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## Bio-Medical Image Segmentation using DC-UNet

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### ABSTRACT

X-rays, CT scans, and MRIs are all examples of medical imaging tools. They may reveal nondestructively information on illness, abnormalities, and anatomical inside the human body. Medical photos include a lot of data and are subject to influence from noise, so it's critical to analyse the images and get the most useful information out of them. The most widely used and productive segmentation of biological images using deep learning up to this point is Dual Channel U-Net (DC-UNet), an improved version of which is called Dual Channel U-Net. The segmentation of medical images will benefit greatly from DC-contribution. UNet's Several medical photos are used to evaluate DC-UNet. According to the findings, DC-UNet consistently outperforms the traditional U-Net model. DCUNet looks to be more dependable and durable. DC-UNet has the ability to detect hazy borders and minimise noise interference.

Keywords: deep learning, DC-UNet, medical picture segmentation, convolution neural network.

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### Introduction

Medical image analysis seeks to provide radiologists and clinicians with an efficient diagnosis and treatment procedure. Diagnostic imaging equipment such as CT, MRI, and radiography can give non-destructive data on illness, abnormalities, and anatomical structures within the human body. Because of the vast quantity of data and noise interference in medical pictures, it is critical to analyse them and extract useful details from them. Processing of medical images has made significant contributions to frequently used medical applications such image segmentation, image registration, and image-guided surgery utilised in medical treatment. Image segmentation, which minimises the area of interest (OI) using some automatic and semi-automatic algorithms, is the most essential approach for processing medical images. Processing is the most significant technology in medical image processing, objective is to use certain automatic and semi-automatic approaches to reduce the area of interest (OI). Many conventional algorithms are created to partition biological organs or tissues. The form, size, and border of the polyps in the CVC-ClinicDB dataset are all completely distinct; certain polyps with hazy edges cannot be spotted using a conventional segmentation method. For a number of computer vision exercises, deep learning approaches have been demonstrated to perform superior than former cutting-edge machine learning techniques.

For implementation Python 3.7, programming language. Google Collab or Jupyter Notebook was used to write scripts. Used other open source python libraries like: Numpy, Scikit-learn, Pandas, Matplotlib, Keras and Tensorflow.

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### Literature Review

In [1] authors the topic of research of computer-aided detection or diagnosis (CAD) has shown promise. Medical image analysis strives to make radiologists and doctors' diagnosis and treatment processes more efficient. This includes breast cancer detection, identifying lung nodules, and locating prostate cancer. This review presents state-of-the-art technologies as of late medical image processing approaches in CAD research, with an emphasis on convolutional neural network (CNN)-based algorithms. There is also a list of the most widely used medical picture databases in the literature. This work is expected to give radiomics, precision medicine, and imaging grouping experts with a systematic overview of the CNN-based methodologies employed in CAD research.

In [2] authors provide a network and training technique that focuses heavily on data augmentation to make better use of the given annotated examples. The UNet design is made composed of a symmetric expanding path and a contracting path for context capture for exact localization. On a modern GPU, segmenting a 512 x 512 picture takes less than a second. They determined that a number of biological segmentation applications for the u-net concept show excellent performance.

In [3] authors offer a straightforward and scalable detection method that increases mean average precision (mAP) by over 30% compared to the previous best VOC 2012 result, obtaining a mAP of 53.3 percent. Their method is based on two essential insights: (1) When there is a lack of labelled training data, supervised pre-training for a secondary task followed by domain-specific fine-tuning results in a noticeable performance improvement; and (2) When there is a lack of labelled training data, supervised pre-training for auxiliary tasks followed by domain-specific fine-tuning results in a noticeable performance improvement. On the 200-class ILSVRC2013 detection dataset, they discovered that R-CNN beats OverFeat by a wide margin.

In [4] authors in this section, we will examine the U-Net model architecture in depth and speculate on some potential options for future upgrades. They explore with various public medical picture datasets of various modalities, and MultiResUNet outperforms them. • We also test a 3D version of MultiResUNet, which outperforms the regular 3D U-Net. They determined that U-Net performs segmentation with amazing accuracy for perfect or near-perfect pictures. In some circumstances, our suggested architecture performs just marginally better than UNet. However, for detailed pictures with disturbances, perturbations, and a lack of defined boundaries, MultiResUNet's performance boost is considerable.

In [5] authors present a new approach for polyp localization in videos of colonoscopies Their method is based on a polyp appearance model that explains polyp borders in terms of valley information. They suggest a comprehensive integration of valley information, promoting complete, concave, and continuous borders typical of polyps. This integration is accomplished through the use of a radial sector window that collect valley information to generate WM-DOVA (Window Median Depth of Valleys Accumulation) energy maps associated with the likelihood of polyp presence. They begin by determining if the greatest number matches to the position of the polyp in the picture. Second, they demonstrate that WM-DOVA energy maps are comparable to saliency maps derived from physicians' fixations using an eye-tracker. Finally, they demonstrate that our strategy beats current computational saliency results. Their approach performs well, particularly for tiny polyps, which are considered to be the major sources of polyp miss-rate, indicating the method's potential for use in clinical practice.

In [6] authors the issue of data augmentation in picture classification is one that we should investigate and compare various ways to. Previous research has shown that simple data augmentation methods like cropping, rotating, and flipping input photos are successful. They intentionally limit our access to a portion of the ImageNet dataset so that they may evaluate each data augmentation method separately. They come to the conclusion that while conventional augmentations still perform about as well as GANs and neural augmentations and take about three times as long to calculate, we can always combine data augmentation approaches. The strength of categorization may be further enhanced by combining classical and neural augmentation.

In [7] authors demonstrate a basic, highly modularized image categorization network architecture Their network is built by repeatedly repeating a construction block that collects a group of modifications having the same topology. Our Simple design results in a homogeneous, multi-branch architecture that requires less configuration of the hyper-parameters. They study ResNeXt further on an Sets for COCO detection and ImageNet-5K, where it outperforms its ResNet cousin.

In [8] authors the performance of three models, the multiresUNet, the UNet, and DC-UNet, was compared using two public medical datasets. Each dataset has some difficult instances. Some pictures in the The dataset for ISBI-2012 electron microscopy includes various interferences such as clamour and other portions of the cell, which will impair the model's ability to distinguish the borders. Polyp borders are exceedingly hazy and difficult to discern in colon endoscopic pictures in CVC-ClinicDB, and polyp forms, sizes, structures, and locations vary. These characteristics make this dataset very difficult. They look for that DC-UNet performed better than MultiResUNet and UNet. By observation, this division findings are substantially closer to the truth.

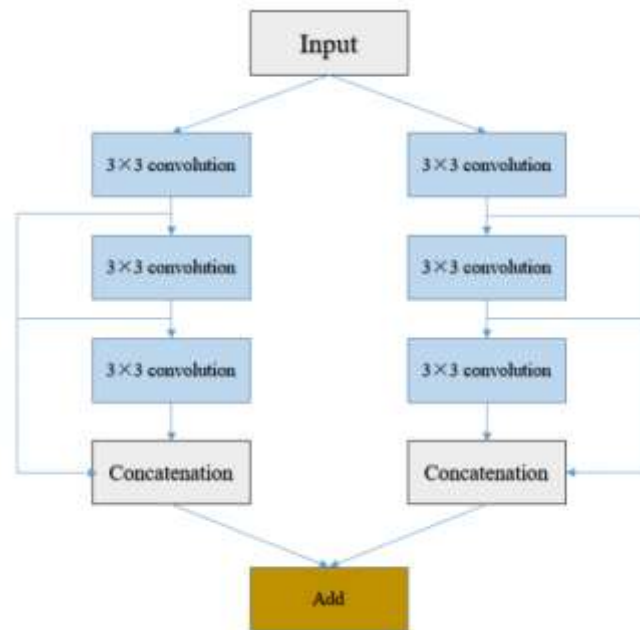
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## Hypothesis

Following a review of the literature, Medical image analysis attempts to assist physicians and clinicians with a diagnosis and treatment process that is more effective. This includes breast cancer detection, detection of lung nodules, and prostate cancer localization. The efficacy of data augmentation techniques such as cropping, rotating, and flipping input photos. The UNet design is made up of a contracting path for context capture and a symmetric extending path for exact localization. On a modern GPU, segmenting a 512x512 picture takes less than a second. There have been studies on many types of data that attempt to predict accuracy levels by comparing photos with various models such as MultiResUnet and UNet. When compared to conventional datasets for computer vision, Datasets for medical imaging today are increasingly challenging. costly medical supplies,, sophisticated picture capture pipelines, expert diagnosis, and time-consuming hand labelling - medical datasets are difficult to construct. There are now various standard datasets for medical imaging that are accessible to the public that feature medical pictures and their ground truth. To evaluate the We used two open datasets to evaluate the performance of the three U-Net-based models. and our proprietary infrared breast dataset. The major goal of the study was to forecast segment pictures with ambiguous borders and segment images with tiny items using biomedical images and the CNN model. The collection includes both ground truth and original photos. The model that is used to identify illnesses in a specific region where they are present.

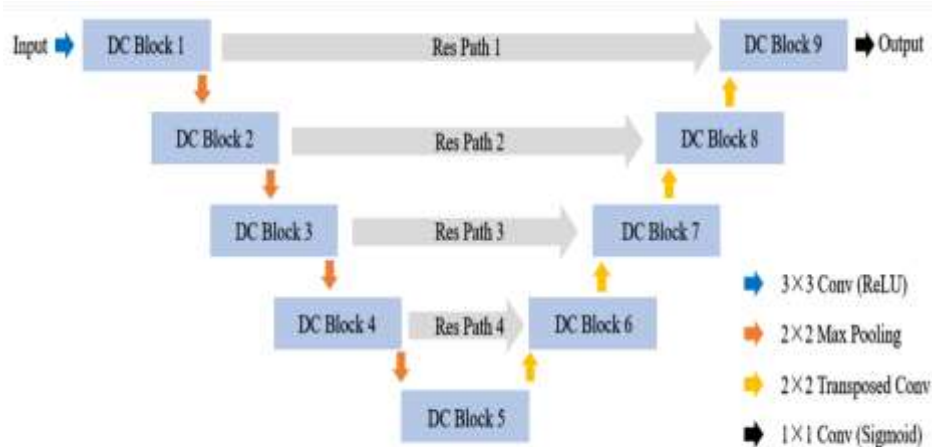
By comparing with a model, it is predicted that Convolutional Neural Networks can categorise and forecast accuracy values. The study done by Washington University Medical Center evaluating and analysing huge medical datasets with multiple models such as UNet, MultiResUNet and obtaining accuracy values by comparing with different models. In this case, we utilised DC-UNet, which is an enhanced version of UNet.

## Architecture Diagram



**Fig. 1:** Dual-Channel block

Three 3 x 3 convolutional layers were utilised in the Dual Channel-UNet (DC-UNet) algorithm. Few extra spatial characteristics are provided by the residual connection in this case, which could not be sufficient for some of the most difficult jobs. Thus, we employed the third convolutional layer.



**Fig. 2:** DC-UNet Architecture

The enhanced version of UNet is called DC-UNet. The U-Net design has been the most effective and widely used in medical picture segmentation. We used three 3 x 3 convolutional layers in succession. Between the encoder and the decoder, we used Res-Path. Dataflow is passed through a series of three-by-three convolutional layers with residual connections before the decoder feature is concatenated. Then, we built a new U-Net architecture called the DC-UNet using the Res-Path and Dual-Channel block. The half filter numbers for each channel in a dual-channel block are 32, 64, 128, 256, and 512. The three-filter number (3 + 3) is also separated into Additionally, Res-path has 32, 64, 128, and 256 filters. The ReLU function activates each convolutional layer in the DC-UNet and For avoiding overfitting, employ batch normalisation. Additionally, the Sigmoid function activates the last output layer.

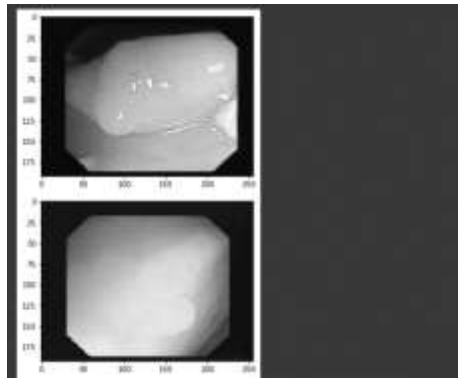
## Methodology

They created an efficient CNN architecture and built the DC-UNet around it. We tested our model on three datasets with difficult scenarios and found that it outperformed traditional U-Net by a factor of 2.90. Furthermore, for gray-to-gray picture comparisons, they employed the Tanimoto similarity instead of the Jaccard similarity.

### *Methodology undergoes in 3 steps:*

#### *1. Data Collection and Preprocessing:*

Bio-Medical photos from several databases, including ISBI-2012 and CVC-ClinicDB. Ground Truth and Mask were assigned to these photographs. The photos in Ground Truth are original, whereas the images in Mask are grayscale. Pre-processing for the thermography database included converting 16-bit pictures to 8-bit and resizing the image to 256X128 pixels. Due to GPU memory constraints, pre-processing for other databases is limited to resizing the size and weight of photos no greater than 256.



**Fig. 3:** Sample images trained to 256 X 192

#### *2. Model Training:*

The CNN is made up of alternating convolutional and max pooling layers, flattening, and a fully linked dense layer. Semantic segmentation attempts to anticipate if a pixel belongs to an item. As a result, this task may be categorized as a Binary classification challenge at the pixel level. The outcome is we picked and reduced the binary cross-entropy loss function. We used the Adam optimizer to train the models with parameters  $\beta_1 = 0.9$  and  $\beta_2 = 0.999$ . Datasets have different epochs.

#### *3. Testing and Validation:*

Every epoch, the data for loss and accuracy for training and validation will be recorded and graphed for verification and overfitting detection. A randomized set of testing photos will be used to generate an accuracy vector that includes correct and erroneous predictions. The accuracy percentage is then determined as the ratio of correct forecasts to total guesses.

#### *4. Measurement metric*

To assess segmentation performance, we required a way to Comparing the divided and the actual region. Because the last layer is activated by a Sigmoid function, its output is in the  $[0, 1]$  range. As a result, we cannot directly compare output to ground truth since ground truth are binary pictures. grayscale to binary conversion of an image (binarization) typically results in significant information loss. There are several techniques for comparing two images:

- a. Jaccard Similarity in Binary versus Binary (JS)
- b. Mean Absolute Error in Gray vs. Gray (MAE)

Taking care of methodology is critical, as is clarity. Designing is the fundamental prerequisite for any type of project development. As a result, having a thorough strategy aids in the smooth growth of the project.

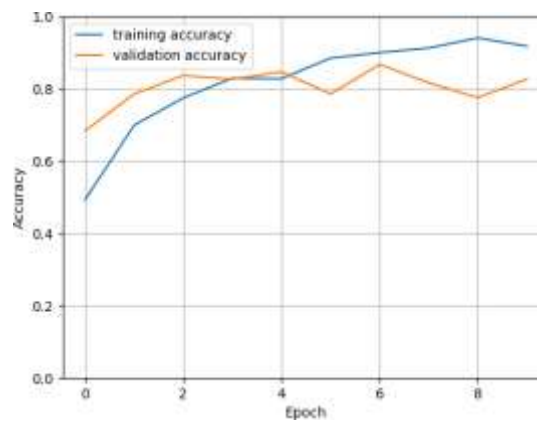
## Result and Analysis

The DC-Unet Model is implemented in this project using CNN. The training data of accuracy and loss is growing with each epoch.

EPOCH	LOSS	ACCURACY
1	73.2%	65.4%
2	71.7%	70.8%
3	71.3%	73.5%
4	70.2%	79.05%
5	69.2%	81.8%
6	68.1%	84.1%
7	67.8%	85.6%
8	66.5%	87.3%
9	66.04%	89.02%
10	65.3%	90.3%

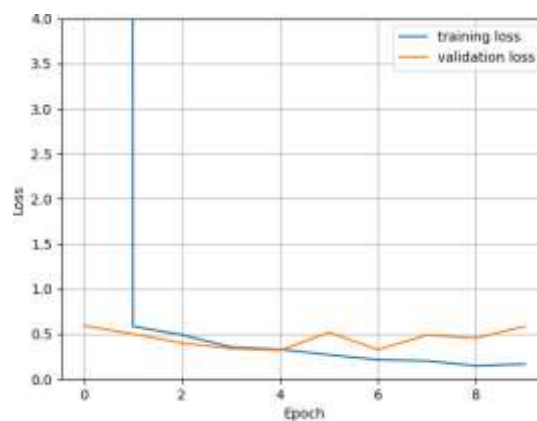
**Table 1:** Details of each epochs in terms of loss and accuracy

The trained CNN has a training accuracy of 90.3 percent and a validation accuracy of 85.73 percent. As the number of epochs increases, so does the training accuracy.



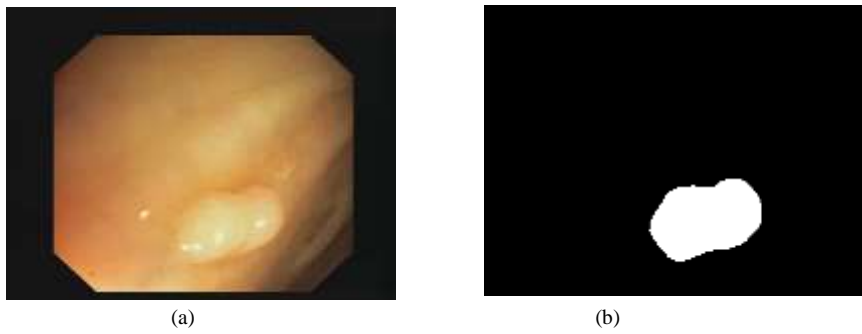
**Fig 4:** The model's training and validation accuracy over epochs

The training and validation losses decrease as predicted, with a tiny rise near the end demonstrating the lack of overfitting.



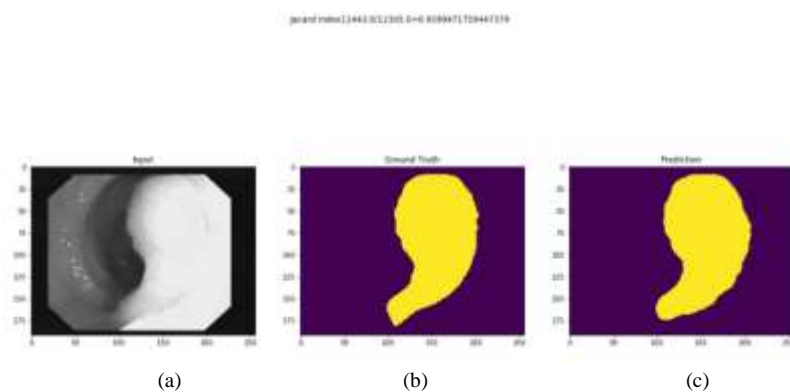
**Fig 5:** Training and validation Loss of the model over the epochs.

We take a look at the CVC- ClinicDB dataset, which contains both original and ground truth photos.

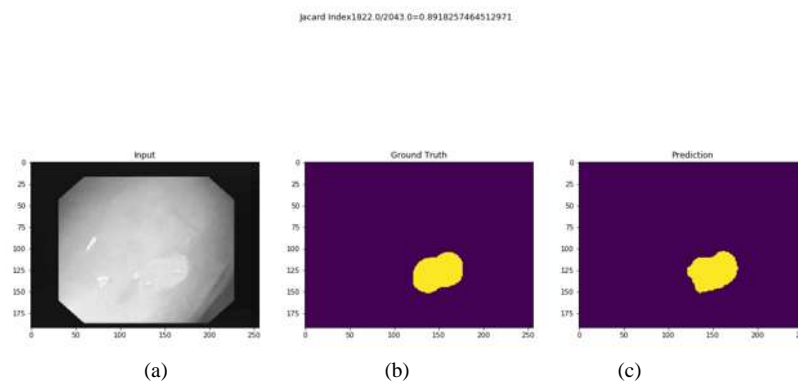


**Fig 6:** Dataset Images (a) Original Image of Polyp (b) Ground Truth/Mask Image of Polyp

The DC-UNet can successfully segment images with vague boundaries and successfully detect small objects in images.



**Fig. 7:** Image segmentation using tiny objects. (a) Original image (b) Ground truth (c) DC-UNet (89.18 %)



**Fig. 8:** Image segmentation using with ambiguous borders. (a) Original image (b) Ground truth (c) DC-UNet (92.99 %)

## Conclusion and Future Work

DC-UNet has a lot of promise in multimodal medical picture segmentation. DC-UNet performs admirably on the CVC- ClinicDB dataset. DC-UNet appears to be more dependable and sturdy. DC-UNet can identify ambiguous limits and avoiding noise interference. Even in difficult circumstances, the DC-UNet has a superior capacity to capture small details. As a result, the DC-UNet architecture may be a useful a medical role model picture segmentation. Data augmentation techniques such as rotating, flipping, and cutting at random to extend datasets and picture improvement are particularly beneficial in producing better results. Data augmentation procedures can assist models in avoiding overfitting during training. In addition to data augmentation and picture enhancement approaches, dual-channel CNN designs have potential. In our trials, we solely employ the segmentation model with two channels. Additional channels, similar to ResNeXt's blocks, will result in more useful features, however it will result in parameter increments and floating point operations (FLOPs). Furthermore, there are alternative versions of the Inception module, such as Inception-v4 and Inception-v3, that demonstrate how to use To swap out the initial convolution kernel, use asymmetric convolution. In order to further minimise the parameters, the 3X3 convolution operator, following a 1X3 convolution, might be replaced with a 3X1 convolution.

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**References**

1. Gao, J., Jiang, Q., Zhou, B., & Chen, D. (2019). An overview of convolutional neural networks for computer-aided identification or diagnosis in medical image processing. 16(6), 6536, *Mathematical Biosciences and Engineering*.
2. Olaf Ronneberger, Philipp Fischer, Thomas Brox. (2015). Convolutional Networks for Biomedical Image Segmentation (U-Net). *Computer Vision and Pattern Recognition International Conference* (pp. 194-403). IEEE
3. Kuruvilla, J., Sukumaran, D., Sankar, A., & Joy, S. P. (2016, March). An examination of image processing and image segmentation 2016 saw the SAPIENCE conference, an international gathering on data mining and advanced computing (pp. 198-203). IEEE.
4. Bernal, J., Sánchez, F. J., Fernández-Esparrach, G., Gil, D., Rodríguez, C., & Vilarino, F. (2015). Validation vs. saliency maps from doctors: WM-DOVA maps for precise polyp highlighting in colonoscopy. 43, 99–111, *Computerized Medical Imaging and Graphics*
5. Song, H., Nguyen, A. D., Gong, M., & Lee, S. (2016). An examination of computer vision techniques for computer-aided diagnostics. *J. Int. Soc. Simul. Surg.* 3, 1–8
6. Voulodimos, A., Doulamis, N., Doulamis, A., & Protopapadakis, E. (2018). A quick overview of deep learning for computer vision. *Neuroscience and computational intelligence*, 2018.
7. Arganda-Carreras, I., Turaga, S. C., Berger, D. R., Cireşan, D., Giusti, A., Gambardella, L. M., ... & Liu, T. (2015). developing image segmentation algorithms using crowdsourcing for connectomics *Neuroanatomical Frontiers* 9, 142.
8. Xie, S., Girshick, R., Dollár, P., Tu, Z., & He, K. (2017). Deep neural network modifications of the aggregated residuals. *IEEE Conference on Computer Vision and Pattern Recognition Proceedings* (pp. 1492-1500).
9. Perez, L., & Wang, J. (2017). The efficiency of data augmentation in deep learning picture categorization. Preprint for arXiv is arXiv:1712.04621.
10. Girshick, R., Donahue, J., Darrell, T., Malik, J.:for precise object identification and semantic segmentation, rich feature hierarchies. In: *Computer Vision and Pattern Recognition (CVPR) Proceedings of the IEEE Conference* (2014)
11. Ange Lou, Shuyue Guan, Murray Loew.: Using Dual Channel Efficient CNN to Rethink the U-Net Architecture for Medical Image Segmentation is called DC-UNet. Preprint AXIIV:2006.00414
12. Cardona, A., Saalfeld, S., Preibisch, S., Schmid, B., Cheng, A., Pulokas, J., ... & Hartenstein, V. (2010). an integrated micro- and macroarchitectural study using computer-aided serial section electron microscopy on the *Drosophila* brain. 8(10), e1000502 in *PLoS Biology*.
13. Song, H., Nguyen, A. D., Gong, M., & Lee, S. (2016). An analysis of computer vision techniques for use in computer-aided diagnostics *International Society for Simulative Surgery Journal*, 3, 1–8.
14. Szegedy, C., Ioffe, S., Vanhoucke, V., & Alemi, A. A. (2017, February). Relative connections' effects on learning are influenced by Inception-v4, Inception-resnet, and other factors

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**Conclusion and Future Work**

Prediction of MoA of novel drugs is a very important task. It improves the usage and trust on the drug. It also makes it easier for doctors to suggest and get to know what areas a drug can affect or what can be its side effects. So, prediction of MoA is gaining a lot of scope in the research. In this project it was checked the capability of Artificial Neural Network for the prediction of the MoA. The model with 3 hidden layers gave the best accuracies and the least losses. If there is more vertical data i.e. more number of drugs that are tested and more horizontal data i.e. more features for the cells being tested then the predictions and accuracies both can improve. There is a lot of future scope for ML in predicting MoA's as other physical and chemical methods for predicting the MoA's are becoming obsolete and as the number of novel drugs being invented is increasing the requirement for better and faster methods like ML is increasing.

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**References**

1. Warchal SJ, Dawson JC, Carragher NO. Evaluation of Machine Learning Classifiers to Predict Compound Mechanism of Action When Transferred across Distinct Cell Lines. *SLAS DISCOVERY: Advancing the Science of Drug Discovery*. 2019;24(3):224-233. doi:10.1177/2472555218820805
2. Moe Elbadawi, Simon Gaisford, Abdul W. Basit, Advanced machine-learning techniques in drug discovery, *Drug Discovery Today*, Volume 26, Issue 3, 2021, Pages 769-777, ISSN 1359-6446, <https://doi.org/10.1016/j.drudis.2020.12.003>
3. Payal Chandak, Nicholas P. Tatonetti, Using Machine Learning to Identify Adverse Drug Effects Posing Increased Risk to Women, *Patterns*, Volume 1, Issue 7, 2020, 100108, ISSN 2666-3899, <https://doi.org/10.1016/j.patter.2020.100108>.
4. Gururaj, H.L., Flammini, F., Kumari, H.A.C. et al. Classification of drugs based on mechanism of action using machine learning techniques. *Discov Artif Intell* 1, 13 (2021). <https://doi.org/10.1007/s44163-021-00012-2>

5. Madhukar, N.S., Khade, P.K., Huang, L. et al. A Bayesian machine learning approach for drug target identification using diverse data types. *Nat Commun* 10, 5221 (2019). <https://doi.org/10.1038/s41467-019-12928-6>
6. Dimitri GM, Lió P. DrugClust: A machine learning approach for drugs side effects prediction. *Comput Biol Chem*. 2017 Jun;68:204-210. doi: 10.1016/j.combiolchem.2017.03.008. Epub 2017 Mar 30. PMID: 28391063.
7. Liu, C., Hogan, A.M., Sturm, H. et al. Deep learning-driven prediction of drug mechanism of action from large-scale chemical-genetic interaction profiles. *J Cheminform* 14, 12 (2022). <https://doi.org/10.1186/s13321022-00596-6>
8. Réda C, Kaufmann E, Delahaye-Duriez A. Machine learning applications in drug development. *Comput Struct Biotechnol J*. 2019 Dec 26;18:241-252. doi: 10.1016/j.csbj.2019.12.006. PMID: 33489002; PMCID: PMC7790737.
9. Chandrasekaran, S.N., Ceulemans, H., Boyd, J.D. et al. Image-based profiling for drug discovery: due for a machine-learning upgrade?. *Nat Rev Drug Discov* 20, 145–159 (2021). <https://doi.org/10.1038/s41573-020-00117-w>
10. Bantscheff M, Eberhard D, Abraham Y, Bastuck S, Boesche M, Hobson S, Mathieson T, Perrin J, Raida M, Rau C, Reader V, Sweetman G, Bauer A, Bouwmeester T, Hopf C, Kruse U, Neubauer G, Ramsden N, Rick J, Kuster B, Drewes G. Quantitative chemical proteomics reveals mechanisms of action of clinical ABL kinase inhibitors. *Nat Biotechnol*. 2007 Sep;25(9):1035-44. doi: 10.1038/nbt1328. Epub 2007 Aug 26. PMID: 17721511.
11. Davis MI, Hunt JP, Herrgard S, Ciceri P, Wodicka LM, Pallares G, Hocker M, Treiber DK, Zarrinkar PP. Comprehensive analysis of kinase inhibitor selectivity. *Nat Biotechnol*. 2011 Oct 30;29(11):1046-51. doi: 10.1038/nbt.1990. PMID: 22037378.
12. Connectivity Mapping: Methods and Applications Alexandra B. Keenan, Megan L. Wojciechowicz, Zichen Wang, Kathleen M. Jagodnik, Sherry L. Jenkins, Alexander Lachmann, and Avi Ma'ayan *Annual Review of Biomedical Data Science* 2019 2:1, 69-92