic one, okay. Now if that is the situation, I start with defining two different clusters centroids over there, so the first one is C0 say this image the randomly got assigned as the centroid for C0. From there I use another centroid which is C1 and that is what got defined as C1.

Now once I have these two as my templates over here or the initial centroid estimates, I have my features as well coming down. So the centroid tow is at C0 is equal to x1 the next centroid is at C1 is equal to x4. These two are my centroid for each of these clusters. Now I am left done with the rest of these three images or basically there will be k number of such images so the rest of them are out over there. Now what I would start is my initial would be this particular one. So with this one I find out what is my distance from the centroid C0 for this particular feature vector x2 and the distance from centroid C1 with this particular vector x2.

Now each of these distances I can find out using a classical Euclidian distance measure as we were doing in our region growing principles over there, use the same concept of finding out the label. Now whatever is the label over there what we are going to is now that you are also bring in this particular element or this particular feature vector into that cluster, so obviously you will need to update the centroid of that particular cluster where it gets assigned, you need to update the centroid of that particular (lab) cluster where the label got assigned over there.

Now similarly you do for the next image over there and you keep on doing till you go to the last image over there. Now once this whole thing is done, now you have a classification available at the end of all of these images which is via clustering. So we did not specify as to which is called as a what would be typically defined as a healthy cell healthy WBC and what will be typically defined as a leukemic WBC's but we just said that it is made up of different classes and by clustering we just came out to conversions of how to segment it out.

So there will be much more exercises which should be detailed over here (())(26:27) how to use say mat lab or python as your programming environment where you can be able to write down codes in order to run down the same solution as well and somewhere down the line in the third week we will be doing much more detailed experiments into deep neural networks where we will be learning into the same data set as to feature extraction and classification in the same pipeline.

So they are much more advanced methods which will guarantee higher and better conversionses and better performances in terms of accuracies when measured out. So in total today we have a good consolidation of some very preliminary methods of segmenting an image from a semi supervised in which a user gives some input from there, you go down to a completely unsupervised one in which you do not need any inputs from the user or you do not need any previous information from a set of different images given down and that is by clustering and from there we also learned how to cluster down images or features together in order to classify images as well.

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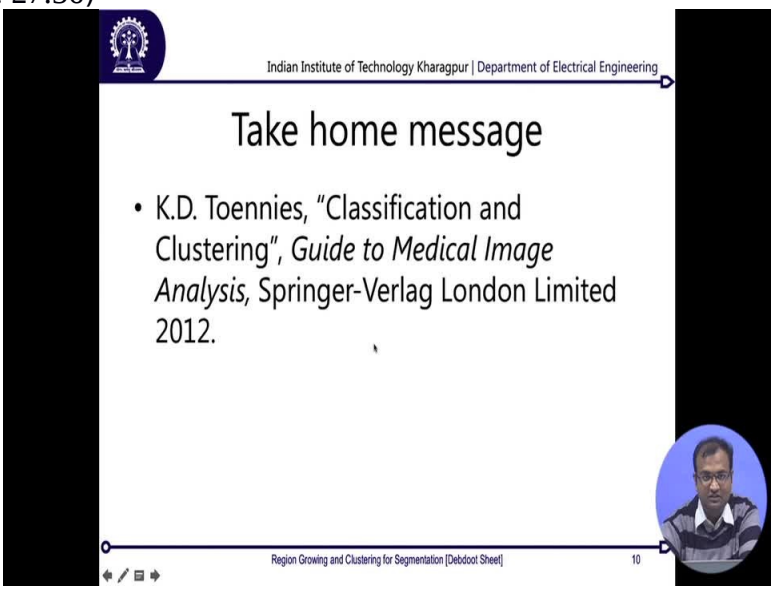

So with this I would come to a conclusion and definitely put you out to a pointer about this particular chapter from the guide to medical image analysis on classification and clustering which you can definitely have a read through as one of the suggested text for this particular chapter, with that it comes to an conclusion and thank you.