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SKIN DATASET ANALYSIS

```
clear all

%loading data

filehere= 'Users/Anna/Documents/MATLAB/Skin_NonSkin.txt';
fid=fopen(filehere);
mydata = textscan(fid,'%f%f%f','delimiter',' ');
fclose(fid);

%naming each feature

Blue = mydata{1};
Green = mydata{2};
Red = mydata{3};
Skin = mydata{4};

X=[Blue Green Red];
labels=Skin;

%Problem: Let's predict the sample to be skin or not skin, based on the B,G,R values
%There are only three features, and in that, all of them have a same scale.

%Plotting data

scatter3(Blue, Green, Red, 30, Skin, 'filled');
title('Skin or not?')
xlabel('Blue')
ylabel('Green')
zlabel('Red')
legend('Not skin pixel')
figure;
%min value of skin colors is around 106.0 and max value of skin colors is 255.0

%Correlation features(color) vs target
r=corr([X labels])
% => So blue has the highest correlation

%mean and standart deviation
mx=mean(X)
stdx=std(X)

% Now I'm gonna visualize the eigenvectors to represent
% my variance
cX =cov(X)
[V,D] = eig(cX)
b=diag(D)
[b idx]=sort(b,'descend'); V=V(:,idx)

plot(V);
```

```

xlabel('x');
ylabel('y');
title('eigen vectors');
set(gca,'XTick',[1 2 3],'XTickLabel',{'Blue', 'Green', 'Red'})
legend('1. Eigvec ','2. Eigvec ','3. Eigvec')

```

r =

1.0000	0.8553	0.4964	0.0920
0.8553	1.0000	0.6601	-0.1203
0.4964	0.6601	1.0000	-0.5700
0.0920	-0.1203	-0.5700	1.0000

mx =

125.0654	132.5073	123.1772
----------	----------	----------

stdx =

62.2557	59.9412	72.5622
---------	---------	---------

cX =

1.0e+03 *		
3.8758	3.1915	2.2423
3.1915	3.5929	2.8711
2.2423	2.8711	5.2653

V =

0.6031	0.5873	0.5398
-0.7767	0.2779	0.5653
0.1819	-0.7602	0.6237

D =

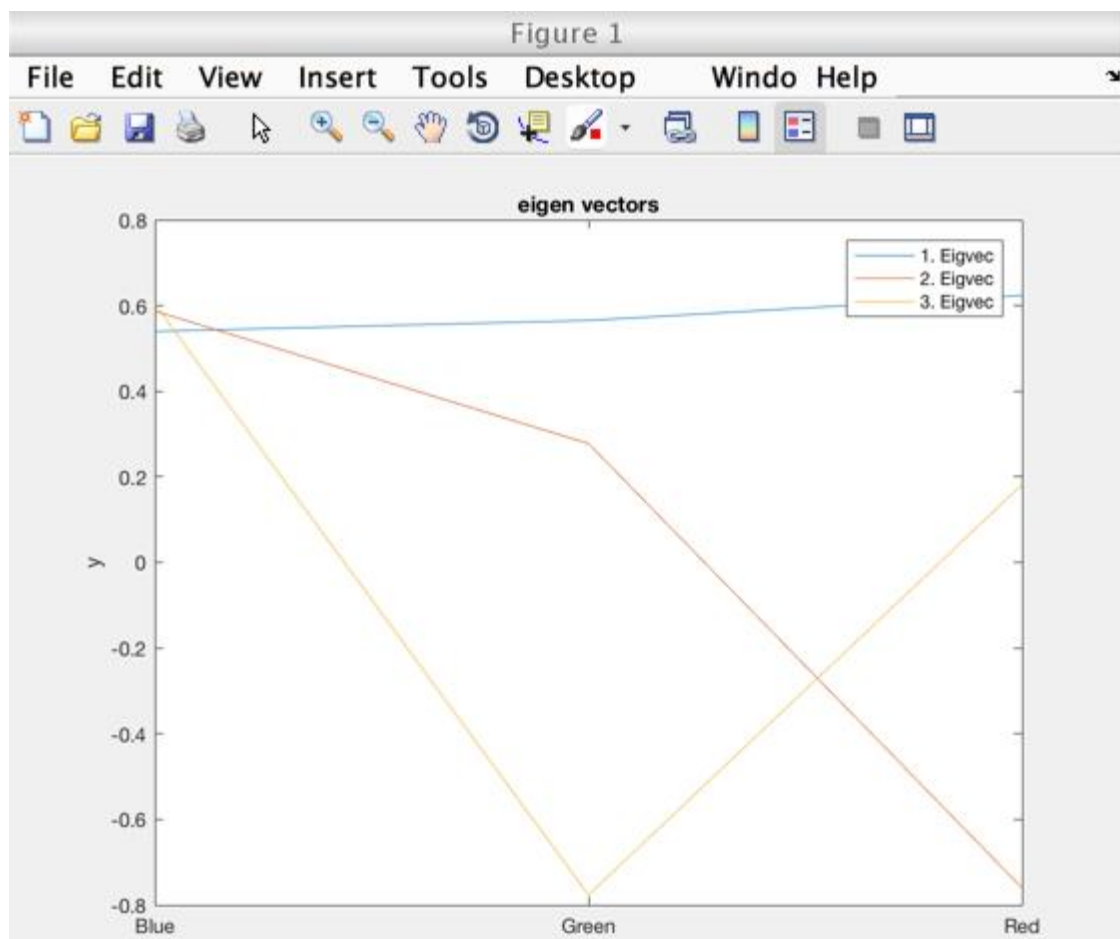
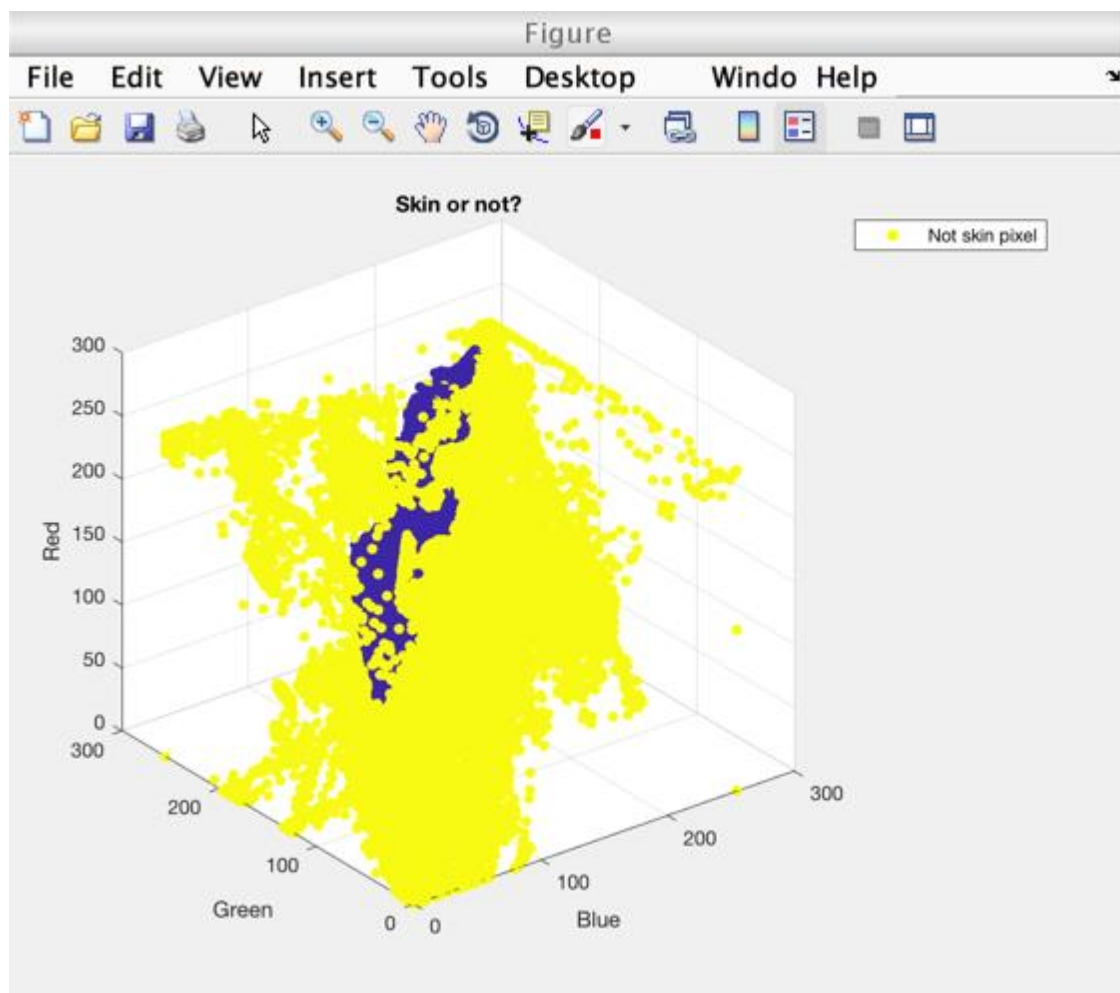
1.0e+03 *		
0.4421	0	0
0	2.4834	0
0	0	9.8084

b =

1.0e+03 *		
0.4421		
2.4834		
9.8084		

V =

0.5398	0.5873	0.6031
0.5653	0.2779	-0.7767
0.6237	-0.7602	0.1819



Principal Component Analysis

```

close all
%calculating sample mean
Xmean = mean(X);

%centering data
Xcentered = X - ones(length(X(:,1)),1)*Xmean;

%calculating covariance
Xcov = cov(Xcentered);

%eigenvalue decompositon
[eigenvect,eigenval] = eig(Xcov);

%eigenvalues from diagonal
eigenval = diag(eigenval);
%sorting
[eigenval, idx]=sort(eigenval, 'descend');
%plotting
eigenvect = eigenvect(idx); V = V (: , idx ) ; %(V is my sorted eigenvetors)

%cumulative sum of eigenvalue percentage
cs = cumsum(eigenval)/sum(eigenval)
f = figure
plot(cs)
title ('RGB:Cumulative Eigenvalues ')
set (gca , 'XTick' ,[1 2 3] , 'XTickLabel' ,{'1. ','2. ','3. '});
xlabel ( ' Eigenvalue ' ) ;
% First eigenvector explains around 77% of the variance in the data, and
% together with the second 96.5%. That means, the skin dataset would be
% well represented by choosing the first two eigenvalues.

V (: ,1:2)
figure
plot ( V (: ,1:2) )

% projection on eigenvectors with highest eigen values(=reduction to 2
% dimensions)

scores = Xcentered*V(:,1:2);

% conversion of scores to prdataset
addpath(['/Users/Anna/Documents/MATLAB/prtools']);

z = prdataset(scores , labels);

figure
scatterd(z)
xlabel('1st eigenvector')
ylabel('2nd eigenvector')
title('Projections onto eignevectors')

%Reconstruction of dataset based on 2 eigenvectors

Xr = scores(:,[1,2])*V(:,[1,2])'+ones(length(Xcentered(:,1)),1)*Xmean;

```

```
% conversion to PRtools

Rdata = prdataset(Xr,labels,...
'featlab',['Blue ','Green';'Red '], 'name','Sample Features');

figure
subplot(2,1,1)
scatterd(X(:,[1,2]));
title ('Original ')
xlabel ('Blue')
ylabel ('Green')

subplot(2,1,2)
scatterd(Rdata(:,[1,2]));
xlabel('Blue')
ylabel('Green')
title('Reconstructed based on 2 eigenvectors')
%Those figures don't tell me much
```

```
cs =
```

```
    0.7703
    0.9653
    1.0000
```

```
f =
```

```
Figure (1) with properties:
```

```
    Number: 1
     Name: ''
   Color: [0.9400 0.9400 0.9400]
 Position: [360 278 560 420]
   Units: 'pixels'
```

```
Use GET to show all properties
```

```
ans =
```

```
    0.6031    0.5873
 -0.7767    0.2779
    0.1819   -0.7602
```

Figure 1

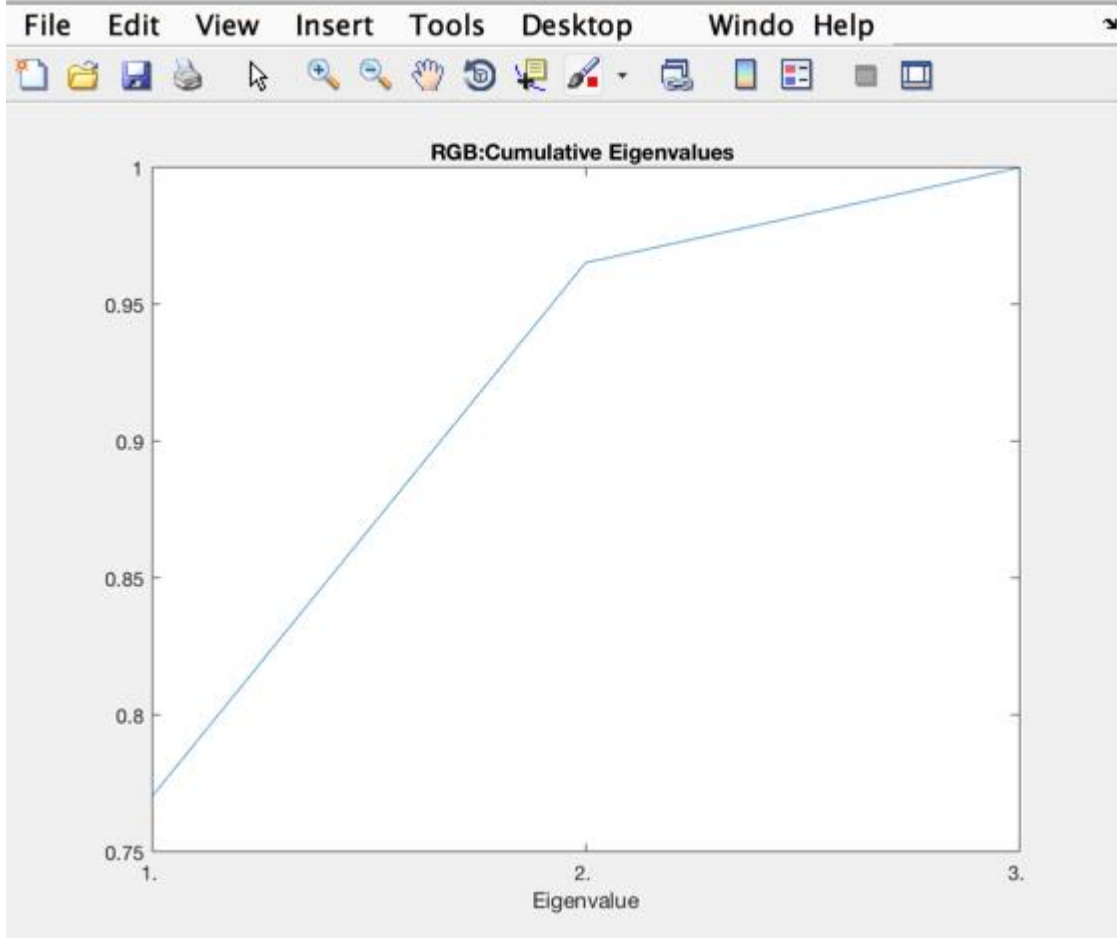


Figure 2

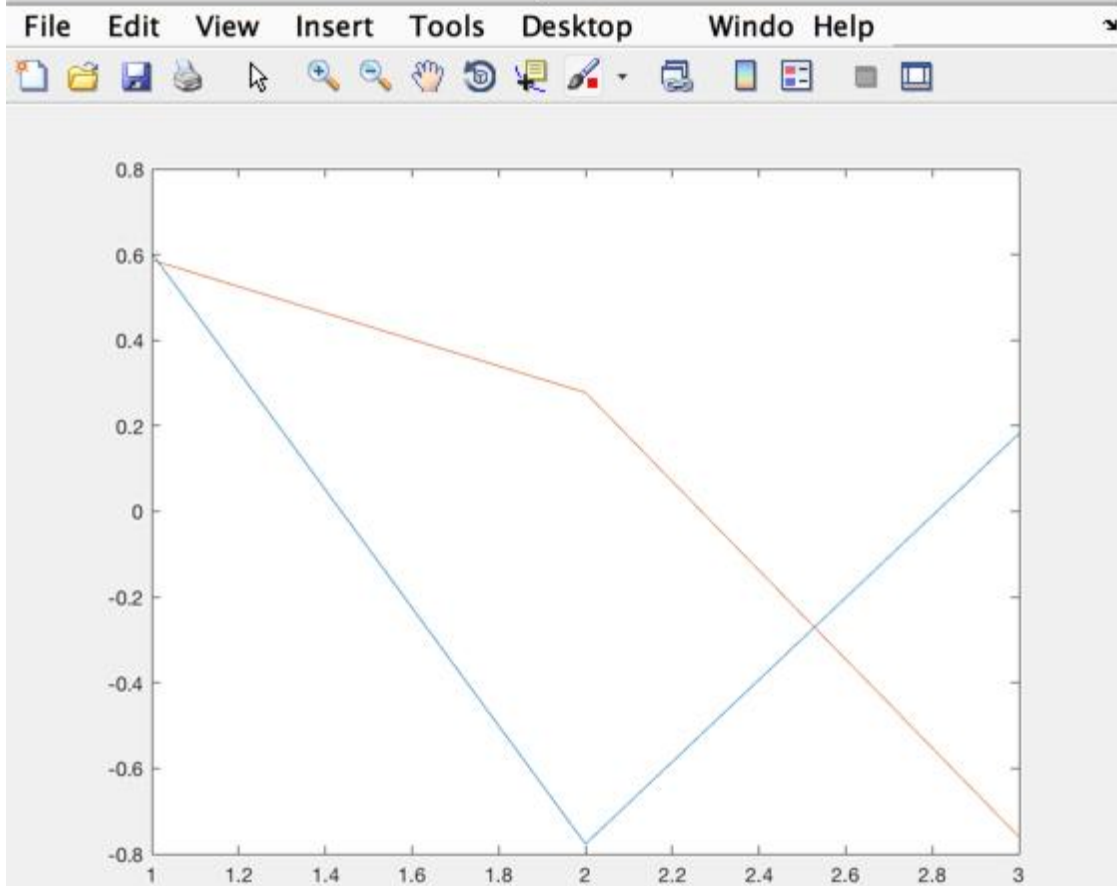
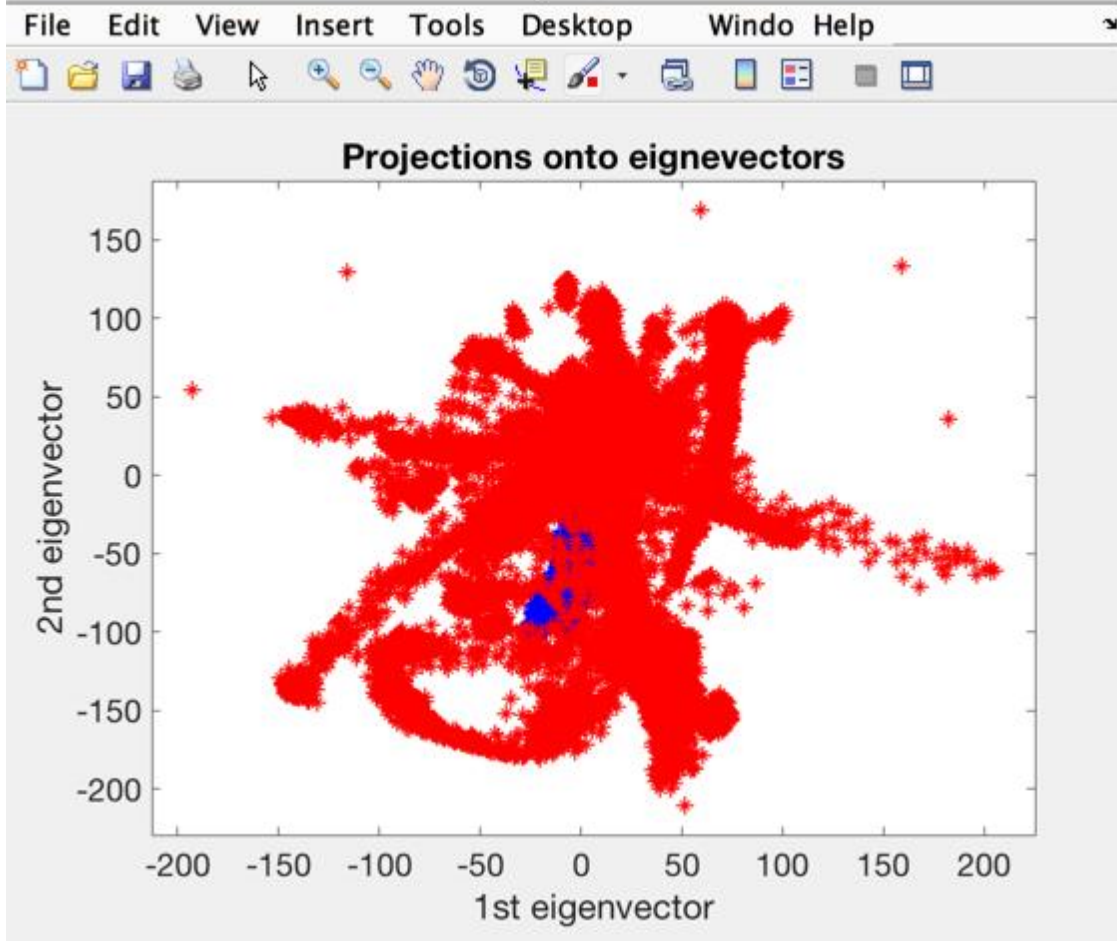
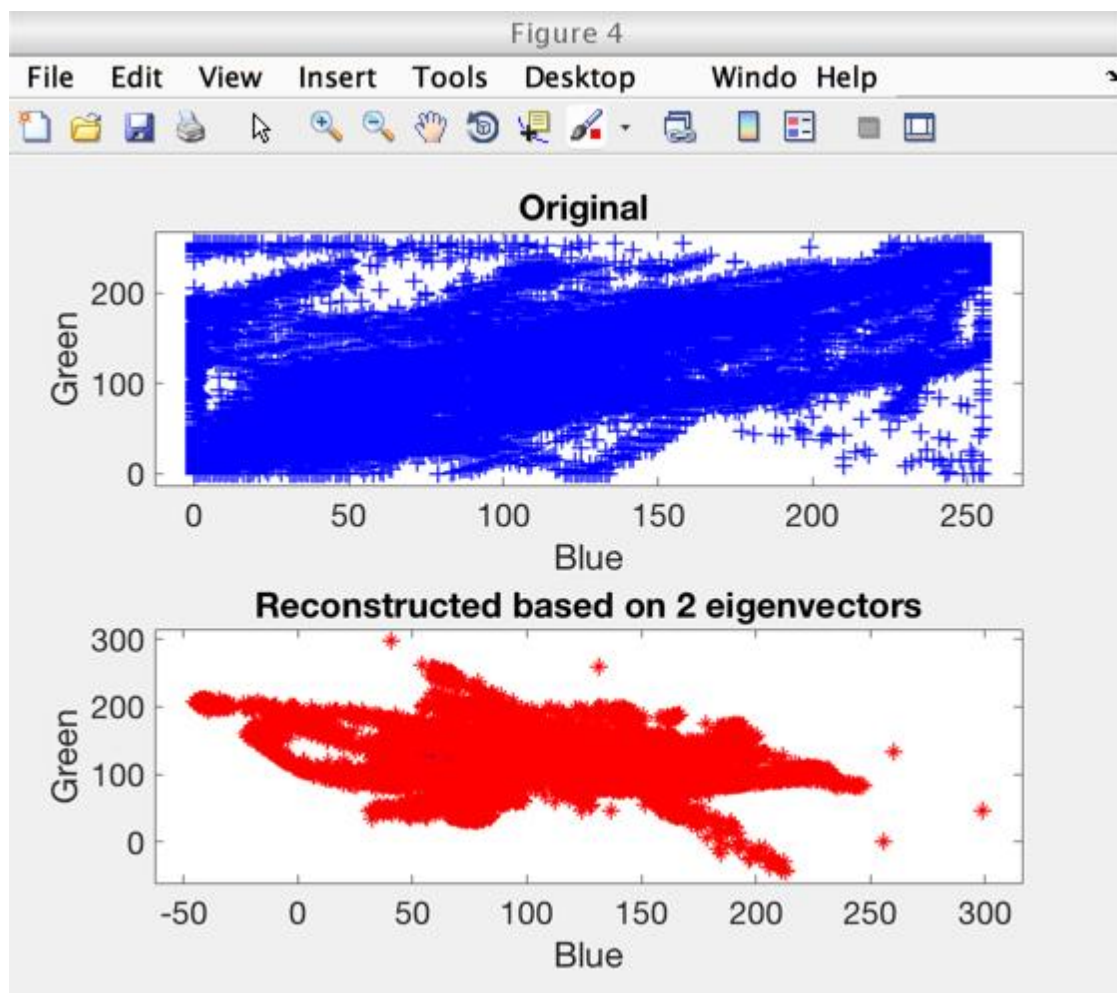


Figure 3





Classification on original data (parametric)

```
clear all

%reloading, naming
filehere= 'Users/Anna/Documents/MATLAB/Skin_NonSkin.txt';
fid=fopen(filehere);
mydata = textscan(fid,'%f%f%f','delimiter',' ');
fclose(fid);

Blue = mydata{1};
Green = mydata{2};
Red = mydata{3};
Skin = mydata{4};

X=[Blue Green Red];
labels=Skin;

labels (labels==1)=0;
labels(labels==2)=1;
[I,J]=size(X);

addpath(['/Users/Anna/Documents/MATLAB/prtools']);

data_all=prdataset(X,labels);
idx_skin=find(labels==0);
idx_noskin=find (labels==1);
```

```

%randomizing order
id_X = randperm(I)';

%Dividing my dataset into training and testing
tr_idx = id_X(1:220551); % training indices 90% of dataset
tst_idx = id_X(220552:245057); %testing indices 10% of dataset

skin_tr = prdataset ( X ( tr_idx ,:),labels ( tr_idx ) );
skin_tst = prdataset ( X (tst_idx,:),labels ( tst_idx ) );

%-----%
%parametric classifiers

confmat(labels,1*ones(I,1));
c_base=confmat(labels,1*ones(I,1));

tp=c_base(1,1); %true positives
fn=0; %always 0
fp=c_base(2,1); %false positives
tn=0; %always 0
acc_base=(tp+tn)/(tp+fp+fn+tn) %also percentage of one class

cv=10; %10 fold cross validation

for classi=1:3
    switch classi,
        case 1,
            %minimum distance classifier
            w=nmisc([]);
        case 2,
            %linear discriminant analysis
            w=ldc([]);
        case 3,
            %quadratic discriminant analysis
            w=qdc([]);
    end

[e dummy pred_labs]=prcrossval(skin_tr,w,cv);
%show confusion matrix

confmat(labels(tr_idx),pred_labs);
c=confmat(labels(tr_idx),pred_labs);
tp=c(1,1); %t=true, p=positives, f=false, n=negatives
fn=c(1,2);
fp=c(2,1);
tn=c(2,2);

acc1(classi)=(tp+tn)/(tp+fp+fn+tn);
p=tp/(tp+fp); %precision
r=tp/(tp+fn); %recall

%f-measure for all 3 classifiers:
f1(classi)=(2*p*r)/(p+r);

end
f1
acc1

%-----%

```

True	Estimated Labels	
Labels	1	Totals
0	50859	50859
1	194198	194198
Totals	245057	245057

acc_base =

0.2075

PR_Warning: GETPRIOR: prcrossval: No priors found in dataset, class frequencies are used instead

True Labels	Estimated Labels		
	1	2	Totals
0	29611	16061	45672
1	11748	163131	174879
Totals	41359	179192	220551

PR_Warning: GETPRIOR: prcrossval: No priors found in dataset, class frequencies are used instead

True Labels	Estimated Labels		
	1	2	Totals
0	41312	4360	45672
1	10772	164107	174879
Totals	52084	168467	220551

PR_Warning: GETPRIOR: prcrossval: No priors found in dataset, class frequencies are used instead

True Labels	Estimated Labels		
	1	2	Totals
0	42278	3394	45672
1	254	174625	174879
Totals	42532	178019	220551

f1 =

0.6805 0.8452 0.9586

acc1 =

0.8739 0.9314 0.9835

PRWAITBAR:

non-parametric knn classifier

```
def_mem=prmemory();
for classi2=1:3,
    switch classi2,
        case 1,
            prmemory(20*def_mem)
            w2=knnc([],1);
        case 2,
            w2=knnc([],2);
        case 3,
            w2=knnc([],3);
    end

[e dummy pred_labs]=prcrossval(skin_tst,w2,cv);
%show confusion matrix

confmat(labels(tst_idx),pred_labs);
c=confmat(labels(tst_idx),pred_labs);
tp=c(1,1); %t=true, p=positives, f=false, n=negatives
fn=c(1,2);
fp=c(2,1);
tn=c(2,2);

acc1(classi2)=(tp+tn)/(tp+fp+fn+tn);
p=tp/(tp+fp); %precision
r=tp/(tp+fn); %recall

%f-measure for all 3 classifiers:
f1(classi2)=(2*p*r)/(p+r);
end
f1
acc1

%calculating errors
errors=pred_labs~=labels(tst_idx);
sum(errors)
```

PR_Warning: GETPRIOR: prcrossval: No priors found in dataset, class frequencies are used instead

True Labels	Estimated Labels		
	1	2	Totals
0	5183	4	5187
1	14	19305	19319
Totals	5197	19309	24506

PR_Warning: GETPRIOR: prcrossval: No priors found in dataset, class frequencies are used instead

True Labels	Estimated Labels		Totals
	1	2	
0	5187	0	5187
1	32	19287	19319
Totals	5219	19287	24506

PR_Warning: GETPRIOR: prcrossval: No priors found in dataset, class frequencies are used instead

True Labels	Estimated Labels		Totals
	1	2	
0	5187	0	5187
1	24	19295	19319
Totals	5211	19295	24506

```
f1 =
    0.9983    0.9969    0.9977
```

```
acc1 =
    0.9993    0.9987    0.9990
```

```
ans =
    24482
```

