CS754 Assignment 4 Report

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Introduction

Welcome to our report on CS754 Assignment 4. We have tried to make this report comprehensive and self-contained. We hope reading this would give you a proper flowing description of our work, methods used and the results obtained.

Also note that we installed the `Image Processing Toolbox` in MATLAB for this assignment. Thus the grader is urged to install it if she wishes to run the code on her on her machine. Also note that some of our code may take a while to run because of the intensive nature of the computations involved.

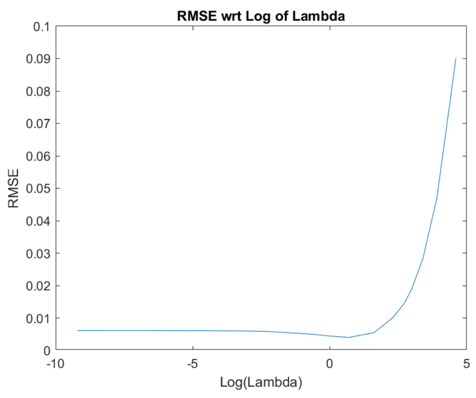
Hope you enjoy reading the report. Here we go!

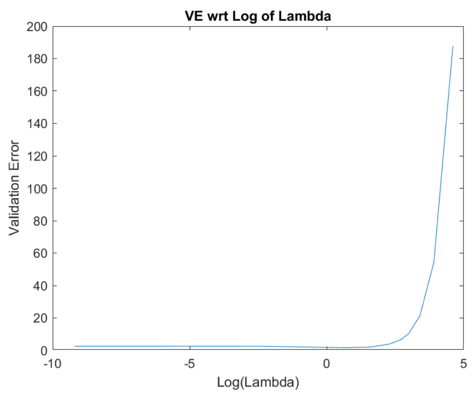
1 Problem 1

In this problem, we try out the cross validation technique and see if we can train and find an optimal value of lambda and then test that value for images that are not in our trained set. This is a very popular technique in machine learning and gives us a measure of robustness of our estimate

1.1 Plots and Graphs of RMSE and VE

Lambda	RMSE	Validation Error
0.0001	0.0061	2.5425
0.0005	0.0061	2.5421
0.0010	0.0061	2.5414
0.0050	0.0061	2.5573
0.0100	0.0061	2.5517
0.0500	0.0060	2.5378
0.1000	0.0059	2.5237
0.5000	0.0050	2.0632
1.0000	0.0044	1.7882
2.0000	0.0040	1.6477
5.0000	0.0054	2.0351
10.0000	0.0101	3.9400
15.0000	0.0143	6.5897
20.0000	0.0190	10.4407
30.0000	0.0283	21.2658
50.0000	0.0470	54.3791
100.0000	0.0901	187.8113





As you can see in the above graphs, the trend of both RMSE and Validation Error matches strongly. At $\lambda = 2$, both the RMSE and VE are at their minimum value. Thus, we can say that our estimates of lambda on the trained set are robust. This is because they match the optimal behaviour also on the new unseen images.

1.2 Coincident V and R

The whole method of cross validation is made to simulate/test out our method in real life like scenarios, where the compressive system would encounter new images, but of the same type/distribution. Since we already train over the R set, there is no point of the V set if it is the same as R.

The Validation error would just be a scaled version of the RMSE. We would not know if we have **underfitted** or **overfitted** to our training set.

In case we are performing cross-validation, it is extremely important to keep the R and V sets of the same distribution for any accurate results, but also disjoint, so as to actually test out the performance.

1.3 Proxying Ability

Theorem 1 in the paper talks about this Proxying ability.

If the number of measurements in the validation set is sufficiently large, the Theorem states that the true recovery error ϵ_r is bounded between $h(\lambda, +)\epsilon_{cv} - \sigma_n^2$ and $h(\lambda, -)\epsilon_{cv} - \sigma_n^2$, with a probability of $erf(\lambda/\sqrt{2})$.

The function $h()$ is defined as-

$$h(\lambda, \pm) \triangleq \frac{m}{m_{cv}} \frac{1}{1 \pm \lambda\sqrt{\frac{2}{m_{cv}}}}$$

The difference between the two bounds is roughly proportional to $1/m_{cv}^{2/3}$. Thus, the bound becomes tighter as the value of m_{cv} increases. This shows that both errors are related strongly.

Since, σ is a measure of the noise variance here, we can say that in case of reasonable amount of noise and sufficiently large m_{cv}, we will have the true error following the same trend as the cross validation error. Thus, we can comfortably use it as a measure of error/inaccuracy in our measurements.

1.4 Theoretical θ vs Cross Validation θ

Cross-Validation method gives us a practical/experimental result, while the last assignment was based on theory. There are always large differences in the approach taken by these two routes. Theoretical results are more general in nature and thus tend to be more conservative. Practical results are often so direct that they give much better results but only on the specific case. We will try to explain some of the points where we thing approaches like cross-validation out perform the results of Theorems.

- Cross Validation is a purely data oriented approach. If we have a statistically significant representative set being used to find λ, then we do not need to worry about it being optimum or not.
  On the other hand, the theoretical result targets the properties of the Sensing Matrix, like Restricted Eigenvalue Property and puts a bound on the noise magnitude. Many of these properties are hard to prove computationally and if at all proven, they are very conservative.

- In cross validation, the optimum value of λ obtained is already tried and tested on the training set and also verified by the validation set. It is also the optimum value since we have tried the several possibilities.
  Following theoretical route gives the results which are very conservative most of the times. This means that we are not working at the efficiency we can. Nor are we utilising the specific properties of the domain we are working in.
- The specific example of the paper in the last assignment just had a lower bound on the λ required. It did not even provide us with an optimum value of λ.
  Testing with a lot of values on the other hand, we can get the optimum value of λ from cross-validation

Thus, we can say that, cross validation is a powerful technique in practice and would tend to outperform the usual theoretical upper bounds. It is good to improve the robustness of our models and obtain better results.

2 Problem 2

Let $D = \{d_1, d_2, ..., d_n\}$ be our dictionary, and let $I \in \mathcal{S}$ be an image in our dataset. Then by the theory of dictionary learning, $I = \sum_{i=1}^{n} \alpha_i d_i$ for some sequence of scalars $\alpha_1, \alpha_2, \ldots, \alpha_n$. In this problem, we are given various transformations T which are applied on the images of $\mathcal{S}$, and we have to propose a modified dictionary D_T such that our transformed images are still expressible as linear combination of "atoms" in D_T.

(a) From the theory taught in class and common image processing literature, we know that derivative filters on an image are obtained through **convolutions** of the image with some known convolution filter, ie:- $I_{\text{filter}} = I * G$, where G is the filter matrix. Now, it's not hard to see that a matrix convolution is a linear mapping, ie:- the **derivative filter 'f' is itself a linear transform** on the image.Then

$$f(I) = f(\sum_{i=1}^{n} \alpha_i d_i) = \sum_{i=1}^{n} f(\alpha_i d_i) = \sum_{i=1}^{n} \alpha_i f(d_i)$$

where all the equalities follow by the properties of linear transforms.
Thus our transformed dictionary is $D_T := \{f(d_1), f(d_2), \ldots, f(d_n)\}$, where f represents our derivative filter.

(b) Once again, note that rotation is a linear transform. In particular, the rotation of an image (matrix) I anticlockwise by an angle θ can be given as below

$$I_{\text{rotated}}(x, y) = I(x \cos\theta + y \sin\theta, y \cos\theta - x \sin\theta)$$

or equivalently as

$$I_{\text{rotated}}([x \;\; y]^T) = I(R_\theta^{-1}[x \;\; y]^T)$$

where the rotation matrix R_θ represents anticlockwise rotation by an angle θ

$$R_\theta = \begin{bmatrix} \cos\theta & -\sin\theta \\ \sin\theta & \cos\theta \end{bmatrix}$$

Thus, once again, we have a linear transform in our hands and thus the new atoms of our transformed dictionary will just be the linear transform applied on the old dictionary itself, ie:- rotated versions of the old atoms. We will have two such dictionaries (for two distinct angles of rotation). Note that we must take the union of both dictionaries as an image, say rotated by β won't be expressible as a linear combination of dictionary atoms rotated by the angle α.

Thus our transformed dictionary is $D_T := \{d_{1\alpha}, d_{2\alpha}, \ldots, d_{n\alpha}, d_{1\beta}, d_{2\beta}, \ldots, d_{n\beta}\}$, where $d_{k\theta}$ represents the k^{th} atom rotated by θ.

(c) Assuming the relation holds pixel-wise, we have

$$I_{\text{new}}(x,y) = \alpha(I_{\text{old}}(x,y))^2 + \beta I_{\text{old}}(x,y) + \gamma$$

But we have

$$I_{\text{old}}(x,y) = \sum_{i=1}^{n} \alpha_i d_i(x,y)$$

$$\implies I_{\text{new}}(x,y) = \alpha(\sum_{i=1}^{n} \alpha_i d_i(x,y))^2 + \beta \sum_{i=1}^{n} \alpha_i d_i(x,y) + \gamma$$

$$\implies I_{\text{new}}(x,y) = \alpha(\sum_{i=1}^{n} \alpha_i^2 d_i^2(x,y) + 2 \sum_{1\le i<j\le n} \alpha_i\alpha_j d_i(x,y)d_j(x,y)) + \beta \sum_{i=1}^{n} \alpha_i d_i(x,y) + \gamma$$

Thus our new dictionary is clear:

- First class of items: $\{d_1^{\circ 2}, d_2^{\circ 2}, ..., d_n^{\circ 2}\}$, where $^{\circ 2}$ denotes **elementwise squaring**.
- Second class of items: $\{d_i \odot d_j\}_{1\le i<j\le n}$, where $\odot$ denotes **elementwise multiplication**.
- Third item: $J_{d\times d}$, where $d_i \in \mathbb{R}^{d\times d}$, where J is the matrix of all ones, ie:- $J =$ `ones(d)`, in MATLAB notation.

Thus our transformed dictionary is $D_T := \{d_1^{\circ 2}, d_2^{\circ 2}, ..., d_n^{\circ 2}, d_1 \odot d_2, \ldots, d_{n-1} \odot d_n, J_{d\times d}\}$.

(d) Blur kernel, like derivative filters, are also convolutions with kernel matrices and hence are linear transforms.

Thus our transformed dictionary is $D_T := \{f(d_1), f(d_2), \ldots, f(d_n)\}$, where f represents our blur kernel transformation.

(e) Similar to the idea used in part (b), we have to take an union of all the dictionaries, each applied with a single blur kernel. Thus let $\mathcal{B} := \{b_1, b_2, ..., b_l\}$ be the set of our blur *transforms*. Then our l dictionaries are $\{b_1(d_1), b_1(d_2), \ldots, b_1(d_n)\}$, $\{b_2(d_1), b_2(d_2), \ldots, b_2(d_n)\}$, ..., $\{b_l(d_1), b_l(d_2), \ldots, b_l(d_n)\}$, and
Thus our final dictionary is $D_T := \{b_1(d_1), \ldots, b_1(d_n), \ldots, b_l(d_1), b_l(d_2), \ldots, b_l(d_n)\}$.

(f) Note that the meaning of the notation for this part is slightly different from all other parts of this problem in the fact that our images and dictionary atoms are now assumed to the vectorized forms of the images they represented.

Now, note that the Radon transform matrix can be denoted as R_θ, which is a square matrix with entries dependent on θ, which when multiplied with our image vectors gives us their Radon transform.

Once again, as above, since this is a linear transform of the vectors, our new dictionary will be the Radon transform of the dictionary atoms. **Thus our new dictionary $D_T := \{Rd_1, Rd_2, \ldots, Rd_n\}$, where R is the Radon transform matrix corresponding to the angle θ.**

(g) Note that translating an image by a certain offset (x, y) basically means that we **pad the image, on the left and downwards, with x columns and y rows of zeros respectively**. Now, since we simply added an extra layer of padding of zeros, the linear combination relations still hold as the zero rows and columns obviously satisfy any linear relation and the old pixels also satisfy the relation too. Thus if we denote translation by the first offset to be t_1 and the second offset to be t_2, then, as we have seen many times before our **new dictionary will be $D_T := \{t_1(d_1), \ldots, t_1(d_n), t_2(d_1), t_2(d_2), \ldots, t_2(d_n)\}$.**

3 Problem 3

3.1 Part 1

We use the **Eckart-Young-Mirsky theorem** to find the **best rank r approximation to the given matrix** $A \in \mathbb{R}^{m \times n}$, ie:- A_r, which, as we have seen in the lecture, states that the best (in terms of the Frobenius norm of the difference in between those two matrices) r-rank approximation is given by $A_r = U\Sigma_r V^*$, where $A = U\Sigma V^*$ is the **Singular Value Decomposition** of A, and Σ_r contains the r maximum singular values in Σ, ie:- we retain the r largest diagonal values of Σ and set the rest to zero.
Thus the minimizer of the objective function $J(A_r) = \|A - A_r\|_F^2$; $\text{rank}(A_r) = r$ is

$$\boldsymbol{A_r = U\Sigma_r V^*}$$

where $A = U\Sigma V^*$ is the SVD decomposition of A and Σ_r contains the r maximum singular values in Σ.
Applications of low rank approximations:

- **Robust PCA**
  - Note that in a surveillance video, the background remains stationary while our object of interest moves. Thus the background of the image can be treated as it's low rank component, which can then be identified using the algorithm outlined above.
  - In a similar vein as the idea above, one can remove occlusion by **completing** a low rank matrix to effectively "cut-out" the occluding object in the image.

3.2 Part 2

We algebraically simplify the objective function $J(R) = \|A - RB\|_F^2$ first to find out the optimum orthonormal R matrix. For that, note the following facts from linear algebra:

- $\|A\|_F^2 = \text{tr}(AA^T)$
- $\text{tr}(AB) = \text{tr}(BA)$, and thus any rearrangement of a matrix multiplication will still yield the same trace.
- $\text{tr}(A) = \text{tr}(A^T)$ for any square matrix A

Then

$$\begin{aligned}\|A - RB\|_F^2 &= \text{tr}((A - RB)(A - RB)^T) = \text{tr}((A - RB)(A^T - B^T R^T)) \\ &= \text{tr}(AA^T - RBA^T - AB^T R^T + RBB^T R^T) \\ &= \text{tr}(AA^T) - \text{tr}(RBA^T) - \text{tr}((RBA^T)^T) + \text{tr}(RBB^T R^T) \\ &= \text{constant} - \text{tr}(RBA^T) - \text{tr}(RBA^T) + \text{tr}(R^T RBB^T) \\ &= \text{constant} - 2 \cdot \text{tr}(RBA^T) + \text{tr}(BB^T) \\ &= \text{constant} - 2 \cdot \text{tr}(RBA^T)\end{aligned}$$

Thus minimizing $\|A - RB\|_F^2$ is equivalent to maximizing $\text{tr}(RBA^T)$.
Now, let BA^T be equal to C, and let $C = U\Sigma V^*$ be the **Singular Value Decomposition** of C. Then

$$\text{tr}(RBA^T) = \text{tr}(RC) = \text{tr}(RU\Sigma V^*) = \text{tr}(V^* RU\Sigma)$$

Now, note that since R, U and V are all orthonormal, $M = V^* RU$ is orthonormal too, and thus

$$\text{tr}(V^* RU\Sigma) = \text{tr}(M\Sigma) = \sum_{i=1}^{n} m_{ii}\sigma_i \leq \sum_{i=1}^{n} |m_{ii}|\sigma_i$$

with the last inequality following by the triangle inequality (and note that $|\sigma_i| = \sigma_i$ since singular values are non-negative).

However, since M is orthonormal, ie:- all of it's column's norms are 1, we have that $|m_{ii}| \leq 1$, and thus the maxima of $\text{tr}(V^* RU\Sigma)$ is achieved when all $|m_{ii}| = 1$. But that can happen only when $M = I$, and thus

$$V^* RU = I$$
$$\implies \boldsymbol{R = VU^*}$$

Thus the best orthonormal transform that maps B to A is given by VU^*, where U and V are obtained from the SVD of $BA^T = U\Sigma V^*$.

This problem is also widely encountered in image processing literature. We ourselves came across one such example in class, namely, in 3D Tomography under unknown angles, wherein we try to determine what rotation best maps one image to another, and there is where we note that orthonormal matrices basically represent unscaled rotation in higher dimensions, from which the problem of minimizing $\|A - RB\|_F^2$ under an orthonormal R constraint arises.

4 Problem 4

Paper Details	
Title of the Paper	Non Negative Matrix Factorization Clustering Capabilities; Application on Multivariate Image Segmentation
Link of the paper	**Click Here**
Author List	Cosmin Lazar, Andrei Doncescu
Publication Date	March 2009
Publication Venue	2009 International Conference on Complex, Intelligent and Software Intensive Systems, Fukuoka, Japan

4.1 Aim of the Paper

The aim is to try to use NMF to perform data clustering. This is compared to the result obtained form the popular Fuzzy K-means algorithm. NMF has already been popular due to its visual clustering capabilities.

Several other algorithms impose constraints on the clusters, but NMF only assumes the constraint of being non-negative, which makes it a good choice.

4.2 Mathematical Formulation

Assume that the data is represented in the form of an $F \times N$ (N points in F dimensions) matrix V with all entries as positive. If we assume that the columns of V are generated from K clusters, we can represent V as $W \times H$, where W is a $\mathbb{R}^{F\times K}$ matrix and H is a $\mathbb{R}^{K\times N}$ matrix. Here W will denote the basis vectors and H will denote the coefficients.

Thus we are using the NMF algorithm to find an optimum dictionary, which will in turn give us the location of the cluster centers.

The NMF based clustering algorithm is as follows-

- Estimate the number of principal directions in the original data space.

This can be done by a greedy approach using tools like OMP or PCA. By setting a threshold, we can get a reasonable estimate of the number of clusters.

- Compute NMF on the new dataset (the number of factors equals the number of the most significant principal directions).

  This can use any algorithm. The approach has not been specified in the paper, but it seems like we can use the alternating method as in the lecture itself.

- The rows of the matrix H are considered to be the data membership degree to a NMF cluster (each cluster is associated to a single direction).

  By normalizing the column vectors of H to have unit length, we can obtain the final result.

- A hard clustering can be obtained by assigning to each data the label corresponding to the line where the maximum value of column vectors lies.

  This approach will work even if there are some values missing in the data. We do not need to perform data imputation in that case.

The clustering number is chosen as the Davies-Bouldin index. In general, the clustering data problem can be solved by trying to find the closest cluster to the observed value if we only look at the correctly observed values.

This error on the feasible set is minimised over all clusters and the remaining indexes are assigned the value according to the cluster's value.

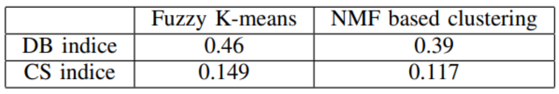
The error metric can be written as-

$$\frac{\|V - W^*H^*\|_F}{\|V\|_F}$$

Here, we are trying to get the basis vectors themselves to represent one cluster each. One limitation is that this approach only works when the clusters are distributed in a convex manner. This means that there are some clusters which this algorithm cannot solve efficiently.

4.3 Results

We observe that this NMF clustering performs better than the popular Fuzzy K-means algorithm and even works better in multispectral images segmentation.



	Fuzzy K-means	NMF based clustering
DB indice	0.46	0.39
CS indice	0.149	0.117

Table 2. Clustering results comparison

Hence, in conclusion, NMF can be considered as a fuzzy clustering approach which performs spectral clustering in case of convex shape clusters efficiently.

5 Problem 5

Note that we have to find the f vector which is most likely to have arisen from the y vector we know under the equation $y \sim \text{Poisson}(I_0 e^{-Rf})$, where all the operations are done element-wise on the vectors. Note that R is the **known** Radon matrix.
Stating this mathematically, we want

$$f = \text{arg max}_{f \in \mathbb{R}^m} P(f|y)$$

Now, note that $P(f|y) \propto P(y|f)P(f)$ by Baye's theorem, where $P(f)$ is a **prior** on f, ie:- a probability distribution on $\mathbb{R}^m$ which tells us how likely a certain point in $\mathbb{R}^m$ is to represent the natural tissue density vector.
But before specifying the functional form of the prior, we'll simplify $P(y|f)$ a bit. Also note that maximizing a certain non-negative function (such as a probability distribution) is equivalent to minimizing it's negative logarithm.
Note that since y varies with f as a Poisson relation

$$P(y|f) = \frac{e^{I_0 e^{-Rf}} (I_0 e^{-Rf})^y}{y!}$$

$$\implies -\log P(y|f) = I_0 e^{-Rf} - y \log(I_0 e^{-Rf}) + \log(y!)$$
$$\implies -\log P(y|f) = \|I_0 e^{-Rf}\|_1 + y^T Rf$$

where we drop all terms not having f in them because we're to define an objective function dependent on f. Note also that we transpose y at the end to make the matrices multipliable. Also note that to convert the vector $I_0 e^{-Rf}$ to a scalar, we take its l_1 norm (note also that the l_1 norm promotes sparsity, which is a desirable quality to have for our objective function), because $y^T Rf$ is also a scalar, and we need to add them both.
Now coming to the prior, note that f denotes natural tissue density. Now, from our study of natural images and other naturally arising phenomena, we know that **their gradients are sparse**. This is only to be expected since consecutive entries for the most part don't change rapidly.
Thus, if we define the **gradient of a vector as follows**

$$\nabla f := \sum_{i=1}^{m-1} |f_i - f_{i+1}|$$

Then

$$P(f) \propto e^{-\nabla f}$$

is a suitable prior. Taking it's negative logarithm we get

$$-\log P(f) = \nabla f$$

, and thus

$$-\log P(f|y) = -\log P(y|f) - \log P(f)$$
$$-\log P(f|y) = \|I_0 e^{-Rf}\|_1 + y^T Rf + \mu \nabla f$$

where μ is a suitable hyperparameter denoting the importance of how much the gradient sparsity is to be tuned.
Thus

$$\boldsymbol{J(f) := \|I_0 e^{-Rf}\|_1 + y^T Rf + \mu \nabla f}$$

Finally, note that for additive white Gaussian noise, we can simply minimize the mean square error (unlike Poisson noise, Gaussian noise is independent of the pixel value it distorts, and thus minimizing the mean square error should suffice). Note that the mean of a Poisson RV is equal to it's parameter, and thus y should be compared to $I_0 e^{-Rf}$, and thus

$$\boldsymbol{J_{\text{Gaussian}}(f) := \|y - I_0 e^{-Rf}\|_2^2}$$

Combining these two together

$$\boldsymbol{J_{\text{complete}}(f) := \|I_0 e^{-Rf}\|_1 + y^T Rf + \mu \nabla f + \lambda \|y - I_0 e^{-Rf}\|_2^2}$$

where λ is another hyperparameter to stress the importance of the Gaussian error function.