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# SKIN CANCER DETECTOR

This code builds a system to automatically detect melanoma histology. To use it, download the folder and use the sample data provided or your own to train the models. These models can be customized adjusting their parameters. Uncomment the last two sections to test the created models with new histological data.

```
clc; close all; clear all;
```

## Upload training images and extract features

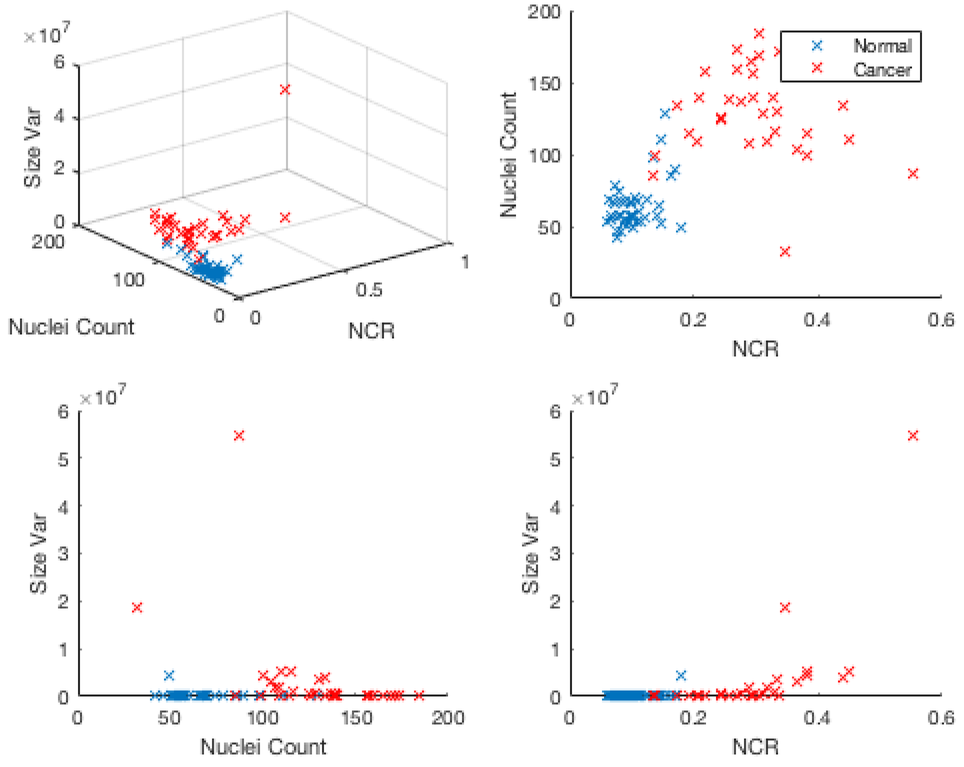
```
% Specify the folder where normal samples are.
myFolder = '/Users/Sergi/Downloads/Skin-Cancer-Detection-using-a-
Computer-based-System-master/Normal';
% Check to make sure that folder actually exists. Warn user if it
 doesn't.
if ~isdir(myFolder)
  errorMessage = sprintf('Error: The following folder does not exist:
\n%s', myFolder);
  uiwait(warndlg(errorMessage));
  return;
end
% Get a list of all files in the folder with the desired file name
 pattern.
filePattern = fullfile(myFolder, '*.bmp'); % Samples images are bmp
 format. Modify it if necessary.
theFiles = dir(filePattern);
% Initialize matrix of normal features
n = length(theFiles);
normal_features = zeros(n,4);
normal_features(:,4) = zeros(n,end);
for i = 1 : n
  baseFileName = theFiles(i).name;
  fullFileName = fullfile(myFolder, baseFileName);
  RGB_sample = imread(fullFileName); % Read RGB image.
  RGB_sample = RGB_sample(:,round(size(RGB_sample,1)/3):end-8,:); %
 Remove black border at the right. Remove line of code if necessary.
  gray_sample = rgb2gray(RGB_sample); % Convert RGB image to gray
 scale.
  threshold= 120; % Threshold value. Modify if necessary.
  BW = gray_sample<threshold; % Convert gray scale image to black and
 white.
```

```
  R = 3; % Disk radius. Adjust if necessary.
  se = strel('disk', R);
  BW = imdilate(BW, se);
  se = strel('disk', R);
  BW = imerode(BW, se);

  % Melanoma features
  % Nuclei to Cytoplasm Ratio (NCR)
  normal_features(i,1) = NCR(BW);

  % Nuclei Count Function
  BW = gray_sample<threshold;
  [nuclei, V] = nuclei_counter(BW); % Adjust intern parameters if
 necessary.
  normal_features(i,2) = nuclei;
  normal_features(i,3) = V;
end


% Specify the folder where cancer samples are.
myFolder = '/Users/Sergi/Downloads/Skin-Cancer-Detection-using-a-
Computer-based-System-master/Cancer';
% Check to make sure that folder actually exists. Warn user if it
 doesn't.
if ~isdir(myFolder)
  errorMessage = sprintf('Error: The following folder does not exist:
\n%s', myFolder);
  uiwait(warndlg(errorMessage));
  return;
end
% Get a list of all files in the folder with the desired file name
 pattern.
filePattern = fullfile(myFolder, '*.bmp'); % Samples images are bmp
 format. Modify it if necessary.
theFiles = dir(filePattern);
% Initialize matrix of normal features
n = length(theFiles);
cancer_features = zeros(n,4);
cancer_features(:,4) = ones(n,end);
for i = 1 : n
  baseFileName = theFiles(i).name;
  fullFileName = fullfile(myFolder, baseFileName);
  RGB_sample = imread(fullFileName); % Read RGB image.
  RGB_sample = RGB_sample(:,round(size(RGB_sample,1)/3):end-8,:); %
 Remove black border at the right. Remove line of code if necessary.
  gray_sample = rgb2gray(RGB_sample); % Convert RGB image to gray
 scale.
  threshold= 120; % Threshold value. Modify if necessary.
  BW = gray_sample<threshold; % Convert gray scale image to black and
 white.
  R = 3; % Disk radius. Adjust if necessary.
  se = strel('disk', R);
  BW = imdilate(BW, se);
  se = strel('disk', R);
  BW = imerode(BW, se);

  % Melanoma features
  % Nuclei to Cytoplasm Ratio (NCR)
  cancer_features(i,1) = NCR(BW);

  % Nuclei Count Function
  BW = gray_sample<threshold;
  [nuclei, V] = nuclei_counter(BW); % Adjust intern parameters if
 necessary.
  cancer_features(i,2) = nuclei;
  cancer_features(i,3) = V;
end
```

## Visualize the extracted features

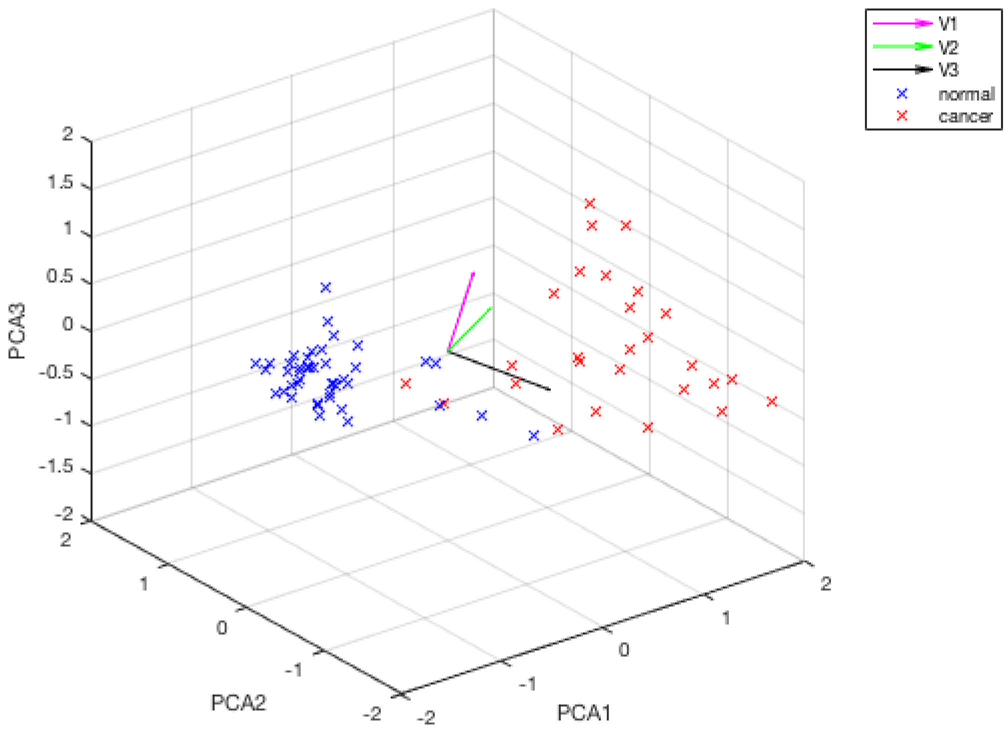
```
close all; clc
n = size(normal_features,1);
features = [normal_features; cancer_features];
Visualize(features,n); % Visualize the extracted features.
[linear_corr,pval] = corr(features(:,1:3)) % Asses correlation in the
 data.
% If p-value is smaller than 0.05, correlation is significantly
 different
% from 0.
```

```

linear_corr =

    1.0000    0.6657    0.5151
    0.6657    1.0000   -0.0329
    0.5151   -0.0329    1.0000


pval =

    1.0000    0.0000    0.0000
    0.0000    1.0000    0.7776
    0.0000    0.7776    1.0000
```



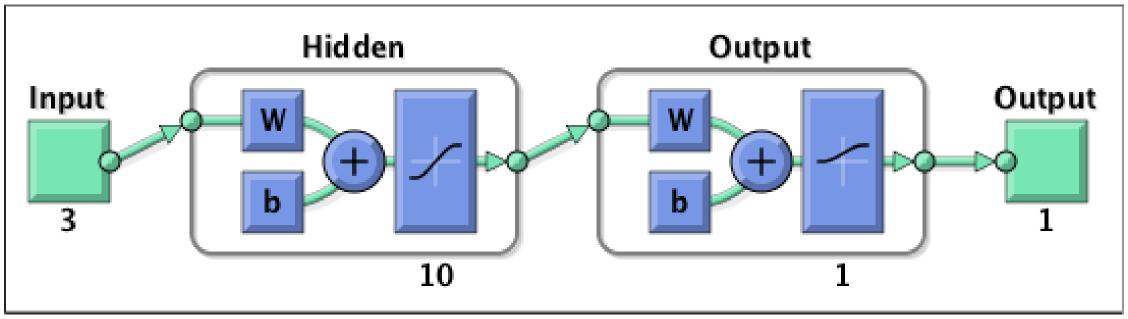
## Perform Principal Component Analysis (PCA)

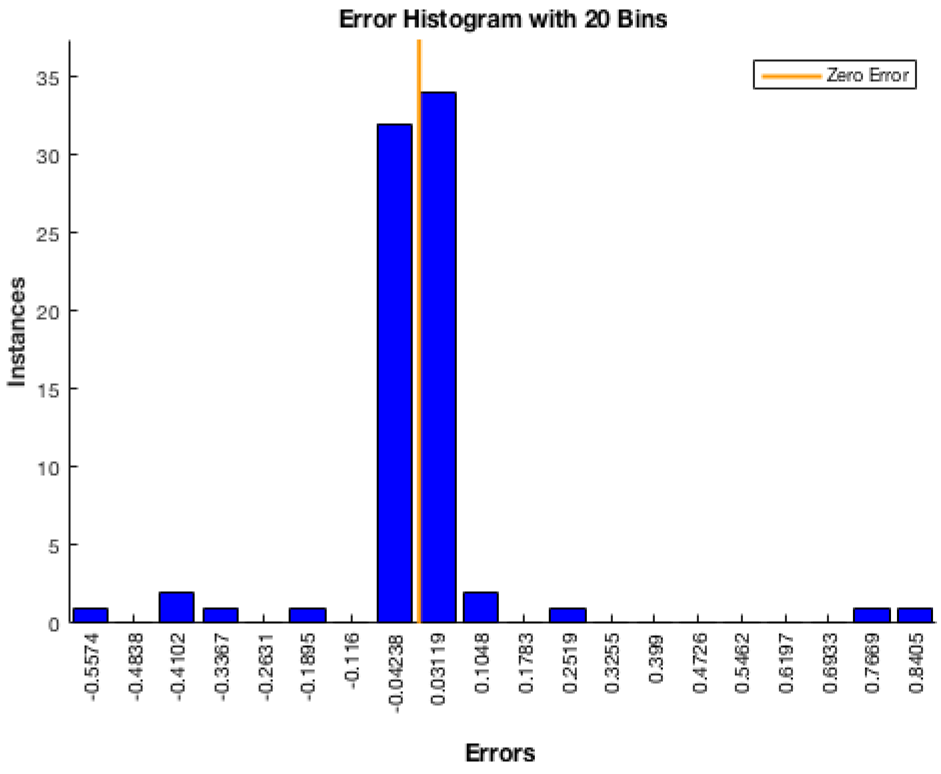
```
% This step may not be necessary (although recommended) if there is no
% correlation in your data.
[V1,V2,V3,pca_3d] = PCA(features,normal_features);
```



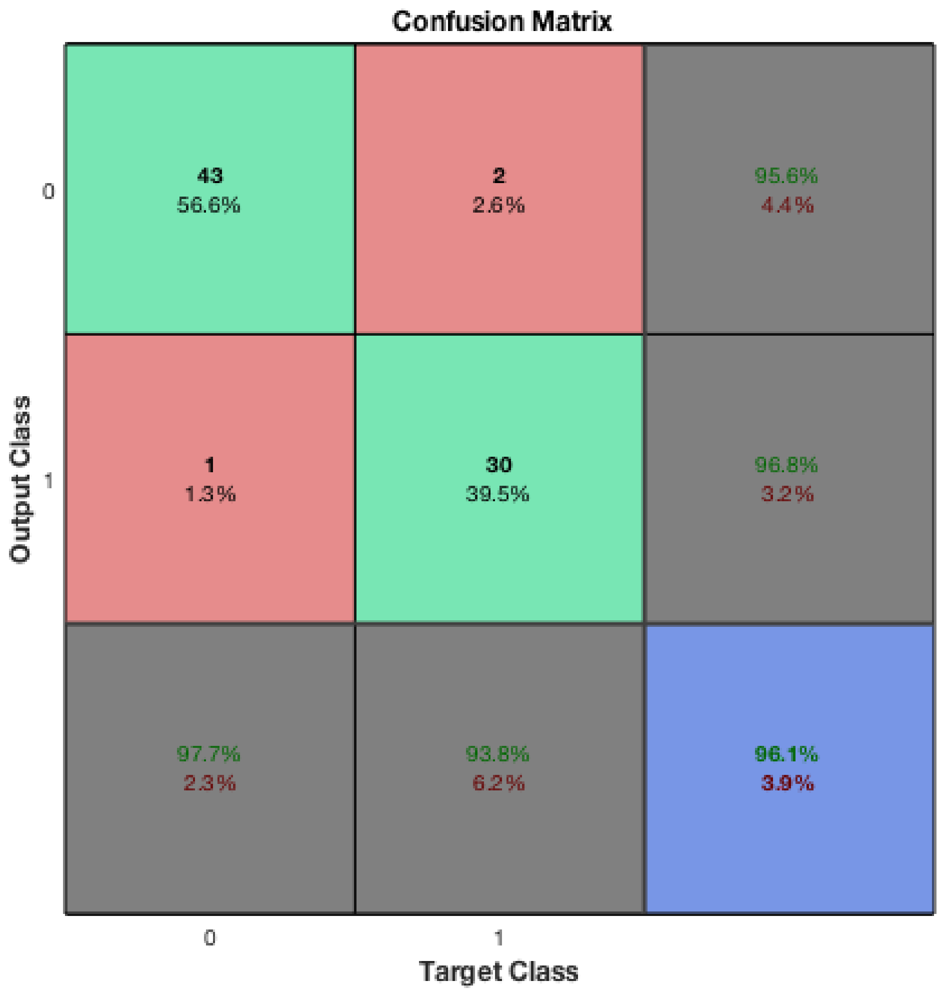
## Machine learning: train and asses model performance

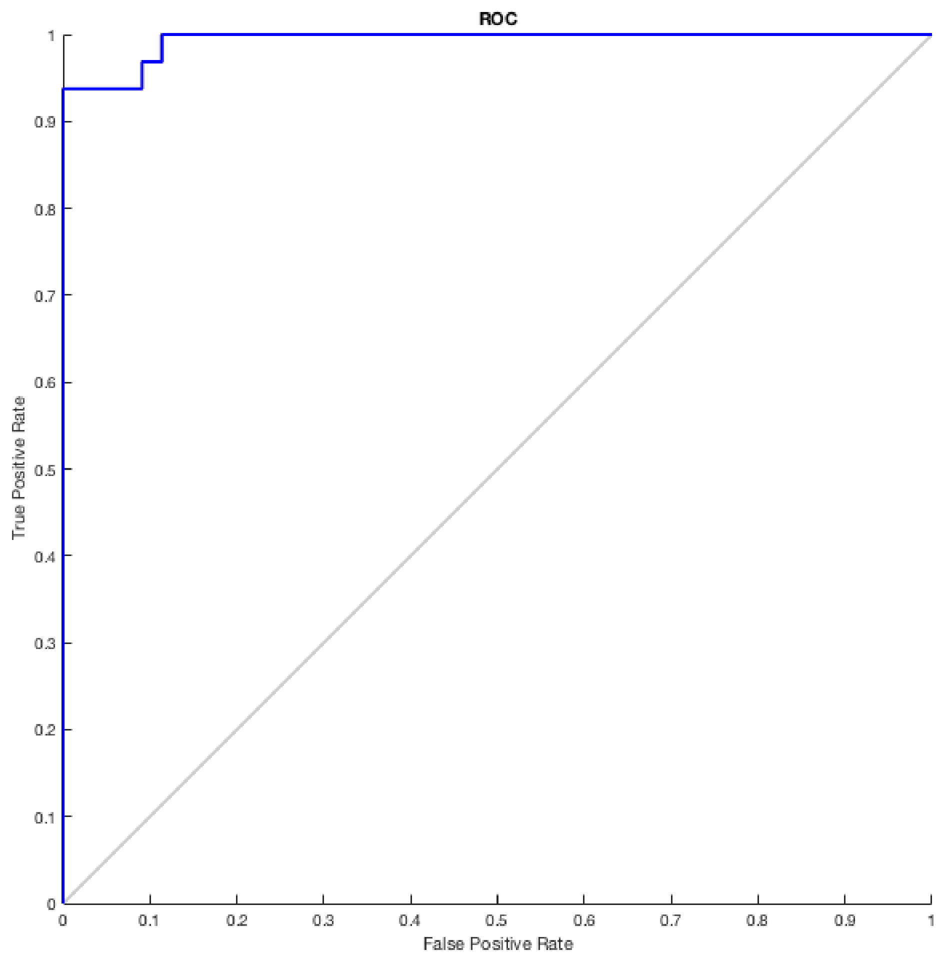
```
n = size(normal_features,1);
c = size(cancer_features,1);
NCR = pca_3d(:,1);
Nuclei = pca_3d(:,2);
Variance = pca_3d(:,3);
Ground_truth = vertcat(repmat(['Normal'],n,1),repmat(['Cancer'],c,1));
data = table(NCR,Nuclei,Variance,Ground_truth);

% Classification Learner
[trainedClassifier1, validationAccuracy1]= trainComplexTree(data)
[trainedClassifier2, validationAccuracy2]=
 trainCoarseGaussianSVM(data)
[trainedClassifier3, validationAccuracy3]=
 trainLinearDiscriminant(data)
[trainedClassifier4, validationAccuracy4]=
 trainSubspaceDiscriminant(data)
% To make predictions with the returned 'trainedClassifier' on new
 data x
% use yfit = trainedClassifier.predictFcn(x);

% Neural Net Pattern Recognition
% Transpose column vector data
x = pca_3d';
t = features(:,4)';
net = NeuralNetwork(x,t);
%  To make predictions with the returned trained network 'net' on new
 data x,
%  use y = net(x);
%  yfit = trainedClassifier.predictFcn(T)


trainedClassifier1 =

            predictFcn: @(x)treePredictFcn(predictorExtractionFcn(x))
     RequiredVariables: {'NCR'  'Nuclei'  'Variance'}
    ClassificationTree: [1x1 ClassificationTree]
                 About: 'This struct is a trained classifier exported
 from...'
           HowToPredict: 'To make predictions on a new table, T,
 use: ...'


validationAccuracy1 =

    0.9474


trainedClassifier2 =

           predictFcn: @(x)svmPredictFcn(predictorExtractionFcn(x))
    RequiredVariables: {'NCR'  'Nuclei'  'Variance'}
    ClassificationSVM: [1x1 ClassificationSVM]
                About: 'This struct is a trained classifier exported
 from ...'
          HowToPredict: 'To make predictions on a new table, T,
 use: ...'


validationAccuracy2 =

    0.9474


trainedClassifier3 =

                   predictFcn: [function_handle]
            RequiredVariables: {'NCR'  'Nuclei'  'Variance'}
    ClassificationDiscriminant: [1x1 ClassificationDiscriminant]
                        About: 'This struct is a trained classifier
 expor...'
                 HowToPredict: 'To make predictions on a new table,
 T, us...'


validationAccuracy3 =
    0.9605


trainedClassifier4 = 

                predictFcn:
 @(x)ensemblePredictFcn(predictorExtractionFcn(x))
         RequiredVariables: {'NCR'  'Nuclei'  'Variance'}
    ClassificationEnsemble: [1x1
 classreg.learning.classif.ClassificationEnsemble]
                     About: 'This struct is a trained classifier
 exported ...'
              HowToPredict: 'To make predictions on a new table, T,
 use: ...'


validationAccuracy4 =

    0.9474


performance =

    0.0978
```





Error Histogram with 20 Bins
Zero Error
Instances
0
5
10
15
20
25
30
35
-0.5574
-0.4838
-0.4102
-0.3367
-0.2631
-0.1895
-0.116
-0.04238
0.03119
0.1048
0.1783
0.2519
0.3255
0.399
0.4726
0.5462
0.6197
0.6933
0.7669
0.8405
Errors


Confusion Matrix
Output Class
Target Class
0
1
0
1
43
56.6%
2
2.6%
95.6%
4.4%
1
1.3%
30
39.5%
96.8%
3.2%
97.7%
2.3%
93.8%
6.2%
96.1%
3.9%



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