KAUNAS UNIVERSITY OF TECHNOLOGY

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Biomedical Image Processing and Analysis

Laboratory work report

Lab 3

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REPORT FOR LABORATORY 3:

A) Introduction and Problem Statement

I am using Matlab and I will solve the below problems:

1. Extraction of regions of interest (segmentation). Read the set of 15 mammograms (size 1024x1024 pixels, size of a pixel 0.2 mm) given in a directory III_lab. Radiologist manually marked two square regions in each mammogram: one of them labels healthy tissue, meanwhile other labels calcification (an example of marking is presented in Fig.1.). The coordinates of squares are given in files Calcification.mat (x, y – coordinates of left upper corner, r – length of a square sides, square labelling region with calcification), and Healthy.mat (x1, y1 – coordinates of left upper corner, r1 – length of a square sides). Extract (crop the square areas) marked regions of healthy and damaged tissue from the images, thus preparing the regions for further evaluation of possibly informative features.

2. Feature extraction. Calculate statistical moments: mean, standard deviation, skewness, entropy [2, 4] of extracted healthy and damaged regions. Try to consider what features of a region reflect these statistical moments from point of view of X – ray and tissue interaction.

3. Feature selection and classification. Try to analyse (try MATLAB: scatter) is it possible to separate (recognize) damaged and healthy tissue regions by using one of the moments or combination of few statistical pixel-level features. Select the most informative features and manually construct decision tree type classifier. Classify all (30) extracted regions into two classes: 1) healthy tissue; 2) calcification.

4. Classification quality assessment. Evaluate classification ratio (correctly classified/all), sensitivity and specificity (%) of your classifier. Consider is it good enough to be used for diagnostics?

B)Figures and Results - C) Comments And Conclusion

1)Firstly, we read the set of 15 mammograms and we cropped them to square regions according to the coordinates which were given in the files Calcification.mat and Healthy.mat .

2) Secondly, we calculated the statistical moments (mean, standard deviation, skewness, entropy) of extracted healthy and damaged regions.

To start with, Mean is the most basic of all statistical measures. In the contest of image processing, the mean is used for noise reduction. From the point of view of X–ray and tissue interaction, mean shows the average pixel value of the region which summarizes the whole region and determines the image by separating the bigger value pixels from the lower value pixels.

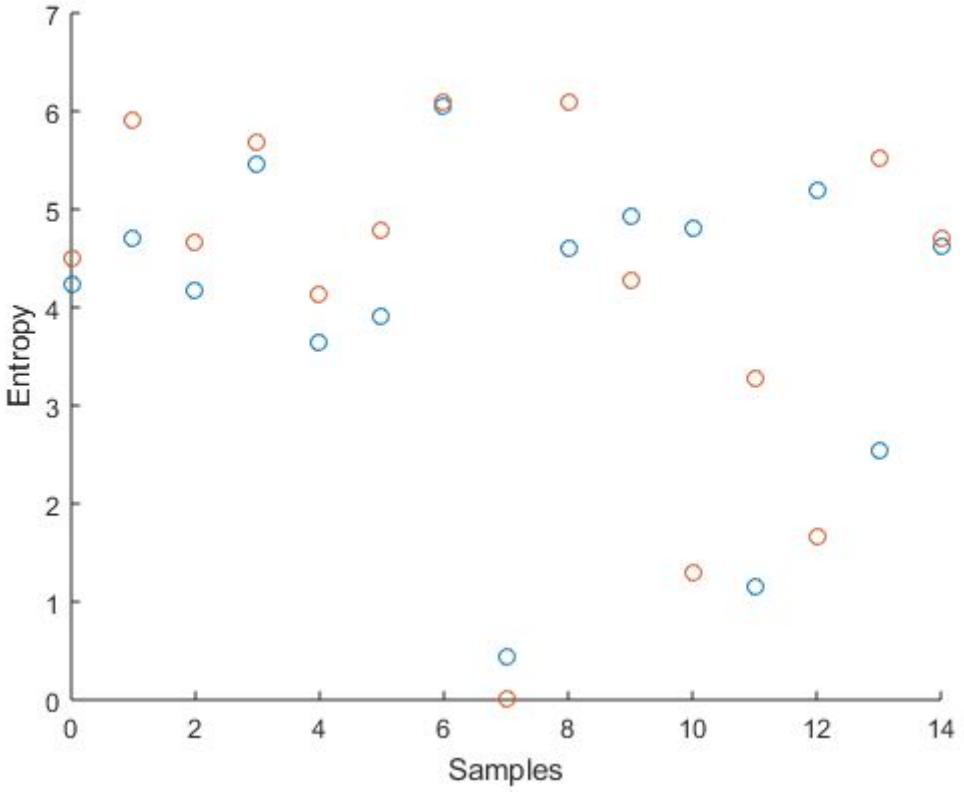
To continue with, in statistics, skewness is a measure of the asymmetry of the probability distribution of a real-valued random variable. The skewness value can be positive or negative, or even undefined . Qualitatively, a negative skew indicates that the tail on the left side of the probability density function is longer than the right side and the bulk of the values (possibly including the median) lie to the right of the mean. Similar attribute applies for the positive skew. A zero value indicates that the values are relatively evenly distributed on both sides of the mean, typically but not necessarily implying a symmetric distribution.

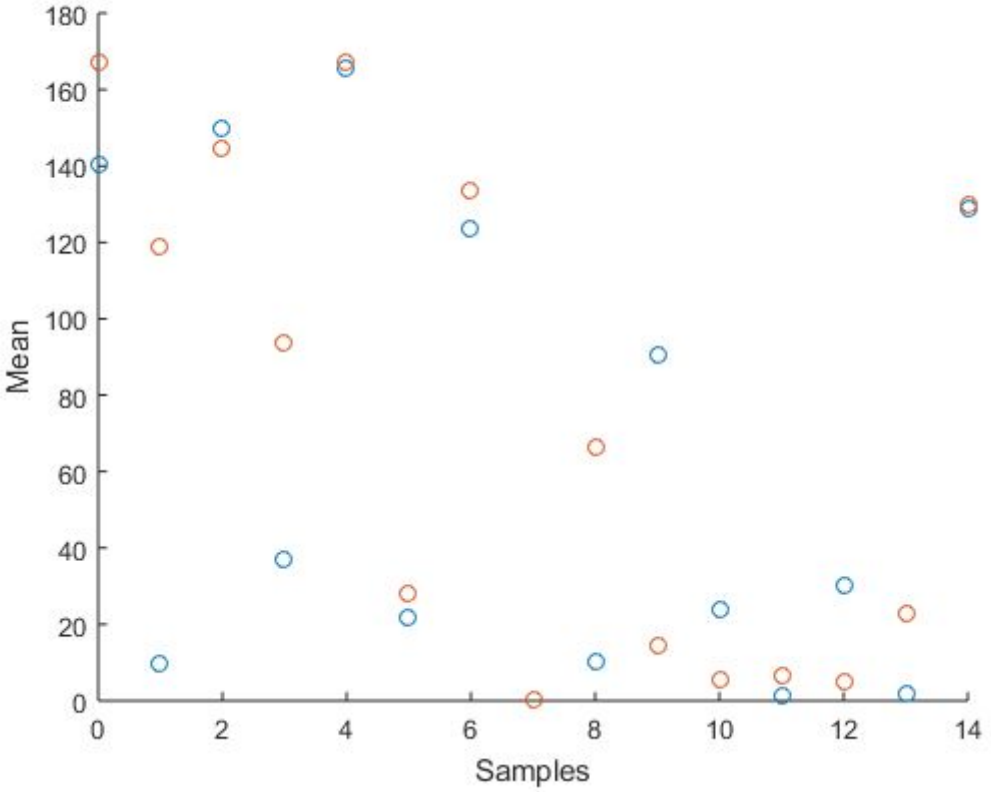
In terms of digital image processing, darker and glossier surfaces tend to be more positively skewed than lighter and matte surfaces. Hence we can use skewness in making judgements about image surfaces - regions.

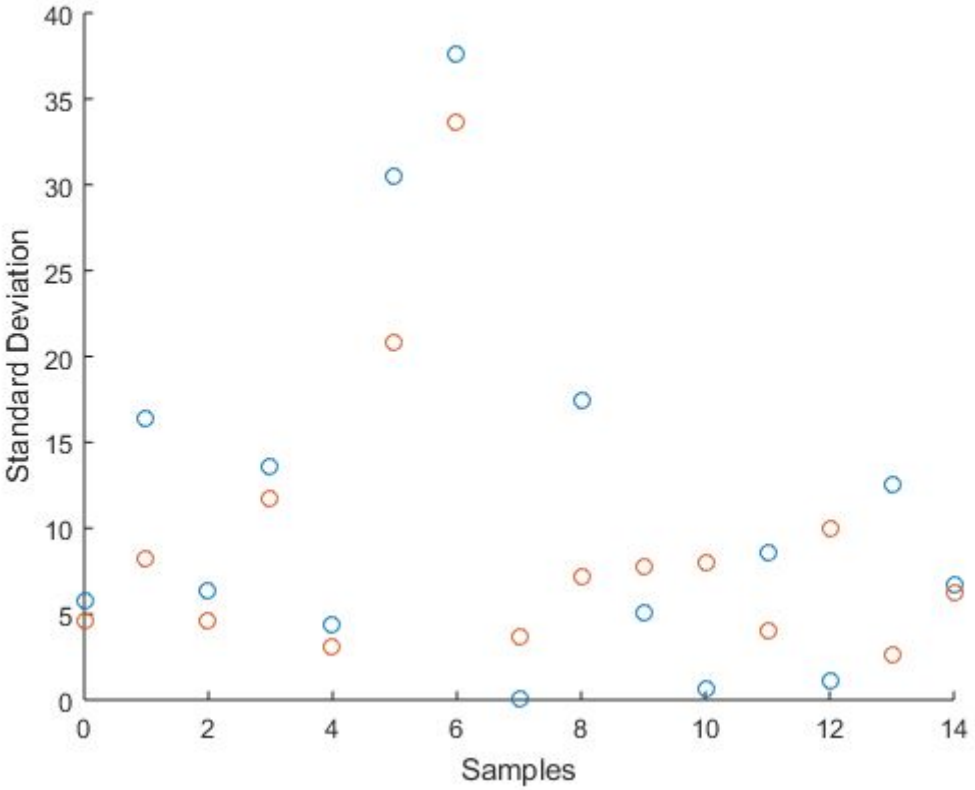
Moving on, standard deviation is the most widely used measure of variability or diversity used in statistics. In terms of image processing it shows how much variation or "dispersion" exists from the average (mean, or expected value). A low standard deviation indicates that the data points tend to be very close to the mean, whereas high standard deviation indicates that the data points are spread out over a large range of values. Therefore, standard deviation shows if the region we are examining shows homogeneity or not.It can also be used in edge sharpening, as intensity level changes at the edge of image by large values. By using standard deviation as a statistical moment, you may be able to recognize some patterns in a region where there is a lot of ‘noise’.
To end with, Entropy is a statistical measure of randomness. As the level of disorder rises, the entropy rises and events become less predictable. It can be used to characterize the texture of the region. In the x-ray analysis of the tissue, entropy might be used to classify textures; meaning that a certain texture might have a certain entropy as certain patterns repeat themselves in approximately certain ways. In this context, low entropy implies low disorder, low variance within a region. A region with low entropy is more homogenous than a region with high entropy, which in combination with other statistical criteria can classify different regions.

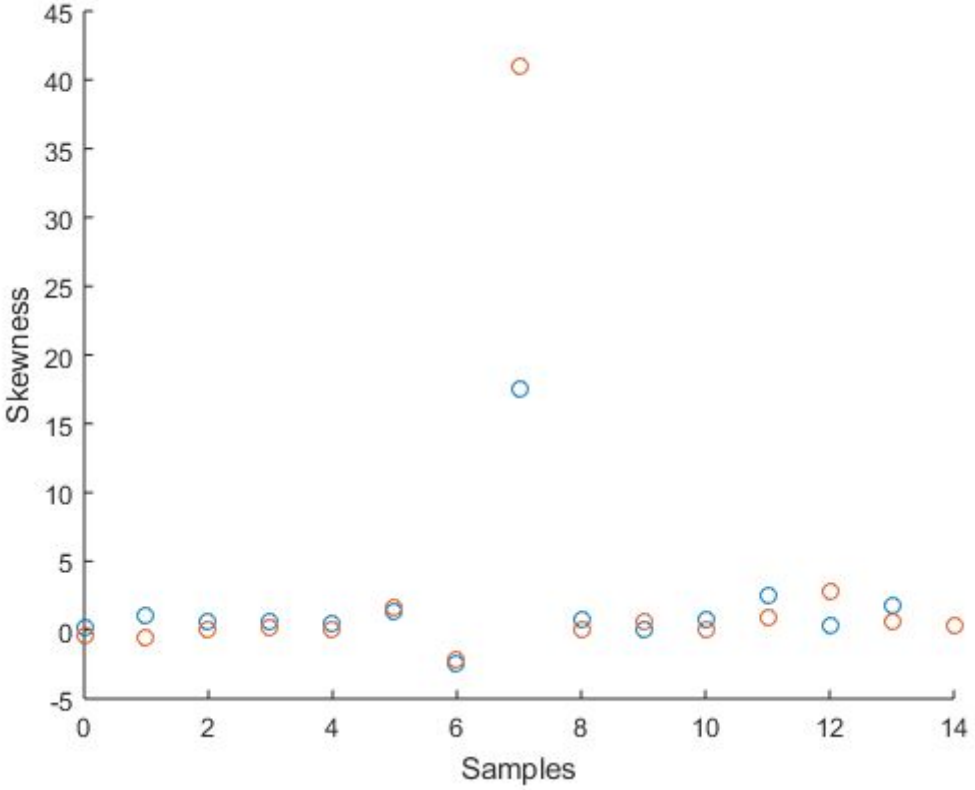
3) Afterwards we analyzed - scattered the above statistical moments.

The blue color shows the statistical moment of the healthy regions while the red color is used for the damaged regions.


Entropy
Samples
0
1
2
3
4
5
6
7
0
2
4
6
8
10
12
14


Mean
Samples
0
20
40
60
80
100
120
140
160
180
0
2
4
6
8
10
12
14





The above plotting will help us in order to choose which features we will isolate in order to create our decision tree. As we can see skewness is almost identical for all the samples, so we chose not to include it in our decision tree predictor. Moreover, Mean should surely be included because it is a very important feature and it determines which pixel value to choose to summarize the whole

image. Mean is very rarely missing from filtering algorithms, so it would not be a smart decision to be left behind. Lastly, between entropy and standard deviation, we cannot exclude none of them , since both of them give us much and different kind of information. Furthermore , I made a test with four different decision trees. In general, if we only had to choose just two statistical criteria , we would have chosen entropy and mean owing to the fact that it is a common practice!
The first one with mean and entropy, the second one with mean and standard deviation , the third one with entropy and standard deviation and the fourth one with mean, entropy and standard deviation. The results are stated below:
First test:

```
ClassRatio =

    0.8000
```

Second test:

```
ClassRatio =

    0.8667
```

Third test:

```
ClassRatio =

    0.8667
```

Fourth test:

```
ClassRatio =

    0.9000
```

Therefore , the tests confirm our first impression that all of these three statistical moments should be taken into account while making the decision tree.
Taking into consideration the Classification Ratio that we produced, we can say that it is indeed possible to recognize damaged and healthy tissue regions with 90% probability of well performing - deciding right. We can even do it with only two statistical moments and have 86.67% probability of performing well. We constructed the decision tree and we classified all of the extracted regions at this step.

4)

```
ClassRatio =

    0.9000

SE =

    0.8667

SP =

    0.9333
```

If we had to evaluate the performance of our classification, we would say that it gives more attention to recognizing healthy subjects than pathology since Specificity is greater than Sensitivity. In general, if we consider that we only used 3 statistical moments and 30 samples , our approach is pretty decent. Nevertheless, we have to keep in mind that the samples examined in order to be classified were again the same as before. This means that the examination was not of a high difficulty, due to the fact that the same samples determined the decision tree.

However, in particular a question arises : Is it good enough to be used for diagnostics?
And the answer is no. Because the error rate in biomedical applications is usually less than 5% and in our case the error rate is 10%. It is not destructive but still it is not a good approach when it comes to diagnostics. In diagnostics we have to deal with life or death situations and the margin for error is not that wide. It should have been at least 95% in

D) Program Code

main.m

```
close all;
clear all;
f=dir('*.pgm');
load('Healthy.mat');
load('Calcification.mat');
Im_array=cell(1,15);
heal_cropped=cell(1,15);
calci_cropped=cell(1,15);
mean_intenHealthy=zeros(1,15);
standard_devHealthy=zeros(1,15);
skHealthy=zeros(1,15);
entrHealthy=zeros(1,15);
mean_intenCalci=zeros(1,15);
standard_devCalci=zeros(1,15);
skCalci=zeros(1,15);
entrCalci =zeros(1,15);
for k=1:15
  thisFileName = f(k).name;
  thisImage = imread(thisFileName);
  Im_array{k}=thisImage;
  healthy = imcrop(Im_array{k},[x1(k) y1(k) r1(k) r1(k)]); %cropped pgm
  calci= imcrop(Im_array{k},[x(k) y(k) r(k) r(k)]); %cropped pgm
  heal_cropped{k}=healthy;
  calci_cropped{k}=calci;
  mean_intenHealthy(k)=mean2(healthy);
  standard_devHealthy(k)=std2(healthy);
  healthy1double=im2double(healthy);
  skHealthy(k)=skewness(healthy1double(:));
  entrHealthy(k) = entropy(healthy);
  mean_intenCalci(k)=mean2(calci);
  standard_devCalci(k)=std2(calci);
  healthy1double=im2double(calci);
  skCalci(k)=skewness(healthy1double(:));
  entrCalci(k) = entropy(calci);
end
%imshow(Im_array{1})
x=linspace(0,14,15);
figure
scatter(x, mean_intenHealthy)
hold on
scatter(x,mean_intenCalci)
xlabel('Samples')
ylabel('Mean')
hold off
figure
```

```
scatter(x, standard_devCalci)
hold on
scatter(x,standard_devHealthy)
xlabel('Samples')
ylabel('Standard Deviation')
hold off
figure
scatter(x, skHealthy)
hold on
scatter(x,skCalci)
xlabel('Samples')
ylabel('Skewness')
hold off
figure
scatter(x, entrHealthy)
hold on
scatter(x,entrCalci)
xlabel('Samples')
ylabel('Entropy')
hold off

%task 3
ResponseY=cell(30,1);
PredictorX=zeros(30,3);
for k=1:15
        ResponseY{k}='healthy';
        PredictorX(k,1)=entrHealthy(k);
        PredictorX(k,2)=mean_intenHealthy(k);
        PredictorX(k,3)=standard_devHealthy(k);

end
for k=16:30
        ResponseY{k}='damaged';
        PredictorX(k,1)=entrCalci(k-15);
        PredictorX(k,2)=mean_intenCalci(k-15);
        PredictorX(k,3)=standard_devCalci(k-15);
end
DecTree=fitctree(PredictorX,ResponseY,'PredictorNames',{'entropy','mean','sd'});
answers=predict(DecTree,PredictorX);

%task 4
TP=0;
TN=0;
FN=0;
FP=0;

for k=1:15
        tf = strcmp(answers{k},'healthy');
        if tf
        TP=TP+1;
        else
```

```
        FN=FN+1;
        end
end

for k=16:30
        tf = strcmp(answers{k},'damaged');
        if tf
        TN=TN+1;
        else
        FP=FP+1;
        end
end

%TP,TN,FN,FP have to be calculated
ClassRatio=(TP+TN)/30;
SE=TP/(TP+FN);
SP=TN/(TN+FP);
ClassRaTio=(SE+SP)/2;
```