RX Basic Implementation

Introduction

This notebook is meant to help implement the RX (and later the SSRX) algorithm on the RIT Blind Test data set.

The RX algorithm is given by: $\mathrm{RX} = \left(\vec{X} - \vec{m}\right)^T \phi^{-1}\left(\vec{X} - \vec{m}\right) > \mathrm{Threshold}$

```
file = 'G:\My Drive\Project\self_test\HyMap\self_test_rad.img';
[mat,hdr] = auto_load_HS(file);
```

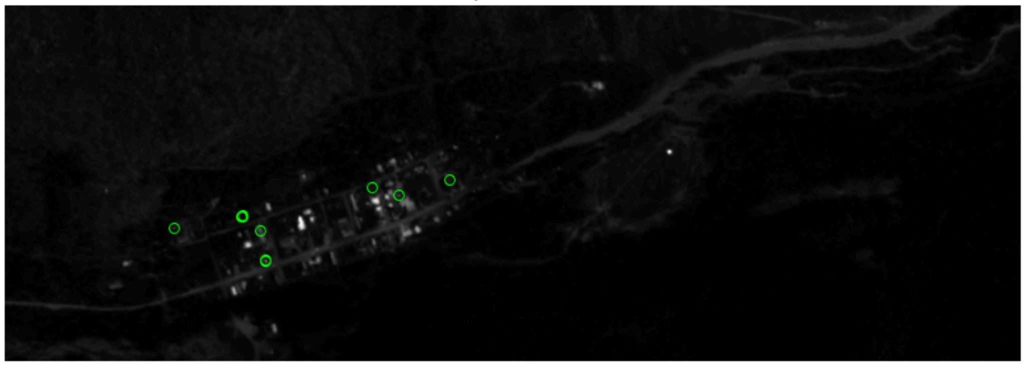
```
Loading ENVI header ...
Loading ENVI image ...
```

```
data=double(permute(mat,[2,1,3]));
[x_size,y_size, num_of_bands]=size(data);
[X_MINUS_M,phi]=HSI_MF_params(data);
phi_inv = pinv(phi);
RX = zeros(x_size,y_size);
for x = 1:x_size
    for y = 1:y_size
        x_minus_m5 = squeeze(X_MINUS_M(x,y,:));
        RX(x,y) = x_minus_m5' * phi_inv * x_minus_m5;
    end
end
RX= RX';
RX_filt = RX > mean(RX(:)) + 3*std(RX(:));
```

visualising results:

```
[~, idxs] = maxk(RX(:), 10);
[row,col] = ind2sub(size(RX),idxs);
figure; imshow(data(:,:,1)',[]); hold on;
plot(col,row,'og')
title('RX Top 10 Anomalies')
```

RX Top 10 Anomalies



SSRX Algorithm

The SSRX algorithm adds a preprocessing step to the RX algrotihm - performing PCA and keeping only low variance PCs.

the formula for PCA is given by:

$$X_{\text{PCA}} = (X - m)\phi^{-1}V_q$$

$m -$ the per channel mean of X
$\phi -$ the covariance matrix
$V_q - a$ matrix where every column is an eigen vector of ϕ while ommiting the q eigen vectors that correspond to the highest varianc

Given X_{PCA} we can now run RX to obtain SSRX:

$$\text{SSRX} = \left(\overrightarrow{X_{\text{PCA}}} - \overrightarrow{m_{\text{PCA}}}\right)^T \phi_{\text{PCA}}{}^{-1}\left(\overrightarrow{X_{\text{PCA}}} - \overrightarrow{m_{\text{PCA}}}\right) > \text{Threshold}$$

```
q = 120;
[V, D] = eigs(phi,126);
V5 = V(:,6:end);    % deleting first 5 PC
V50 = V(:,51:end);  % deleting first 50 PC
V120 = V(:,121:end);% deleting first 120 PC
data_pca2D5 = reshape(X_MINUS_M,x_size*y_size,num_of_bands) * V5;
data_pca2D50 = reshape(X_MINUS_M,x_size*y_size,num_of_bands) * V50;
data_pca2D120 = reshape(X_MINUS_M,x_size*y_size,num_of_bands) * V120;

data_pca5   = hyperConvert3d(data_pca2D5', x_size,y_size,num_of_bands);
data_pca50  = hyperConvert3d(data_pca2D50', x_size,y_size,num_of_bands);
data_pca120 = hyperConvert3d(data_pca2D120', x_size,y_size,num_of_bands);
```

Now that we have the preprocessed data, we can run the RX algorithm on it to get SSRX:

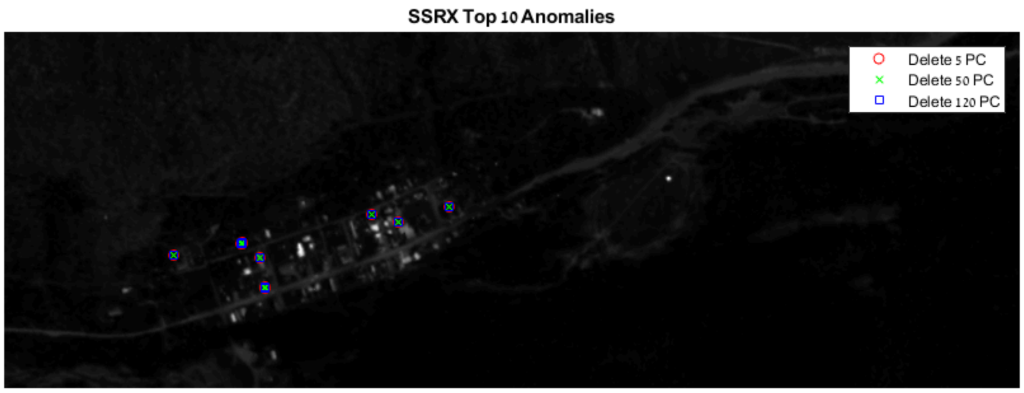
```
%calc phi_inv
[X_MINUS_M_PCA5,phi_pca5]=HSI_MF_params(data_pca5);
```

```
[X_MINUS_M_PCA50,phi_pca50]=HSI_MF_params(data_pca50);
[X_MINUS_M_PCA120,phi_pca120]=HSI_MF_params(data_pca120);

phi_pca_inv5 = pinv(phi_pca5);
phi_pca_inv50 = pinv(phi_pca50);
phi_pca_inv120 = pinv(phi_pca120);

%init empty results matrices
SSRX5   = zeros(x_size,y_size);
SSRX50  = zeros(x_size,y_size);
SSRX120 = zeros(x_size,y_size);

for x = 1:x_size
    for y = 1:y_size
        x_minus_m5 = squeeze(X_MINUS_M_PCA5(x,y,:));
        x_minus_m50 = squeeze(X_MINUS_M_PCA50(x,y,:));
        x_minus_m120 = squeeze(X_MINUS_M_PCA120(x,y,:));

        SSRX5(x,y) = x_minus_m5' * phi_pca_inv5 * x_minus_m5;
        SSRX50(x,y) = x_minus_m50' * phi_pca_inv50 * x_minus_m50;
        SSRX120(x,y) = x_minus_m120' * phi_pca_inv120 * x_minus_m120;
    end
end
SSRX5= SSRX5';
SSRX50= SSRX50';
SSRX120= SSRX120';
SSRX5_filt = SSRX5 > mean(SSRX5(:)) + 3*std(SSRX5(:));
SSRX50_filt = SSRX50 > mean(SSRX50(:)) + 3*std(SSRX50(:));
SSRX120_filt = SSRX120 > mean(SSRX120(:)) + 3*std(SSRX120(:));
```

Top 10 Anomalies

Let's look at the top 10 results of the RX and the SSRX. Firstly, let's compare the different flavours of SSRX to see if there's any change in top anomalies:

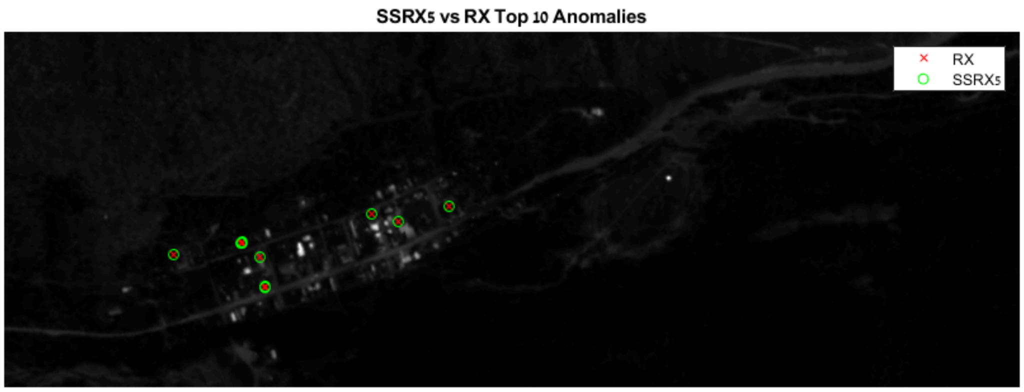
```
[~, idxs_pca5] = maxk(SSRX5(:), 10);
[~, idxs_pca50] = maxk(SSRX50(:), 10);
[~, idxs_pca120] = maxk(SSRX120(:), 10);
[row_pca5,col_pca5] = ind2sub(size(SSRX5),idxs);
[row_pca50,col_pca50] = ind2sub(size(SSRX50),idxs);
[row_pca120,col_pca120] = ind2sub(size(SSRX120),idxs);
figure; imshow(data(:,:,1)',[]); hold on;
plot(col_pca5,row_pca5,'or')
plot(col_pca50,row_pca50,'xg')
plot(col_pca50,row_pca50,'sb')
legend('Delete 5 PC', 'Delete 50 PC', 'Delete 120 PC')
title('SSRX Top 10 Anomalies')
```



Conclusion: top 10 SSRX anomalies stay the same regardless of how many PCs we cut off.

Now let's compare one the SSRX flavours to RX:

```
figure; imshow(data(:,:,1)',[]); hold on;
plot(col,row,'xr')
plot(col_pca5,row_pca5,'og')
title('SSRX5 vs RX Top 10 Anomalies')
legend('RX','SSRX5')
```



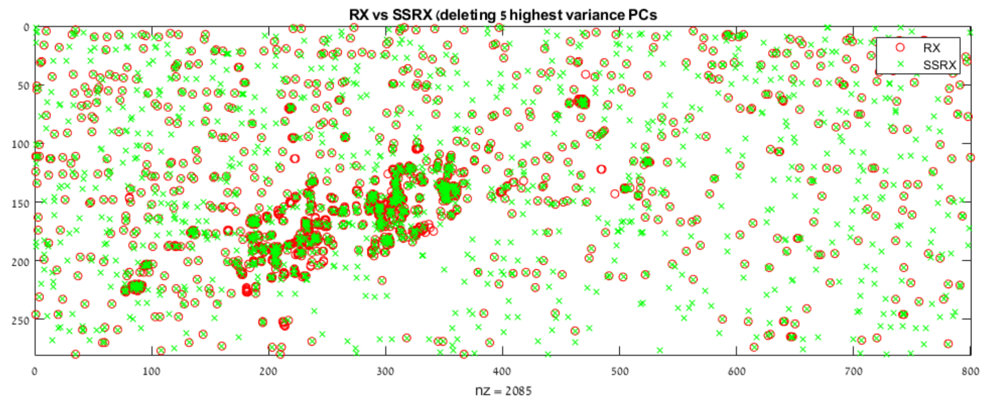
Conclusion: top 10 RX anomalies remain for SSRX as well.

Scatter Plot Comparison

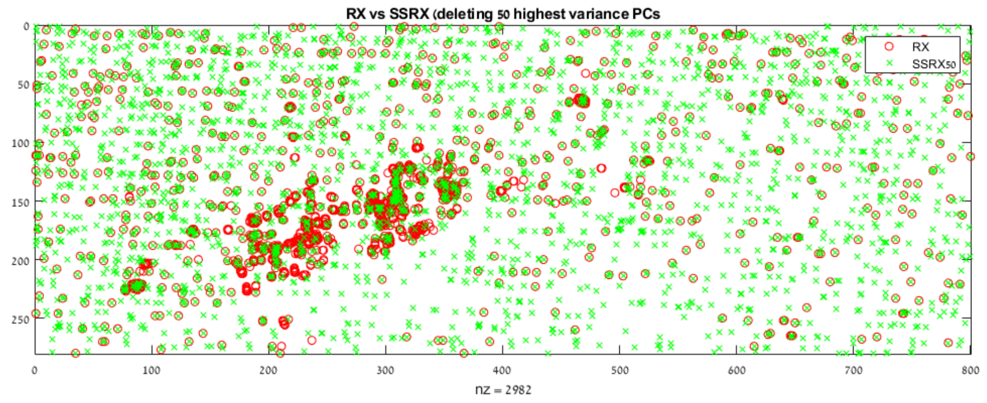
Based on the results above, the difference between the 2 algorithms (if exists) is in the lower scored anomalies. Let's try to look at that:

```
h1=figure;
spy(RX_filt,'or');
```

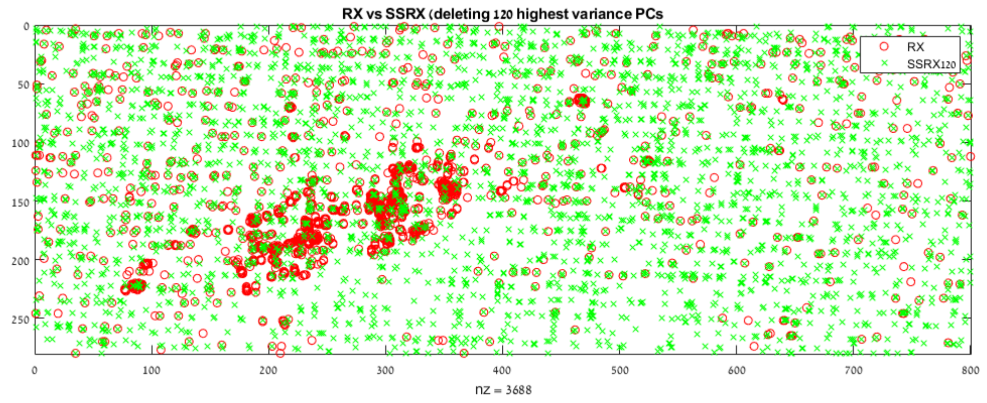
```
hold on;
spy(SSRX5_filt,'xg');
legend('RX','SSRX');
title('RX vs SSRX (deleting 5 highest variance PCs');
set(h1, 'Position', [0 0 1200 600])
```



```
h2=figure;
spy(RX_filt,'or');
hold on;
spy(SSRX50_filt,'xg');
legend('RX','SSRX50');
title('RX vs SSRX (deleting 50 highest variance PCs');
set(h2, 'Position', [0 0 1200 600])
```



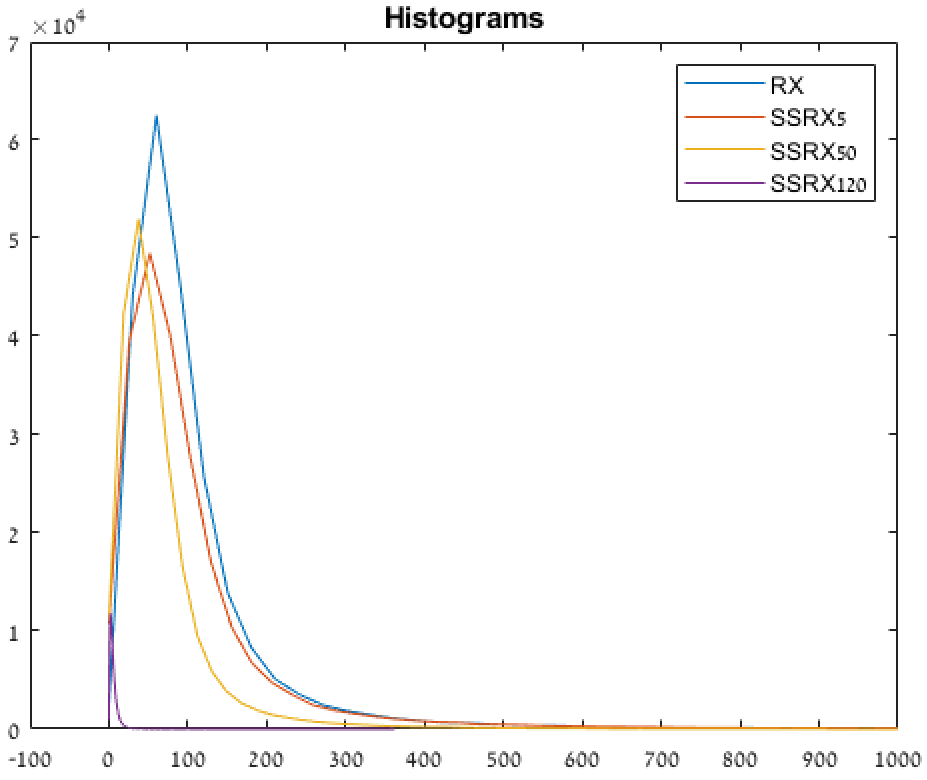
```
h2=figure;
spy(RX_filt,'or');
hold on;
spy(SSRX120_filt,'xg');
legend('RX','SSRX120');
title('RX vs SSRX (deleting 120 highest variance PCs');
set(h2, 'Position', [0 0 1200 600])
```



Conclusion: Seems like RX provides best results over all SSRX variants, and that the best SSRX variant is obtained by deleting only 5 hig variance PCs.

Histogram of all scores

```
[RX_val,RX_bins]=histcounts(RX,1000);
[SSRX5_val,SSRX5_bins]=histcounts(SSRX5,1000);
[SSRX50_val,SSRX50_bins]=histcounts(SSRX50,1000);
[SSRX120_val,SSRX120_bins]=histcounts(SSRX120,1000);
figure;
plot(RX_bins(1:1000),RX_val);
hold on;
plot(SSRX5_bins(1:1000),SSRX5_val);
plot(SSRX50_bins(1:1000),SSRX50_val);
plot(SSRX120_bins(1:1000),SSRX120_val);
xlim([-100 1000]);
legend('RX','SSRX5','SSRX50','SSRX120');
title('Histograms');
```


Histograms
×10^4
7
6
5
4
3
2
1
0
-100
0
100
200
300
400
500
600
700
800
900
1000
RX
SSRX5
SSRX50
SSRX120