Original Article

Exploring the Cervical Cancer Prediction by Machine Learning and Deep Learning with Artificial Intelligence Approaches

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Abstract - Cervical cancer is among the most prevalent and lethal tumours that affect women. Despite this, this cancer is completely curable if diagnosed at a precancerous stage. A standard diagnostic method for cervical cancer detection is the Pap smear system. Due to negligence, the hand-operated screening technology has a significant false-positive rate. Deep learning-based computer-aided diagnostic approaches are widely developed to divide and classify cervical cytology images automatically to improve the efficiency and effectiveness of manual screening. This survey presents an overview of deep learning and machine-learning algorithms for evaluating cervical cancer. To begin, we will discuss deep learning and machine learning, the various simple models employed in this subject. This paper provides a summary of previous research and even its methodology.

Keywords - Machine Learning (ML), Support Vector Machine (SVM), Deep Learning (DL), Cervical Cancer, Random Forest (RF), Logistic Regression (LR), K- Nearest Neighbor (KNN), Gestational Diabetes Mellitus (GDM).

1. Introduction

The most frequent malignant tumour in women is cervical cancer. It is the 4th largest reason for mortality from cancer. It can be spread through touch or distant metastases, providing a serious health risk to women. Furthermore, due to low awareness and proper medical facilities, underdeveloped countries are more prone to cancer mortality, which makes up nearly 90% of cervix cancer-related deaths. Cervical cancer is becoming less common in developing countries, although it is becoming more common among young women. As a result, it is critical to make a clear diagnosis for early-stage cancer detection and use dependable approaches, which are in high demand. As a result, precise and timely histopathological image analysis is critical in clinical investigation. A physician who can examine histology images must undergo extensive training and devote 100% of their attention to the task at hand, including the time it takes to analyze the sample.

HPV is the main cause of this condition, which causes a tumor in the contaminated area. Health professionals say the condition can be cured with timely screening and vaccination. Furthermore, it is one of the most common tumours. In 2013, an estimated 527,000 instances were reported in women. Current cancer research necessitates rapid diagnosis and precise disease identification.

Every day, the ordinary human body produces 40 to 60 billion cells to replace those that have died or become damaged. Human cells can sometimes overgrow and produce a Tumor, benign or malignant. Only malignant tumours are described as cancer cases. This paper is about a kind of cancer known as cervical cancer. Two main variables cause cancer: adjustable elements such as first, there's sexual activity, and then there are non-modifiable things like mutational hormones. Every patient with cervical cancer is unique. Cancer Treatment Centers of America has vast experience correctly evaluating and diagnosing the disease and designing a treatment plan suited to each patient's kind of cervical cancer. Cervical cancer develops when cells lining the cervical begin to alter abnormally. These aberrant cells may grow malignant or return to their original over

time. The majority of women do not acquire cancer as a result of aberrant cells.

Cervical cancer is categorized into two types: adenocarcinoma and squamous cell carcinoma. The look of cells under a microscope distinguishes each. Squamous cell carcinomas develop from the thin, flat cells that border the cervix's bottom. According to the American Cancer Society, this form of cancer accounts for almost 90% of cervical malignancies. Cervical adenocarcinomas form in the glandular cells that border the upper part of the cervix.
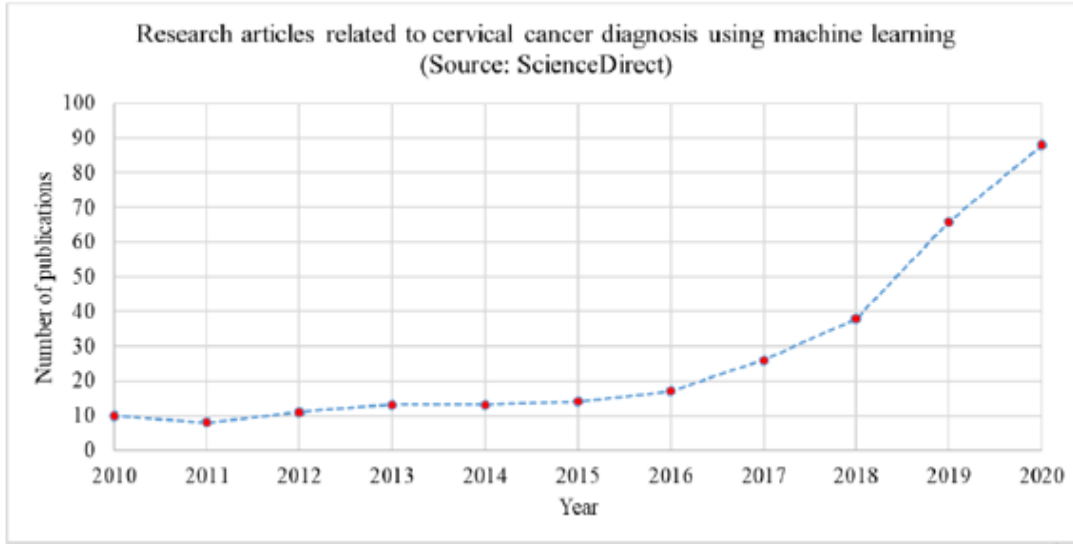

Fig. 1 Articles on the use of machine learning to diagnose cervical cancer

2. Three Levels of Cervix Cancer

For women of reproductive age, cervical cancer monitoring is divided into three tiers. Cervical cytology is the most prevalent early cancer screening, referred to as narrow liquid-based cytology. An aberrant cervix can be detected early by examining a highly porous vaginal cell smear under a microscope. The second phase of electronic colposcopy is essential if the patient's TCT test indicates suspicious high-grade malignancy. Colposcopy is a procedure that involves using a microscope with a source of light and filter to enlarge the epidermis tissues of the cervix or genitals to monitor minute changes in the cervix epithelium with veins; several biopsies of suspicious lesions should be obtained and then sent to histological investigation under the supervision of acetic as well as iodine solutions staining if anomalies are identified during colposcopy.

3. Related Work

Y. Song et al. [1] approach such as cervical cell identification, super-pixel segmentation, and Convolution neural segmentation are proposed. Because there is no cytoplasm contrast in the backdrop. Then, to identify the region of interest, CNN is used. They obtain the data in this experiment in a confidential manner. They train the network with 1200 cell samples and test it with 200 cell units. They use 21 photos to assess performance. 1024 1360 pixels is the image size. The trim mean filter minimizes the image's noise during preprocessing. They got an F1 score of more than

0:89. Y. Song et al. [2] proposed extracting features and graph partitioning for nucleus segmentation, which the author devised using a multi-resolution convolutional neural network. Cytoplasm, nuclei, and background can be separated using the MSCN and graph partitioning techniques. However, a new resilient nuclei clump approach is proposed to solve the cell image's overlapped nuclei. They collect the dataset for this experiment in private, comprising 21 photographs (15 abnormal and six normal). They achieved cytoplasmic and nuclear segmentation results of 90% and 85%, respectively, utilizing MSCN and graph partitioning. Xue, Dan, et al. [3] studies on the usefulness of ensembles learning approaches in processing cervical histopathology pictures have been conducted in recent years. Finally, using the Herlev dataset, an examination - related to distinguishing benign from malignant cells is conducted, with an accuracy rate of 98:37 percent. Ilyas et al. [4] presented in this study suggest an Ensemble classification approach. The researchers tested a variety of classifiers, including DT, SVM, NB, J48 Trees, RF, LR, and KNN. The study shows a 94 percent increase in prediction accuracy, which beats the accuracy of individual methods performed on the benchmark datasets. As a result, the suggested paradigm gives health practitioners a second opinion on disease detection and treatment. Yu, Suxiang, et al. [5] examined the ability of a deep learning network to detect aberrant cells in this research. The Thin Prep cytologic test data is gathered from Baoding's fourth central hospital. The

second model improved on the first by adding a spatially pyramidal pooled layer to handle cell pictures according to their sizes. Based on the first, the third model replaces the CNN layer with the fully–connected. On the other hand, the fourth model combined the SPP layers and the conception modules into the first framework.

Abdoh, Sherif F. [6] discovered that deep learning had shown considerable promise when applied to biological challenges, such as medical image processing, disease prediction, and picture segmentation. As a result, in needed to execute cervical cancer screening, very high residual learning-based networks are constructed. Furthermore, we emphasize the effect of activation functions on the result of a residual setup represented in this research. As a result, three residual networks with distinct activation functions of the same structure are formed. Huang, Pan, et al. [7] proposed the lowest relative shrinking and selecting operator and support vector machine is used in this paper to provide a technique for cervical biopsy tissue image classification (EL-SVM). The receiver operating curve and errors curve has been used to assess the classifier's generalization capacity after detecting and categorizing 468 biopsy tissue pictures using the EL-SVM classifier. According to tests, the accuracy of regular cancer classification was 99.64 percent.

Wu, Wen, et al. [8] discovered cervical cancer is currently diagnosed using only a few approaches. This research introduces the SVM technique for cervix cancer diagnosis. To diagnose cancer samples, two enhanced SVM approaches are proposed to use support vector machine-recursive feature reduction & (SVM-PCA). After that, evaluate the 3 methodologies that the risk factor results in the underlying data. The SVM-PCA technique has been shown to outperform the others. Zhang, Huiting, et al. [9] proposed the genuine Raman spectrum signals of precancerous cervical tissue are obtained in this work, and the signal properties of the spectrum were extracted using the PLS and Relief techniques. Then, after developing and comparing KNN and ELM classification models, we could detect cervical cancer early. In this experiment, the first and 2nd derivative features were used to develop a feature-based fusion approach in feature extraction. ELM has a 90.81 % accuracy rate without feature fusion and a 93.51 percent average accuracy after fusion. The findings show that feature matching accuracy has improved and will be used as a creative spectrum information fusion method.

Lin, Haoming, et al. [10] investigated this research to provide a CNN-based technique for segmenting cervical cells in Pap smears that integrates cells' image appearance and morphology. The cervical cell dataset's training consists of coarsely centred picture patches that have been adaptively re-sampled. For comparison, multiple Neural network models pre-trained databases are on the dataset. The proposed strategy is tested using 5 cross-validations at client splitting on the Herlev cervix dataset. Improved classification results

can be attained by including cytoplasm and nucleus mask as baseline morphological information in appearance-based CNN learning. Senthilkumar, Geeitha, et al. [11] states that the LASSO algorithm was developed to predict repeated specific gene in body parts. The recurring genetic code is obtained from Geo Datasets. To evaluate feature selection, the Hilbert-Schmidt independence criteria are paired only with HSDAFS. This technique incorporates a component based on genetic value, and lncRNA ratings are determined via AI. The prognosis factor of 300 samples in GSE44001 was calculated using a risk factor of 9 lncRNA features.

Lu, Jiayi, et al. [12] proposed that this research presents a novel ensembles approach to predicting cancer risk. To increase the prediction's performance, a data rectification mechanism is presented. To evaluate the proposed procedure, multiple measurements are taken. The findings suggest that by utilizing the voting technique, the chance of having cervical cancer can be accurately predicted. The suggested technique is much more flexible and practical than other ways.

Zhang, Shuailei, et al. [13] introduced the ResNet50 versions of the cnn model are used as a featured extractor in this experiment. This experiment presents the Stacking Generalization categorization technique to expand the model's accuracy, adaptability, and stability. In the SK classification model, the first-layer base learner possibilities include CNN-KNN, CNN-RF, and CNN-SVM, while Multilayer Perceptron is the second-layer classifier option (MLP). MLP, for example, gets the result by studying the base learner's label discrimination classification performance; the classification model's efficiency after ensemble methods is over 90%. CNN was used to determine cervical cancer cells. Cell photos are fed into an Intelligence model to obtain deep learning cervical cancer features. An ELM classifier is used to classify the input photographs. CNN's methodology employs transfer learning and fine-tuning [14].

Kim et al. [15] designed women who had a severe hysterectomy at the beginning period were prospects for this treatment, according to a proposed classifier for precise Method Mortality over a 5 period. The monogram was evaluated by bootstrap, and performance was evaluated with the concord index and calibration curves. With a p-value below 0.05, the infection phase, the number of major nodes, and the invading depth were all recognized as risk variables for cervical illness recurrence. Yoshida et al. [16] state that the PRS of patients with RUCC was developed in an estimated cervical cancer study. PRS had an impact on clinic pathological indications as well. Some individual and multivariable analyses were agreed with using the Kaplan Meier and Cox regression models. Patients with cervical cancer.

Mabuchi et al. [17] introduced a new work that developed a novel technique for determining the length of life in people living with recurring cancer who had previously received radiotherapy to discover predictive indicators. The study cited relapse site, disease state, initiating chemoradiotherapy, and treatment approach as predictive factors. Doctors can accurately assess cervical cancer using these four clinical factors. Lora et al. [18] investigated by identification of patients with localized cervical cancer based on spectral considerations, and the model, including prognostic indicators, was validated (LACC). The general face time of the models with elements was considered when discriminating, calibrating, and evaluating the efficiency of different metrics.

On an individual basis, I'm committed to designing and constructing a prediction model for cervical cancer patients that have had a full hysterectomy.[19] Predictive models for all people with cancer are developed early on, including overall disease-free survival. A Kaplan-Meier graph was utilized in the proposed approach to highlight the variations in survival prediction for each risk group. Liu, Jun, et al. [24] proposed that fuzzy reasoning methodology could improve sensitivity much more without requiring more features. The automatic CIN categorization technique suggested here could be a useful test in the future. Cervical cancer prevention is a topic that has received a lot of attention recently. Cervical epithelial cells are recognized and classified using Artificial Intelligent (AI) and the Random Forest method based on the Artificial Fish Swarms Algorithm. Using 200+ cervical Pap smear pictures, the proposed approaches [25] were tested. The experiments reveal that cervical cells can be separated with a good segmentation outcome. With the smallest feature number, the proposed method approach attained an efficiency of 81.31 percent. Under fivefold cross-validation, the modified RF with 2 and 7 classifications achieves the greatest classification accuracy of 96.86 percent.

Tatsuya et al. [26] determine the goal of this study is to learn more about the current practice of 3D image-guided brachytherapy for cervical cancer treatment in Japan, as well as the problems associated with its implementation. A 30-item questionnaire was given to 171 Japanese businesses that use high-dose-rate brachytherapy equipment in 2012. For review, a total of 135 responses were received. Fifty-one hospitals had purchased 3D imaging modalities with applicator insertion, with CT and MRI used in 51 and 3 hospitals, respectively. X-ray films, CT scans, and MRI scans were used for actual treatment planning at 113, 20, and 2 facilities, respectively. Due to a lack of time, 29 of the 43 sites that utilized an applicator to collect X-ray images and CT or MRI still used X-ray films. Zhang et al. [27] proposed to develop an AI architectural style for automating the removal of difficult-to-understand representations from contrast-enhanced ultrasound (CEUS) videos and assess the AI design for identifying benign and malignant cervical

lymph nodes. A total of 127 lymph glands (39 normal and 88 malignant) from 88 patients were evaluated quantitatively using five-fold cross-validation. Normal and malignant cervical lymph nodes showed a substantial variation in SVM probability. The PGBM-based AI architecture has demonstrated good classification accuracy and could be used in the future to clinically diagnose cervical lymph node cancer.

Diffusion-weighted images (DWI) of 98 patients with advanced cancer were obtained for this investigation. We used 2D and 3D U-Net to train an automatic tumour contour segmentation model to see if such a model may be used in clinical practice. The training used 98 examples [28] that were then forecasted by switching the train and test images. Six predictions images were acquired after six pieces of training for one case to predict tumour outlines. The six pictures were combined and binarized using automatic contour segmentation to create a final image. The Dice similarity coefficient (DSC) & Hausdorff distance were used to investigate the disparity between radiation oncologists' tumour contour delineation and the output image (HD). As a result, the analysis revealed that the outline of cervical tumor tissue might be segmented accurately and automatically. Liu, Yiming, et al. [29] suggest a cervical nucleus feature extraction technique in which pixel-level prior information is used to provide supervisory information after training a mask regional convolutional neural network, which will be used to achieve the nuclei's multiscale characteristics, and the nuclei's coarse segmentation and set of points, using Mask-RCNN forward propagation. We tested our method using cervical nuclei from the Herlev Pap smear data set and discovered the precision and recall. Similarity indexes all were higher than 0.95 to low standard deviations, demonstrating that our model is more effective and trustworthy than current condition methods.

Asiedu et al. [30] present automatic extraction of features for acetic acid & Lugol's iodine cervigrams and approaches for merging features/diagnosis of distinct cervigram contrasts for increased performance. The features were used to create a support vector machine model for visually assessing cervigrams based on related diseases. The conceptual methodology is found to be valid to the tune of 80.0 percent. Luo, Yan-Min, et al. [31] suggested For the diagnosis and classification of cervical lesions, this research provides a deep learning-based strategy based on multi-CNN decision feature integration. In data preprocessing, the suggested methodology employs the k-means technique to group training data into specified classes, which is then educated in cross-validation to increase the model's generalization capacity. Based on the combination of the two techniques, two unique integrating methods (inner-to-outer and outer-to-inner) are developed as the final product. The proposed multi-decision feature fusion technique and the K-means preprocessing stage method may improve the learning

of neural networks. The suggested K-means preprocessing stage method can better get computer-aided diagnosis findings that meet the clinical diagnosis needs.

Wang, Tao, et al. [32] propose a tree domain structure with an insight screening approach for locating probable nucleus locations in cervical cytology photos using circumferential grouping features of nuclei deeper data. The projected nucleus regions are meticulously segmented using an iterative level set approach based on evolutionary radius morphological dilation. The ISBI2015 open dataset is used to evaluate the research findings. The recommended nucleus segmentation method outperforms state-of-the-art approaches regarding its potential prognostic accuracy, diagnostic accuracy, specificity, and recollection of something like cervical nucleus segmentation. Ghoneim et al. [33] investigate a CNN-based cervical tumour cell detection and diagnosis method in this research. The cell pictures are loaded into a CNNs model to extract deep-learned features. The input photos are then classified using an extreme learning machine (ELM)-based classifier. Transfer learning and fine-tuning are utilized to implement the CNN model. The Herlev database is used in the experiments. In the detection task, the suggested CNN-ELM-based method achieves 99.5 percent accuracy and 91.2 percent in the classification challenge.

Akbulut et al. [34] created a predictive model using assistive e-Health applications that pregnant women and practitioners' data can use was processed using machine learning and deep learning algorithms to predict the status of foetal anomalies based on maternal and clinical information. During development tests using the Decision Forest model, the maximum prediction accuracy was 89.5 percent. Kopanitsa, Georgy, et al. [35] determines maternal sepsis is responsible for 11% of all maternal deaths globally. It is the third leading cause of maternal death. Machine learning analyzes massive amounts of data to uncover underlying correlations and regularities. We are building actual world-proof data-driven methods that will be able to recognize the danger of sepsis in pregnancy at an early stage of its development, taking into account the potential of machine learning in the prediction and risk management of sepsis. At last, the derived performance model was 95% accurate. Decision Tree Classification was employed as the methodology, including well-suited algorithms for medical diagnosis. The C4.5 Decision Tree approach was one of the research's most widely used and successful classifiers for pregnant data classification. [36] The purpose of this report is to highlight the value of collecting data parameter standardization in the research, to measure performance from the C4.5 classification model across both un-standardized and standardized sets of data, and to assess the effectiveness of the proposed method in terms of computation time once

implemented to a dataset obtained from accumulated and standardized maternity statistics.

Alsmariy, et al. [37] purposed the study to use machine learning techniques to create a model that can diagnose cervical cancer effectively and sensitively. The classification model was built using the UCI's cervical cancer health risk data using a voting approach that combined classification methods: decision tree, logistic regression, and random forest. Finally, by comparing our findings to previous research, we discovered that these models were more effective at diagnosing cervical cancer based on key evaluation criteria. Divakar et al. [38] provide an integrated strategy for diagnosing cervical cancer that combines ontology-driven algorithms with neural networks. The MATLAB deep learning toolbox is frequently employed to identify the obtained features from cytology pictures used to analyze different cancer stages. The interaction between the core and the cytoplasm and the form and colour strength of the nucleus region, perimeter, and eccentricity are all important diagnostic criteria. Using the Scaled Conjugate Gradient (SCG.) Training Algorithm, this article reports a 95.6 percent efficiency using the deep-leaning technique.

The most frequent birth abnormality is congenital heart disease (CHD). An ensemble of neural networks was trained to identify recommended cardiac images and distinguish between normal and complicated CHD hearts. Finally, we calculated conventional fontal cardiothoracic measures using segmentation models. The model had a 95 percent AUC of 0.99[39]. The author proposes a Bayesian weight gain forecasting method that efficiently deals with the restricted data available for earlier detection. The findings were validated using a variety of European and Chinese groups; by using individual data mid-way through the trimester [40], the greatest state-of-the-art returns were 8.17 & 6.60 kgs in corresponding communities. The prediction model can track a woman's weight growth during pregnancy and help her fulfil her GWG goals, preventing excessive or insufficient weight gain. Du, Yuhan, et al. [41] created an ML-based clinical decision support system that can be used to identify at-risk women who require targeted prenatal intervention. 5 ML techniques were used to optimize the balanced accuracy after suitable data preprocessing, synthetic minority oversampling methodology, and feature selection. This model was implemented as a publicly accessible web server for academic usage.

After limited fine-tuning, the model was trained on a diversified data set of 741 developmentally normal foetal brain images aged between 19 to 39 weeks maternal age, and performance and generalizability were demonstrated using individual data sources from four academic universities and institutes in Turkey, with R2 results of 0.81–0.90. The described statistical technique could establish a robotic tool to assess prenatal neurogenesis and direct authentic maternal time of life prediction from the first pregnancy [79]. This

study provides a comparison of Bayesian ML algorithms. Depending on the patient's risk indicators exhibited by the patients, networks are capable of recognizing at-risk pregnancies. The finest method for the prediction was established by comparing the performance of numerous Bayes-based ML techniques. [43] Detection and treatment of hypertension problems in pregnant women. This study's contribution focuses on creating clever classifiers for new mobile devices that provide consistent results in detecting pregnancy-related issues. As a result, this research may help to reduce maternal and foetal deaths. To see if including nonalcoholic fatty liver disease-related variables improves the model's performance, [44] researchers constructed earlier forecasting models in gestational diabetes mellitus with machine learning. RF, LR, SVM, and deep neural networks were used to build the predictive methods. This thesis aimed to evaluate the results of machine learning algorithms to logistic regressions in predicting GDM. To predict the occurrence of GDM [45], eight standard machine learning methods and two common regressions, stepwise logistic regression and logistic regression were used. The DT model outperformed the other machine learning approaches (AUC 0.74, 95 percent CI 0.71-0.76), with only minor differences.

Zhang et al. [46] discuss using ultrasound imaging throughout various pregnancy phases and examining malignancies discovered in lactation or pregnancy. Advanced Machine Learning techniques use logistic regression classifiers plus convolution neural networks to translate a basic image as input to the desired output image. The findings of the experiments suggest that the LRC based on CNN can be used to forecast the output of an obstetric ultrasound with enhanced maternal and neonatal mobility rates. For diabetes mellitus disease diagnosis and severity level estimation, this research developed an optimum weighted oriented deep artificial neural network approach. [47]. The suggested system is divided into two phases, one for disease prediction and the other for severity level estimate. Preprocessing for the Pima dataset is done during the illness prediction phase. The features are taken from the preprocessed data, and then OWDANN is used to complete the classification phase. Akhtar et al. [48] goal of this research is to find the most predictable biochemical indicators for predicting gestational age in large animals with the least computational effort. Tenfold cross-validation was used on a large dataset for gestational age to train some machine learning algorithms. When compared to certain other machine learning classifiers, the support vector machine outperformed them all, with an 85 percent prediction precision score.

The cost-sensitive hybrid model (CSHM) and five classic machine learning algorithms are used to create prediction models that capture the future hazards of GDM in temporally aggregated EHRs. The experimental data came from a nested case-control research cohort. Even though positive sample efficiency is just 62.16 percent, the data show that the vast majority (98.4%) of those expected positive occurrences are actual positives [49]. Akbulut et al. [50] created a predictive model with supportive e-Health applications that pregnant women and practitioners can use. The performance of nine binary classifier models was examined after they were trained using a test data set of 89 pregnant women. They were then used to forecast fetal abnormality status based on maternal and clinical data. During development tests using the Decision Forest model, the maximum prediction accuracy was 89.5 percent. The author aimed to produce various ML models to forecast small-for-gestational-age (SGA) infants in women exposed to radiation before conception. For the classification model of SGA prediction, eight different machine learning models were examined. ML algorithms can create robust models to predict SGA babies in pregnant women exposed to radiation before conception and hence can be used as a tool to predict SGA infants in high-risk pregnant women [79]. Gudigar et al. [52] proposed a software diagnoses tool that used foetal sonography of moms with typical pregnancy-induced hyperglycemia and gestational diabetes mellitus (GDM). Compared to deep learning techniques, the shearlet-based characteristics produced encouraging results under the LPCS framework. Using an SVM classifier, the suggested technique attained a higher precision of 98.15 percent. As a result, doctors may be able to use this paradigm to detect foetal cardiac hypertrophy in women who have pre-GDM or GDM.

The purpose of this study was to establish forecasting models for embryonic development using ml algorithms. To develop prediction models, six sample machine learning methods were used: Logistic Regression, Support Vector Machine, Decision Tree, Back Propagation Neural Network, XGBoost, and Random Forest. Random Forest [53] was the most accurate of the six predictive models, with a recall ratio and F1 of 97 percent and an AUC of 0.97. This research presents a novel ensemble approach for predicting the risk of cervical cancer. This method overcomes the limitations of prior cervical cancer studies by employing a voting strategy. To increase the prediction's performance, an A data correcting mechanism is proposed [54]. A gene-assistance mechanism is an optional technique to improve the prediction's robustness. To evaluate the proposed procedure, multiple measurements are taken. The findings suggest that the chance of having cervical cancer can be accurately predicted utilizing the voting technique. The presented scheme is more flexible and practical than other ways. The author provides a unique strategy for successfully deconstructing a separate pregnant abdominal Electrocardiogram into a mother Electrocardiogram and a foetus Electrocardiogram without numerous steps, based on an end-to-end deep learning network infrastructure on W-net. Using a dataset from a simulation, then, from a live maternal abdominal ECG, a foetus ECG is extracted, and the

architecture's performance is evaluated to other deep learning methods [55] that recognize QRS complexes.

Sammali et al. [56] According to machine learning, a new method for extracting EHG and TVUS features is proposed here, built upon singular value decomposition of both the obtained EHG and TVUS recordings. Sixteen women were assessed during three stages of Fertility treatments: follicular stimulation, embryogenesis, and 5 to 7 days after ET. Following feature space reduction using correlations filtering, 3 machine-learning algorithms, namely SVM, KNN, and Gaussian mixture model, were refined and assessed for their capacity that forecast successful embryo implantation using nested leave-one-out cross-validation. KNN had the maximum accuracy of 93.8 percent in all phases, whereas SVM had the highest accuracy in FS and ET1 phases. It provides a hybrid methodology for a specialized system built on Bayesian networks, a multicriteria decision-making approach, and artificial intelligence, in such approach, based on symptoms of diseases that appear in tandem or develop due to the favorable environment created by the progression of undiagnosed diabetes. The disorders and symptoms investigated [57] were taken from medical journals. Federated learning can assist solve this problem by delivering a copy of trained models rather than raw data to the central server and aggregating them. We share our findings in this publication, a federated learning strategy that protects privacy. Users collaborate to learn and update the global information model in [58].

Furthermore, we demonstrate that this model revision can be done in stages without the need to save the data. Local changes are made indefinitely. The approach we propose achieves a mean of the absolute inaccuracy of 4.455 kgs while maintaining confidentiality 2.572 kgs were achieved by a centralized technique involving individual efforts. Data up to day 140 of training.

Participants had to submit the segmentation findings and measurements from the segmented objects to complete the challenge. A detailed quantitative and qualitative evaluation was conducted to compare the outcomes of a probable set of existing techniques offered to the problem. [78] Several experts (three for the head sub-challenge and two for the femur sub-challenge) manually identified those things of interest to define the actual data used by the assessment framework. Several teams produced results for the head sub-challenge comparable to manual delineations and may be used in clinical settings. The femur sub-challenge fared lower than the head sub-challenge because it is a more challenging segmentation task.
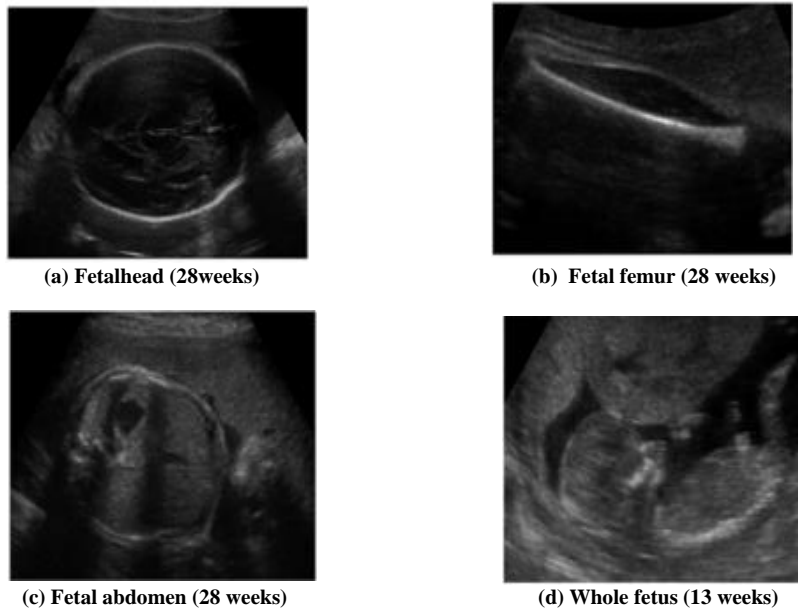

(a) Fetalhead (28weeks)

(b) Fetal femur (28 weeks)

(c) Fetal abdomen (28 weeks)

(d) Whole fetus (13 weeks)

Fig. 2 Ultrasound images of (a) the fetal head, (b) the fetal femur, (c) the fetal femur, and (d) the whole fetus.

Nucleolus, et al. [60] focused on reducing the societal and financial costs of early-pregnancy prenatal diagnostics testing for fetal aneuploidies by developing a noninvasive aneuploidy diagnostic technique. We offer a system based on artificial neural networks constructed using data on singleton pregnancy occurrences for first-trimester screening. This research employed three different datasets1, totaling 122 362 euploids and 967 aneuploid occurrences. This research aims to look into the promising prospects of using ml algorithms like ANN strategies for noninvasively assessing the amount of euploidy, trisomy 21, and other chromosomal aneuploidies (OCA) at 11–13 weeks gestation using sonographic,

biochemical, and other relevant data. [61] The information was randomized and split into training, which guided the construction of several ANN techniques, SVM classifiers, and k closest neighbor models. Using a thermal image captured with a smartphone, we describe a new approach for predicting SSI. Images taken as part of the clinical trial involving 530 women from rural Rwanda that undergone cesarean section surgery were used to construct machine learning algorithms. Thermal images were taken about 10 days following surgery, together with a wound check by a skilled doctor, to establish the wound's state (infected or not). Infected wounds were discovered in 30 of the 530 women. The data was utilized to create two Convolutional Neural Network (CNN) models, with specific attention paid to minimize fitting & address the problem of binary classification class imbalance. Fletcher et al. [62] Using a thermal image captured with a smartphone, we describe a new approach for predicting SSI. Images taken as part of the clinical trial involving 530 women from rural Rwanda that undergone caesarean section surgery were used to construct machine learning algorithms. Thermal images were taken about 10 days following surgery, together with a wound check by a skilled doctor, to establish the wound's state (infected or not). Infected wounds were discovered in 30 of the 530 women. The data was utilized to create two Convolutional Neural Network (CNN) models, with specific attention paid to minimize fitting & address the problem of binary classification class imbalance. The current research compares the performance of bagging and boosting classification models using birth data collected from government hospitals in Muzaffarabad, Kashmir. The experiments are carried out with the R package caret, a comprehensive platform for developing machine learning models. The accuracy-based results are presented together with other evaluation measures. Regarding accuracy, precision, and recall, bagging functions such as Adabag and BagFda fared somewhat better. There are improvements compared to a previous study on the same dataset [63].

According to the data, a real PPH diagnosis has a 96.7 percent accuracy rate, and a whole disseminated intravascular coagulation (DIC) prognosis has a 90.3 percent accuracy rate. In light of this, we may infer that the proposed machine learning model will help us properly forecast PPH risk, estimate the crucial stage of PPH patients, and anticipate that the findings of our study will contribute to a reduction in the rate of maternal death [64]. Ling et al. [65] determine a set of maternal serum screening data is analyzed with different evaluation settings; the experimental findings reveal that this framework outperforms some machine learning approaches. The best-indicated combination of inputs includes alpha-fetoprotein, human chorionic gonadotropin, unconjugated estriol, and maternal age. For DS screening, there are a few aspects to consider. Furthermore, our technique has the potential to produce much more precise forecasts for Unbalanced and feature-correlated data, resulting in a novel and successful method for the analysis of particular illnesses.
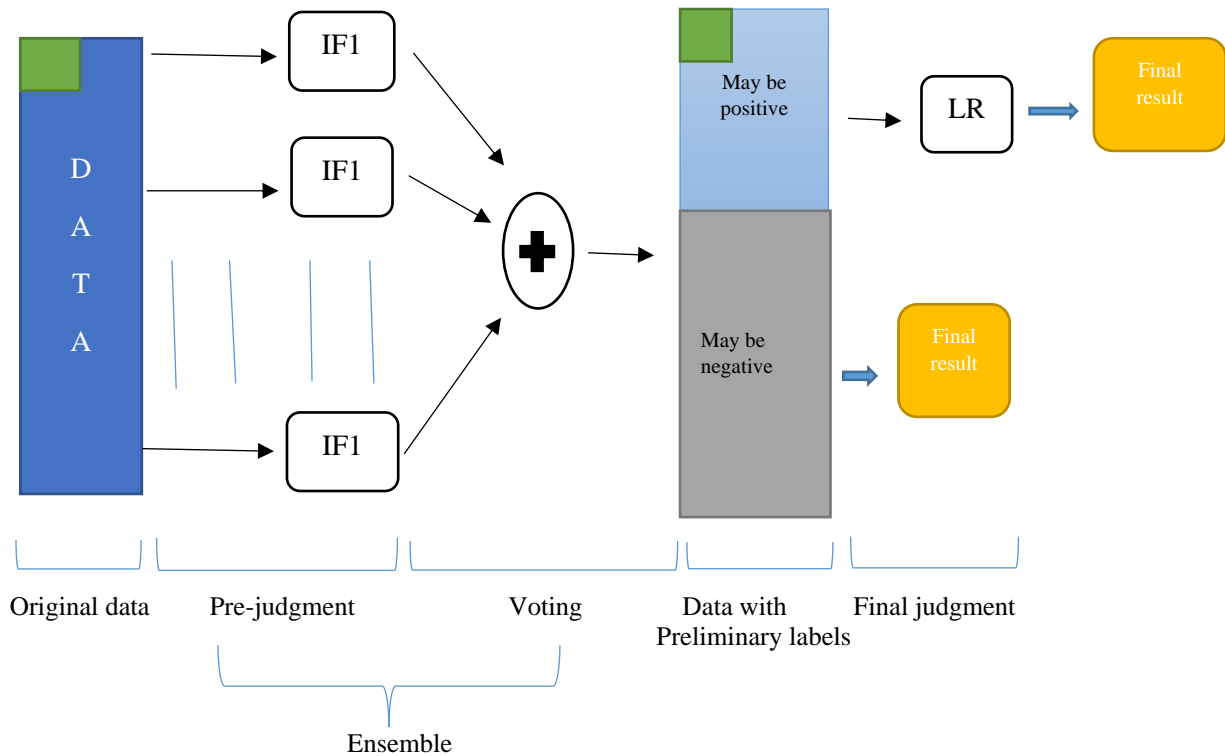

Fig. 3 Schematic representation of CVIFLR.

Image classification algorithms on deep learning methodology enhance the precision of identifying photos of disabled persons. Convolutional neural networks have been used to help persons with mental and physical limitations improve their picture classification. Images of persons with various disabilities were utilized in this study to extract hidden traits that represent each handicap. Authors implemented a technique that effectively improves image prediction for visually impaired people and improves image mobility security in cloud systems [66]. In addition, results from 19 studies in smears from individuals with neoplasia are provided. MN rates rose with neoplasia severity that was considerably increased in CC patients. Our meta-analysis reveals that the MN assay, which may be used with Pap tests and is straightforward to administer, might help define and predict CC. However, even before MN tests [67] are used in regular screening, they must be standardized (including the specification of the ideal cell counts & stains) and then further validated. The author created a model that can emphasize important traits in a low-dimensional space, making patient classification easier. We used deep learning architectures to implement the suggested method and obtained effective predictive results that outperformed previously developed methods [68].

Timpka et al. [69] study were to see how much a past of these pregnancy problems can improve CVD risk prediction over and beyond traditional predictors. In Sweden, pregnant women had standardized clinical appointments. The data were linked to delivery and CVD registries. Women with prenatal problems are more likely to have CVD later in life. When combined with other risk factors, however, having a history of HDP and having had LBW infants did not significantly enhance 10-year CVD early identification in women aged 50 and up. Most women (87.7%) were under 40, making the 10-year risk estimates advocated by American and European nations useless. All women could be tested for FRS-CVD. The ASCVD (81.5 percent) and JBS3 assessed much fewer people (91.6 percent. When assessing maternal cardiovascular disease and the requirement for postpartum follow-up, we believe that pregnancy problems should be assessed individually. Risk of cardiovascular disease in the mother and the requirement for postpartum follow-up [70].

Multiple assessment markers and regulated experimental models are used to assess the impact of predictive model creation. The RF model is used in this paper to rank the relevance of the output feature's feature importance based on the value of the input feature's classification result. The absolute mean errors to measure the reliability of the prediction of insulin levels [71] are based on the accuracy of logistic prediction. Sammali et al. [72] state that there are problems with self-reported weight measures, such as a lack of data and non-uniformity. To deal with limited data availability, it offers and compares two innovative parametric and non-parametric techniques that combine self-training data with population data. We continuously identify the subset of population weight gain data closest to a given person. The self-reported weight measures of a given person are then forecasted using a regression model learned on the specified subset. Our innovative approach forecasts end-of-pregnancy weight growth with an accuracy rate of 73.65 percent halfway through pregnancy.

In contrast, a strategy is only 53.75 percent accurate and has an MAE of 16.22 kgs. The authors suggested a multi-modal, multipara metric technique, outperforming alternative solutions based on the qualitative clinical assessment indicators. However, an effective dataset is needed to better classifier training and evaluate their clinical use within the context of IVF treatments [73].

Pregnancy is also renowned for its hyperglycaemic state, which is especially important for Fontan flow people. Furthermore, medications have the potential to pass the placental barrier and enter the foetal circulation. The available evidence for medicine during pregnancy is provided by European Medicine Agency & US Food and Drug Administration (FDA), which is useful for considering or changing drug therapy throughout pregnancy and breastfeeding [74]. The author devised a logistic regression gradient boosting technique-based information blood sugar strategy to assess multiple aspects of postprandial glycemic reactions in this study. The portion of food data from the smartphone app diary, food environment, patient factors, and patient behavioural surveys were all combined to create the model. A set of rules was devised and implemented to detect inaccurate meal entries and filter defective data. Analyses were done on the overall food diary information, specifically the information largely on current meals from which postprandial blood sugar reactions were computed [75]. Several monograms have been found to outperform standard staging methods. Their usage has been suggested as a supplement to, or even a replacement for, disease stage or other known prognosticators. A monogram to determine overall survival (OS) for cervical cancer patients in stages I–IV has yet to be reported. This research aimed to create and evaluate a monogram for forecasting patient survival in invasive cancer patients. The various classification approaches establish the four most regularly employed characteristics of models. ML approaches for predicting GDM [76] are more appealing than current screening strategies. The necessity of evaluation and consistent clinical diagnosis should be emphasized to increase their utilisation [77].
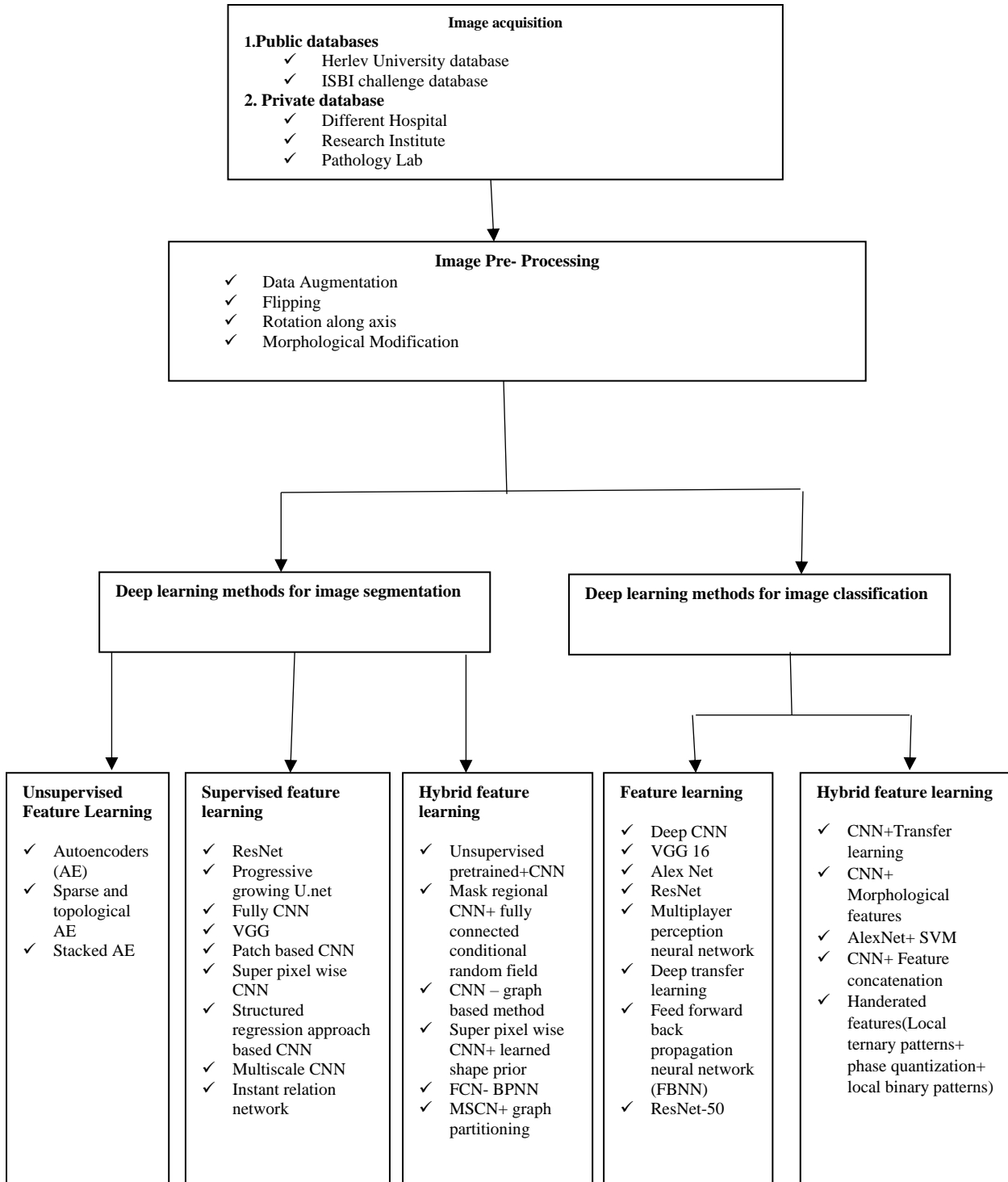
Image acquisition
1.Public databases
- ✓ Herlev University database
- ✓ ISBI challenge database

2. Private database
- ✓ Different Hospital
- ✓ Research Institute
- ✓ Pathology Lab

Image Pre- Processing
- ✓ Data Augmentation
- ✓ Flipping
- ✓ Rotation along axis
- ✓ Morphological Modification

Deep learning methods for image segmentation

Deep learning methods for image classification

Unsupervised Feature Learning
- ✓ Autoencoders (AE)
- ✓ Sparse and topological AE
- ✓ Stacked AE

Supervised feature learning
- ✓ ResNet
- ✓ Progressive growing U.net
- ✓ Fully CNN
- ✓ VGG
- ✓ Patch based CNN
- ✓ Super pixel wise CNN
- ✓ Structured regression approach based CNN
- ✓ Multiscale CNN
- ✓ Instant relation network

Hybrid feature learning
- ✓ Unsupervised pretrained+CNN
- ✓ Mask regional CNN+ fully connected conditional random field
- ✓ CNN – graph based method
- ✓ Super pixel wise CNN+ learned shape prior
- ✓ FCN- BPNN
- ✓ MSCN+ graph partitioning

Feature learning
- ✓ Deep CNN
- ✓ VGG 16
- ✓ Alex Net
- ✓ ResNet
- ✓ Multiplayer perception neural network
- ✓ Deep transfer learning
- ✓ Feed forward back propagation neural network (FBNN)
- ✓ ResNet-50

Hybrid feature learning
- ✓ CNN+Transfer learning
- ✓ CNN+ Morphological features
- ✓ AlexNet+ SVM
- ✓ CNN+ Feature concatenation
- ✓ Handerated features(Local ternary patterns+ phase quantization+ local binary patterns)

Fig. 4 DL methods for the analysis of cervical cancer

4. Datasets And Method Analysis

We'll go through several popular datasets and method analyses in this section.

4.1. Cervical Cytology Datasets

The Herlev and ISBI challenge databases were determined to be the most often used publically available databases in our research. The Herlev and ISBI databases are primarily used to segregate data. On the other hand, the Herlev database is mostly utilized for classification. We discovered a new publically accessible database called "SIPAKMED" that can be used for classification.

4.1.1. Pap smear benchmark database (herlev dataset)

The team at Herlev Medical University in Denmark produced and examined a Pap smear benchmark database. They created the database by segmenting photos with a commercially available software suite called CHAMP (Dimac). They created two databases, one from 2003 and the other from 2005, each containing 501 and 917 single cell photos, including an overall image size of 158 140. The previous dataset had 140 photographs of actual cells and 340 images of abnormal cells, but the existing dataset contains 252 and 665 images of malignant cells, respectively.

4.1.2. ISBI challenge database

The dataset consists of 17 multi-layer cervical cell volumes, with 8 being used for training and 9 for testing. Eight annotated multi-layered cytology volumes, four from the training dataset and four from the testing set, have been released. Each cervical cell is delineated in this annotation (cytoplasm and nucleus). The remaining nine multi-layered cytology volumes will be released. Only the training volumes will receive manual annotation.

4.1.3. Sipakmed database

The SIPaKMeD database contains 4049 photos of isolated cells that were painstakingly cropped from 966 Pap smear slide cluster cell images. These photographs were taken with a CCD camera attached to a microscope. Normal, abnormal, and benign cells are separated into five groups in the cell pictures.

4.2. Method Analysis

As stated in section IV, most of the study work has been undertaken using publicly available databases. Nucleus segmentation is exclusively performed by the scientist that uses the Herlev database. The Zijdenbos similarity index is a popular way to assess segmentation results. A greater ZSI number denotes more precise precision. In [20], the author uses a neural network to extract features with C-Means clustering to segment the nucleus with the ZSI value of 0.8. The author of [22] recommends combining Mask-RCNN with LFCCRF to partition and get a ZSI score of 0:94. As a result, the method described below is more effective for segmenting cervical cancer cell nuclei.

Private and CPS or ISBI challenge datasets are used in studies that segment overlapping cervical cells. Both the cytoplasm and the nucleus are segmented into overlapping cells. The overlapped nucleus and cytoplasm segmentation work that includes pixel-wise CNN and a learned prior achieves maximum accuracy, recall, and ZSI value [22]. In addition, the segment of the CPS database using IR-Net [23] is identified as a task. As a result, these are the best methods for segmenting overlapping cervical cells.

5. Conclusion and Future Work

In this work, we looked at research that used DL and ML approaches to differentiate & classifying cervical cytopathology pictures. In addition, popular deep learning ideas and common architectures are discussed. Cervical cytopathology image processing is a growing issue, according to the review. The majority of the segmentation and classification approaches that have been proposed have been applied to the same dataset. As a result, it's easy to tell which algorithm is superior to others. More complex models can be developed in the future to bring more accuracy.

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