

Image Classification using Topological Data Analysis

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Goals

- ▶ Dimension Reduction for Classification Models
 - ▶ Fight the overfitting problem
 - ▶ Speed up the training process
 - ▶ Common dimension reduction methods
 1. Convolution in Convolutional Neural Networks (CNN)
 2. Principle Component Analysis (PCA)
 3. Topological Data Analysis (TDA)
 4. TDAsweep
 5. Etc.
- ▶ Example : CNN

"C" in CNN

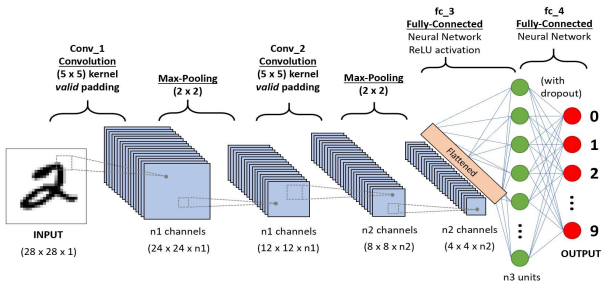


Figure – CNN Workflow

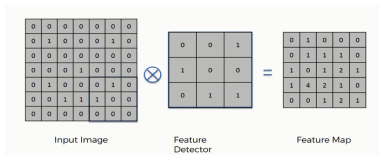


Figure – Convolution in CNN

Examples of TDA

- *Topological data analysis of high resolution diabetic retinopathy images* (Kathryn,G.,Robin,H.,Irina,M.,Cristina,M. May 24, 2019)

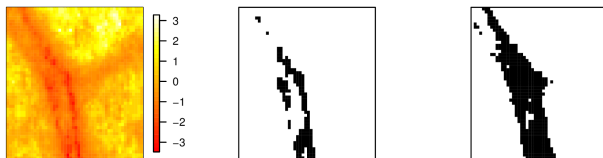


Figure – Persistent Homology on 50x50 Fundus Images

TDA_{sweep}

- ▶ Components
 - ▶ Number of isolated pixel value(s)
 - ▶ e.g. there are 3 components in "1011101"
 - ▶ The 1s are the results after thresholding the pixel values
- ▶ The Sweeps
 - ▶ Finds the number of components in a pixel value matrix with respect to :
 1. Rows
 2. Columns
 3. Diagonals (NW to SE)
 4. Diagonal (NE to SW)

TDAsweep on MNIST

Output of TDAsweep on a random image from MNIST :

```
> ncol(img[1,])
> 784
> res <- test_one_img(img,label,28,28,F,20,2)
> res
> 0 0 0 1 2 2 2 2 1 1 1 1 1 0 0 0 0 0 0.5 2
2.5 2 2 1 0.5 0 0 0 2 2 2 2 2 1 1 0 0 0 0
0 0 2 1.5 1.5 1.5 1 1 1 0.5 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0.5 1 2 2 1.5 1 1 1 0.5
0 0 0 0 0 0 0 0 0 9      # last column is label
> ncol(res)
> 85
```

tdaImage

1. Specify images as a pixel intensity matrix, and labels as a vector.
2. Specify threshold for feature extraction.
3. Specify interval width, further decreasing the number of features.
4. Outputs a string of component counts in the row, column, and diagonals directions.
5. The set of output can then be fed into a ML method.

Threshold Value

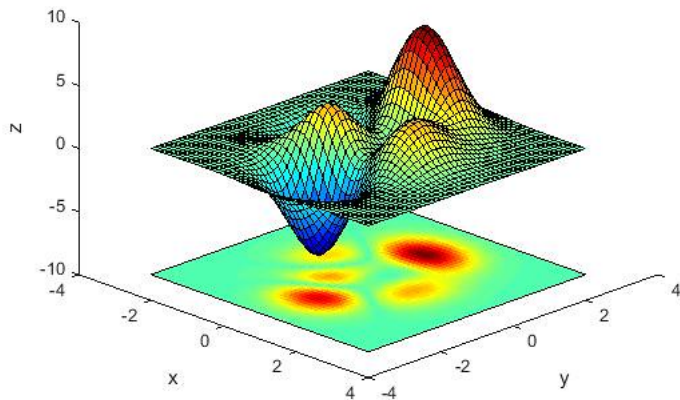


Figure – Slicing a Mountain

Example of Threshold

Threshold = 0:

0 0 70 25 80 0 -> 1 component

Threshold = 26:

0 0 70 0 80 0 -> 2 components

Threshold = 71:

0 0 0 0 80 0 -> 1 component

Example of intervalWidth

#intervalWidth=1	#intervalWidth=2
...	...
3 3 2 0 0 1	1.5 2.5 2 0.5 0.5 1
0 2 2 1 1 1	...
...	

Takes the mean of every 2 rows, therefore further reducing the number of features in one direction by half.

TDA + SVM on MNIST

```
tstidx <- sample(nrow(mnist), 5000)
mn.tst <- mnist[tstidx,]
mn.trn <- mnist[-tstidx,]
# get TDA output
tdaout.trn <- tda_wrapper_func(mn.trn[,-785],
                               mn.trn[,785], 28, 28, F, 100, 2)
tdaout.tst <- tda_wrapper_func(mn.tst[,-785],
                               mn.tst[,785], 28, 28, F, 100, 2)
...
library('e1071')
system.time(svmout <- svm(labels~., data=tdrn, scale=F))
preds <- predict(svmout, tdst[, -85])
mean(preds == tdst$labels) # 0.9602
```

Analysis

TDAsweep Analysis			
Parameters	MNIST(no sweep)	MNIST	MNIST
No. of Features	784	84	168
intervalWidth	NA	2	2
thresholds	NA	(100)	(100,175)
TDAsweep total time	NA	42min	78min
SVM train time	123min	14min	24min
Accuracy	97.9%	97%	97.86%

Table – Speed comparison of SVM before and after TDAsweep

- ▶ Note that the time for training has drastically decreased in exchange for a low cost of accuracy.
- ▶ TDAsweep is still time costly but is highly parallelizable

Analysis(Cont.)

- ▶ In general, for a $n \times m$ image ($n \times m$ features), TDAsweep reduced it to :

$$t \times \left(\left\lceil \frac{n}{i} \right\rceil + \left\lceil \frac{m}{i} \right\rceil + 2 \times \left\lceil \frac{n + m - 1}{i} \right\rceil \right) \quad (1)$$

- ▶ where i and t denotes `intervalWidth` and `|thresholds|` respectively

Example of dimension reduction on one MNIST image :

```
> dim(test_set[1,])  
[1] 1 784  
tda_test_set <- tda_wrapper_func(test_set[1,],  
test_y_true[1], nr=28, nc=28, rgb=FALSE, thresh=c(100)  
, intervalWidth = 1)  
> dim(tda_test_set) # with label attached in the end  
[1] 1 167
```

Next Step

- ▶ Try on colored image set, e.g., CIFAR-10.
- ▶ Make it faster with parallel computation - introduce clusters to distribute pre-processing work.
- ▶ Figures tend to be ragged. Add a minimum value for component length.