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Applied Article

Classification of Skin lesions By Tda Alongside Xception Neural Network

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Abstract

In this paper, we use the topological data analysis (TDA) mapper algorithm alongside a deep convolutional neural network in order to classify some medical images.
Deep learning models and convolutional neural networks can capture the Euclidean relation of a data point with its neighbor data points like the pixels of an image and they are particularly good at modeling data structures that live in the Euclidean space and not effective at modeling data structures that live in the non-Euclidean spaces.
Topological data analysis-based methods have the ability to not only extract the Euclidean, but also topological features of data.
For the first time in this paper, we apply a neural network as one of the filter steps of the Kepler mapper algorithm to classify skin cancer images. The major advantage of this method is that Kepler Mapper visualizes the classification result by a simplicial complex, where neural network increases the accuracy of classification. Furthermore, we apply TDA mapper and persistent homology algorithms to analyze the layers of Xception network in different training epochs. Also, we use persistent diagrams to visualize the results of the analysis of layers of the Xception network and then compare them by Wasserstein distances.

1. Introduction

The incidence of skin cancer and skin problems in the world has increased dramatically over the last few years. Despite preventative public health measures, rates are continuing to hit new records. Skin cancer can be divided into some major types like melanoma, Basal cell carcinoma (BCC) and Squamous cell carcinoma (SCC).
However, skin cancer grows very quickly but the process of treatment would be much easier and also faster if it can be diagnosed as soon as possible. Machine learning can help doctors with proper and accurate methods to diagnose skin cancer with high accuracy. In the last few years, many papers have been published to propose methods for detection of the skin cancer with remarkable results. For more information, we encourage readers to check out [1]. Artificial neural networks especially deep neural networks are among the best algorithms for image classification hence skin lesions. However, there is an issue with deep neural networks, namely the black box problem. Here we try to explain the black box problem with an example: Imagine a doctor after several observations and experiments came to the decision that a patient has skin cancer, this decision has been made in a special framework based on some predefined rules, for instance at the first step the patient must take test1, if the result of test1 is positive then he must take test 2 and so on; at the end after taking several such tests doctor comes to his decision. But when a neural net classifies a patient as a person who has cancer there is no such benchmark or framework in order to understand why it came to this decision despite the fact that its decision is exact and accurate. In deep learning, we call this problem as the black-box problem [2].

Convolutional neural networks are designed in a way that can only capture Euclidean relations of data points and they cannot capture topological and geometrical relation of data points. For example, take an image into account, convolutional neural networks can capture the relation of one pixel with its surrounding pixels which are all in Euclidean $\mathbb{R}^2$ space (in the case of grayscale image) or in Euclidean $\mathbb{R}^3$space (in the case of RGB image). With advances in technology, more and more complex data structures like graphs and simplicial complexes have emerged. These data structures are not Euclidean and have lots of important non-Euclidean (topological and geometrical) properties, the goal of topological data analysis is to extract and use those features to further build stronger deep learning and machine learning models. Here in this article we used TDA based methods to build a pipeline to use both features from deep learning (Euclidean) and non-Euclidean to analysis and classify skin cancer images. Topological data analysis (TDA) is one of the brand-new and fast-growing fields of data science which is trying to analyze data by studying its shape and also reducing the dimensionality of data [3]. TDA is based on two very important branches of mathematics including Statistics and Algebraic Topology. Because of its methodology, TDA can solve some serious problems in data science. Some goals of TDA are reducing the dimensionality of high dimensional data and also analyzing the topological structure or shape of data and finally clustering complex data. TDA also provides innovative data mining methods that can improve the efficiency of machine learning techniques. Persistent homology and Mapper are significant algorithms in TDA. In Persistent homology by constructing a filtration of simplicial complexes that is established from dataset, main topological structures of data are derived. Some visualization tools such as ``Persistent Diagram", ``Barcode" and `` Persistent Landscape" are invented to indicate the main topological features of data. Persistent homology had been previously used in image analysis [4,5] and text mining [6,7]. Converting a high-dimensional data into a simplicial complex that sums up the topological structure of the data as it reduces the dimensionality of data is the main goal of TDA-Mapper. TDA Mapper has been previously applied to classify clinical data [8,9,10].

Automated classification of skin lesions using images is a challenging task because of the structure of skin images. In this paper first, we demonstrate classification of skin lesions using TDA Mapper from images directly, using only pixels and disease labels as inputs. We use neural networks as one of filters in mapper to gain better results. Second we will explain how topological data analysis can help to obtain insight in understanding how convolutional neural networks (CNN's) work that means TDA can propose some ways to make black-box problem easier. In section preliminaries, we introduce some backgrounds about artificial intelligence and novel methods in TDA. Then we describe the HAM10000 data set [11] that consists of images of seven different types of skin diseases by sketching some diagrams like chord diagrams to compare the relation between different types of skin cancer and gender or position of cancer. Next, we apply mapper alongside a neural network to classify this dataset (HAM10000). At last, we analyze the weights of the layers of Xception neural network that is trained with HAM10000 dataset and visualize the results of this analysis by the means of mapper and persistent diagrams.

2. Preliminaries

In this section first, we introduce some concepts about neural networks, then we describe the Architecture of the Xception neural net as the main part of our pipeline, next we provide some explanation of persistent homology and TDA mapper methods in the topological data analysis field.

2.1. AI and neural networks

Artificial intelligence (AI) is a branch of computer science inspired by the human brain and its ability to learn new concepts and solve problems. Artificial neural net (ANN) learns to perform tasks and solve problems by considering and other predefined rules. In our brain neurons has organized in layers and information and biological signals transfer from one layer to another. Based on this architecture ANNs also made up of several different layers including input, hidden and output layers. Typically, a neural network is initially trained or fed with large amounts of data. Training consists of providing input and telling the network what the output should be with respect to the given input. By giving outputs to the network, it will update its weights in order to get the right predictions.

2.1.1. Convolutional Neural Networks

Convolutional Neural Network (CNN) is a class of neural networks which has been designed to work with visual data like images.

In CNN the layers are organized in 3 dimensions: width, height and depth in addition to that, the neurons in one layer do not connect to all the neurons in the next layer but only to a small fraction of them.

In the case of a CNN, the convolution operation is performed on the input data (pixels of an image) with the use of a filter to then produce a feature map. We execute a convolution by sliding the filter over the input. At every location, matrix multiplication is performed and sums the result onto the feature map. Figure1 shows the mechanism of convolution operation. You can see the filter is sliding over our input and the sum of the convolution goes into the feature map. The area of our filter is also called the receptive field the size of this filter is 3x3.

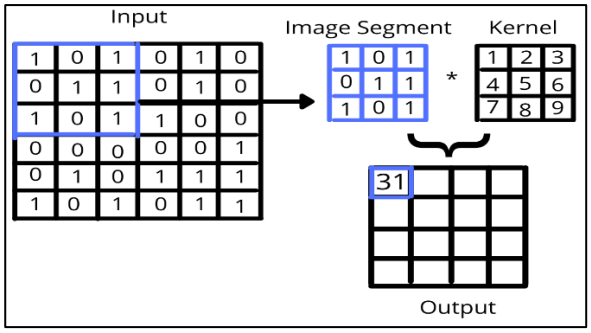

Figure 1. Single CNN with filter size of 3

2.1.2. Depthwise Convolution

In depthwise convolution, we use each filter channel only at one input channel. In Figure 2 from [12] we have 3 channel filter and 3 channel image. The algorithm first breaks the filter and image into three different channels and then convolves the corresponding image with the corresponding channel and then stack them back, next it uses the 1 by 1 convolutional filters called pointwise convolution in the context of depthwise separable convolution. The benefit of depthwise convolution is that it has fewer computations than regular convolution.

2.1.3 Architecture of Xception neural net

In simple convolutional neural networks, for filtration we can use one filter each time. For example, a filter of size 3 by 3 or 5 by 5 but a Inception block can use different sizes of filters, let us say (3 by 3, 5 by 5) and also a max-pooling and then we concatenate the results together as an output as shown in Figure 3 from [13]. Xception network architecture uses the extreme version of Inception Figure 4 from [13], which first uses a 1 by 1 convolution to map cross channel correlations and then separately maps the spatial correlations of every output channel.

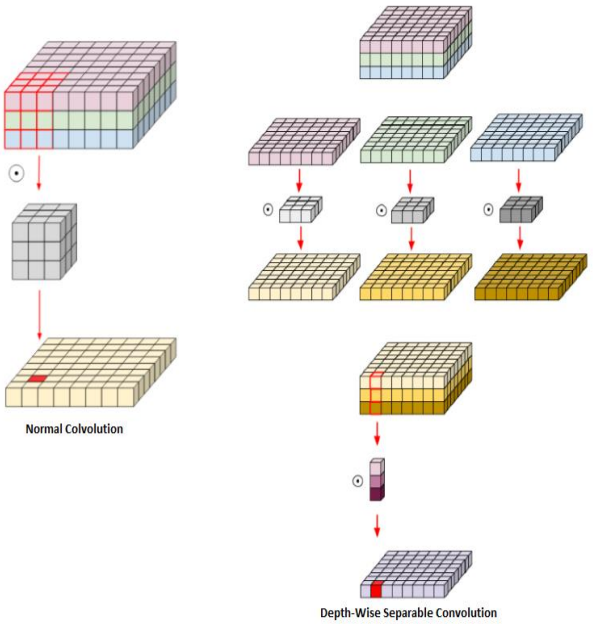

Figure 2. In this depthwise convolution we have 3 channel filter and 3 channel image. The algorithm first breaks the filter and image into three different channels and then convolves the corresponding image with the corresponding channel and then stacks them back, next it uses the 1 by 1 convolutional filters called pointwise convolution in the context of depthwise separable convolution.

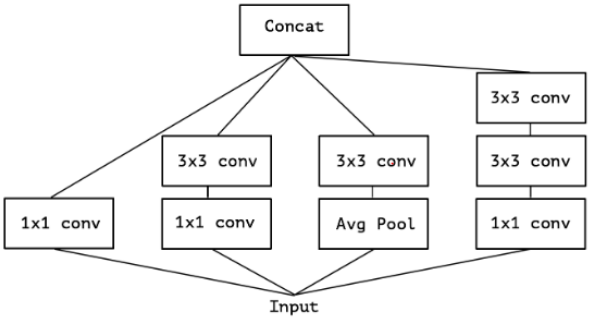

Figure 3. Inception Block.

The extreme version of Inception is just as same as depthwise separable convolution.

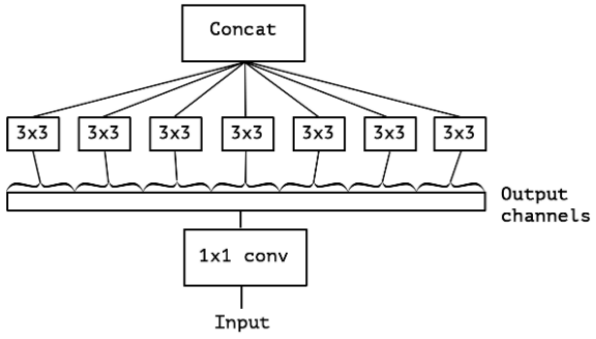

Figure 4. Extreme Inception Block.

However, there are some slight differences between them including:
-The order of occurrence of depthwise and pointwise convolutions are different,
- In depth wise separable convolutions, they usually do not have any non-linearities but in extreme inception, we have some non-linearities like RELU.

2.2. Persistent homology algorithms

A classical way to represent discretized objects is using simplicial complexes, a collection of well-glued blocks called simplices. Formally, a k-simplex σ is the convex hull of k+1 affinely independent points. A 0-simplex is a single point, a 1-simplex is an edge, a 2-simplex is a triangle, a 3-simplex is a tetrahedron, and so on. Any simplex which is the convex hull of a nonempty subset of the points generating σ is called a face of σ. A simplicial complex $\mathbb{K}$ is a finite set of simplices that each face of a simplex in $\mathbb{K}$ belongs to $\mathbb{K}$, and each nonempty intersection of any two simplices in $\mathbb{K}$ is a face of both.
Simplicial homology is a powerful tool in shape analysis, providing invariants for shape description and characterization.
For a simplicial complex, it is possible to define some concepts like chain complex, filtration of a simplicial complex and homology groups that their ranks count connected components, tunnels and holes of simplicial complex. Persistent homology allows for detecting the changes in the homology of a simplicial complex to detect changes in topological properties of simplicial complex with the help of the filtration concept.
Summarizing the persistent homology method is as follows:
Let $\mathbb{P}$ be a point cloud data. First, we construct the Vietoris-Rips complex for $\mathbb{P}$ as follows:
consider an increasing sequence of positive real numbers $\varepsilon_1 \leq \varepsilon_2 \leq \varepsilon_3 \ldots$, then we construct a cover of circles with centers of points in $\mathbb{P}$ and diameter ε_1, so we have as many circles as the number of data points in point cloud data, next we draw an edge between the center of each two circles which have any intersection and therefore we have a simplicial complex $\mathbf{VR}(\varepsilon_1)$. We do the same process for all i = 1,2,3,…, as a result we have a filtration of complexes $\mathbf{VR}(\varepsilon_i)$. The reader can see one Vietoris-Rips complex constructed for a data set in Figure 5 of [6].

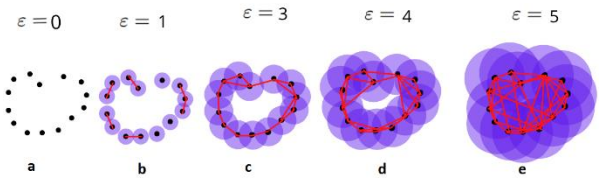

Figure 5. Different Vietoris-Rips complexes constructed for a data set is shown in (a) to (e).

Now for analyzing the connection between points of the dataset we compute different Betti numbers of homological groups corresponding to filtration. These computations can be found in [14].
Since it is very hard to analyze the information about homological groups and holes we can use some visualization methods for detecting persistent homology like barcode, persistent diagram and landscape. A barcode represents each persistent generator(hole) with a horizontal line beginning at the first filtration level where it appears, and ending at the filtration level where it disappears, while a persistence diagram plots a point for each generator with its x-coordinate the birth time and its y-coordinate the death time.
In other words persistent diagram can be explain as follows.
The p-persistent diagram D of a filtration … is defined as follows.
Let be the number of independent p-dimensional classes that are Born in and die entering K_j, then D is obtained by drawing a set of points (i,j) with multiplicity μ_p, where the diagonal is added with infinite multiplicity.
For comparing two persistent diagrams some metrics like bottleneck and Wasserstein distances are defined.
Let D_1, D_2 be two persistent diagrams and B be the set of all bijective functions $\varphi: D_1 \longrightarrow D_2$. If be the supremum norm, then the bottleneck distance between two persistent diagrams $_1$, denoted by (D_1, D_2) is defined as follows.
$(D_1, D_2) = inf$ ∞.
Let D_1, be two persistent diagrams and B be the set of all bijective functions , then the Wasserstein distance between two persistent diagrams D_1, D_2 denoted by $W_p(D_1,$) is defined as follows.
$W(D_1, D_2) = [inf_{\varphi \in B} \sum$ –
Reader can found more about persistent homology in [15].

2.3. TDA Mapper method

Mapper is a tool from Topological Data Analysis (TDA) that provides a topological summary of the data.

The Mapper algorithm was introduced by Singh, Mémoli and Carlsson [16] as a geometrical tool for analyzing and visualizing datasets.
Here we introduce a table of notations to explain the mathematics of mapper method.

Table 1. Notation and symbols that have been used to describe TDA mapper algorithm.

Symbol	Explanation
	Underlying space of point cloud data
$\mathbb{P}$	Point cloud data ($\mathbb{P}\subseteq \mathbb{X}$
$\mathbb{Z}$	Parameter space (usually $\mathbb{Z}=\mathbb{R}$)
$\mathbb{F}$	Filter function ($\mathbb{F}$: $\mathbb{P}\subseteq \mathbb{X} \longrightarrow \mathbb{Z}$)
	Range of $\mathbb{F}$ restricted to $\mathbb{P}$
$\mathbb{U}$	A covering of $\mathbb{P}$
	Collection of subintervals of Γ which overlap

-Then we find the range of $\mathbb{F}$ restricted to $\mathbb{P}$ and call it Γ.Then partition Γ into subintervals ξ in order to create a covering of $\mathbb{P}$ by inverse image $\mathbb{F}^{-1}$ in the next step;
-For every subinterval we find the inverse image of under filter function and call it that is the following set ={ x | $\mathbb{F}$ (x) ∈ ξ_i}. The set $\mathbb{U}$ ={X_i}$ form a covering for $\mathbb{P}$ ($\mathbb{P}$ $_i$);
- For ever y element of we cluster the points of by single linkage clustering algorithm with a suitable metric, i.e for every we have the set of clusters X_{ij};
- Every cluster X_{ij} would be represented as a vertex in simplicial complex where a family of vertexes X_{ij} spans a simplex if and only if the corresponding clusters have a point in common.
The intuitive idea behind Mapper is illustrated in Figure 6 that is brought from [17] and can be explained as follows: suppose we have a point cloud data representing a shape, for example, a hand.
First, we project the whole data $\mathbb{X}$ on a coordinate system with fewer dimension.
in order to reduce complexity via dimensionality reduction (here we project the data on the hand to the parameter space $\mathbb{Z}$).
Now we partition the parameter space into several bins with an overlapping percentage. Next, put data into overlapping bins.
Afterward, we use clustering algorithms in order to classify the points of each bin into several clusters. Once the previous stage is done, we can create our interactive graph.

Summarizing the mapper algorithm with respect to the above notations is as follows:
- First we start with a filter function $\mathbb{F}$: $\mathbb{P}\subseteq \mathbb{X}$ $\mathbb{Z}$;

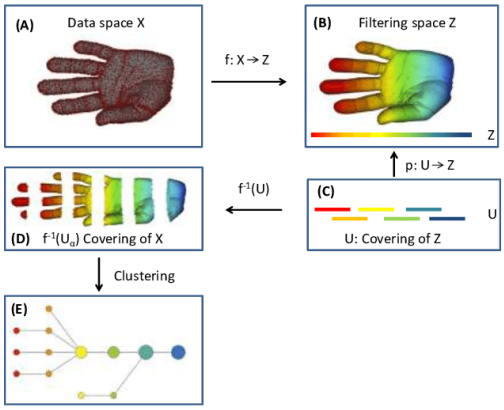

Figure 6. Mapper algorithm on hand shape data cloud B) .First, we project the whole data cloud to parameter space. C) Then we partition the parameter space into overlapping bins (here shown as colored intervals). D) Then we find a cover of overlapping bins by computing inverse function of colored intervals . E) Next, we use any clustering algorithm to cluster the points in the bins which each cluster would represent as a vertex of the graph (generally simplicial complex) and we draw an edge between two vertexes if they share a common data point.

3. Results

In this section first, we provide some details about the dataset that we used. We explain the evaluation metrics and results of our model and compare the proposed model with other available models. problem with our proposed method.

4. Data set

In this paper, we have applied our method to two different datasets of skin lesions for showing its accuracy and efficiency. At first, we have used the HAM10000 data set [11], which includes 10015 dermatoscopic images of skin lesions labeled with their respective types of skin diseases.

The images in the data set are separated into the following seven types of skin diseases:

- Actinic keratosis is considered to be a noncancerous (benign) type of skin disease. However, if left untreated, it usually develops into squamous cell carcinoma (SCC).
- Basal cell carcinoma is a cancerous type of skin lesion that develops in the basal cell layer located in the lower part of the epidermis. It is the most common type of skin cancer accounting for 80 percent of all cases.
- Benign keratosis is a noncancerous and slow-growing type of skin disease. They can be left untreated as they are typically harmless.
- Dermatofibromas are also noncancerous and usually harmless, thus no treatment is required. It is commonly found pinkish in color and appears like a round bump.
- Melanoma is a type of malignant skin cancer that originated from melanocytes, cells that are responsible for the pigment of your skin.
- Melanocytic nevi are a benign type of melanocytic tumor. Patients with melanocytic nevi are considered to be at a higher risk of melanoma.
- Vascular lesions are composed of a wide range of skin lesions including cherry angiomas, angiokeratomas, and pyogenic granulomas. They are similarly characterized as being red or purple in color and are usually a raised bump.

Secondly, we applied our algorithm to the skin cancer ISIC dataset.

This dataset consists of 2357 images of malignant and benign oncological diseases, which were formed from The International Skin Imaging Collaboration (ISIC). This dataset is available in [https://www.kaggle.com/datasets/nodoubttome/skin-cancer9-classesisic]. The Skin Cancer ISIC consists of nine classes of skin diseases, including

-actinic keratosis
- basal cell carcinoma
- dermatofibroma
- melanoma
- nevus
- pigmented benign keratosis
- seborrheic keratosis
- squamous cell carcinoma
- vascular lesion

Here we present some chord diagrams that show the weighted relation between different types of skin diseases and the other variables like the gender of patient. For example in Figure 7 we present the relation between skin diseases and gender of patient or in Figure 8 relation between the location of the lesion and gender of patient and in Figure 9 the relation between the location of the lesion and type of the lesion are shown by diagrams.

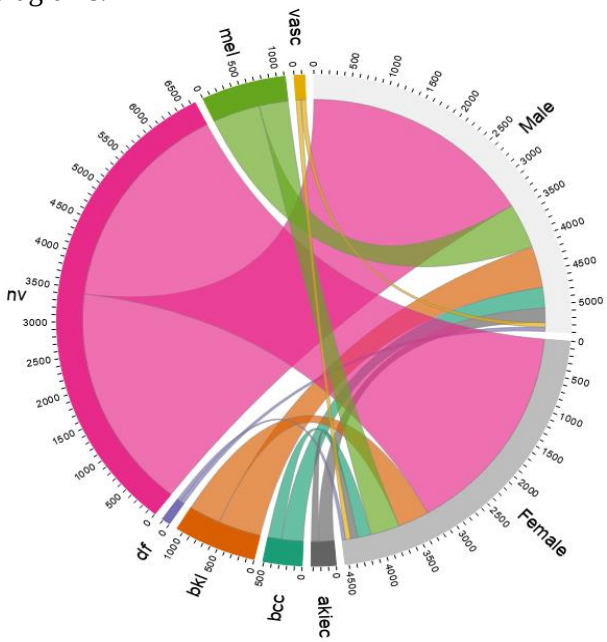

Figure 7. Chord diagram of Skin Diseases Related to Each Gender.

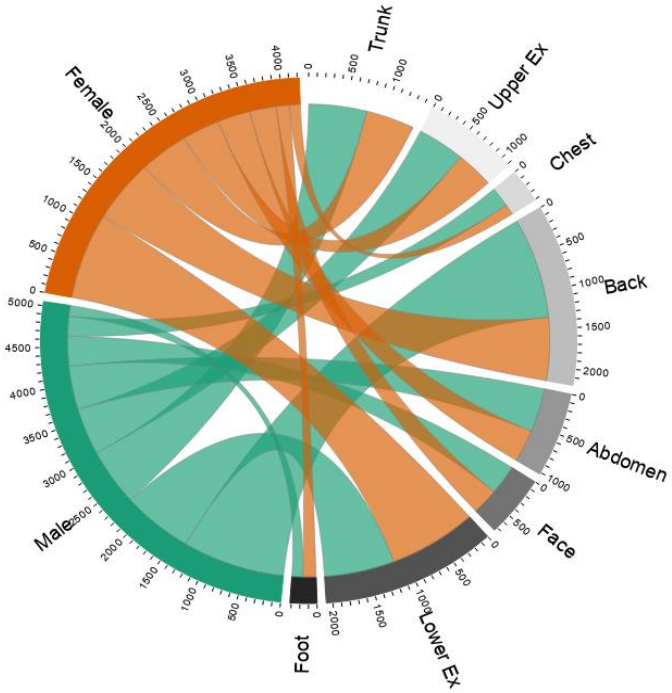

Figure 8. Chord diagram of the gender of the patient and the location of lesion.

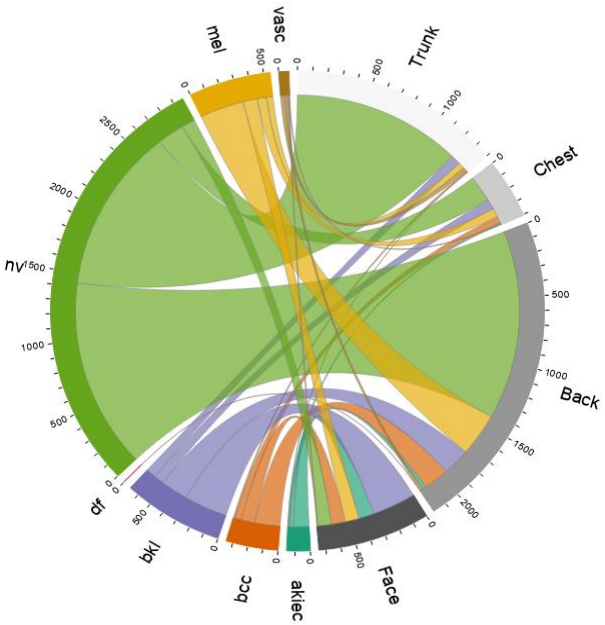

Figure 9. Chord diagram of the type and location of lesion.

3.2. Main method as a combination of TDA-Mapper algorithm and Xception neural net

Implementation of mapper algorithm is already available in python packages like ``Mapper" and `` Kepler Mapper" [18]. In this article we used ``Kepler Mapper" alongside other python packages like Keras and Sikit-Learn, all experiments and runs have been done on Google Colab with 12.69 Gigabytes of RAM and Tesla T4 GPU and the whole runtime took about 4 hours. First, we resize each image of our dataset into 100 by 100 pixel image, then we fed the dataset to a simple neural net, next we fed the output of neural net to kepler mapper, for clustering we used ``Agglomerative Clustering" available in ``sklearn" package with ``cosine" similarity and complete linkage. Finally, mapper makes a simplicial complex for visualizing classification that has been shown in Figure 10.

To encapsulate the low-dimensional representation generated by the filtering step (neural net), Mapper employs binning (or partitioning), followed by partial clustering within each bin. The binning step partitions the low-dimensional space into overlapping bins by using two parameters—the number of bins (or resolution (R=6)) and the percentage of overlap between bins (or gain (G=0.4)). Within each bin, complete linkage clustering is performed to condense the time frames into a set of one or more clusters, Figure of our proposed pipeline can be found in Figure 11.

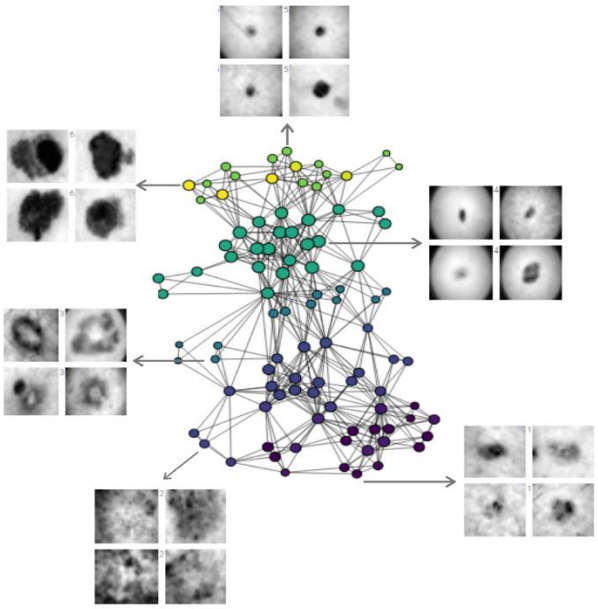

Figure 10. Some sample images of nodes of simplicial complex induced from mapper.

Talking about learning, the combination of mapper and neural networks (using neural networks as filter function in mapper) can be both supervised and un-supervised at the same time, supervised because Xception algorithm that we used is supervised since we use images with their labels, and also unsupervised since we used Agglomerative clustering for mapper visualization.

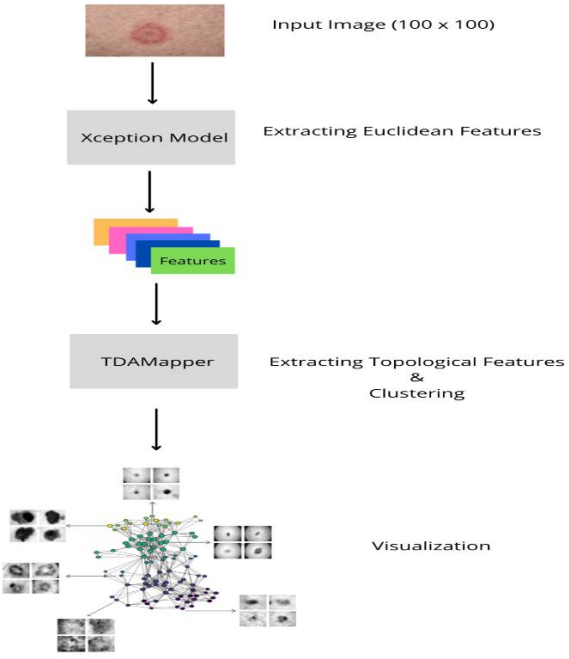

Figure 11. Pipline of our proposed method. First of all image data will be fed to Xception neural network in order to extract features from the data, and then after that, we use image and all those extracted features from a deep model to feed into TDA mapper. Next, TDA mapper extract extra topological features as well as visualizing the result of classification.

3.3. Evaluation Metrics

For the evaluation step, we use over all accuracy, sensitivity, and specificity. Sensitivity evaluates the portion of correctly predicted positive samples among all positive ones and specificity evaluates the portion of correctly predicted negative samples among all negative samples.

In [19] authors performed a classification task on dataset Ham10000 with three different methods namely: artificial intelligence(ResNet50), 112 dermatologists, and a combination of both methods called fusion method, a summary of their results can be seen in Table 2. In our method, we used Xception model, out of 10015 images we used 1002 images for testing and 9003 for training. We used the pretrained Xception model with Imagenet weights and transferred learning in order to minimize the computational cost and training time, we also used Adam optimizer with the learning rate of 0.001. After 60 epochs the model reached to stability in accuracy in comparison with [19]. The result was acceptable with the accuracy of over 83 percent. As in Table 3, someone can check the accuracy of our model. Also Figures 13 and 14 show the accuracy of our model over on Ham10000 dataset which is about 85percent.

Also it is worth mentioning that the sudden fall in the first 5 epochs is because our dataset is unbalanced (about 85 percent of images belong to three classes of nevi, Benign keratosis, and melanoma out of 10000 images and only 15 percent of images belong to other 4 classes as in Figure 12 has been shown. however it recovers soon after the model sees more images of every class.

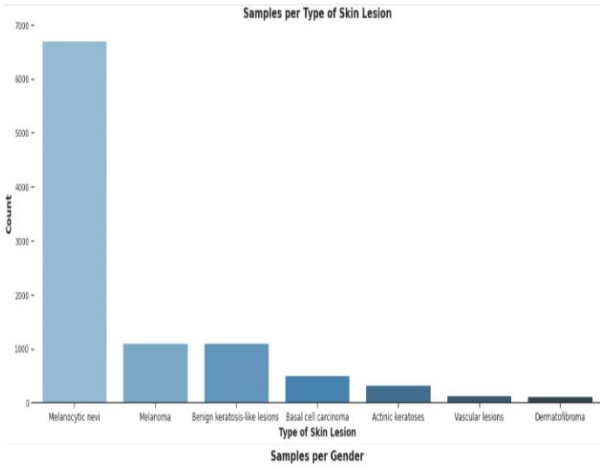

Figure 12. Ham10000 dataset distribution.

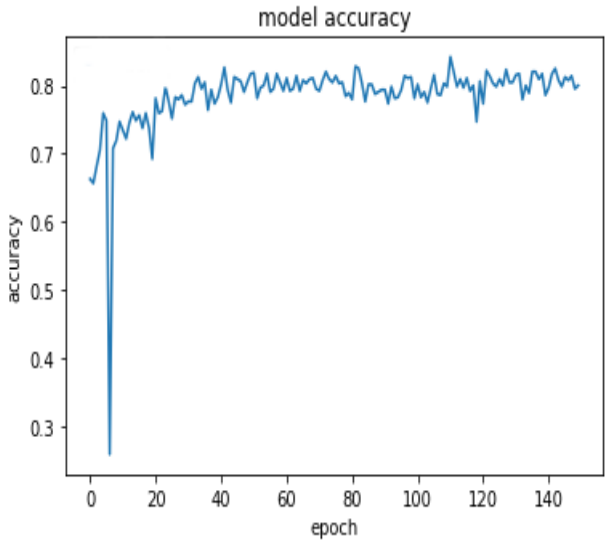

Figure 13. Accuracy of our model on Ham10000 dataset which is about 85 percent.

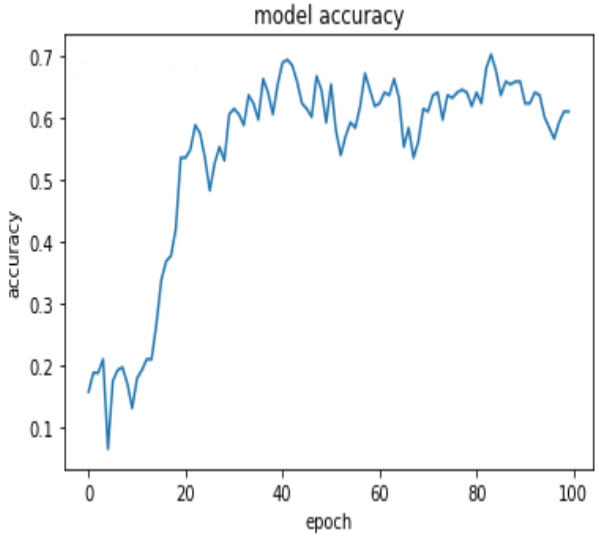

Figure 14. Accuracy of our model on Skin Cancer ISIC dataset which is about 70 percent.

In [20] authors used a dataset of 13000 dermoscopic images, including HAM10000 which had been collected from clinical centers around the world [21]. They separated 10015 of those images (the Ham10000 part) and used this dataset for two main tasks including lesion segmentation and melanoma disease classification, the summary of their proposed method to compare with our work is as follows:

First, they applied a segmentation algorithm to get an image mask and they applied the image mask to the image in order to get the exact disease location, next they extracted information from each channel via RGB transformation, after that, they used persistent homology to compute persistent diagrams as features and feed all those features to a multi-class SVM with a "one-

against-one" approach and the result of their proposed methods can be found at Table 4.

Table 1. Accuracies of models on HAM10000 with different methods proposed in \cite{[23]}, including CNN, doctors, and fusion method with different number of dermatologists with different numbers ranging from 17 to 30.

Questionnaire (doctor's number)	Mean accuracy doctor	Mean accuracy CNN	Mean accuracy fusion method
1 (n = 17)	36.59%	78%	80.95%
2 (n = 14)	**47%** &	**82%**	80.89%
5 (n = 21)	46.29%	80%	80.60%
6 (n = 30)	42.20%	80%	**83.20%**
Overall	42.94%	81.59%	82.95%

Table 3. shows the result (precision, recall, f1-score) of Xception model on HAM10000 dataset for classification task.

Type	**F1-Score**	**Recall**	**Precision**
nv	78%	42%	55%
Mel	73%	71%	72%
Bkl	72%	69%	70%
Bcc	78%	58%	67%
Akiec	89%	97%	93%
Vasc	75%	50%	60%
Df	100%	93%	96%
Accuracy	85.2%		

Table 4. Result of three main models proposed in [20], on 13000 dermoscopic images. Models are as follows: Model 1, Model 2, Model 3.

	Features	**Validation Score**
Model1	**XYZ curves, XYZ stats**	65.6%
Model2	**XYZ CURVES, XYZ STATS, RGB stats**	**67.2%**
Model3	**XYZ curves, XYZstats, RGB stats, HSV stats**	66.0%

3.4. Addressing blcak box problem

Convolutional neural networks are well adapted to image data. In this case, the input nodes are arranged in a square grid corresponding to the pixel array of Image. The nodes are composed in a collection of layers. A layer is called convolutional if it is made up of a collection of square grids identical to the input layer, and it is understood that the weights at the nodes in each such square grid involve only nodes in the previous layer that are very near to the corresponding node. Sometimes intermediate layers called pooling layers are introduced between convolutional layers, and in this case the higher convolutional layers are smaller square grids. Xception is a neural network that is combination of the layers which has been trained on more than a million images from the ImageNet database. It can classify images into different categories. In fact the network has learned rich feature representations for a wide range of images. To train the neural network model of analysis, we used HAM10000 dataset with Xception neural network.

To better understand the functionality of each layer during each epoch we used mapper and persistent to detect changes.

Here we choose Second last dense layer of Xception network for epochs 10, 50, 100 and then visualize the weights of them by both mapper and

persistent diagram. The results of These calculation has been brought in Figures 15, 16, 17 and 19.

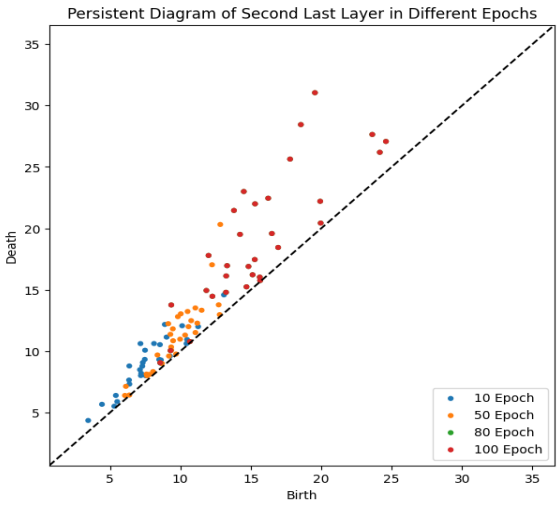

Figure 15. Persistent Diagram of Second Last Dense Layer in Different Epochs.

Mapper diagrams show that changes in weights of second last dense layer in epochs 50 and 100 is very significant.

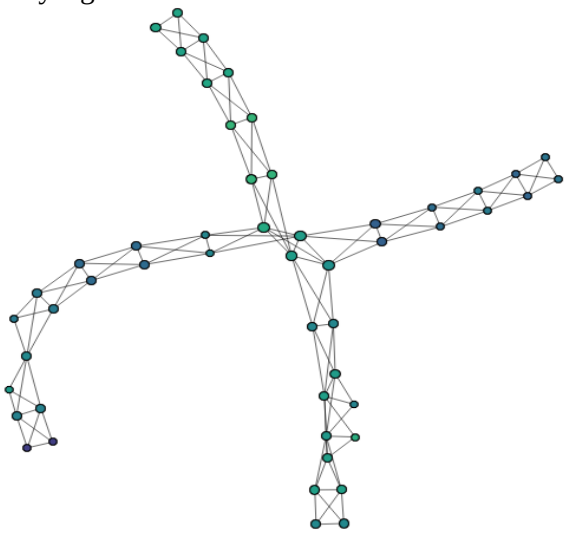

Figure 16. Detecting changes in weights of second last dense layer in epoch 10.

We will bring the results of computing Wasserstein distances for different epochs in Table 5. This demonstrates the capability of using topological data analysis to monitor and provide insight into the learning process of a neural network.

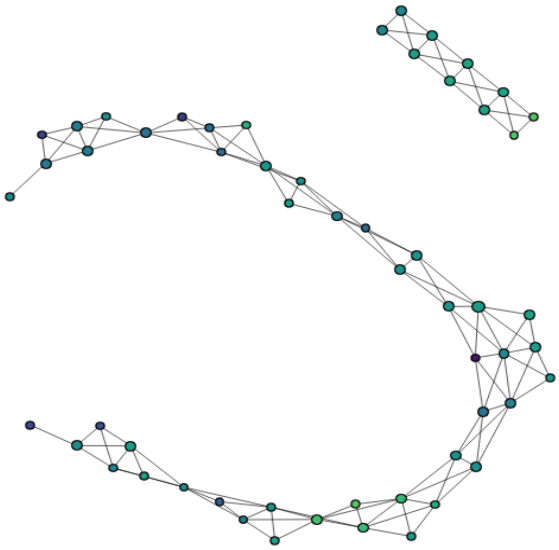

Figure 17. Detecting changes in weights of second last dense layer in epoch 50.

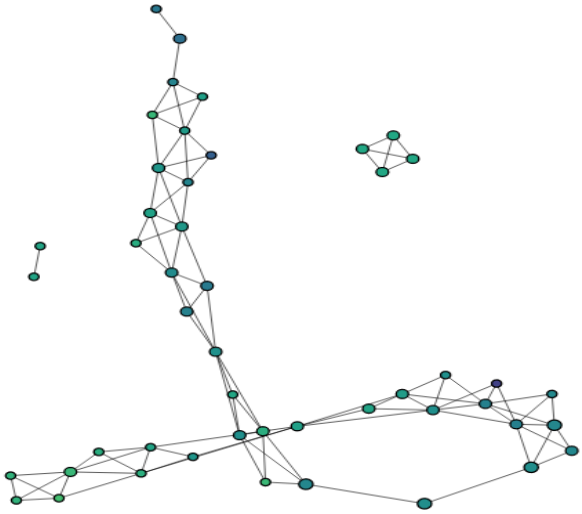

Figure 18. Detecting changes in weights of second last dense layer in epoch 80.

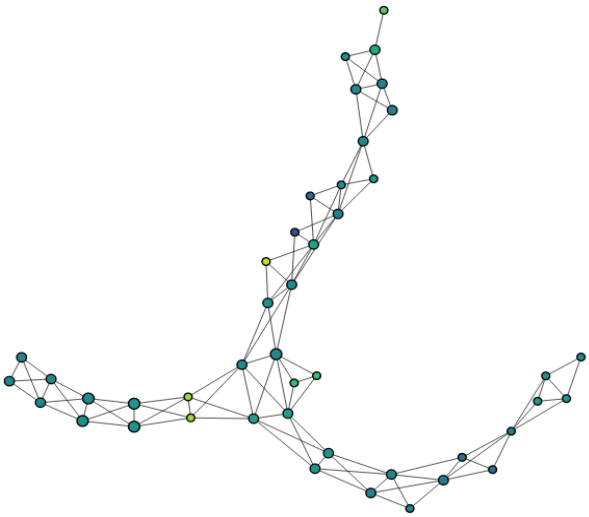

Figure 19. Detecting changes in weights of second last dense layer in epoch 100.

Table 5. Table below shows Wasserstein distance of second last dense layer weights between different epochs which as numbers suggest decreases as the number of epochs increase (since the model starts to converge).

Different epochs	Wasserstein Distance
epoch 10 and epoch 50	21.83638785530654
epoch 50 and epoch 80	8.865006495262655
epoch 80 and epoch 100	25.1911944614468
epoch 10 and epoch 100	59.9561201103112

4. Conclusion

In this manuscript, we reviewed TDA algorithms like mapper and persistent homology and neural networks. Then for better visualization of the classification problem with Xception neural net we used mapper algorithm alongside Xception algorithm on the dataset Ham10000.The accuracy of this visualization in comparison with other classifications of this dataset shows that classification problems can be done better by TDA algorithms alongside neural nets. Also, TDA algorithms helped us to detect the weights of layers of Xception in different epochs that can be generalized for every neural network. These pieces evidences show the power of TDA in solving machine learning problems.

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طبقه‌بندی ضایعات پوستی توسط تحلیل توپولوژیکی داده به همراه شبکه عصبی Xception

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چکیده:

در این مقاله، ما از الگوریتم نگاشت‌گر در تحلیل توپولوییکی داده به همراه یک شبکه عصبی کانولوشن عمیق برای طبقه‌بندی برخی عکس‌های پزشکی استفاده می‌کنیم. مدل‌های یادگیری عمیق و شبکه‌های عصبی کانولوشنی، روابط اقلیدسی یک نقطه از داده با نقاطی از داده در همسایگی آن مانند پیکسل‌های های یک عکس را درمی‌آورند و این الگوریتم‌ها به خصوص درمدل کردن ساختارهای داده‌ای که در فضای اقلیدسی زندگی می‌کنند خوب هستند و در فضاهای نااقلیدسی موثر نیستند. روشهایی که بر اساس تحلیل توپولوژیکی داده بنا نهاده شده‌اند نه تنها توانایی استخراج صفات اقلیدسی بلکه صفات توپولوژیکی داده را نیز دارند. برای اولین بار در این مقاله، ما یک شبکه عصبی را به عنوان یک گام پالایش الگوریتم "کپلر مپر" به منظور طبقه‌بندی عکس‌های سرطان پوست به کار می‌بریم. مزیت اساسی این روش این است که "کپلر مپر" نتایج طبقه‌بندی را با یک همبافت سادکی بصری‌سازی می‌کند، درحالی که شبکه عصبی دقت طبقه‌بندی را افزایش می‌دهد. به علاوه ما الگوریتم‌های نگاشت‌گر وهومولوژی پایا را به منظور تحلیل لایه‌های شبکه اکسپشن در دوره‌های مختلف یادگیری به کار می‌بریم. همچنین ما نمودارهای پایا را به منظور بصری‌سازی نتایج تحلیل لایه‌های شبکه اکسپشن استفاده می‌کنیم و آنها را از طریق متریک واسرشتاین مقایسه می‌کنیم.

کلمات کلیدی: تحلیل توپولوژیکی داده، نگاشت‌گر، هومولوژی پایا، شبکه عصبی.