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Pattern recognition
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Report

Practical assignment

Introduction

This paper reports the result of our analysis of a data set of handwritten digits. We have divided the paper into paragraphs, where each paragraph describes a step in our analysis. All the experiments have been conducted in R language. To allow the reader to replicate the experiments, we have included the code in the "Appendix" paragraphs. All the code runs in Rstudio.

Exploratory analysis of the data

The data are composed of 784 features, which correspond to the 784 pixels an image has. We have in total 42000 images where the corresponding class (the digit that is written in the image) has been hand labelled in the data set as first column. The values of the feature represent the colour of the pixel on the grayscale, where 0 represents completely white, and 255 represents completely black. For each of them, we extract the minimum value it takes in the data set, the maximum, the average, the number of times the pixel takes value 0 (it's "white") and the number of times it takes value 255 (it's "black").

Then we compute the mean of all these vectors.

Mean.minValue	Mean.maxValue	Mean.avgValue
0	217.676	33.40891

Mean.nwhite	Mean.nblack
33955.76	284.8342

After that, we compute:

- The number of pixels which take value 0 at least once: 784 (all of them)
- The number of pixels which take value 255 at least once: 591

All these results suggest that we are dealing with a sparse matrix, where there are some pixels which always take value 0. In some sense they are "useless", i.e. they do not bring any information we can use to build our predictive model. Moreover, we define as useless all the pixels who always take the same value in the data set.

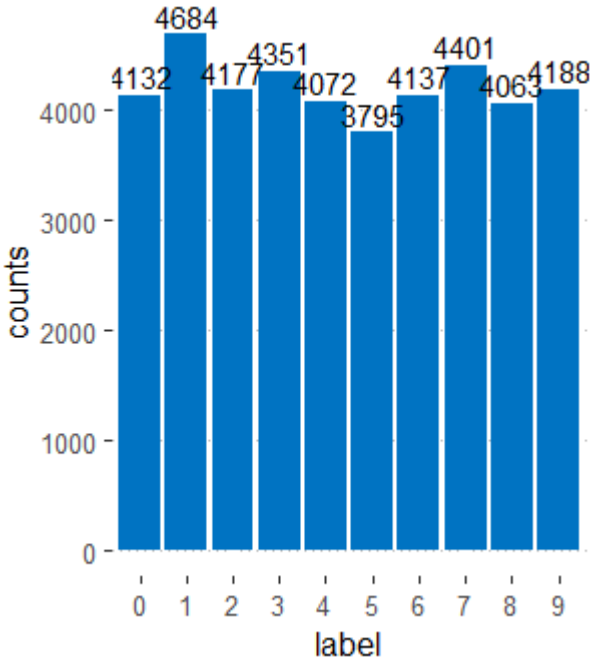
We do so some analysis to spot those useless pixels. They are the following:

```
"pixel0"   "pixel1"   "pixel2"
"pixel3"   "pixel4"   "pixel5"
"pixel6"   "pixel7"   "pixel8"
"pixel9"   "pixel10"  "pixel11"
"pixel16"  "pixel17"  "pixel18"
"pixel19"  "pixel20"  "pixel21"
"pixel22"  "pixel23"  "pixel24"
"pixel25"  "pixel26"  "pixel27"
"pixel28"  "pixel29"  "pixel30"
"pixel31"  "pixel52"  "pixel53"
"pixel54"  "pixel55"  "pixel56"
"pixel57"  "pixel82"  "pixel83"
"pixel84"  "pixel85"  "pixel111"
```

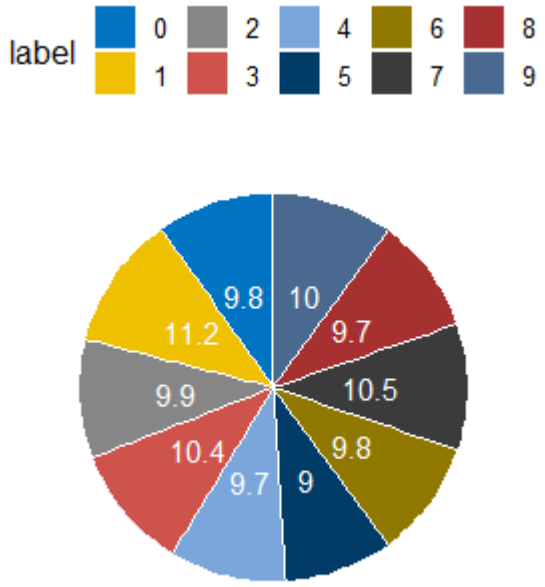
```
"pixel112" "pixel139" "pixel140"
"pixel141" "pixel168" "pixel196"
"pixel392" "pixel420" "pixel421"
"pixel448" "pixel476" "pixel532"
"pixel560" "pixel644" "pixel645"
"pixel671" "pixel672" "pixel673"
"pixel699" "pixel700" "pixel701"
"pixel727" "pixel728" "pixel729"
"pixel730" "pixel731" "pixel754"
"pixel755" "pixel756" "pixel757"
"pixel758" "pixel759" "pixel760"
"pixel780" "pixel781" "pixel782"
"pixel783"
```

They are 76 in total. All of them take always value 0. By, inspection, we find that there are no pixels which take always the same non-zero value.

Then we analyse the class distribution: we have in total 9 classes, each corresponding to a digit. We plot the following graph, with the classes on the x-axis and the counts of images with that digit on the y-axis.

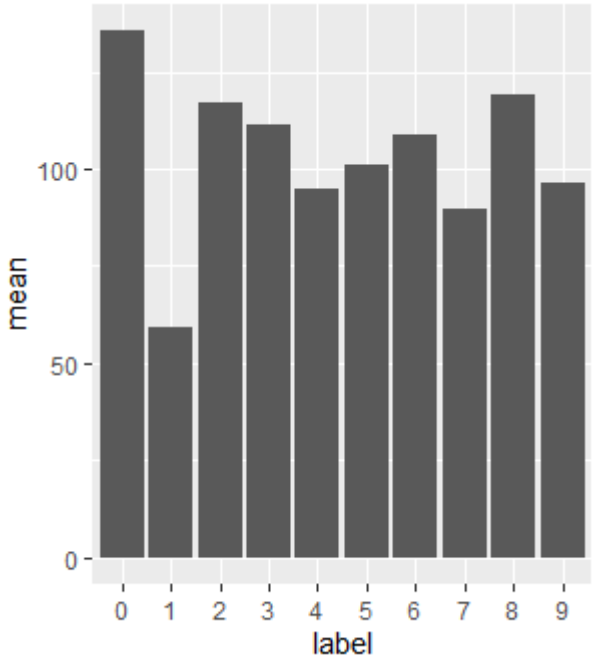


We plot a pie chart as well, where “label” stands for “class”



The majority class is the class corresponding to the digit “1”: if we predicted only that class, we would have a percentage of correct classifications of 11,2%.

Moreover, we do some analysis taking into consideration the images in the data set and aggregating the results per each class of belonging (i.e., per row instead of per column, as we have always done before). We define “dark pixels” the pixels whit a value greater than 128. Per each image, we compute the number of “dark pixels” and then compute the mean per each class. The results are in the following graph. There are few (consider that they each image has 784 pixels).



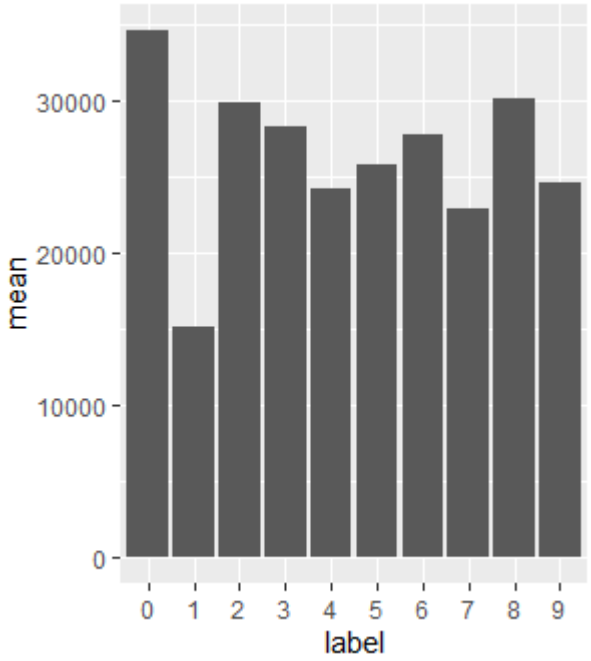
We feel that dark pixels are useful to spot the skeleton of a handwritten digit, eliminating all the remaining ink which has simply spread in the paper where the digit was written. As an example, we compare the image number 380 in the data set and the same image where we have shrunk to 0 out all the pixel which take values between 0 and 128. Note: in these images white and black are inverted.

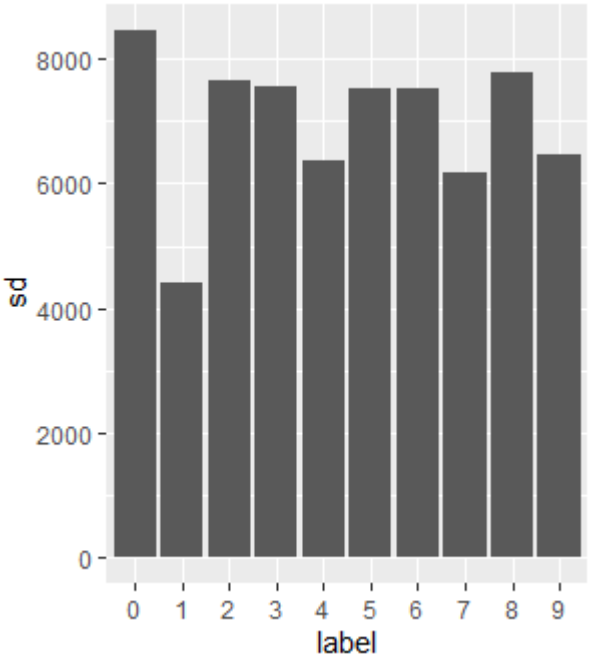
Figure 1: filteredl image

Figure 2: actual image

How much ink

To measure “how much ink” a digit costs, we sum all the feature values per each element of the data we have (i.d., per each row of the dataframe). The results can be then in the interval [0; 255*784 = 199920]. Then we aggregated the results per each digit, plotting the mean and the standard deviation. We called this feature “density”. As before, “label” means “class”.





label		mean
1	0	34632.41
2	1	15188.47
3	2	29871.10
4	3	28320.19
5	4	24232.72
6	5	25835.92
7	6	27734.92
8	7	22931.24
9	8	30184.15
10	9	24553.75

Label		sd
1	0	8462.916
2	1	4409.932
3	2	7653.922
4	3	7574.975
5	4	6375.416
6	5	7527.595
7	6	7531.413
8	7	6169.042
9	8	7778.354
10	9	6466.003

This feature allows us to distinguish correctly between four groups: {class 1} [which has a mean below 20000], {class 4, class 7, class 9} [which have a mean between 20000 and 25000], {class 2, class 3, class 5, class 6, class 8} [which have a mean between 25000 and 3000 and more or less the same sd], {class 0} [which has a mean over 30000]. Moreover, we feel that only class 1 can be correctly distinguished from the other ones. However, big values of standard deviations (at least 20% for all the classes) among with the fact that all the mean values are comparable (per each class, almost 7 of the other are within the standard deviation) suggest that the feature is not very relevant to spot a class.

We add to our data set a column with density values as a new feature. We scale it. Then we train a multinomial logistic regression model with only the density of all the 42000 images as a feature. We test it using the same density values.

We get the following confusion matrix, where the rows represent the prediction of the model, and the columns the actual values. As expected, the model has the best performances on class 1, while it never predicts classes 4,5,6,8. Class 0 is predicted very often: that's why it's predicted correctly many times (it has high recall but small precision)

The correct predictions are highlighted in yellow.

	0	1	2	3	4	5	6	7	8	9	sums
0	2420	10	1496	1246	440	728	1057	325	1430	484	9636
1	83	3823	280	408	829	671	450	1190	192	763	8689
2	322	5	326	335	196	197	296	149	343	197	2366
3	805	101	1039	1037	886	846	982	819	1047	869	8431
4	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0
7	384	722	874	1141	1496	1190	1145	1700	879	1651	11182
8	0	0	0	0	0	0	0	0	0	0	0
9	118	23	162	184	225	163	207	218	172	224	1696
sums	4132	4684	4177	4351	4072	3795	4137	4401	4063	4188	42000

The overall accuracy of the model is `0.2269048`.

As an example, this the confusion matrix of the class 1 against all the others.

		Image is of class 1	
		True	False
Model predicts class 1.	yes	3823	4866
	no	861	32450

Accuracy	Precision	Recall
0.8636	0.4400	0,8162

New feature

To elaborate a new feature given an image, we deal with pixels as if they were points in a cartesian space. We try to find out a way of measuring different distributions of points, since each distribution corresponds to a different digit. Firstly, we associate to each pixel two cartesian coordinates which are, for simplicity sake, the row and column numbers, since the distribution doesn't depend on the reference system, but only or the reference point around which we are measuring the distribution. Then, we consider only dark points, according to the definition previously given. Then, we select as a reference point the first dark point we encounter in the image's pixels, i.e. the one with smallest row and column values. Then we compute the mean square distance between this point and all the other dark points. We repeat this procedure for each image, and then we have a new feature we can use in our multinomial model. By picking up this new feature, we must make some decisions between different possibilities, besides the general intuition of considering. We discuss them hereunder.

The reason for filtering out non dark points has already been explained in the section "Exploration of the data". We hope in this way to filter out some noise in the input data.

The selection of the reference point is crucial in our model. There are some other possible choiches:

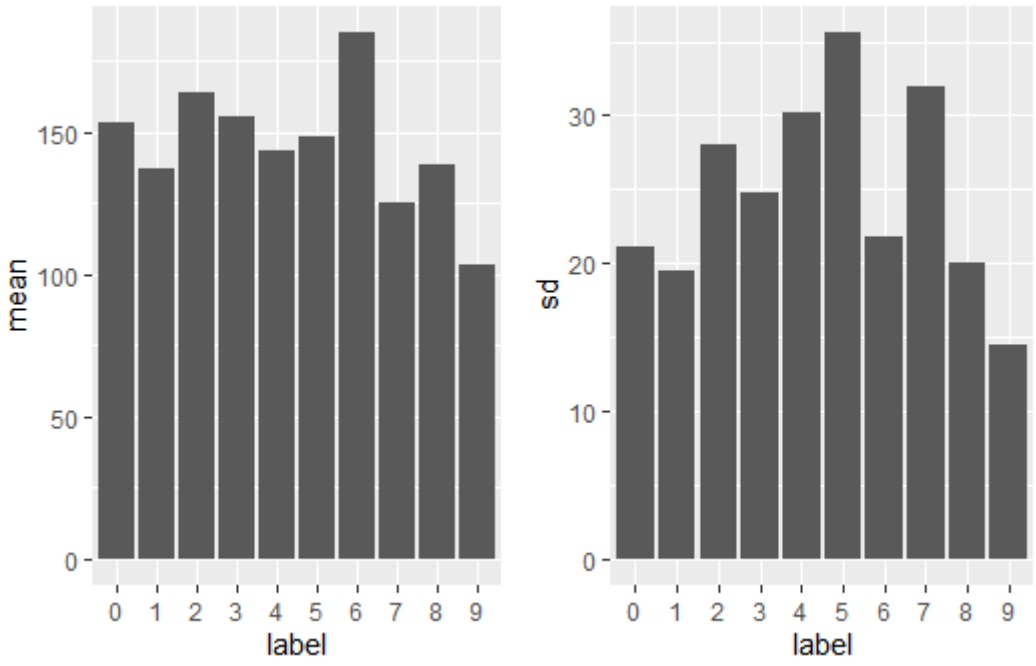
- The point (0,0). We discarde this option since we feel that sometimes the same digit is written in different positions in the cell on the paper sheet, i.e. it could be written more to the left or more to the right, near to the top border or to the bottom border. This would affect the measure of the distance and create problems to our model.
- The point (mean.row, mean.column), where mean row and mean column are computed per each image as the mean on the dark points. This allows to treat in the correct way the digits which are not at the centre of the grid of pixels. Unfortunately, this does not prevent some points from having the same distribution with respect to this reference point,because of some kind of symmetry. For example, the digit “3” and “8” would have the same distribution.
- The first dark point, on the other side, is always located in the same relative position with respect to the others, so it permits a correct measure.

Taking the sum of the squared distances instead of the squared mean values would allow to differentiate more between different classes. However, we avoid that because the number of dark points per each class is not equal (see the exploration of the data). This affects the sum of the distances (if we have more points, we have more addends in the sum), and it’s correlated to the amount of ink each digit costs. Since we already have a measure of the amount of ink (the density), we would have two correlated variables, which is not desirable, especially considering the next section, where we put together the two features.

We square the distance to avoid some sort of “netralization” between two points with high distance and low distance and two points with medium distance.

After having taken the feature, we draw some statistics of this new feature, as done for the density. A positive aspect of this feature is the small values of standard deviation (with respect to the mean, around 10% for all the classes, except for class 5), which is better than the density model (which was more or less the double).

Nonetheless, class 0, class 3 and class 5 appear to have the same feature, as well as class 1 ad 8.




```
label     mean
1     0 153.2546
2     1 136.9092
```

```
3       2 164.0622
4       3 155.5612
5       4 143.2583
6       5 148.1774
7       6 184.8624
8       7 125.0244
9       8 138.2670
10      9 103.5335

label       sd
1       0 21.09303
2       1 19.46680
3       2 28.01959
4       3 24.74468
5       4 30.20623
6       5 35.61966
7       6 21.78778
8       7 31.90288
9       8 20.01939
10      9 14.47188
```

As done before, we scale these values, we train a multinomial logistic model on the data set and we test it on the same data set. We have the following confusion matrix, which unfortunately confirms our negative expectations: classes 0, 4, 5, 8 are never predicted. Classes 6 and 9, which have a distinctive feature value and low sd, are predicted very well. Class 1 is predicted correctly many times, but it's predicted many times as well (it has relatively high recall, 0,4468, but low precision, 0,2002). Maybe that's because it has included the predictions for class 0 and 8.

	0	1	2	3	4	5	6	7	8	9	sums
0	0	0	0	0	0	0	0	0	0	0	0
1	1177	2093	621	1319	1111	1025	115	720	2039	235	10455
2	697	204	829	591	316	381	775	157	163	8	4121
3	1342	523	931	1194	524	698	417	289	542	34	6494
4	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0
6	508	248	1415	811	667	760	2814	391	183	2	7799
7	254	1361	185	316	883	385	10	923	970	631	5918
8	0	0	0	0	0	0	0	0	0	0	0
9	154	255	196	120	571	546	6	1921	166	3278	7213
sums	4132	4684	4177	4351	4072	3795	4137	4401	4063	4188	42000

The overall accuracy is `0.2650238`.

Both features

We then repeat the same training and test set using both features and obtain the following results. It improves the performances, but still never predicts class 5, which was never predicted also in the two previous separated models.

	0	1	2	3	4	5	6	7	8	9	sums
0	1911	7	947	818	193	420	438	96	807	76	5713
1	79	3781	230	434	707	486	389	732	184	194	7216
2	381	9	478	325	135	184	384	45	94	3	2038
3	499	44	496	639	286	368	247	155	315	22	3071
4	217	211	273	540	443	388	163	232	349	38	2854
5	0	0	0	0	0	0	0	0	0	0	0
6	337	148	1181	690	634	690	2470	375	161	3	6689
7	97	436	145	340	812	398	10	857	711	484	4290
8	448	26	233	450	371	364	33	277	1227	259	3688
9	163	22	194	115	491	497	3	1632	215	3109	6441
sums	4132	4684	4177	4351	4072	3795	4137	4401	4063	4188	42000

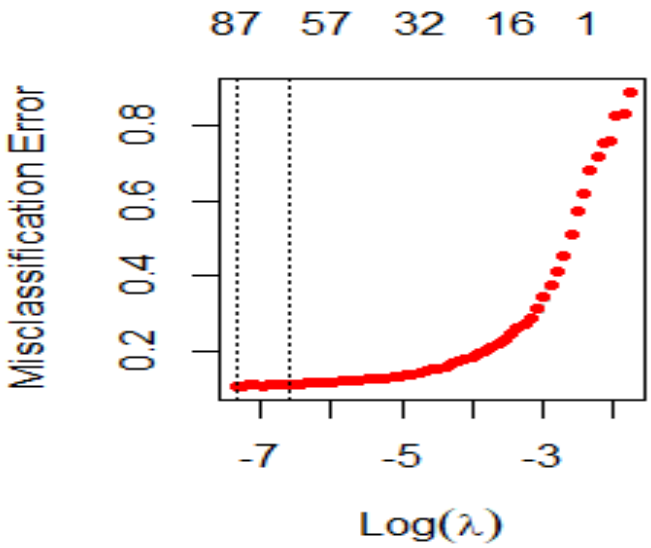
The overall accuracy is `0.355119`, which is anyway better.

Using the pixels as features themselves

In this part we use the pixels as features. First of all, we reduce the number of pixel (and then the level of detail of the image) scaling the image from a grid of 28 x 28 pixels to a grid of 14 x 14 pixels. We recompute the useless pixels in these images and remove them to have faster computation. They are the numbers 2, 3, 4, 5, 9, 10, 12, 14, 15, 16, 29, 30, 44, 58, 72, 114, 128, 142, 156, 170, 184, 185, 197. Unlike the previous experiments, we select a sample of 5000 elements (without replacement) as training set and use the rest as test set. We use the same training set and test set for all the experiments.

Regularized multinomial logit model (using the LASSO penalty)

We apply 10 folds cross validation on the training set to find out the best lambda value to use in the LASSO penalty. Lambda is simply a coefficient which indicates how much we want to penalize big weights (and so overfitted models) in the multinomial model. Lambda is the only complexity para meter of this model. We obtain the value `0.0006389703`. For completeness, this is the plot of lamb da log values against classification errors. As expected, increasing lambda improves the performanc es since it avoids overfitting. This is valid until a critical value, above which the model is too simple and starts performing terribly bad. In our case, this critical value, which is the best value indeed, is very small.



We then test the model with the test set, obtaining the following confusion matrix (where the rows are the predictions of our model, the columns are the actual values).

	0	1	2	3	4	5	6	7	8	9	sums
0	3455	0	11	8	11	34	38	20	33	32	3642
1	2	3979	45	27	25	42	20	41	113	40	4334
2	30	22	3198	114	26	46	34	79	56	7	3612
3	23	22	78	3342	3	151	2	14	154	62	3851
4	8	4	37	8	3235	58	52	69	30	150	3651
5	57	24	21	149	10	2747	43	6	111	23	3191
6	41	8	66	21	36	87	3426	4	31	7	3727
7	6	15	72	59	13	29	13	3470	18	134	3829
8	28	38	76	73	32	119	24	8	2942	48	3388
9	2	3	39	47	184	40	1	182	87	3190	3775
sums	3652	4115	3643	3848	3575	3353	3653	3893	3575	3693	37000

The overall accuracy is `0.8914595`

Support Vector Machine

The complexity parameters to determine in this model are gamma and Cost. Gamma is a parameter for nonlinear hyperplanes (the free parameter for a Gaussian radial basis kernel function), and it indicates how the model shapes its decision boundary. Higher values of gamma lead to overfitting. C is the cost function for misclassification error for points which are on the wrong side of the decision boundary. We try different values of gamma and C and pick the best ones to build the model: for gamma all the powers of 10 between -5 and -1, for cost between -3 and 1. We get the following matrix.

```
   gamma  cost  error dispersion
1  1e-05 1e-03 0.8862 0.01245258
2  1e-04 1e-03 0.8862 0.01245258
3  1e-03 1e-03 0.8862 0.01245258
4  1e-02 1e-03 0.8862 0.01245258
5  1e-01 1e-03 0.8862 0.01245258
6  1e-05 1e-02 0.8862 0.01245258
7  1e-04 1e-02 0.8862 0.01245258
8  1e-03 1e-02 0.8862 0.01245258
9  1e-02 1e-02 0.8862 0.01245258
10 1e-01 1e-02 0.8862 0.01245258
11 1e-05 1e-01 0.8240 0.01720465
12 1e-04 1e-01 0.8862 0.01245258
13 1e-03 1e-01 0.8862 0.01245258
14 1e-02 1e-01 0.8862 0.01245258
15 1e-01 1e-01 0.8862 0.01245258
16 1e-05 1e+00 0.5068 0.04096828
17 1e-04 1e+00 0.8818 0.02294825
18 1e-03 1e+00 0.8862 0.01245258
19 1e-02 1e+00 0.8862 0.01245258
20 1e-01 1e+00 0.8862 0.01245258
21 1e-05 1e+01 0.4590 0.03380007
22 1e-04 1e+01 0.8816 0.02350981
23 1e-03 1e+01 0.8862 0.01245258
24 1e-02 1e+01 0.8862 0.01245258
25 1e-01 1e+01 0.8862 0.01245258
```

The best one is the 21st. We pick then gamma = 1e-05 and C = 1e+01. We find anyway other useless pixels (they could have become useless due to the sampling of 5000 images in the training set, so

that they do not take always value zero in the test set, but they do in the training set. We remove them only for this experiment (we need them for the cross validation of the following experiment). They are the numbers 6, 8, 13, 17, 18, 31, 86, 100, 196. We train a new model with these values. We predict on the test set. We get the following confusion matrix.

	0	1	2	3	4	5	6	7	8	9	sums
0	3252	0	17	16	4	32	62	9	32	26	3450
1	3	4034	164	147	74	202	153	235	263	132	5407
2	27	13	2965	119	15	32	26	18	50	7	3272
3	50	16	84	3249	0	579	8	13	246	53	4298
4	22	3	108	12	2940	84	66	102	30	196	3563
5	123	5	5	30	20	2109	72	1	108	5	2478
6	95	7	98	13	19	56	3258	2	15	0	3563
7	2	2	54	36	1	10	1	3115	10	178	3409
8	61	34	116	146	22	110	7	71	2657	68	3292
9	17	1	32	80	480	139	0	327	164	3028	4268
sums	3652	4115	3643	3848	3575	3353	3653	3893	3575	3693	37000

The overall accuracy is `0.8272162`.

Feed forward neural networks

The two parameters of this model are size and decay. Size is the number of units in hidden layer and decay is the regularization parameter to avoid over-fitting. We do 10 folds cross validation to compute the right values of these parameters. We try values from 1 to 10 for size and from 0.1 to 0.5 for decay. We find that size = 10 and decay = 0.4 are the best models.

We get the following confusion matrix.

	0	1	2	3	4	5	6	7	8	9	sums
0	3438	0	19	17	9	46	26	13	21	27	3616
1	0	3979	56	34	26	15	12	46	86	17	4271
2	39	29	3228	101	19	41	35	56	44	7	3599
3	21	17	97	3378	2	145	1	14	113	40	3828
4	14	3	50	3	3296	40	88	77	30	169	3770
5	61	19	24	139	14	2795	48	11	89	31	3231
6	41	17	39	17	59	91	3407	2	39	12	3724
7	11	10	67	45	5	39	1	3533	13	83	3807
8	20	37	48	63	25	84	35	17	3083	44	3456
9	7	4	15	51	120	57	0	124	57	3263	3698
sums	3652	4115	3643	3848	3575	3353	3653	3893	3575	3693	37000

The overall accuracy is `0.9027027`.

Discussion of the differences

The feed forward neural network is the best model, according to the computed accuracies.

To find out in a rigorous way whether the differences between the three models are statistically significant a McNemar test has been performed between the three models, splitting the predictions in correct ones and incorrect ones. We order the models according to their accuracy and we test each model against the ones with better accuracy. The McNemar test performs a chi-squared test to indicate if there is evidence that marginal probabilities of the table are the same (the null ipothesis)

Svm vs Multinomial

		Multinomial	
		Correct	Incorrect
Svm	Correct	29581	1026
	Incorrect	3403	2990

```
McNemar's chi-squared = 1274.6, df = 1, p-value < 2.2e-16
```

We refuse the null ipothesis (the differences are not significant) with an error probability near 0. We conclude that the multinomial model is significantly better.

Svm vs Neural Network

		Neural	Networks
		Correct	Incorrect
svm	Correct	29475	1132
	Incorrect	3925	2468

```
McNemar's chi-squared = 1541.5, df = 1, p-value < 2.2e-16
```

We refuse the null ipothesis (the differences are not significant) with an error probability near 0. We conclude that the neural network model is significantly better.

Multinomial vs Neural Networks

		Neural	Netwokrs
		Correct	Incorrect
Multinomial	Correct	31894	1090
	Incorrect	1506	2510

```
McNemar's chi-squared = 66.342, df = 1, p-value = 3.79e-16
```

We refuse the null ipothesis (the differences are not significant) with an error probability near 0. We conclude that the neural network model is significantly better (even if the accuracies are comparable)

Appendix 1: Set up code

This code installs all the packages needed for the experiments and calls all the libraries. Then creates the dataframe in the environment, and changes the class values as factors, to handle them

```
#-----------------install packages---------------------#
install.packages("OpenImageR")
install.packages("ggplot2")
install.packages("ggpubr")
install.packages("dplyr")
install.packages("nnet")
install.packages("raster")
install.packages("e1071")
install.packages("caTools")
install.packages("glmnet")
install.packages("caret")
#-----------------libraries---------------------#
library( OpenImageR)
library(ggplot2)
library(ggpubr)
library(dplyr)
theme_set(theme_pubr())
library(nnet)
library(raster)
library(e1071)
library(caTools)
library(glmnet)
library(caret)
#----------------set up code) ---------------------#
mnist.dat <-
read.csv("C:/Users/ponti/Documents/GitHub/DataMining/pattern
recognition/mnist.csv")
mnist.dat$label<-factor(mnist.dat$label) #Converting label to
factor
```

Appendix 2: Code for the exploration of the data

This code is used to draw the graphs and extract the results contained in the section Exploration of the data.

```
#-----------------class distribution---------------------#
ggplot(data=mnist.dat, aes(label)) +geom_bar(fill = "#0073C2FF")
+theme_pubclean()

frequency.dataframe <- mnist.dat %>%
  group_by(label) %>%
  summarise(counts = n())
frequency.dataframe

ggplot(frequency.dataframe, aes(x = label, y = counts)) +
  geom_bar(fill = "#0073C2FF", stat = "identity") +
  geom_text(aes(label = counts), vjust = -0.3) +
  theme_pubclean() # histrogram with quantity of the bars

frequency.dataframe <- frequency.dataframe %>%
  arrange(desc(label)) %>%
  mutate(prop = round(counts*100/sum(counts), 1),
         lab.ypos = cumsum(prop) - 0.5*prop)
frequency.dataframe
```

```
ggpie(frequency.dataframe, x = "prop", label = "prop",
  lab.pos = "in", lab.font = list(color = "white"),
  fill = "label", color = "white",
  palette = "jco"
) #pie chart


#-----------------summary statistics----------------------#
pixel.minValue <- apply(mnist.dat[,-1], 2, min) #2 means by column
pixel.maxValue <- apply(mnist.dat[,-1], 2, max) #1 means by row
pixel.avgValue <- apply(mnist.dat[,-1], 2, mean)

pixel.nwhite <- apply(mnist.dat[,-1], 2, function(pixel){
  return (length(pixel[pixel ==0]))
})
pixel.nblack <- apply(mnist.dat[,-1], 2, function(pixel){
  return (length(pixel[pixel ==255]))
})
mean.minValue <- mean(pixel.minValue)
mean.maxValue <- mean( pixel.maxValue)
mean.avgValue <- mean(pixel.avgValue)
mean.nwhite <- mean(pixel.nwhite)
mean.nblack <- mean(pixel.nblack)
summary <- cbind(pixel.minValue, pixel.maxValue, pixel.avgValue,
pixel.nwhite, pixel.nblack)
summary <- as.data.frame(summary)
useless.pixels <- summary[summary$pixel.minValue ==
summary$pixel.maxValue, ]
useless.pixels.name <- row.names(useless.pixels)
bottom.pixels <- summary[summary$pixel.minValue == 0, ]
top.pixels <- summary[summary$pixel.maxValue == 255, ]
num.bottom.pix <- nrow(bottom.pixels)
num.top.pix <- nrow(top.pixels)
```

Appendix 3: code for black points

```
#-----------------analysis of the dark points----------------------
#
mnist.dat$darks <- apply(mnist.dat[,c(2:785)], 1, function(
sample){
  return (length(sample[sample > 128]))
} )
blacks.mean <-
aggregate(mnist.dat$blacks,by=list(mnist.dat$label),FUN=mean)
colnames(blacks.mean) <- c("label", "mean")
ggplot(data=blacks.mean,
aes(x=label,y=mean))+geom_bar(stat="identity") #Depicting average
number of black points.
imageShow(matrix(as.numeric(mnist.dat[380,-
c(1,786)]),nrow=28,ncol=28,byrow=T)) #image with no filter
#verifying the filter
sample.image <- as.numeric(mnist.dat[380,-c(1,786)])
sample.image <- sapply(sample.image, function(pixel){
  if (pixel > 128){
    return (pixel)
  }
  else return (0)
})
```

```
imageShow(matrix(sample.image,nrow=28,ncol=28,byrow=T)) #image with
no filter
```

Appendix 4:code for "how much ink"

```
#-----------------how much ink ("density") ( mean and standard
deviation)----------------------#
mnist.dat$density <- apply(mnist.dat[,c(2:785)], 1, sum)
density.mean <-
aggregate(mnist.dat$density,by=list(mnist.dat$label),FUN=mean)
colnames(density.mean) <- c("label", "mean")
print(density.mean)
ggplot(data=density.mean,
aes(x=label,y=mean))+geom_bar(stat="identity") #Depicting average
intensity.
#standard deviation
density.sd <-
aggregate(mnist.dat$density,by=list(mnist.dat$label),FUN=sd)
print(density.sd)
colnames(density.sd) <- c("label", "sd")
ggplot(data=density.sd,
aes(x=label,y=sd))+geom_bar(stat="identity") #Depicting standard
deviation.

#-----------------simple multinomial model ("density")-------------
---------#
mnist.dat$density <- as.vector(scale(mnist.dat$density))
input <- as.data.frame(mnist.dat$density, row.names = NULL,
optional = TRUE)
colnames(input) <- "density"
multinom.model<-multinom(label~density,data = mnist.dat, maxit =
1000)
summary(multinom.model)
multinom.pred <- predict(multinom.model, input, type = "class")
multinom.conf.mat <- table(multinom.pred,mnist.dat$label)
#confusion matrix
multinom.accuracy <-
sum(diag(multinom.conf.mat))/sum(multinom.conf.mat)
print (multinom.conf.mat)
print(multinom.accuracy)
```

Appendix 5: code for new feature

```
#-----------------new feature multinomial model ( distance of the
dark points)----------------------#
mnist.dat$mean.distance <- apply(mnist.dat[,c(2:785)],1,
function(current.example){
  current.example <- unlist(current.example)
  current.example <- as.vector(current.example)
  index.row <- lapply(c(0:27), function(row){
    rep(row, 28)
  })
  index.row <- unlist(index.row, recursive = FALSE)
  index.column <- lapply(c(0:27), function(column){
    c(0:27)
  })
  index.column <- unlist(index.column, recursive = FALSE)
  current.example.with.indexes <- cbind(current.example, index.row,
index.column)
```

```
  current.example.points <-
current.example.with.indexes[current.example.with.indexes[,1] >
128, ]
  mean.row <- current.example.points[1,2]
  mean.column <- current.example.points[1,3]
  point.distances <- lapply(c(1:nrow(current.example.points)),
function(point){
    example <- current.example.points[point,]
  return ( ((pointDistance(current.example.points[point,-1],
cbind(mean.row,mean.column), lonlat = FALSE))^2))
  })
  point.distances <- unlist (point.distances, recursive = FALSE)
  return (mean(point.distances))
})
#average value
mean.distance.mean <-
aggregate(mnist.dat$mean.distance,by=list(mnist.dat$label),FUN=mean
)
colnames(mean.distance.mean) <- c("label", "mean")
print(mean.distance.mean)
ggplot(mean.distance.mean,
aes(x=label,y=mean))+geom_bar(stat="identity") #Depicting average
distance to the center.
#standard deviation
mean.distance.sd <-
aggregate(mnist.dat$mean.distance,by=list(mnist.dat$label),FUN=sd)
colnames(mean.distance.sd) <- c("label", "sd")
print(mean.distance.sd)
ggplot(data=mean.distance.sd,
aes(x=label,y=sd))+geom_bar(stat="identity") #Depicting standard
deviation.
#-----------------simple multinomial model ( with the second
feature)----------------------#
mnist.dat$mean.distance <-
as.vector(scale(mnist.dat$mean.distance))
input <- as.data.frame(mnist.dat$mean.distance, row.names = NULL,
optional = TRUE)
colnames(input) <- "mean.distance"
multinom.model<-multinom(label~mean.distance,data = mnist.dat,
maxit = 1000)
summary(multinom.model)
multinom.pred <- predict(multinom.model, input, type = "class")
multinom.conf.mat <- table(multinom.pred,mnist.dat$label)
#confusion matrix
multinom.accuracy <-
sum(diag(multinom.conf.mat))/sum(multinom.conf.mat)
print (multinom.conf.mat)
print(multinom.accuracy)
```

Appendix 6: code for both features

This code is used to train a multinomial logistic model and test it on the same dataset used. It prints on the console a summary of the model, the confusion matrix between the predicted values and the actual values, and the overall accuracy.

```
#-----------------multinomial model with both features-----------
---------#
data.training <- mnist.dat[, cbind("label", "mean.distance",
"density")]
```

```
multinom.model<-multinom(label~.,data = data.training, maxit =
1000)
summary(multinom.model)
multinom.pred <- predict(multinom.model, data.training[,-1], type =
"class")
multinom.conf.mat <- table(multinom.pred,data.training$label)
#confusion matrix
multinom.accuracy <-
sum(diag(multinom.conf.mat))/sum(multinom.conf.mat)
print (multinom.conf.mat)
print(multinom.accuracy)
```

Appendix 7: set up code for the last 3 models

```
#reducing the dimensions of the image by half
mnist.dat.reduced<- apply(mnist.dat[ , -1], 1, function(image){
  image.matrix <- matrix(image,nrow = 28, ncol = 28, byrow = TRUE)
  image.reduced <- down_sample_image(image.matrix, 2, gaussian_blur
= FALSE)
  return (image.reduced)
})
mnist.dat.reduced <- t(mnist.dat.reduced)
mnist.dat.reduced <- cbind(mnist.dat[,1], mnist.dat.reduced)
mnist.dat.reduced <- as.data.frame(mnist.dat.reduced)

mnist.dat.reduced[,1]<-factor(mnist.dat.reduced[,1])
pixel.minValue <- apply(mnist.dat.reduced[,-1], 2, min) #2 means by
column
pixel.maxValue <- apply(mnist.dat.reduced[,-1], 2, max) #1 means by
row
summary <- cbind(pixel.minValue, pixel.maxValue)
summary <- as.data.frame(summary)
useless.pixels <- summary[summary$pixel.minValue ==
summary$pixel.maxValue, ]
mnist.dat.reduced <- mnist.dat.reduced[,-
c(2,3,4,5,9,10,12,14,15,16,29,30,44,58,72,114,128,142,156,170,184,1
85,197)]
#drawing 500 random samples
training.rows<-sample(nrow(mnist.dat.reduced),5000)
training.set<-mnist.dat.reduced[training.rows,]
#using the remaining samples as a test set
test.set <-mnist.dat.reduced[-training.rows,]
```

Appendix 8: code for multinomial model

```
#-----------------the regularized multinomial logit model (using
the LASSO penalty)----------------------#
lasso.model<-cv.glmnet(as.matrix(training.set[,-
1]),training.set[,1],family="multinomial",type.measure ="class")
print(lasso.model$lambda.min) #Best lambda value 0.001246766
plot(lasso.model)

lasso.pred<-predict(lasso.model,as.matrix(test.set[,-
1]),s="lambda.min", type="class")

lasso.confmat<- table(lasso.pred,test.set[,1])
lasso.accuracy <- sum(diag(lasso.confmat))/sum(lasso.confmat)

print(lasso.confmat)
print(lasso.accuracy)
```

Appendix 9: code for support vector machine model

```
#--------------------------------------svm-----------------------
-------------------------

tuned.parameters <- tune.svm(training.set[,-
1],training.set[,1],gamma = 10^(-5:-1), cost = 10^(-3:1))
tuned.parameters$performances
summary (tuned.parameters)
#training.set <- training.set[, -c(6,8,13,17,18,31,86,100,196)]
#test.set <- test.set[, -c(6,8,13,17,18,31,86,100,196)]
training.set <- training.set[, -c(2,4,6,7,8,19,71,85,174)]
test.set <- test.set[, -c(2,4,6,7,8,19,71,85,174)]
mnist.svm.tuned <- svm(training.set[, -1],training.set[,1],cost =
1e+01, gamma = 1e-05)
mnist.svm.pred <- predict(mnist.svm.tuned,test.set[,-1])
mnist.svm.confmat <- table(mnist.svm.pred, test.set[,1])
mnist.svm.accuracy <-
sum(diag(mnist.svm.confmat)/sum(mnist.svm.confmat))
```

Appendix 10: code for neural network model

```
#-----------------feed forward neural network----------------------
#
x.train_labels<-mnist.dat.reduced[training.rows,1]
x.test_labels<-mnist.dat.reduced[-training.rows,1]
x.train_labels<-as.factor(x.train_labels)
x.test_labels<-as.factor(x.test_labels)
train_norm <- as.data.frame(lapply(mnist.dat.reduced[training.rows,
-1], function(x) {
  return(x / 255)
}))
test_norm <- as.data.frame(lapply(mnist.dat.reduced[-
training.rows,-1], function(x) {
  return(x / 255)
}))
train_labels_matrix = class.ind(x.train_labels)
head(x.train_labels)
TrainingParameters <- trainControl(method = "cv", number = 10)
grid_nn <- expand.grid(size = seq(from = 1, to = 10, by = 1),
                       decay = seq(from = 0.1, to = 0.5, by = 0.1))
nn <- train(train_norm, x.train_labels,
            trControl= TrainingParameters,
            method = "nnet",
            tuneGrid = grid_nn,
            MaxNWts = 20000
)
nn
NNPredictions <-predict(nn, test_norm)
mnist.dat.nnet.confmat<- table(NNPredictions,x.test_labels)
sum(diag(mnist.dat.nnet.confmat))/sum(mnist.dat.nnet.confmat)
```

Appendix 11: code for McNemar test

```
#-----------------Mc Nemar test---------------------#
NNPredictions.is.correct <-
sapply(c(1:length(NNPredictions)),function(index){
  if(NNPredictions[index] == x.test_labels[index]){
    return (1)
  }
```

```
  else (return (0))
})

lasso.pred.is.correct <-
sapply(c(1:length(lasso.pred)),function(index){
  if(lasso.pred[index] == x.test_labels[index]){
    return (1)
  }
  else (return (0))
})

mnist.svm.pred.is.correct <-
sapply(c(1:length(mnist.svm.pred)),function(index){
  if(mnist.svm.pred[index] == x.test_labels[index]){
    return (1)
  }
  else (return (0))
})
svm.vs.multinomial.conf.matrix <- table(mnist.svm.pred.is.correct,
lasso.pred.is.correct)
mcnemar.test(svm.vs.multinomial.conf.matrix)
svm.vs.nn.conf.matrix <- table(mnist.svm.pred.is.correct,
NNPredictions.is.correct)
mcnemar.test(svm.vs.nn.conf.matrix)
multinomial.vs.nn.conf.matrix <- table(lasso.pred.is.correct,
NNPredictions.is.correct)
mcnemar.test(multinomial.vs.nn.conf.matrix)
```