

Principal Component Analysis with R

Objective: To get acquainted with how data can be filtered and visualized using principal component analysis (PCA). Upon completing this exercise it is expected that you:

- Can apply and interpret principal component analysis (PCA) for data visualization.

R Help: R help for a function is obtained by typing `?<function name>` in the R command prompt. In practice, the fastest and easiest way to get help in R is often to simply Google your problem. For instance: "How to add legends to a plot in R" or the content of an error message. In the later case, it is often helpful to find the *simplest* script or input to script which will raise the error.

Piazza discussion forum: You can get help by asking questions on Piazza: piazza.com/dtu.dk/fall2019/october2019

Software installation: Extract the R toolbox from the Dropbox folder . Start R and go to the `<base-dir>/02450Toolbox_R/` directory by setting the working directory through `setwd(<base-dir>/02450Toolbox_R/)` and run `source('setup.R')`. Remember the purpose of the exercises is not to re-write the code from scratch but to work with the scripts provided in the directory `<base-dir>/02450Toolbox_R/Scripts/`
Representation of data in R:

	R var.	Type	Size	Description
	X	Numeric	$N \times M$	Data matrix: The rows correspond to N data objects, each of which contains M attributes.
	attributeNames	Cell array	$M \times 1$	Attribute names: Name (string) for each of the M attributes.
	N	Numeric	Scalar	Number of data objects.
	M	Numeric	Scalar	Number of attributes.
Classification	y	Numeric	$N \times 1$	Class index: For each data object, y contains a class index, $y_n \in \{0, 1, \dots, C - 1\}$, where C is the total number of classes.
	classNames	Cell array	$C \times 1$	Class names: Name (string) for each of the C classes.
	C	Numeric	Scalar	Number of classes.

2.1 PCA on the Nanose dataset

As an example dataset we will consider chemical sensor data obtained from the NanoNose [1] project, see also [2]. The data contains 8 sensors named by the letters

A–H measuring different levels of concentration of Water, Ethanol, Acetone, Heptane and Pentanol injected into a small gas chamber. The data will be represented in matrix form such that each row contains the 8 sensors measurements (i.e. sensor A–H) of the various compounds injected into the gas chamber.

- 2.1.1 Inspect the file `<base-dir>/02450Toolbox_R/Data/nanonose.xls` and make sure you understand how the data is stored in Excel. We will load the Nanose dataset from the file

`<base-dir>/02450Toolbox_R/Data/nanonose.xls` into R using the `read.csv` function, and get it into the standard data matrix form as we learnt how to do it in Exercise 1. Make sure to use “,” as the cell separator when saving as .csv. See `ex2_1_1.R` for details. There are 90 data objects with 8 attributes each. Do you get the correct data matrix X of size 90×8 ?

- 2.1.2 The data resides in an 8 dimensional space where each dimension corresponds to each of the 8 NanoNose sensors. This makes visualization of the raw data difficult, because it is difficult to plot data in more than 2–3 dimensions.

Plot the two attributes A and B against each other in a scatter plot using `ex2_1_2.R`.

Script details:

- *Type `?plot` to learn how the R plot function works.*
- *The attributes A and B are the first and second columns of the matrix X .*
- *You can use indexing to get the columns out of the matrix, e.g., `x=X[,1]`; `y = X[,2]`;*

Try to change the dimensions that are plotted against each other.

We will use principal component analysis to reduce the dimensionality of the data. PCA is computed by subtracting the mean of the data, $\mathbf{Y} = \mathbf{X} - \mathbf{1}\boldsymbol{\mu}$ (where $\boldsymbol{\mu}$ is a (row) vector containing the mean value of each attribute and $\mathbf{1}$ is a N by 1 column vector of ones in all entries) and then calculating the singular value decomposition (SVD) of the zero mean data, i.e. $\mathbf{Y} = \mathbf{U}\mathbf{S}\mathbf{V}^\top$.

From PCA we can find out how much of the variation in the data each PCA component accounts for. This is given by

$$\rho_m = \frac{s_{mm}^2}{\sum_{m'=1}^M s_{m',m'}^2},$$

i.e. the squared singular value of the given component divided by the sum of all the squared singular values.

- 2.1.3 Compute the PCA of the NanoNose data and plot the percent of variance explained by the principal components as well as the cumulative variance explained using `ex2_1_3.R`.

Script details:

- You can use the function `colMean` to compute the column means of the data.
- You should compute the mean for each attribute, i.e., the vector of means should have M elements.
- You cannot directly subtract a vector from a matrix. One way to accomplish this is through the `apply` function. Try typing `?apply`.
- Try the command `apply(datfinal,1,'-',colMeans(datfinal))`. Notice that the function `apply` returns a matrix with M rows, where M is the length of the vector returned by the minus operation applied to each row, i.e. the number of columns in the data matrix. To get a matrix of the same dimensions as the original data matrix, transpose the result from `apply` using the function `t()`.
- You can use the function `svd` to compute the SVD.

Can you verify that more than 90% of the variation in the data is explained by the first 3 principal components? How many components would be needed for 95 %?

- 2.1.4 Plot principal component 1 and 2 against each other in a scatterplot, see the script `ex2_1_4.R` for details.

Script details:

- Data can be projected onto the principal components using $Z = Y*V$ or equivalently computed directly from the SVD as $Z = U*S$, where Y is the zero mean data, U is the matrix of left singular vectors, S is the matrix with the singular values in the diagonal, and V is the matrix containing right singular vectors.
- The matrix Z contains the projections of observations in the rows, and each column corresponds to a PC. Thus the i 'th row and j 'th column contains the projection of the i 'th observation onto the j 'th PC.
- You learned how to make a scatter plot in Exercise 2.1.2.

What are the benefits of visualizing the data by the projection given by PCA over plotting two of the original data dimensions against each other? Compare with the scatter plots of attributes you made in Exercise 2.1.2.

- 2.1.5 Interpret the principal directions (V) obtained using the PCA. Consider the script `ex2_1_5.R`. Which of the original attributes does the second principal component mainly capture the variation of and what would cause an observation to have a large negative/positive projection onto the second principal component? (remember both the attributes and the principal component has a sign and a magnitude)

Script details:

- The columns of V gives you the principal component directions
- The data is projected onto the second principal components by `Y%*%V[,2]`

We can correct for differences in scale by standardization. When doing PCA on data with attributes of different scales, it can be very important to standardize the

dataset. We standardize a dataset by ensuring each attribute has a mean of zero (as before), but also has a variance of one (i.e. zero mean and unit variance).

In `ex2_1_5.R` you saw that we can interpret the principal directions by investigating the coefficients in the vectors of \mathbf{V} . Another way to approach interpreting the principal directions is to plot the coefficients as vectors in the principal component space. In the PC1/PC2-space, we can for instance interpret the relationship between PC1, PC2 and a given attribute by drawing a line from Origo to the coefficients in PC1 and PC2 corresponding to the attribute. The direction and magnitude of such a vector defines how the data from that attribute is projected onto the PC1/PC2-space—e.g. if the vector points in positive direction of PC1, then positive values of that attribute contributes to a positive projection onto PC1. Since the vectors in \mathbf{V} are unit-vectors, all coefficients will lie within the unit-circle.

- 2.1.6 Investigate the standard deviation of the NanoNose attributes and try to determine if some of the attributes have higher variance than the others using `ex2_1_6.R`. Which attribute has the highest standard deviation? Use the script to visualize the difference between either only subtracting the mean or both subtracting the mean and dividing by the standard deviation (visualize: the projection, attribute coefficients, and the variance explained of a PCA for the two). How did the attribute with the highest standard deviation change in terms of its direction and magnitude in the attribute coefficients? How did the variance explained change? Lastly, try multiplying one of the attributes with a factor 100 and see how that changes the PCA.

2.2 Tasks for the report

For the report, complete the following sections:

- **A detailed explanation of the attributes of the data.**
 - Describe if the attributes are discrete/continuous, Nominal/Ordinal/Interval/Ratio,
 - give an account of whether there are data issues (i.e. missing values or corrupted data) and describe them if so

If your data set contains many similar attributes, you may restrict yourself to describing a few representative features (apply common sense).

- **Tasks from PCA section**

There are three aspects that needs to be described when you carry out the PCA analysis for the report:

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- The amount of variation explained as a function of the number of PCA components included,
 - the principal directions of the considered PCA components (either find a way to plot them or interpret them in terms of the features),
 - the data projected onto the considered principal components.

If your attributes have very different scales it may be relevant to standardize the data prior to the PCA analysis.

References

- [1] Nanonose project.
- [2] Tommy S Alstrøm, Jan Larsen, Claus H Nielsen, and Niels B Larsen. Data-driven modeling of nano-nose gas sensor arrays. In *SPIE Defense, Security, and Sensing*, pages 76970U–76970U. International Society for Optics and Photonics, 2010.