**Readme for the Programs/Data used for the Sparse SVD paper**

1. Main function (R/Matlab): ssvd.R (ssvd.m), thresh.R (thresh.m)
2. Input variables:
3. X= argument (n x d matrix)
4. threu = type of penalty (thresholding rule) for the left singular vector

1 = (Adaptive) LASSO (default)

2 = hard thresholding

3 = SCAD

1. threv = type of penalty (thresholding rule) for the right singular vector

1 = (Adaptive) LASSO (default)

2 = hard thresholding

3 = SCAD

1. gamu = weight parameter in Adaptive LASSO for the left singular vector

nonnegative constant (default = 0, LASSO)

1. gamv = weight parameter in Adaptive LASSO for the right singular vector

nonnegative constant (default = 0, LASSO)

1. u0, v0 = initial values of left/right singular vectors (default = the standard SVs)
2. merr = threshold to decide convergence (default = 10^(-4))
3. niter = maximum number of iterations (default = 100)
4. Output:
5. u = left sparse singular vector
6. v = right sparse singaulr vector
7. iter = number of iterations to achieve the convergence
8. Lung cancer data

The data.txt file is a 12625 x 56 matrix; each column (row) of X corresponds to the individual case (gene).

Among the 56 cases,

Columns 1~20: pulmonary carcinoid samples (Carcinoid);

Columns 21~33: colon cancer metastasis samples (Colon);

Columns 34~50: normal lung samples (Normal);

Columns 51~56: small cell carcinoma samples (SmallCell).