Dimension Reduction

```
> library(swirl)

| Hi! Type swirl() when you are ready to begin.

> swirl()

| Welcome to swirl! Please sign in. If you've been here before, use the same
name as you did then. If you are new,
| call yourself something unique.

What shall I call you? Stephen

| Please choose a course, or type 0 to exit swirl.

1: Data Analysis
2: Exploratory Data Analysis
3: Getting and Cleaning Data
4: Mathematical Biostatistics Boot Camp
5: Open Intro
6: R Programming
7: Regression Models
8: Statistical Inference
9: Take me to the swirl course repository!

Selection: 2

| Please choose a lesson, or type 0 to return to course menu.

 1: Principles of Analytic Graphs   2: Exploratory Graphs             3: Gra
phics Devices in R
 4: Plotting Systems                5: Base Plotting System           6: Lat
tice Plotting System
 7: Working with Colors             8: GGPlot2 Part1                  9: GGP
lot2 Part2
10: GGPlot2 Extras                 11: Hierarchical Clustering       12: K M
eans Clustering
13: Dimension Reduction            14: Clustering Example            15: Cas
eStudy


Selection: 13

| Attempting to load lesson dependencies...

| Package ‘fields’ loaded correctly!

| Package ‘jpeg’ loaded correctly!

| Package ‘datasets’ loaded correctly!
```

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| Dimension_Reduction. (Slides for this and other Data Science courses may be
found at github
| https://github.com/DataScienceSpecialization/courses/. If you care to use t
hem, they must be downloaded as a zip
| file and viewed locally. This lesson corresponds to 04_ExploratoryAnalysis/
dimensionReduction.)

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| In this lesson we'll discuss principal component analysis (PCA) and singula
r value decomposition (SVD), two
| important and related techniques of dimension reduction. This last entails
processes which finding subsets of
| variables in datasets that contain their essences. PCA and SVD are used in
both the exploratory phase and the more
| formal modelling stage of analysis. We'll focus on the exploratory phase an
d briefly touch on some of the
| underlying theory.

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| We'll begin with a motivating example - random data.

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| This is dataMatrix, a matrix of 400 random normal numbers (mean 0 and stand
ard deviation 1).  We're displaying it
| with the R command image. Run the R command head with dataMatrix as its arg
ument to see what dataMatrix looks
| like.

> head(dataMatrix)
            [,1]       [,2]       [,3]       [,4]       [,5]       [,6]
[,7]       [,8]       [,9]       [,10]
[1,]  0.5855288  1.1285108  0.6453831  1.5448636 -0.4876385 -1.4361457 -0.700
0758 -1.5138641  0.3803157 -0.37582344
[2,]  0.7094660 -2.3803581  1.0431436  1.3214520  0.3031512 -0.6292596 -0.567
4016  0.1642810  0.6051368 -1.81283376
[3,] -0.1093033 -1.0602656 -0.3043691  0.3221516 -0.2419740  0.2435218 -0.261
3939 -0.8708652  1.0196741  0.28860021
[4,] -0.4534972  0.9371405  2.4771109  1.5309551 -0.4817336  1.0583622 -1.063
8850  1.5933290  0.4749430 -0.18962258
[5,]  0.6058875  0.8544517  0.9712207 -0.4212397 -0.9918029  0.8313488 -0.106
3687  0.6465975 -2.1859464  0.01786021
```

```
[6,] -1.8179560  1.4607294  1.8670992 -1.1588210 -0.2806491  0.1052118  0.771
1037  0.3573697  0.9331922  0.65043024

| You are really on a roll!

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| So we see that dataMatrix has 10 columns (and hence 40 rows) of random numb
ers. The image here looks pretty
| random. Let's see how the data clusters. Run the R command heatmap with dat
aMatrix as its only argument.

> heatmap(dataMatrix)

| That's a job well done!

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| We can see that even with the clustering that heatmap provides, permuting t
he rows (observations) and columns
| (variables) independently, the data still looks random.

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| Let's add a pattern to the data. We've put some R code in the file addPatt.
R for you. Run the command myedit with
| the single argument "addPatt.R" (make sure to use the quotation marks) to s
ee the code. You might have to click
| your cursor in the console after you do this to keep from accidentally chan
ging the file.

> myedit("addPatt.R")

| Great job!

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|   8%

| Look at the code. Will every row of the matrix have a pattern added to it?

1: Yes
2: No

Selection: 2

| Keep up the great work!

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|  10%

| So whether or not a row gets modified by a pattern is determined by a coin
flip. Will the added
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| pattern affect every column in the affected row?

1: Yes
2: No

Selection: 2

| You nailed it! Good job!

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| So in rows affected by the coin flip, the 5 left columns will still have a
mean of 0 but the right
| 5 columns will have a mean closer to 3.

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| Now to execute this code, run the R command source with 2 arguments. The fi
rst is the filename (in
| quotes), "addPatt.R", and the second is the argument local set equal to TRU
E.

> source("addPatt.R", local = TRUE)

| You're the best!

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| Here's the image of the altered dataMatrix after the pattern has been added
. The pattern is clearly
| visible in the columns of the matrix. The right half is yellower or hotter,
indicating higher
| values in the matrix.

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| Now run the R command heatmap again with dataMatrix as its only argument. T
his will perform a
| hierarchical cluster analysis on the matrix.

> heatmap(dataMatrix)

| Excellent job!

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| Again we see the pattern in the columns of the matrix. As shown in the dend
rogram at the top of the
```

| display, these split into 2 clusters, the lower numbered columns (1 through 5) and the higher
| numbered ones (6 through 10). Recall from the code in addPatt.R that for rows selected by the
| coinflip the last 5 columns had 3 added to them. The rows still look random.

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| Now consider this picture. On the left is an image similar to the heatmap of dataMatix you just
| plotted. It is an image plot of the output of hclust(), a hierarchical clustering function applied
| to dataMatrix. Yellow indicates "hotter" or higher values than red. This is consistent with the
| pattern we applied to the data (increasing the values for some of the right most columns).

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| The middle display shows the mean of each of the 40 rows (along the x-axis). The rows are shown in
| the same order as the rows of the heat matrix on the left. The rightmost display shows the mean of
| each of the 10 columns. Here the column numbers are along the x-axis and their means along the y.

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| We see immediately the connection between the yellow (hotter) portion of the cluster image and the
| higher row means, both in the upper right portion of the displays. Similarly, the higher valued
| column means are in the right half of that display and lower columnn means are in the left half.

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| Now we'll talk a little theory. Suppose you have 1000's of multivariate variables X_1, ... ,X_n. By
| multivariate we mean that each X_i contains many components, i.e., X_i = (X_{i1}, ... , X_{im}.
| However, these variables (observations) and their components might be correlated to one another.

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| Which of the following would be an example of variables correlated to one a
nother?

1: Heights and weights of members of a family
2: The depth of the Atlantic Ocean and what you eat for breakfast
3: Today's weather and a butterfly's wing position

Selection: 1

| You are amazing!

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| 23%

| As data scientists, we'd like to find a smaller set of multivariate variabl
es that are uncorrelated
| AND explain as much variance (or variability) of the data as possible. This
is a statistical
| approach.

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| In other words, we'd like to find the best matrix created with fewer variab
les (that is, a lower
| rank matrix) that explains the original data. This is related to data compr
ession.

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| Two related solutions to these problems are PCA which stands for Principal
Component Analysis and
| SVD, Singular Value Decomposition. This latter simply means that we express
a matrix X of
| observations (rows) and variables (columns) as the product of 3 other matri
ces, i.e., X=UDV^t. This
| last term (V^t) represents the transpose of the matrix V.

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| Here U and V each have orthogonal (uncorrelated) columns. U's columns are t
he left singular vectors
| of X and V's columns are the right singular vectors of X. D is a diagonal
matrix, by which we mean

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| that all of its entries not on the diagonal are 0. The diagonal entries of
D are the singular
| values of X.

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| To illustrate this idea we created a simple example matrix called mat. Look
at it now.

> mat
     [,1] [,2] [,3]
[1,]    1    2    3
[2,]    2    5    7

| You are really on a roll!

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|  29%

| So mat is a 2 by 3 matrix. Lucky for us R provides a function to perform si
ngular value
| decomposition. It's called, unsurprisingly, svd. Call it now with a single
argument, mat.

> svd(mat)
$d
[1] 9.5899624 0.1806108

$u
           [,1]       [,2]
[1,] -0.3897782 -0.9209087
[2,] -0.9209087  0.3897782

$v
           [,1]       [,2]
[1,] -0.2327012 -0.7826345
[2,] -0.5614308  0.5928424
[3,] -0.7941320 -0.1897921


| You got it!

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|  30%

| We see that the function returns 3 components, d which holds 2 diagonal ele
ments, u, a 2 by 2
| matrix, and v, a 3 by 2 matrix. We stored the diagonal entries in a diagona
l matrix for you, diag,
| and we also stored u and v in the variables matu and matv respectively. Mul
tiply matu by diag by
| t(matv) to see what you get. (This last expression represents the transpose
of matv in R). Recall
| that in R matrix multiplication requires you to use the operator %*%.
```

```
> matu %*% diag %*% t(matv)
     [,1] [,2] [,3]
[1,]    1    2    3
[2,]    2    5    7

| Great job!

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|  31%

| So we did in fact get mat back. That's a relief! Note that this type of dec
omposition is NOT
| unique.

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|  33%

| Now we'll talk a little about PCA, Principal Component Analysis, "a simple,
non-parametric method
| for extracting relevant information from confusing data sets." We're quotin
g here from a very nice
| concise paper on this subject which can be found at http://arxiv.org/pdf/14
04.1100.pdf. The paper
| by Jonathon Shlens of Google Research is called, A Tutorial on Principal Co
mponent Analysis.

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| Basically, PCA is a method to reduce a high-dimensional data set to its ess
ential elements (not
| lose information) and explain the variability in the data. We won't go into
the mathematical
| details here, (R has a function to perform PCA), but you should know that S
VD and PCA are closely
| related.

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| We'll demonstrate this now. First we have to scale mat, our simple example
data matrix.  This means
| that we subtract the column mean from every element and divide the result b
y the column standard
| deviation. Of course R has a command, scale, that does this for you. Run sv
d on scale of mat.

> svd(scale(mat))
$d
[1] 1.732051 0.000000
```

```
$u
           [,1]      [,2]
[1,] -0.7071068 0.7071068
[2,]  0.7071068 0.7071068

$v
          [,1]       [,2]
[1,] 0.5773503 -0.5773503
[2,] 0.5773503  0.7886751
[3,] 0.5773503 -0.2113249


| You're the best!

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|  36%

| Now run the R program prcomp on scale(mat). This will give you the principa
l components of mat. See
| if they look familiar.

> prcomp(scale(mat))
Standard deviations (1, .., p=2):
[1] 1.732051 0.000000

Rotation (n x k) = (3 x 2):
           PC1        PC2
[1,] 0.5773503 -0.5773503
[2,] 0.5773503  0.7886751
[3,] 0.5773503 -0.2113249

| You are quite good my friend!

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| Notice that the principal components of the scaled matrix, shown in the Rot
ation component of the
| prcomp output, ARE the columns of V, the right singular values. Thus, PCA o
f a scaled matrix yields
| the V matrix (right singular vectors) of the same scaled matrix.

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| Now that we covered the theory let's return to our bigger matrix of random
data into which we had
| added a fixed pattern for some rows selected by coinflips. The pattern effe
ctively shifted the
| means of the rows and columns.

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| Here's a picture showing the relationship between PCA and SVD for that bigg
er matrix.  We've
| plotted 10 points (5 are squished together in the bottom left corner). The
x-coordinates are the
| elements of the first principal component (output from prcomp), and the y-c
oordinates are the
| elements of the first column of V, the first right singular vector (gotten
from running svd). We
| see that the points all lie on the 45 degree line represented by the equati
on y=x.  So the first
| column of V IS the first principal component of our bigger data matrix.

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| To prove we're not making this up, we've run svd on dataMatrix and stored t
he result in the object
| svd1. This has 3 components, d, u and v. look at the first column of V now.
It can be viewed by
| using the svd1$v[,1] notation.

> svd1$v[,1]
 [1] -0.01269600  0.11959541  0.03336723  0.09405542 -0.12201820 -0.43175437
-0.44120227 -0.43732624
 [9] -0.44207248 -0.43924243

| You are quite good my friend!

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|  42%

| See how these values correspond to those plotted? Five of the entries are s
lightly to the left of
| the point (-0.4,-0.4), two more are negative (to the left of (0,0)), and th
ree are positive (to the
| right of (0,0)).

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|  43%

| Here we again show the clustered data matrix on the left. Next to it we've
plotted the first column
| of the U matrix associated with the scaled data matrix. This is the first L
EFT singular vector and
| it's associated with the ROW means of the clustered data. You can see the c
lear separation between
| the top 24 (around -0.2) row means and the bottom 16 (around 0.2). We don't
show them but note that
| the other columns of U don't show this pattern so clearly.
```

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| 45%

| The rightmost display shows the first column of the V matrix associated wit
h the scaled and
| clustered data matrix. This is the first RIGHT singular vector and it's ass
ociated with the COLUMN
| means of the clustered data. You can see the clear separation between the l
eft 5 column means
| (between -0.1 and 0.1) and the right 5 column means (all below -0.4). As wi
th the left singular
| vectors, the other columns of V don't show this pattern as clearly as this
first one does.

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| 46%

| So the singular value decomposition automatically picked up these patterns,
the differences in the
| row and column means.

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| 47%

| Why were the first columns of both the U and V matrices so special? Well a
s it happens, the D
| matrix of the SVD explains this phenomenon. It is an aspect of SVD called v
ariance explained.
| Recall that D is the diagonal matrix sandwiched in between U and V^t in the
SVD representation of
| the data matrix. The diagonal entries of D are like weights for the U and V
columns accounting for
| the variation in the data. They're given in decreasing order from highest t
o lowest. Look at these
| diagonal entries now. Recall that they're stored in svd1$d.

> svd1$d
 [1] 12.458121 7.779798 6.732595 6.301878 5.860013 4.501826 3.921267 2
.973909 2.401470
[10] 2.152848

| Excellent work!

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| 48%

| Here's a display of these values (on the left). The first one (12.46) is si
gnificantly bigger than
| the others. Since we don't have any units specified, to the right we've plo
tted the proportion of

| the variance each entry represents. We see that the first entry accounts fo
r about 40% of the
| variance in the data. This explains why the first columns of the U and V ma
trices respectively
| showed the distinctive patterns in the row and column means so clearly.

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| 49%

| Now we'll show you another simple example of how SVD explains variance. We'
ve created a 40 by 10
| matrix, constantMatrix. Use the R command head with constantMatrix as its a
rgument to see the top
| rows.

```
> head(constantMatrix)
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
[1,]    0    0    0    0    0    1    1    1    1     1
[2,]    0    0    0    0    0    1    1    1    1     1
[3,]    0    0    0    0    0    1    1    1    1     1
[4,]    0    0    0    0    0    1    1    1    1     1
[5,]    0    0    0    0    0    1    1    1    1     1
[6,]    0    0    0    0    0    1    1    1    1     1
```

| That's correct!

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| 51%

| The rest of the rows look just like these. You can see that the left 5 colu
mns are all 0's and the
| right 5 columns are all 1's. We've run svd with constantMatrix as its argum
ent for you and stored
| the result in svd2. Look at the diagonal component, d, of svd2 now.

```
> svd2$d
 [1] 1.414214e+01 1.293147e-15 2.515225e-16 8.585184e-31 9.549693e-32 3.33003
4e-32 2.022600e-46
 [8] 4.362170e-47 1.531252e-61 0.000000e+00
```

| You are amazing!

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| 52%

| Which index holds the largest entry of the svd2$d?

1: 1
2: 5
3: 9
4: 10

Selection: 1

| Your dedication is inspiring!

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|   53%

| So the first entry by far dominates the others. Here the picture on the lef
t shows the heat map of
| constantMatrix. You can see how the left columns differ from the right ones
. The middle plot shows
| the values of the singular values of the matrix, i.e., the diagonal element
s which are the entries
| of svd2$d. Nine of these are 0 and the first is a little above 14. The thir
d plot shows the
| proportion of the total each diagonal element represents.

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|   54%

| According to the plot, what percentage of the total variation does the firs
t diagonal element
| account for?

1: 90%
2: 100%
3: 0%
4: 50%

Selection: 2

| Excellent job!

  |=============================================================
|   55%

| So what does this mean? Basically that the data is one-dimensional. Only 1
piece of information,
| namely which column an entry is in, determines its value.

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|   57%

| Now let's return to our random 40 by 10 dataMatrix and consider a slightly
more complicated example
| in which we add 2 patterns to it. Again we'll choose which rows to tweak us
ing coinflips.
| Specifically, for each of the 40 rows we'll flip 2 coins. If the first coin
flip is heads, we'll add
| 5 to each entry in the right 5 columns of that row, and if the second coinf
lip is heads, we'll add
| 5 to just the even columns of that row.

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|   58%

| So here's the image of the scaled data matrix on the left. We can see both
patterns, the clear
| difference between the left 5 and right 5 columns, but also, slightly less
visible, the alternating
| pattern of the columns. The other plots show the true patterns that were ad
ded into the affected
| rows. The middle plot shows the true difference between the left and right
columns, while the
| rightmost plot shows the true difference between the odd numbered and even-
numbered columns.

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|   59%

| The question is, "Can our analysis detect these patterns just from the data
?" Let's see what SVD
| shows. Since we're interested in patterns on columns we'll look at the firs
t two right singular
| vectors (columns of V) to see if they show any evidence of the patterns.

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| Here we see the 2 right singular vectors plotted next to the image of the d
ata matrix. The middle
| plot shows the first column of V and the rightmost plot the second. The mid
dle plot does show that
| the last 5 columns have higher entries than the first 5. This picks up, or
at least alludes to, the
| first pattern we added in which affected the last 5 columns of the matrix.
The rightmost plot,
| showing the second column of V, looks more random. However, closer inspecti
on shows that the
| entries alternate or bounce up and down as you move from left to right. Thi
s hints at the second
| pattern we added in which affected only even columns of selected rows.

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  |=============================================================
|   61%

| To see this more closely, look at the first 2 columns of the v component. W
e stored the SVD output
| in the svd object svd2.

> svd2$v[,1:2]
            [,1]         [,2]
 [1,] 0.06154540  0.142468636
 [2,] 0.26433096  0.504510087
```

```
 [3,] 0.04987554  0.316470664
 [4,] 0.27693897  0.524499356
 [5,] 0.14275820 -0.282921362
 [6,] 0.43252652 -0.002280468
 [7,] 0.37724057 -0.354403893
 [8,] 0.43280767  0.039226153
 [9,] 0.34912246 -0.376485206
[10,] 0.43379723 -0.031422705

| Great job!

  |=======================================================================
|  63%

| Seeing the 2 columns side by side, we see that the values in both columns a
lternately increase and
| decrease. However, we knew to look for this pattern, so chances are, you mi
ght not have noticed
| this pattern if you hadn't known if was there. This example is meant to sho
w you that it's hard to
| see patterns, even straightforward ones.

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|  64%

| Now look at the entries of the diagonal matrix d resulting from the svd. Re
call that we stored this
| output for you in the svd object svd2.

> svd2$d
 [1] 14.084918  8.257842  6.458184  6.100500  5.538262  2.266358  1.955790  1
.609508  1.078566
[10]  1.054146

| Great job!

  |=======================================================================
|  65%

| We see that the first element, 14.55, dominates the others. Here's the plot
of these diagonal
| elements of d. The left shows the numerical entries and the right show the
percentage of variance
| each entry explains.

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  |=======================================================================
|  66%

| According to the plot, how much of the variance does the second element acc
ount for?

1: 11%
2: 18%
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3: 53%
4: .1%

Selection: 2

| Keep working like that and you'll get there!

  |===
| 67%

| So the first element which showed the difference between the left and right halves of the matrix
| accounts for roughly 50% of the variation in the matrix, and the second element which picked up the
| alternating pattern accounts for 18% of the variance. The remaining elements account for smaller
| percentages of the variation. This indicates that the first pattern is much stronger than the
| second. Also the two patterns confound each other so they're harder to separate and see clearly.
| This is what often happens with real data.

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| 69%

| Now you're probably convinced that SVD and PCA are pretty cool and useful as tools for analysis,
| but one problem with them that you should be aware of, is that they cannot deal with MISSING data.
| Neither of them will work if any data in the matrix is missing. (You'll get error messages from R
| in red if you try.) Missing data is not unusual, so luckily we have ways to work around this
| problem. One we'll just mention is called imputing the data.

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= | 70%

| This uses the k nearest neighbors to calculate a values to use in place of the missing data. You
| may want to specify an integer k which indicates how many neighbors you want to average to create
| this replacement value. The bioconductor package (http://bioconductor.org) has an impute package
| which you can use to fill in missing data. One specific function in it is impute.knn.

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== | 71%

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| We'll move on now to a final example of the power of singular value decompo
sition and principal
| component analysis and how they work as a data compression technique.

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| Consider this low resolution image file showing a face. We'll use SVD and s
ee how the first several
| components contain most of the information in the file so that storing a hu
ge matrix might not be
| necessary.

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  |=======================================================================
=====                               |   73%

| The image data is stored in the matrix faceData. Run the R command dim on f
aceData to see how big
| it is.

> dim(faceData)
[1] 32 32

| That's a job well done!

  |=======================================================================
======                              |   75%

| So it's not that big of a file but we want to show you how to use what you
learned in this lesson.
| We've done the SVD and stored it in the object svd1 for you. Here's the plo
t of the variance
| explained.

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  |=======================================================================
=======                             |   76%

| According to the plot what percentage of the variance is explained by the f
irst singular value?

1: 40
2: 15
3: 100
4: 23

Selection: 1

| You are really on a roll!

  |=======================================================================
=========                           |   77%
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| So 40% of the variation in the data matrix is explained by the first component, 22% by the second,
| and so forth. It looks like most of the variation is contained in the first 10 components. How can
| we check this out? Can we try to create an approximate image using only a few components?

...

  |=== | 78%

| Recall that the data matrix X is the product of 3 matrices, that is X=UDV^t. These are precisely
| what you get when you run svd on the matrix X.

...

  |=== | 80%

| Suppose we create the product of pieces of these, say the first columns of U and V and the first
| element of D. The first column of U can be interpreted as a 32 by 1 matrix (recall that faceData
| was a 32 by 32 matrix), so we can multiply it by the first element of D, a 1 by 1 matrix, and get a
| 32 by 1 matrix result. We can multiply that by the transpose of the first column of V, which is the
| first principal component. (We have to use the transpose of V's column to make it a 1 by 32 matrix
| in order to do the matrix multiplication properly.)

...

  |=== | 81%

| Alas, that is how we do it in theory, but in R using only one element of d means it's a constant.
| So we have to do the matrix multiplication with the %*% operator and the multiplication by the
| constant (svd1$d[1]) with the regular multiplication operator *.

...

  |=== | 82%

| Try this now and put the result in the variable a1. Recall that svd1$u, svd1$d, and svd1$v contain
| all the information you need. NOTE that because of the peculiarities of R's casting, if you do the
| scalar multiplication with the * operator first (before the matrix multiplication with the %*%

```
| operator) you MUST enclose the 2 arguments (svd1$u[,1] and svd1$d[1]) in pa
rentheses.

> a1 <- svd1$u[,1] %*% t(svd1$v[,1]) * svd1$d[1]

| Excellent work!

  |=======================================================================
===============                      |  83%

| Now to look at it as an image. We wrote a function for you called myImage w
hich takes a single
| argument, a matrix of data to display using the R function image. Run it no
w with a1 as its
| argument.

> View(myImage)

| Not quite! Try again. Or, type info() for more options.

| Type myImage(a1) at the command prompt.

> myImage(a1)

| You are amazing!

  |=======================================================================
================                     |  84%

| It might not look like much but it's a good start. Now we'll try the same e
xperiment but this time
| we'll use 2 elements from each of the 3 SVD terms.

...

  |=======================================================================
==================                   |  86%

| Create the matrix a2 as the product of the first 2 columns of svd1$u, a dia
gonal matrix using the
| first 2 elements of svd1$d, and the transpose of the first 2 columns of svd
1$v. Since all of your
| multiplicands are matrices you have to use only the operator %*% AND you DO
N'T need parentheses.
| Also, you must use the R function diag with svd1$d[1:2] as its sole argumen
t to create the proper
| diagonal matrix. Remember, matrix multiplication is NOT commutative so you
have to put the
| multiplicands in the correct order. Please use the 1:2 notation and not the
c(m:n), i.e., the
| concatenate function, when specifying the columns.

> a2 <- svd1$u[,1:2] %*%  diag(svd1$d[1:2])  %*% t(svd1$v[,1:2])

| Excellent job!
```

```
  |=================================================================================
==================              |  87%

| Use myImage again to see how a2 displays.

> myImage(a2)

| You are amazing!

  |=================================================================================
===================             |  88%

| We're starting to see slightly more detail, and maybe if you squint you see
a grimacing mouth. Now
| let's see what image results using 5 components. From our plot of the varia
nce explained 5
| components covered a sizeable percentage of the variation. To save typing,
use the up arrow to
| recall the command which created a2 and replace the a2 and assignment arrow
with the call to
| myImage, and change the three occurrences of 2 to 5.

> myImage(svd1$u[,1:5] %*%  diag(svd1$d[1:5])  %*% t(svd1$v[,1:5]) )

| All that practice is paying off!

  |=================================================================================
====================            |  89%

| Certainly much better. Clearly a face is appearing with eyes, nose, ears, a
nd mouth recognizable.
| Again, use the up arrow to recall the last command (calling myImage with a
matrix product argument)
| and change the 5's to 10's. We'll see how this image looks.

> myImage(svd1$u[,1:10] %*%  diag(svd1$d[1:10])  %*% t(svd1$v[,1:10]) )

| That's a job well done!

  |=================================================================================
=====================           |  90%

| Now that's pretty close to the original which was low resolution to begin w
ith, but you can see
| that 10 components really do capture the essence of the image. Singular val
ue decomposition is a
| good way to approximate data without having to store a lot.

...

  |=================================================================================
======================          |  92%

| We'll close now with a few comments. First, when reducing dimensions you ha
ve to pay attention to
| the scales on which different variables are measured and make sure that all
your data is in
```

| consistent units. In other words, scales of your data matter. Second, princ
ipal components and
| singular values may mix real patterns, as we saw in our simple 2-pattern ex
ample, so finding and
| separating out the real patterns require some detective work. Let's do a qu
ick review now.

...

  |===
========================= | 93%

| Which of the following cliches LEAST captures the essence of dimension redu
ction?

1: separate the wheat from the chaff
2: find the needle in the haystack
3: see the forest through the trees
4: a face that could launch a 1000 ships

Selection: 4

| You are amazing!

  |===
========================== | 94%

| A matrix X has the singular value decomposition UDV^t. The principal compon
ents of X are ?

1: the rows of V
2: the rows of U
3: the columns of V
4: the columns of U

Selection: 3

| Keep up the great work!

  |===
========================== | 95%

| A matrix X has the singular value decomposition UDV^t. The singular values
of X are found where?

1: the columns of D
2: the diagonal elements of D
3: the columns of U
4: the columns of V

Selection: 2

| That's the answer I was looking for.

  |===
========================== | 96%

```
| True or False? PCA and SVD are totally unrelated.

1: True
2: False

Selection: 2

| Nice work!

  |=========================================================================
==============================    |  98%

| True or False? D gives the singular values of a matrix in decreasing order
of weight.

1: False
2: True

Selection: 2

| You're the best!

  |=========================================================================
================================ |  99%

| Congratulations! We hope you enjoyed making faces and that this lesson didn
't reduce the dimensions
| of your understanding.

...

  |=========================================================================
================================| 100%

| Would you like to receive credit for completing this course on Coursera.org
?

1: Yes
2: No
```

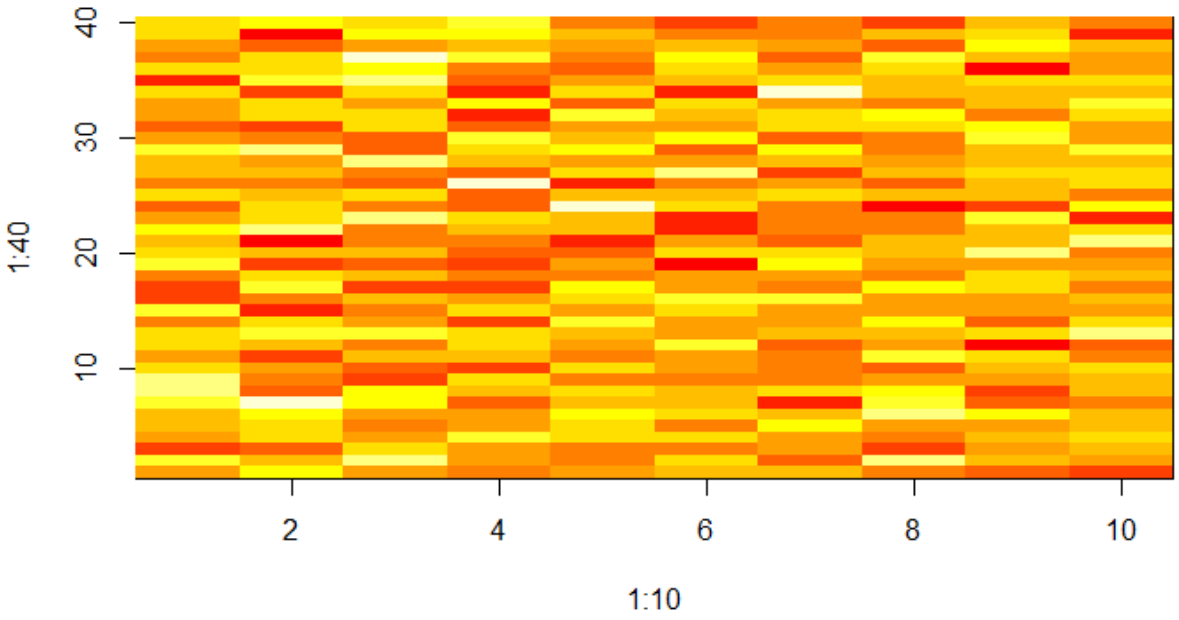
Codes

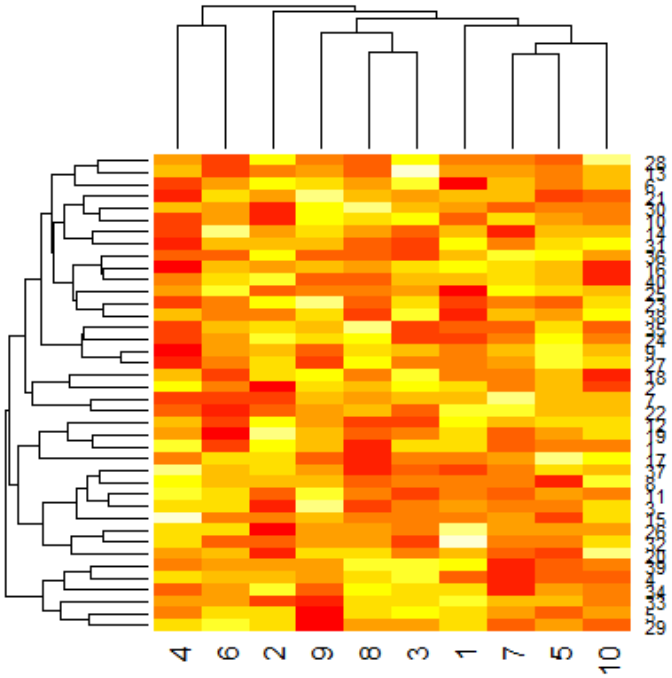
addPatt.R

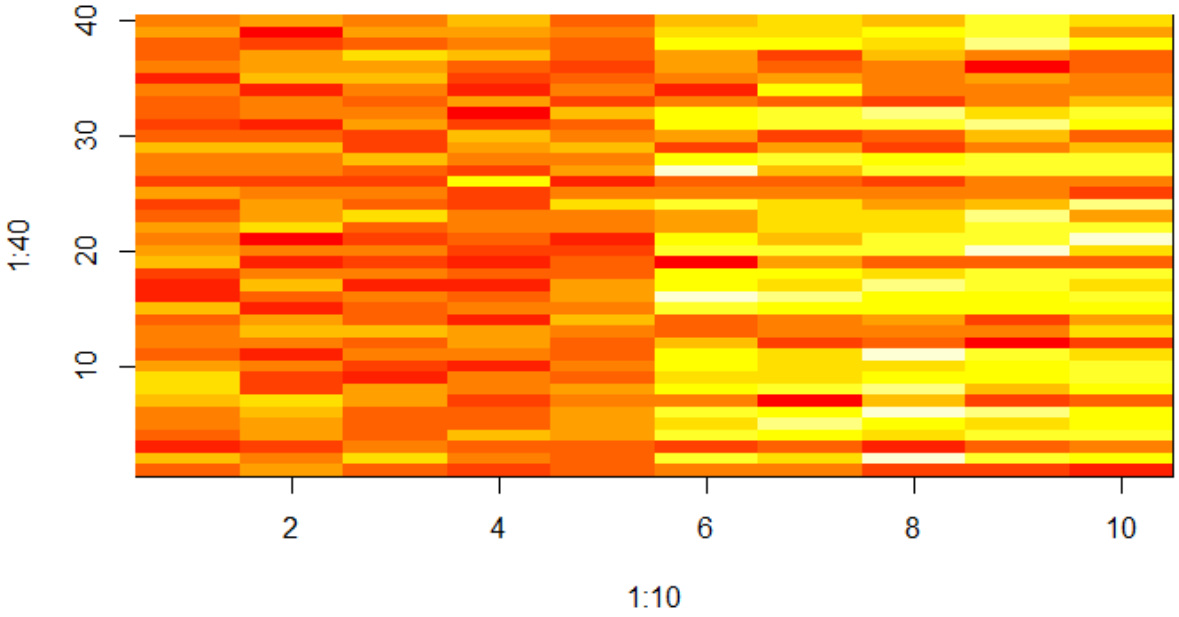
```
set.seed(678910)

for(i in 1:40){

 # flip a coin

 coinFlip <- rbinom(1,size=1,prob=0.5)

 # if coin is heads add a common pattern to that row
```

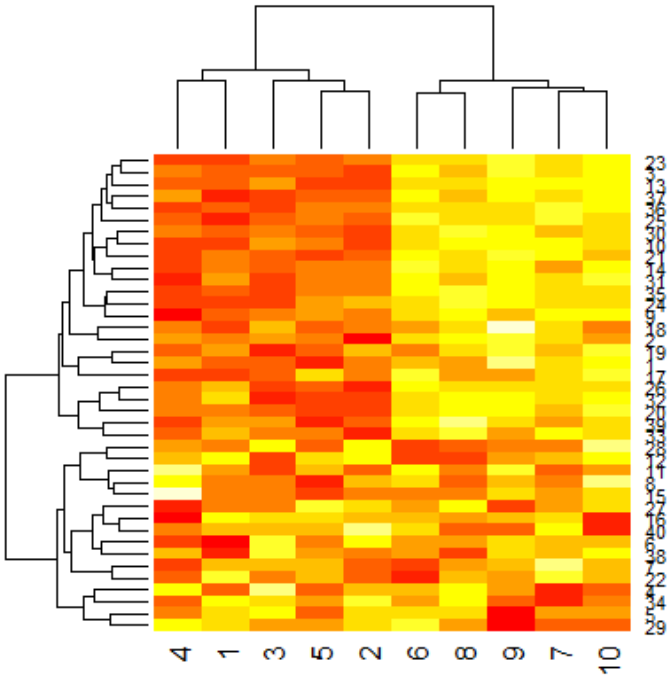
```
  if(coinFlip){
    dataMatrix[i,] <- dataMatrix[i,] + rep(c(0,3),each=5)
  }
}
```

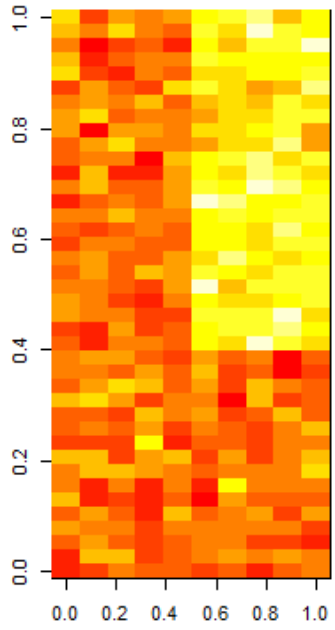
Plots

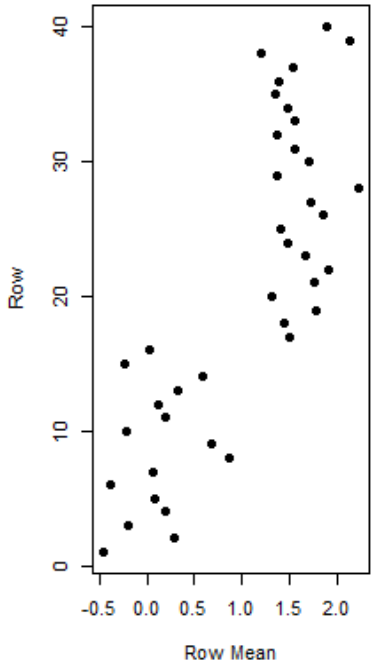


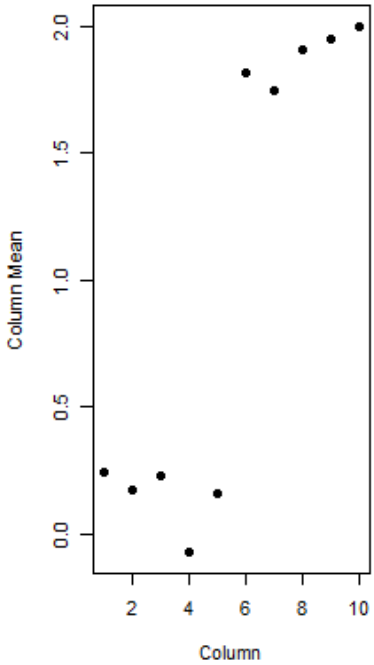

4 6 2 9 8 3 1 7 5 10

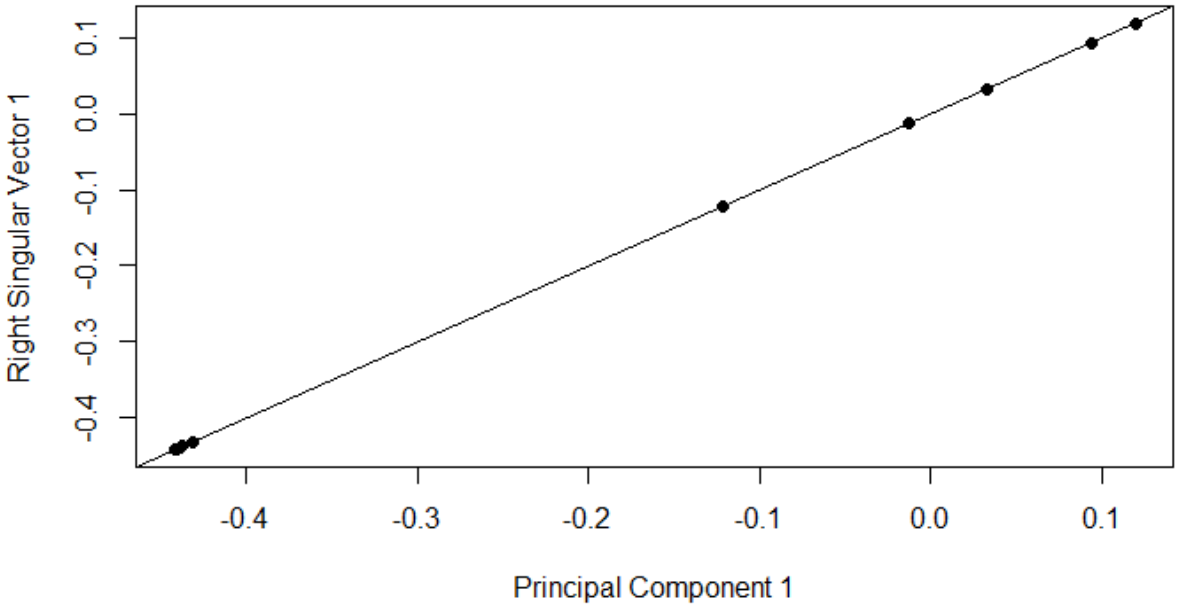

1:40
10
20
30
40
2
4
6
8
10
1:10

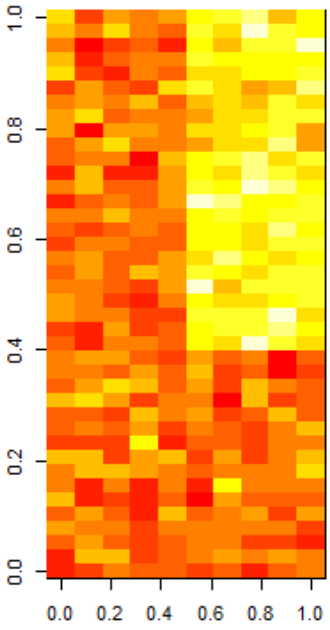

4 1 3 5 2 6 8 9 7 10

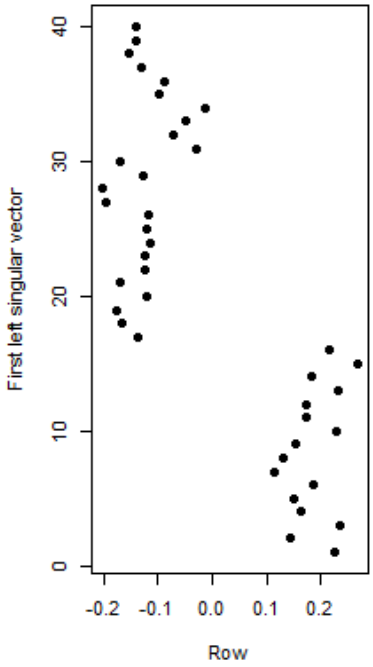

0.0 0.2 0.4 0.6 0.8 1.0

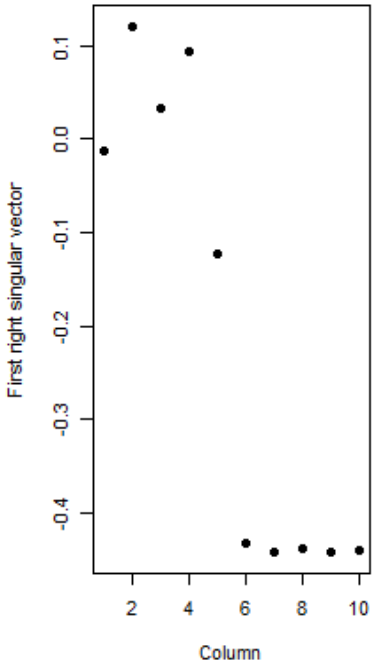

Row
Row Mean
0 10 20 30 40
-0.5 0.0 0.5 1.0 1.5 2.0

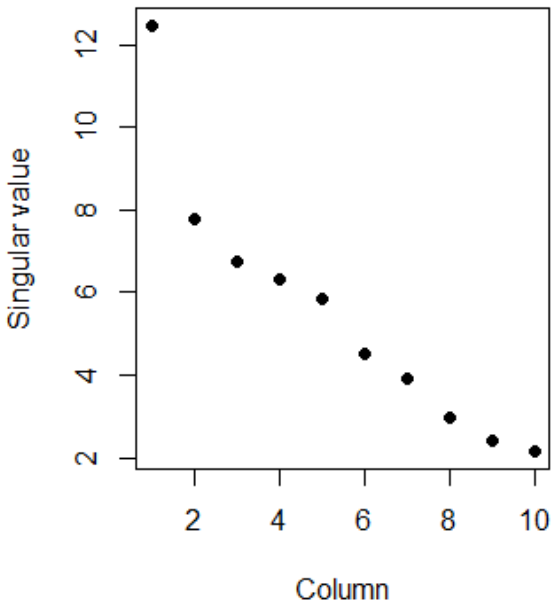

Column Mean
Column
0.0 0.5 1.0 1.5 2.0
2 4 6 8 10

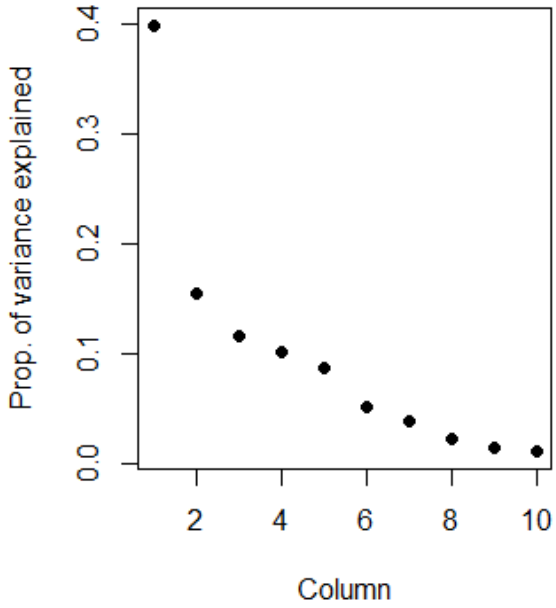

Right Singular Vector 1
-0.4
-0.3
-0.2
-0.1
0.0
0.1
Principal Component 1

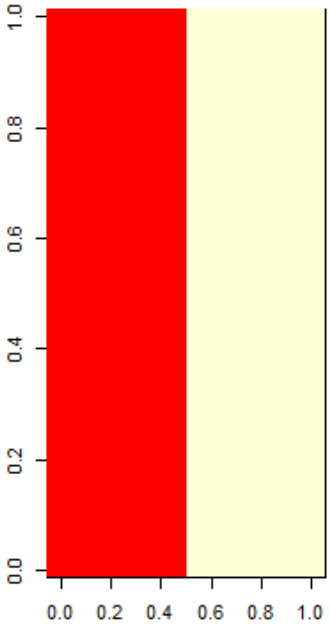

0.0
0.2
0.4
0.6
0.8
1.0

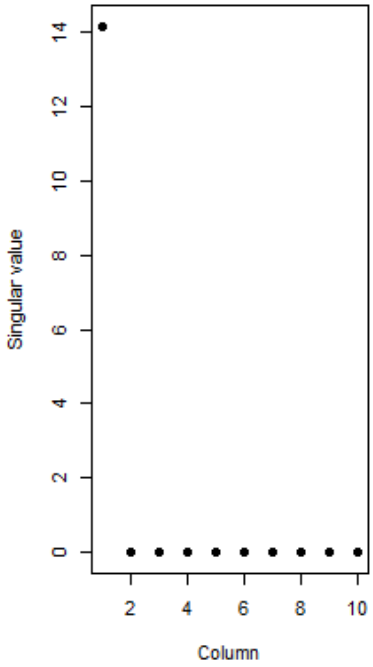

First left singular vector
0
10
20
30
40
-0.2
-0.1
0.0
0.1
0.2
Row

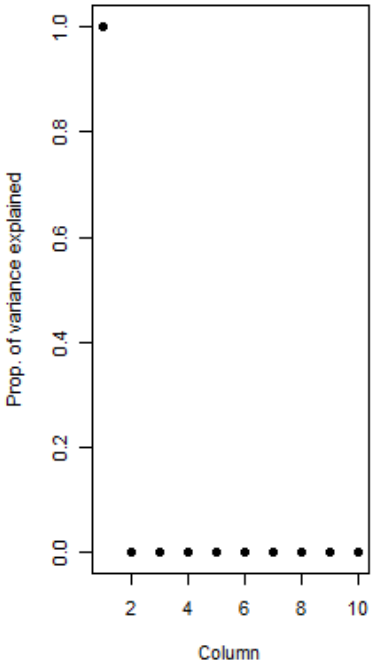

First right singular vector
-0.4
-0.3
-0.2
-0.1
0.0
0.1
2
4
6
8
10
Column

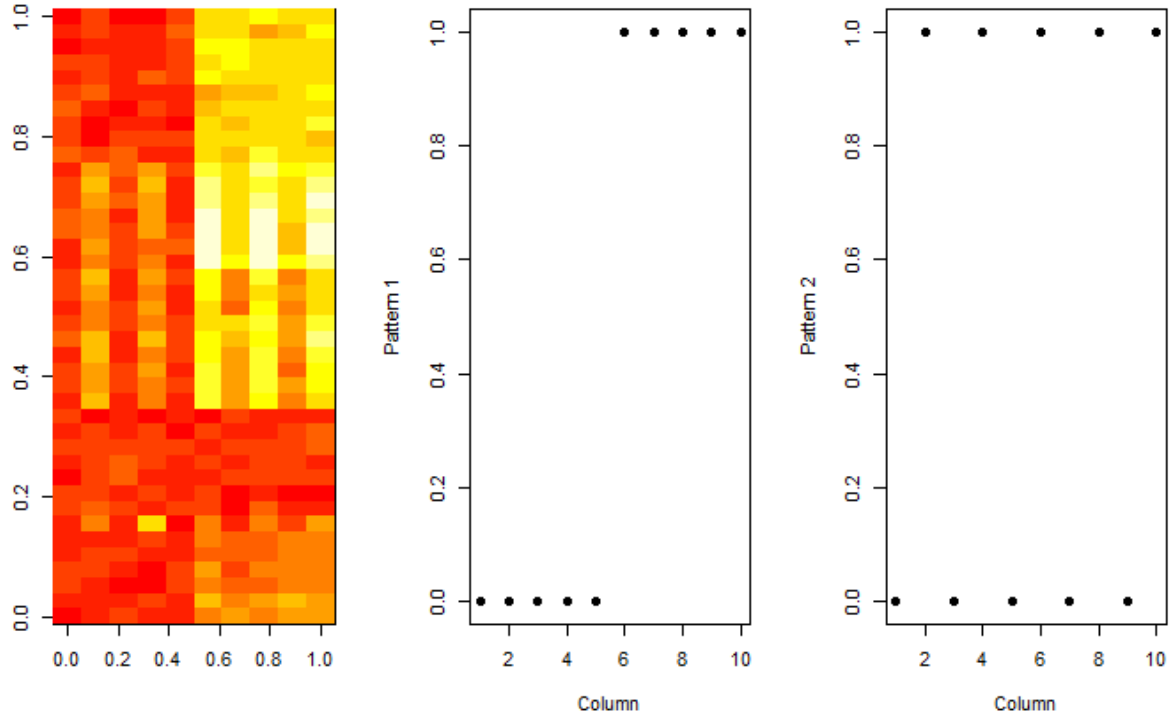

Singular value
Column
2
4
6
8
10
12


Prop. of variance explained
Column
0.0
0.1
0.2
0.3
0.4

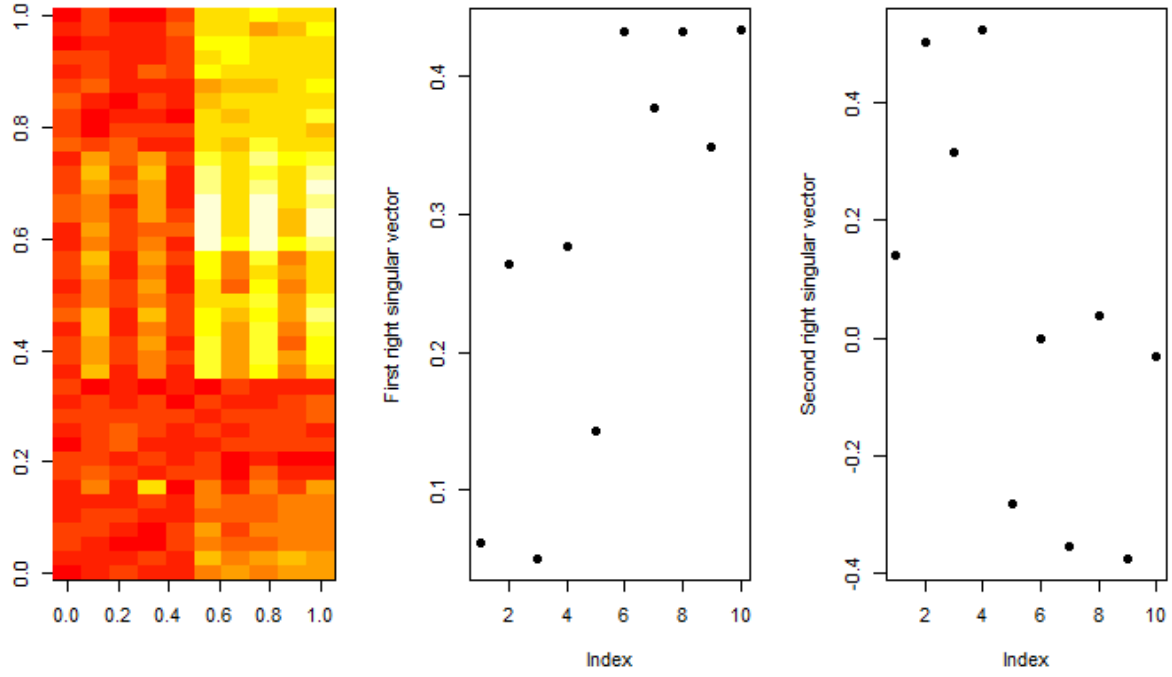

0.0
0.2
0.4
0.6
0.8
1.0

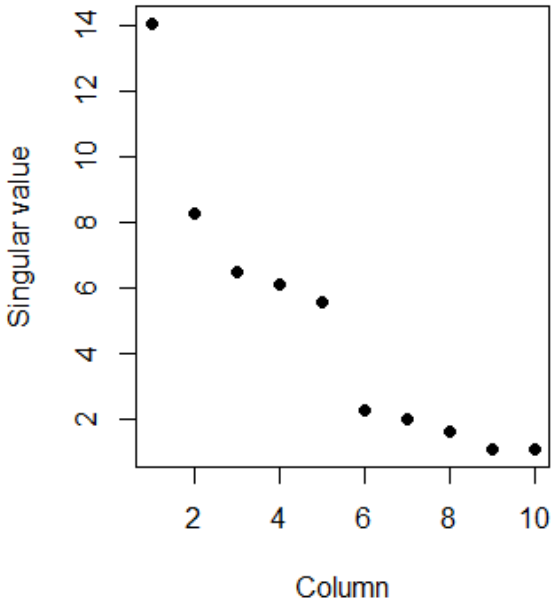

Singular value
Column
0
2
4
6
8
10
12
14

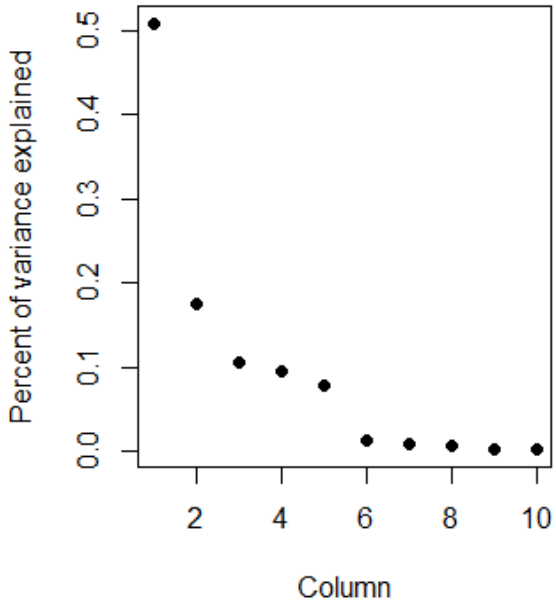

Prop. of variance explained
Column
0.0
0.2
0.4
0.6
0.8
1.0

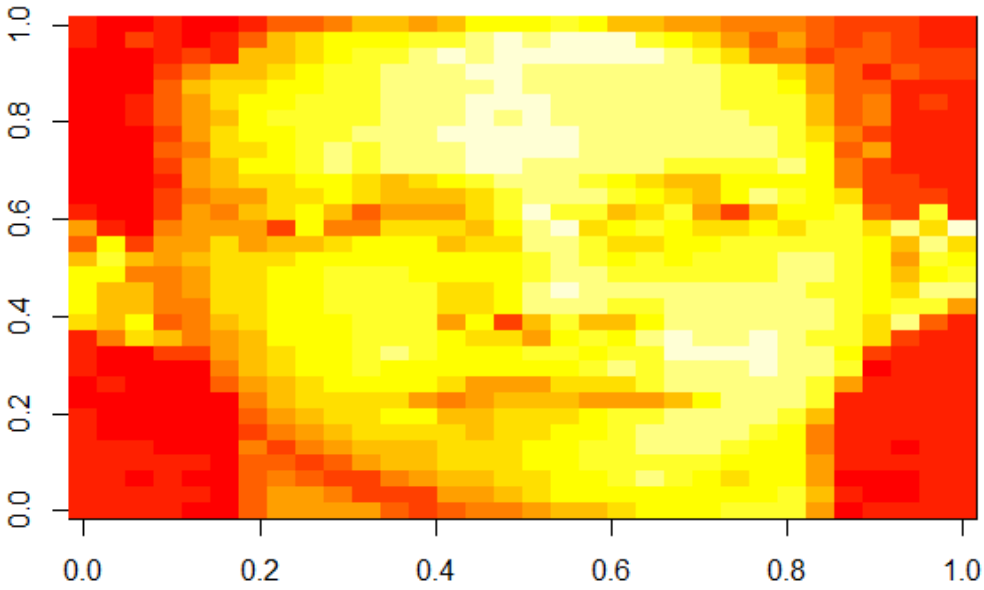


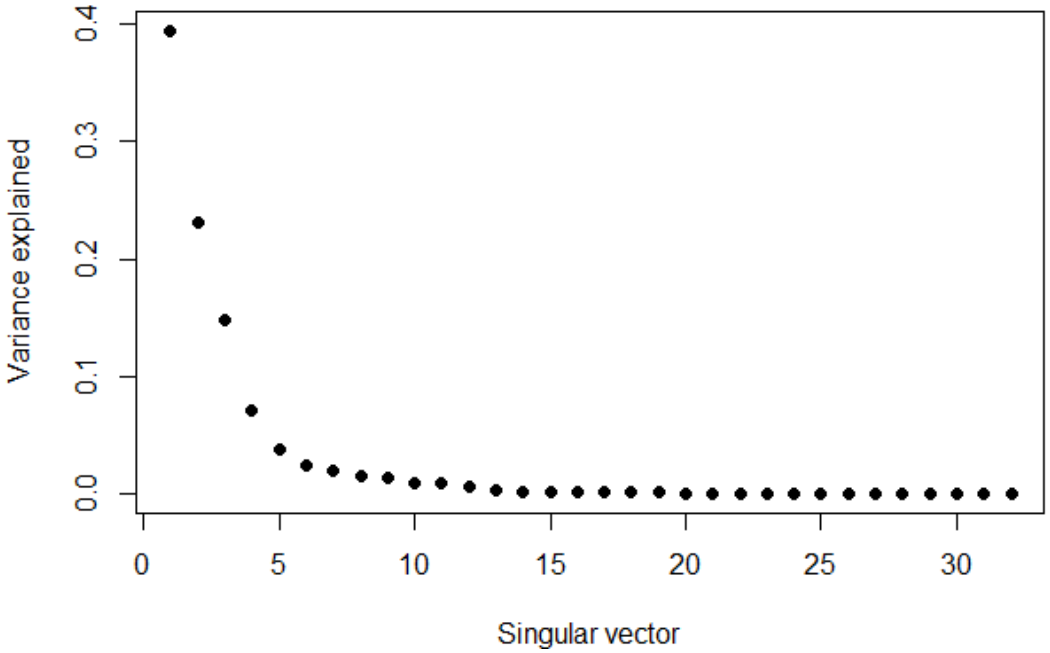
v and variation in columns

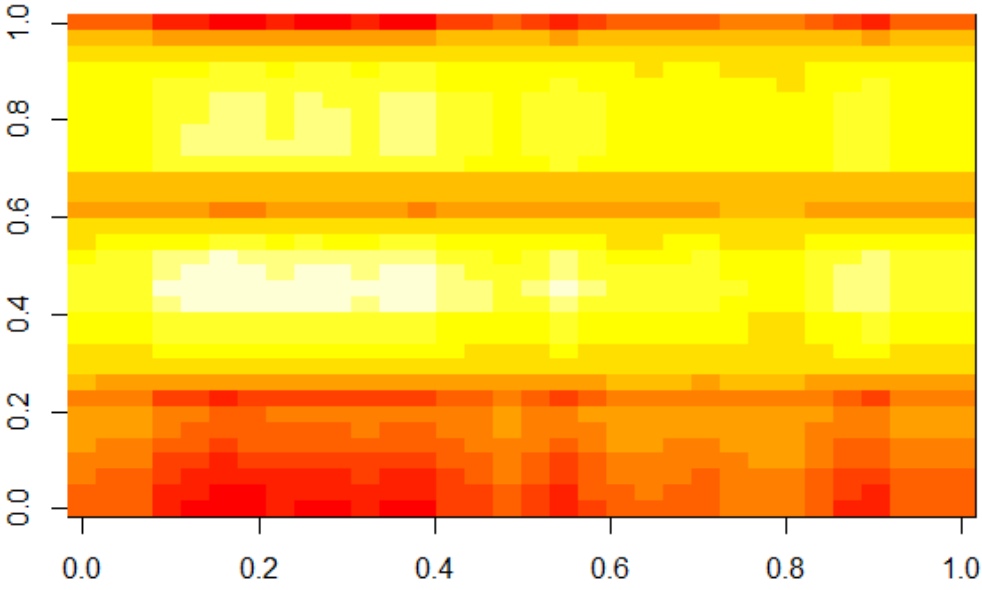


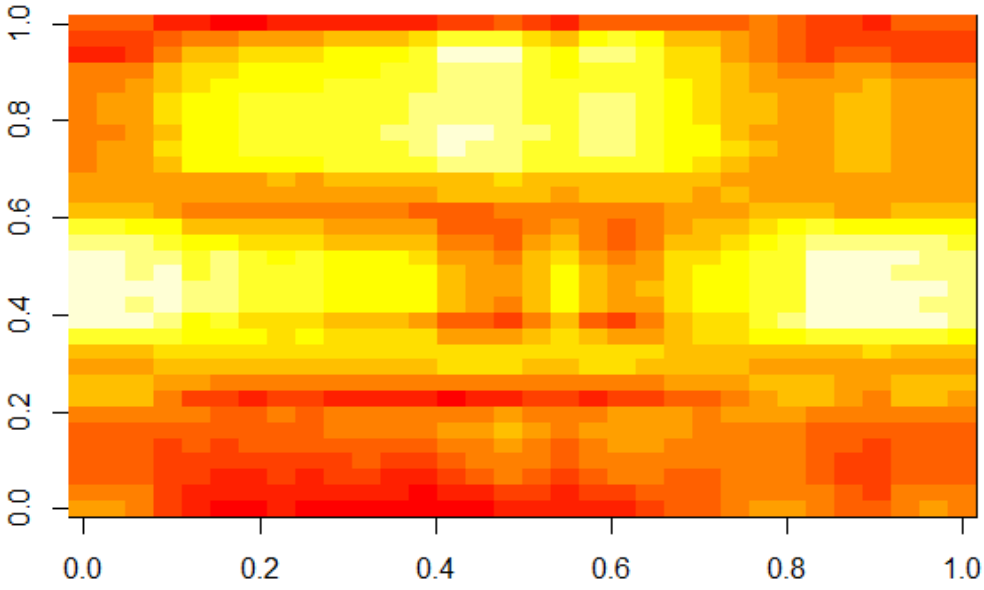

Singular value
2
4
6
8
10
12
14
2
4
6
8
10
Column

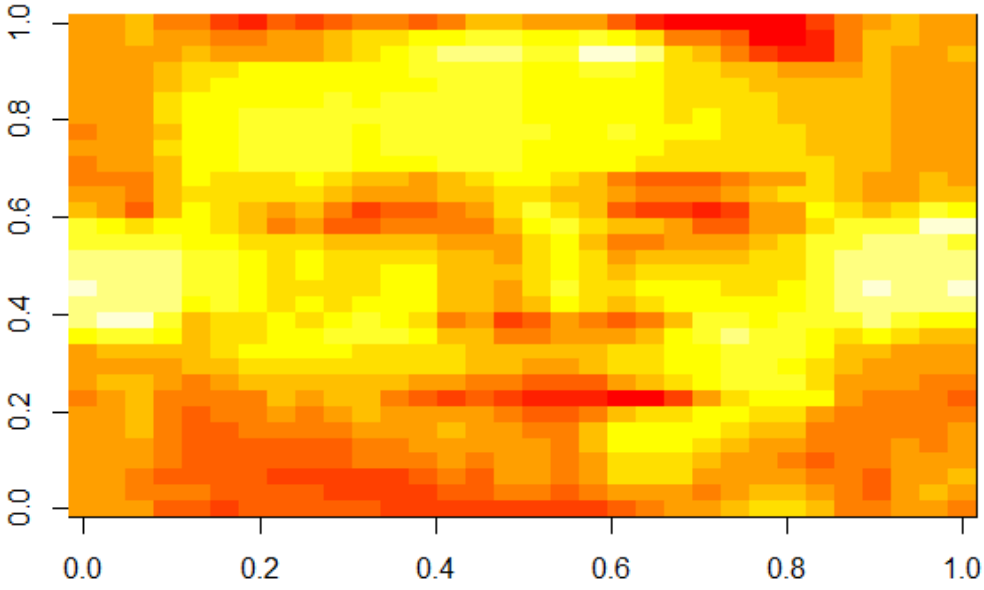

Percent of variance explained
0.0
0.1
0.2
0.3
0.4
0.5
2
4
6
8
10
Column

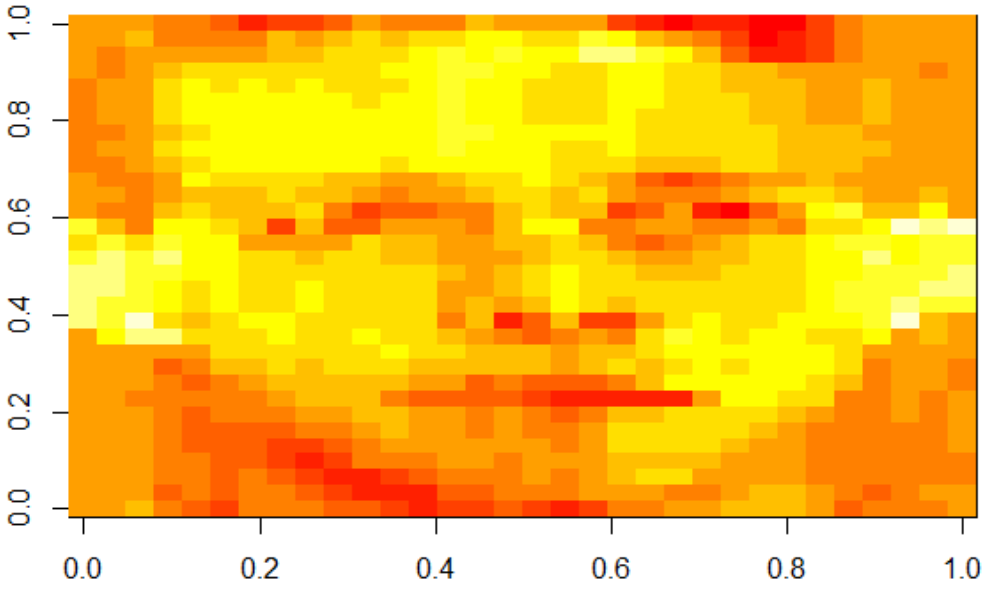

0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0


Variance explained
0.0
0.1
0.2
0.3
0.4
0
5
10
15
20
25
30
Singular vector


0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0


1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0


1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0


0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0