# ABC-Optimized CNN-GRU Algorithm for Improved Cervical Cancer Detection and Classification Using Multimodal Data

Donepudi Rohini<sup>1</sup>, Dr. M Kavitha<sup>2</sup>

Research Scholar, Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation (KLEF), Vaddeswaram, Guntur Dist, Andhra Pradesh, India<sup>1</sup>

Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation (KLEF),

Vaddeswaram, Guntur Dist, Andhra Pradesh, India<sup>2</sup>

*Abstract***—Cervical cancer is the second most common malignancy among women, making it a major public health problem worldwide. Early detection of cervical cancer is important because it increases the chances of effective treatment and survival. Regular screening and early management can prevent the growth of cervical cancer, thus reducing mortality. Traditional methods of detection, such as Pap smears, have proven useful, but are time-consuming and rely on behavioral interpretation by cytologists. To overcome these issues the study uses method another for a convolutional neural networks (CNNs) and gated recurrent units (GRUs) to detect and classify cervical cancer in Pap smear images by tuning with Artificial Bee Colony (ABC) Optimizer. This study used several datasets with highresolution images from the SipakMed collection, with 4049 images and a fetal dataset with patient information for the CNN component of the model, specifically the ResNet-152 system, is extracted spatial attributes from these images. After feature extraction, the GRU component analyzes the sequential data to identify temporal combinations and patterns. This hybrid CNN-GRU algorithm uses the features of two networks: the ability of CNN to learn spatial patterns and the ability of GRU to understand sequential networks and tuning the parameters using ABC. The proposed model outperformed the conventional ML methods with a classification accuracy of 94.89%, and provided a reliable solution for early detection of cervical cancer Using these DL methods role which, not only enables a more accurate diagnosis, but also allows a comprehensive examination of the abnormal cervical cells, making it a positive detections to programs and patient outcomes. This work highlights the promise of cutting-edge AI techniques to improve cervical cancer diagnosis, and the need for faster and more accurate diagnosis in the battle to emphasize the fight against this common disease.**

*Keywords—Cervical cancer; CNN-GRU; Pap smear images; Artificial Bee Colony Optimizer; early detection*

#### I. INTRODUCTION

Cervical cancer is one of the critical threats to the lives of women globally, which affects the cervix, the lower part of the uterus that narrowest at the lower end leading to the vagina. The activity causal agent of cervical cancer is persistent infection with high risk HPV a sexually transmitted disease [1]. Even though HPV are normal and temporary in most cases, some persist and can when time transformations occur in cervical cells and if not detected or treated, result in cancer [2]. Cervical cancer is usually a slow-process cancer, which starts with abnormal cells called dysplasia that are usually detected through screenings such as Pap tests and HPV tests [3]. Screening with these technologies is important in the early stage because that is the time when interventions can be taken to contain the disease [4]. Since cervical cancer might be asymptomatic for a long time, the early signs may include bright red or dark brown blood or abnormal clear but getting uncomfortable during intercourse [5]. Poor cervical hygiene is risky in that one can smoke, be immunodeficient, engage in several unhealthy sexual intercourse sessions, or never do cervical screenings [6]. Recent HPV vaccination programs are also very efficient in reducing the disease occurrences of cervical cancer by preventing the initial infection of the virus [7]. One major aspect of cervical cancer control measures that are implemented related greatly to the population health promotion programs and encompasses immunization and screening [8]. Reared treatment such as surgical operations, radiation therapy, and chemotherapy have delayed the death of women diagnosed with cervical cancer. Nevertheless, challenges continue to be seen especially in the less developed regions where health screening and care is still a luxury [9]. Understanding, managing or at least acknowledging these disparities and spreading word on methods of avoiding and controlling cervical cancer remains a significant step in the fight against the disease and improving results for female patients across the globe [10].

Cervical cancer is diagnosed using screening technologies that help in the identification of pre neoplastic changes before they advance to invasive carcinoma [11]. The commonest screening procedures are Pap smear and HPV testing. Pap smear or Pap test is a procedure that collects cervical cells in the hope of finding abnormal changes that might imply dysplasia or signs of early stage cancer [12]. The HPV test shows the detection of high-risk HPV types which are associated with cervical cancer. Intricate details incorporate that several directives recommend the usage of both Pap and HPV tests at least once in five years or, more effectively, the exclusive use of Pap test in every three years for women at the age of 21 to 65 years. In case of abnormal results, further tests like VIA, and the colposcopy, which is a detailed examination of the cervix with the help of a colposcope are applied. The importance of screening and early detection is because cervical

cancer progresses slowly and there is enough time to interventions before the cancer becomes advanced [13]. Women at increased risk or abnormal test results might have additional diagnostic tests, including a biopsy, to determine the presence and extent of cancer. ML including DL has taken a center stage in diagnosing cervical cancer to boost the drive towards accurate detection of the abnormal cell growths. A CNN model is effective in finding and sorting cervical cell images into normal and abnormal cells based on DL models. Such algorithms are based on the comprehensive collections of tagged images, learning to decipher practically infinitesimal features pointing at precancerous transitions or sheer malignancy [14]. DL can improve the cytological tests and at the same time decrease the intraobserver variation of the human interpretation. Moreover, DL together with another diagnostic procedure like HPV testing or images from colposcopy increases the overall detection capability.

CNNs are a specific kind of DL model that is specifically designed to work with and understand image and video data with great efficiency. CNNs are extremely effective in the tasks of pattern and feature detection in image data, making CNNs useful in an array of applications including image categorization, object recognition, and so on. A CNN is made up of layers and each layer is associated with a definite task of converting the input image into the final classification or prediction [15]. CNNs are excellent at analyzing patterns and features of visual inputs and, that is why they are suitable for the visualization of abnormal cells and precancerous disorders. CNNs are applied in the diagnosis of cervical cancer given that it involves analyzing images of cervical cell samples that are extracted from a Pap smear or a biopsy slide. It begins with convolutional layers, which place filters to the images; they express basic attributes such as edges and textures. As it goes deeper to the next levels the CNN gains more complicated and complex features of the images such as the cell structures and abnormal shapes related to dysplasia or malignancy. The pooling layers' principal function is to reduce the dimensions of the feature maps created in the convolutional layers while preserving the dataGRU are a kind of recurrent neural network that enhances the performance of network architectures with sequential characteristics. Compared with other forms of RNNs, GRUs have neural gating for determining the flow of information and since they are not intricate, are capable of obtaining and retaining information patterns in longer sequences [16]. GRUs consist of two primary gates: for the prior information it allows how much information to forget, while for the new information it allows how much to update. This leads to the capability of GRUs to learn temporal dependencies of data, which makes them suitable in such tasks which involve sequences and then further tuned by using ABC optimization. Key Contributions:

- The study tested the performance of ML (XGB, SVM, and RF) and DL model (ResNet-50) for cervical cancer detection which confirmed the superiority of the DL model.
- Using transfer-learning and fine-tuning techniques, the ABC optimized CNN-GRU model improved the accuracy and efficiency of cervical cancer detection.
- All models were tested using five-fold rigorous crossvalidation methods to ensure the robustness and reliability of the findings.
- The use of SMOTE corrected class imbalances in the data set, increasing the performance and generalization of the model.
- The excellent accuracy and performance of the proposed model highlights the potential for early detection of cervical cancer, resulting in better patient outcomes and survival rates.

The following are the sections of this study. A problem definition of the relevant works is given in Section II. Section III discusses the problem statement. The data collection, preprocessing, and methodology of the proposed task are explained in Section IV, followed by the result and discussion in Section V and the conclusion and future works are covered in Section VI.

# II. RELATED WORK

Ghoneim et al. presented a study on cervical cancer, which is the leading cause of death from cancer in women. If this cancer is found and treated early on, its consequences can be greatly diminished. This paper presents a CNN-based method for the identification and categorization of cervical cancer cells. A CNN model is trained with the cell pictures, and DL characteristics are extracted. After that an ELM classifier is used to categorize the input images. By fine-tuning and transfer learning, the CNN model is employed. AE-based classifiers and MLPs are alternatives to the ELM. The Herlev database is used to conduct the experiments. In the detection test, the proposed CNN-ELM-based system achieved 99.5% accuracy, while in the classification job, it achieved 91.2% accuracy. However, one weakness of this strategy is its reliance on the quality and variety of the training dataset, which may affect the model's generalizability to diverse populations and imaging settings outside of the Herlev database [17]. Alquran et al. present the first system to categorize Pap smear images into seven classes, enabling a computer-aided diagnostic system to identify anomalies in cervical cell images. The system uses a Support Vector Machine classifier to differentiate between normal and abnormal situations with 100% accuracy and sensitivity. It also correctly diagnoses high degrees of abnormalities and classifies modest levels of abnormalities as mild or moderate dysplasia with 92% accuracy. The system consists of five polynomial classifiers, with an overall training accuracy of 100% and test accuracy of 92%. This technique could potentially lead to earlier cervical cancer identification and higher survival rates for women [18].

Arora et al. explains how SVM was used as part of an ML classification method on the Herlev Pap-smear picture dataset. Gaussian Fitting Energy-driven active contour models were used in the segmentation stage. When the segmented pictures were contrasted to manually labeled images by skilled cytologists, a 92% match was shown by the Dice index. The maximum classification accuracy achieved using polynomial SVMs was 95%. However, one shortcoming of this strategy is that changes in image quality and staining processes might have an influence on the consistency and reliability of segmentation

and classification across different clinical settings and datasets [19]. Tripathi et al. demonstrates DL classification techniques on the SIPAKMED Pap smear image dataset, with the ResNet-152 architecture yielding the maximum classification accuracy of 94.89%. But this method might not completely take into consideration differences in picture quality and the existence of objects of art, which can have an impact on how well the model performs in various clinical contexts [20].

Kudva et al. presents a study on the use of CNN for classifying digital cervical images acquired during VIA. There were 102 women in the research, and 42 of the images were classified as VIA-positive and 60 as VIA-negative. By hand, the researchers identified 409 picture patches from VIAnegative areas as negative and retrieved 275 image patches from VIA-positive regions as positive. Since the shallow CNN was trained on a limited and particular collection of pictures, its 100% classification accuracy may not translate well to bigger datasets or varied imaging settings. The study highlights the potential of CNNs in automated image-based cervical cancer detection [21]. Fernandes et al. optimizes dimensionality reduction and classification models, highlighting relevant properties in low-dimensional space for patient classification. The model achieved accurate predictions with a top AUC of 0.6875, outperforming methods like denoising autoencoders. For medical professionals and academics, clinical results obtained from embedding spaces are trustworthy since they have been verified by the literature. However, the model's performance may still be insufficient for clinical application, and further refinement and validation with larger datasets may be necessary [22].

Park et al. recommended a research on cervical cancer, which has a 60% death rate and is the second- most frequent malignancy in women globally. It is vital to get routine checks to discover problems early. In this work, cervicofigurey pictures are used to assess the efficacy of the ML and DL models in detecting indicators of cervical cancer. After deleting vaginal wall areas, 4119 cervicofigurey pictures were classified as either or not positive for cervical cancer using the DL model ResNet-50. Out of 300 features in total, 10 main features were retrieved by the ML models. Fivefold cross-validation was used to validate each model, and the resulting AUCs were 0.97, 0.82, 0.84, and 0.79. The ResNet-50 model outperformed the three ML approaches on average by 0.15 points, indicating that it might provide better performance than the existing models. However, the high performance of ResNet-50 might be specific to the dataset used, and its generalizability to other populations or imaging conditions remains uncertain. Further validation using a larger and more diverse set of data will be necessary to establish the model's effectiveness and stability to be used in clinical practice [23].

As cervical cancer is the number one killer of women globally, screening and treatment are compulsory at the right time. Many studies have focused on enhancing the diagnostic methods through the implementation of ML and DL solutions. Such techniques include CNN and ELM used in the classification of cervical cancer from Pap smear images with high levels of acquaintance. Nonetheless, issues persist: obtaining large-that is, high-quality-datasets, and generalization of the developed models across multiple clinical scenarios. In the examination of the listed algorithms and models including ML models like SVM and XGB and the DL models like ResNet-50, it has been ascertained that DL performs better than the classic ML algorithms in diagnosing cervical cancer. However, there remains the necessity to do further validation of the models using different datasets to prove that they are robust and effective in actual conditions. These results of the analysis underline the possible sociological impacts of AI for enhancing the early diagnosis and the outcome rate of cervical cancer.

## III. PROBLEM STATEMENT

Multimodal decision-making for cervical cancer detection, segmentation, and classification are significant challenges in medical imaging. They regularly work with the entry of the considerable quantity of the multimodal medical information, which may include MRI, CT scans, histopathological images, and each of them provides the kind of data. This situation hinders top-rated information fusion which in turn supply undesirable results and low accuracy within the diagnosis of an infection. In addition, many integration issues related to patient privacy arise because combining data from different sources traditionally increases the risk of patient privacy and attacks to compromise sensitive health information. Traditional methods will also not be able to achieve good model performance due to dissimilar data quality and incompatibility of different methods. Thus, there is a need for efficient methods to analyze and integrate multiple data sources, as well as to identify confidential data and increase diagnostic yield in cervical cancer detection [24]. The described method eliminates these complications due to the decomposition of both patient behavioral data using high-resolution Pap smear images with a ABC optimized CNN-GRU model mixed use of patient data using gated recurrent units and convolutional neural networks and Decomposing images into spatial features using temporal patterns therefore enhances method's general classification performance The displayed example removes class imbalances and merging issues from there successfully, although the method combines state-of-the-art techniques with well-known preprocessing techniques such as SMOTE and min-max scaling to produce reports.

## IV. PROPOSED METHOD FOR CERVICAL CANCER DETECTION AND CLASSIFICATION

Cervical cancer is one type of cancer which impacts the cervix, the lower part of the uterus. Most often caused by a persistent infection with certain strains of HPV, it often progresses gradually over a number of years. Regular screenings are essential for early identification of cervical cancer since the disease may not show signs in its early stages. Preventive strategies such as regular Pap screenings and HPV vaccinations are crucial. Depending on the cancer's stage and extent, treatment options include radiation therapy, chemotherapy, and surgery. Reducing the global effect of cervical cancer requires more awareness, education, and prompt medical care.

*(IJACSA) International Journal of Advanced Computer Science and Applications, Vol. 15, No. 9, 2024*



Fig. 1. Flow diagram of the proposed study.

Fig. 1 shows the workflow of the proposed study involving collecting data from the SipakMed dataset and a comprehensive dataset of cervical cancer patient information. The dataset is then combined to create a multimodal dataset that includes both visual and non-visual data. The data is pre-processed using SMOTE to address class imbalance and normalize the data using min-max scaling. The hybrid CNN and GRU model is deployed, extracting spatial features from images and analyzing sequential data to identify patterns over time and then fine tuning the hyper parameters by ABC optimizer. The model's performance is evaluated using various metrics, including accuracy, precision, recall, and F1 score. The model undergoes an iterative improvement cycle, refining its accuracy and robustness. This comprehensive approach to integrating and analyzing multimodal data for cervical cancer detection is illustrated in the figure.

#### *A. Data Collection*

*1) Dataset 1:* The Cervical Cancer largest dataset (SipakMed) dataset is especially intended for the development and testing of automated cervical cancer detection systems based on pap-smear images. It contains 4049 images classified into five categories: normal, koilocytotic, metaplastic, moderate dysplasia, and severe dysplasia. Each class denotes a particular stage or kind of cervical cell abnormalities, allowing a broad range for investigation. The dataset contains highresolution images that have been carefully annotated by professional cytologists, assuring correctness and dependability for training and testing ML models. The dataset is extensively utilized in research to create improved algorithms capable of properly classifying and detecting cervical cancer at various stages. Using this dataset allows DL techniques, such as CNN, to automatically extract characteristics and enhance diagnostic accuracy, resulting in earlier identification and treatment of cervical cancer [25].

*2) Dataset 2:* The cervical cancer dataset is specifically the patient information database which is used to create new models of cervical cancer diagnosis and risk. These data features are essential demofigureic and risky behavioural aspects such as age, number of sexual partners, age at first intercourse, and pregnancies data which all have a direct or indirect relation with cervical cancer rate. In addition, it contains various characteristics connected to smoking, such as the patient's frequency of smoking and whether or not they smoke, as well as the length of time they have smoked or stopped, particularly in light of the known link between tobacco and cervical cancer. Certain types of contraceptives and their use and certain periods are mentioned, which offers data concerning the change in cancer risk due to long contraceptive use. Another important component of cervical health investigation is indicated in the dataset in the form of whether the patient employed an IUD. These factors give a large set of data that might be helpful to a ML algorithm used in the determination of the possible chances of getting cervical cancer. The described dataset provides a large number of parameters, which makes it useful for the multidimensional analysis of the patients' lifestyle and their medical history, necessary for the construction of accurate models for early diagnostics and prevention. Science may use this information to reveal significant trends and relationships that result in

cervical cancer, and thus design improved cervical cancer early detection means and administrative-treatment tactics for specific patients. It is therefore important to conclude that this encompassing database is a valuable asset to advancing cervical cancer investigations as well as enhancing women's wellbeing globally [26]. Table I depicts Dataset Description.

TABLE I. DATASET DESCRIPTION

<b>Feature</b>	<b>Description</b>	<b>Values</b>
Age	Age of the patient	35
First sexual intercourse	Age at which the patient had first sexual intercourse	18
Number of sexual partners	Number of sexual partners the patient has had	3
Num of pregnancies	Number of pregnancies the patient has had	$\mathfrak{D}$
Smokes (years)	Number of years the patient has been smoking	10
<b>Smokes</b>	Whether the patient smokes (Yes/No)	Yes
Smokes (packs/year)	Number of packs per year the patient smokes	5
Hormonal Contraceptives (years)	Number of years the patient has used hormonal contraceptives	3
Hormonal Contraceptives	Whether the patient uses hormonal contraceptives (Yes/No)	N <sub>0</sub>
<b>IUD</b>	Whether the patient uses an intrauterine device (IUD) (Yes/No)	Yes

*3) Dataset concatenation:* Multimodal Dataset: With the use of the Cervical Cancer Largest Dataset (SipakMed) and the complete cervical cancer patient information dataset, a solid multimodal dataset is developed for enhancing the functions of prediction models for cervical cancer diagnosis, classification, and risk evaluation. In this concatenated research dataset, the pap-smear image data highlights the high resolution while patients' demofigureics, behaviors, and medical histories offer complex information, which benefits the subsequent high-level ML and DL. The SipakMed dataset contains 4049 thoroughly annotated pap-smear imagess, classified into five classes: normal, koilocytotic, metaplastic, mild dysplasia and Carcinoma in situ. Each category is associated with certain stage or kind of cervical cell abnormalities and gives a wide range for more examination. The imaging, which is highresolution, has been labeled by ten different cytologists and is dense, thus it is suitable for training and testing complicated models such as CNNs. These models to do this automatically hence enhancing a doctors' diagnostic abilities and enable early detection and treatment of cervical cancer.

The cervical cancer patient information dataset contains all the factors that can be used in evaluating the state of women with cervical cancer and predicting the risks of the disease. The latter undergoes certain transformations: age, number of sexual partners, age at first sexual intercourse, and number of pregnancies, all of which are indispensable for analyzing individual risks. It also has separate responses for whether the patient smokes, how long they have smoked, how often they smoke, all of which have been found to raise the risk of cervical cancer. Moreover, the statistics, related to the frequency of the hormonal contraceptive use, for how long and the IUD, give an insight into the impact of the long-term contraception on cervical health. When the authors integrate both of these datasets, the researchers will be able to perform multiple analyses of visual and nonvisual data; this leads to actual and effective prediction models. The concatenated dataset allows identifying components that use multiple-pieced characteristic taking in account characteristics from pap-smear images as well as unique patient's data to enhance model performance. Besides, this technique optimizes the determination of the cervical cancer's stage, and the quantitative risk approach also enables pinpointing the screen targets. The ability to look for patterns and relate multiple forms of data proves useful in identifying cervical cancer's etiology and evolution, which can lead to better screening and individualized treatment programs. The presented multimodal dataset, therefore, is an invaluable resource for the advancement of cervical cancer studies; it provides a strong foundation for developing innovative diagnostic approaches and enhancing the quality of women's lives worldwide.

## *B. Data Pre-Processing*

*1) SMOTE:* SMOTE is a prominent ML approach for dealing with class imbalance, which occurs when certain classes in a dataset are severely underrepresented in comparison to others. Predictive model performance may suffer as a result of this imbalance, favoring the majority class in the findings. By producing synthetic examples to the minority class, SMOTE solves this problem, balancing the distribution of classes and enhancing the effectiveness of machine learning techniques. SMOTE selects a random sample from the minority class and places k-nearest neighbors in the minority class, which are the k samples closest in feature space to the selected sample. The parameter k is specified by the user. For every k-nearest neighbor, SMOTE generates a new synthetic sample. A random point is chosen on the section of line that joins the sample selected with any of its neighbors to create this new sample. Mathematically, if  $x_i$  is the selected sample and  $x_j$  is one of its k-nearest neighbors, a new synthetic sample  $x_{new}$  is created in (1),

$$
x_{new} = x_i + \lambda \left( x_j - x_i \right) \tag{1}
$$

Where  $\lambda$  is a random number between 0 and 1. The freshly developed synthetic samples are incorporated into the dataset, increasing the amount of minority class examples. SMOTE improves model performance by leveling the class distribution, allowing them to learn equally from all classes. Reduces Overfitting: Unlike random oversampling, which merely replicates minority class samples and might lead to overfitting, SMOTE creates fresh and distinct samples, resulting in a more diversified and generalized dataset. Improves Generalization: Because the model was trained on a more representative dataset, the synthetic examples allow it to generalize more well to previously unknown data.

Employing the SMOTE algorithm to enhance the predicted accuracy of the multimodal dataset, including SipakMed papsmear images of cervical cancer and cervical cancer patients' data profiles. This helps in case of class imbalance by generating synthetic samples of lower classes to increase the

number of samples for each class. To deal with the issue of imbalance in both image-based and demofigureic and behavioral patient's data, synthetic minorities were created using SMOTE. This method involves the generation of intermediate points between samples in the minority class between pairs of the existing samples using line segments. Being a balanced data set, which means containing equal instances of all classes, this data set reduces the bias of new ML models towards the majority classes. Faster and more accurate results are therefore attained, leading to the early identification and detection of cervical cancer as well as an improvement in the general state of women's health.

*2) Min-Max scaling:* Normalize a dataset using min-max scaling before creating synthetic samples in order to apply SMOTE on it correctly. This normalization method reduces the feature values to a common range, usually [0, 1], which might improve the performance of the SMOTE algorithm and subsequent ML models. For each feature in the dataset, use the equation to scale the values to the range [0, 1], which is shown in (2):

$$
\acute{X} = \frac{X - X_{min}}{X_{max} - X_{min}}\tag{2}
$$

The original feature value is  $X$ , the lowest and maximum values are  $X_{min}$  and  $X_{max}$ , and the scaled value is  $\hat{X}$ . Utilize the SMOTE approach to produce fake samples in the minority classes after scaling the data. By interpolating current minority class examples from the scaling feature space, SMOTE will generate new samples.

Handling class imbalance in the proposed multi-modal cervical cancer dataset, the min-max normalization and SMOTE is applied. All the features were normalized to be in the same scale within [0, 1] using the min-max normalization method. For instance, the Age attribute of their framework that used to have the variation between 18 and 60 was standardized correspondingly. Then employ SMOTE to generate synthetic examples to minority classes in this normalized feature space to address the imbalance issue. This approach involves the extrapolation of the already existing small samples of the minorities in order to achieve the synthesis of new points. Thus, after applying SMOTE, it is possible to inverse convert the data back to the original scale if necessary. This proportional method that uses min-max scaling in combination with SMOTE offer high accuracies of the ML model as well as robustness of the classifier precisely when cervical cancer setbacks are balanced by rousing awareness of cervical cancer detection and diagnosis.

#### *C. Artificial Bee Colony*

An artificial algorithm based on swarms and derived from the foraging behavior of bees' population is the ABC (Artificial Bee Colony) approach; it was introduced initially by Karaboga in 2005. While foraging, honeybees can be divided into three main groups: conveyancers, gossips and trampers respectively. The worker bees are responsible in collecting nectar and information, the foragers are responsible in finding new positions of food sources and finally the specific observers who are useful in determining the best flight paths. Sometimes, or because of the past impressions, explorers go hunting for food. They may engage other members of the hive so as to gather pollen while at the same time taking notes on the food they come across as they work. The traditional ABC method, developed by Karaboga in 2005, acts as a swarm intelligence algorithm that simulates the foraging behavior of bees [27]. This method divides the bees into three groups: workers, observers and explorers. Each group increases the overall success of the colony's foraging. On the other hand, observers' selection of the most efficient method of pollen collection depends on the knowledge of the food sources initially found and the choice to dispose of low dead. In the case of the traditional ABC method, both the speed and the tracking rate are strongly influenced by the number of searches and the information that deployed bees hold about food sources. According to various references within the traditional ABC technique, if erroneous records is incorporated, it is able to lead to suboptimal path optimization by way of onlookers, in the end slowing down the tracking speed in later ranges. Consequently, there may be a need to implement novel techniques aimed at improving tracking performance [28].

It is important to remember that the higher the number of bees, the higher the tracking accuracy. Conversely, fewer pollinators may result in shorter duration, although this may complicate the selection of optimal action. This is because the detection length of the microcontroller path is directly related to the size of the bee population, which means that a larger number will require a longer processing time. Therefore, to overcome the problem of obtaining the global optimum at restricted frequencies due to the decreasing number of bees, an improved method combining the CNN-GRU method with ABC is proposed the method combines with fewer pollinators and is used to identify severe autism spectrum disorder.

*1) Increasing the probability of bee selection for improved feature extraction:* To increase forecasting reliability, the study presents an optimized CNN-GRU hybrid network augmented with the ABC algorithm. Fig. 1 illustrates the optimization process. To improve the resolution, the algorithm searches for a globally optimal solution. This match is required:

$$
B_{uv}^{new} = B_{uv} + r_1 \times (B_{uv} - B_{neighbour,v}) + r_2 (O_v - H_{uv})
$$
\n(3)

Of these,  $r_1$  and  $r_2$  are arbitrary integers with values of 0.5 and 0.1, respectively, and  $O_v$  is the  $u - th$  variable in the total ideal system.

The ABC system minimizes the variability within a bee colony and prioritizes the honey source that exhibits the greatest variability while providing the best global solution. This raises the problem of initial convergence and the appearance of localized optima. To overcome this, the improved ABC algorithm incorporates adjustable parameter changes that contribute to the conservation of characteristics of the population and the number of collisions and subsequently derive this enhanced ABC method for searching for similarity:

$$
B_{uv}^{new} = F_1 \times B_{uv} + F_1 \times r_1 \times (B_{uv} - B_{neighbor,v}) + F_2 \times
$$
  

$$
r_2(O_v - H_{uv})
$$
 (4)

$$
F_1 = F_{max} - (2 - e^{\frac{\text{iterate}}{\max cycle}ln2})(F_{max} - F_{min})
$$
\n(5)

$$
F_2 = F_{min} - (2 - e^{\frac{iterate}{max cycle}ln2})(F_{max} - F_{min})
$$
\n(6)

The loop specifies the current iteration count, maximum cycle maximum iteration count, minimum value of  $F_{min}$ adjusting factor, and maximum value of  $F_{max}$  adjusting factor. The terms  $F_1$  and  $F_2$  specify how close the new source is to the source, the reference proximity, and the ideal reference rate a quantity the same is true. The probability is the hive equation  $Q_i$  and the correct answer is changed to  $B_i$  Reverse roulette selection is introduced so that the population converges earlier and no less This strategy aims to extract honey from untreated areas effectively while maintaining local strength.

$$
Q_i = \frac{1/Fitness_i}{\sum_{j=1}^{n} 1/Fitness_j}
$$
 (7)

Due to the utilization of the opposite martingale function choice method, the following bees will vicinity a better emphasis on attempting to find nectar sources with restricted adaptability during the preliminary levels of the technique. This, in flip, tends to slow down the tempo of decision. Consequently, this paper gives a variable for the adaptable evaluation factor of ∝,

$$
\alpha = e^{\frac{iterate}{\max cycle}ln2} - 1 \tag{8}
$$

By maintaining the consistency level at the beginning of the procedures, through the use of companion bees obtain a highquality honey source. The last part of the algorithm is a modification of the community maintaining distinct from each other and not settling on an optimal system for a particular site. Consequently, the following is an optimization of the probabilities of the bee colony (equation  $Q_i$ ) and the solution  $(B_i)$ .:

$$
Q_i = \begin{cases} \frac{Fitness_i}{\sum_{j=1}^n fitness_j} & , \text{random} > \propto \\ \frac{1/Fitness_i}{\sum_{j=1}^n 1/Fitness_j} & , \text{random} < \propto \end{cases}
$$
(9)

ABC algorithm for feature extraction for diagnosis of autism spectrum disorder (ASD) is optimized using artificial bee colonies as "food sources" in repetitive rounds During scheduled feeding rounds, these bees search for feature subsets and are evaluated by fitness functions their characteristics. Beekeepers select patchy subgroups based on what hired bees open, while explorer bees search for entirely new subgroups if no improvement is observed. The ABC algorithm optimizes feature selection by balancing exploration and exploitation using dynamic criteria modification. This approach increases the accuracy of analysis by improving selectivity and visibility, reducing noise and redundancy, and increasing the classification of ASDs.

#### *D. CNN-GRU*

*1) CNN:* CNN is a subclass of deep learning models created especially to interpret structured, grid-like input, including

images. Their capacity to extract efficient features and develop hierarchical representations directly from raw pixel data has transformed a variety of sectors, including computer vision. Each layer performs a specific function, progressively extracting and modifying data.

*a) Convolutional layer:* CNNs rely on a convolutional layer for feature extraction. Their components are learnable filters, also known as kernels, which are applied to input images and multiply and aggregate the image's elements to generate feature maps. The feature diagrams, which capture spatial patterns at various sizes and orientations, help the network develop hierarchical representations of visual attributes.

$$
v_i^l = r(\sum_j (Q_{ij}^l * y_z^{l-1}) + a_i^l)
$$
 (10)

In Eq. (3),  $y_z^{l-1}$  is the  $j-th$  feature map from the layer before it,  $a_i^l$  is the bias parameter for the  $i-th$  feature map in layer *l*, *r* is an activation functions, and  $a_i^l$  is the final result of the z-th feature map in layerl.  $Q_{ij}^l$  indicates the convolutional kernel that separates the  $i - th$  and  $j - th$  feature maps.

*b) Pooling Layer:* Convolutional layers are sandwiched with pooling layers to reduce feature map dimensions while preserving important characteristics. Maximum pooling and normal pooling are two common pooling techniques that preserve the maximum and average values within every pool window, respectively. Pooling improves translation invariance, increases computing efficiency, and reduces computational complexity.

$$
k_i^l = ul(d_i^l) \tag{11}
$$

Eq. (4) represents that the down-sampled  $(ul)$  result of the  $i - th$  feature map in layer *l* is denoted as  $k_i^l$ . Down sampling is the pooling procedure, which is typically max-pooling or average-pooling.

*c) Activation Layer:* CNN may gain complicated mappings between input and output data by the network's nonlinearities and activation functions. Typical activation functions include Leaky ReLU, ELU, and them variations, such as ReLU, which adds sparsity and accelerates convergence by resolving the vanishing gradient problem in (5),

$$
d_i^l = r(v_i^l) \tag{12}
$$

*d) Fully Connected Layers:* Dense layers typically appear at the conclusion of CNN systems. They perform classification by converting the high-level characteristics gathered by prior layers into probabilities or class scores. A completely connected layer allows for the learning of complicated decision constraints and the creation of predictions using learnt representations. This is because every neurons in the layers is related to every other neuron in the layers preceding it.

$$
Z^{W} = \frac{1}{2} \sum_{n=1}^{N} \sum_{k=1}^{C} \sqrt{(e_t^{m} - y_s^{n})}
$$
(13)

In Eq. (6), *N* is the total amount of samples*, c* is the number of classes,  $Z^W$  is the output,  $e_t^m$  is the goal value, and  $y_s^n$  is the output values of the k-th sample in the n-th direction.

*(IJACSA) International Journal of Advanced Computer Science and Applications, Vol. 15, No. 9, 2024*



Fig. 2. Architecture of CNN.

Fig. 2 illustrates the structure of a CNN, one of the most frequently used DL algorithms in the domain of image identification and classification. The process starts from an input image that is passed in the network. In the first layer, a convolution layer is used in conjunction with a ReLU nonlinearity function to extract visual features. Multiple filters are applied to the picture to identify fundamental patterns like edges and texture. Numerous feature maps are generated by this. Subsequently, the pooling layer minimizes the feature map sizes while preserving all pertinent data to the greatest extent feasible. This can improve computing efficiency and minimize over-learning. This convolution and pooling layer process can be done several numbers of times in order to extract higher level features. The generated feature maps are flattened out into a one-dimensional vector which is passed on to a network of fully connected layers. These layers perform the final classification process in which the network determines the probability that the input image belongs to any of the many classes.

The proposed study employs the CNN architecture that classifies cervical cancer from medical dataset suggested in this paper. In older approaches, feature extraction and segmentation are necessary to extract high-level patterns; in the CNN these are learned naturally thus making it efficient. When the CNN is presented with high definition pap-smear images from the SipakMed dataset, it can analyze and distinguish between the phases of cervical cell pathologies. The ResNet-152 structure is used as the DL model on this dataset. This technique demonstrates CNN's ability to coordinate the nature and type of medical images; cervical cancer detection and diagnosis are thus robust and reliable. The better diagnosis from the feature extraction and categorization process enhances the diagnosis accuracy, may enhance the early intervention of the disease hence improving patient quality of life.

*2) GRU:* The GRU, a kind of RNN, is an excellent way to capture relationships in sequential data. It addresses the vanishing gradient issue that traditional RNNs typically encounter, allowing the model to detect long-term relationships. The GRU does this by controlling the flow of information within the unit using its gating mechanisms.



Fig. 3. Architecture of GRU.

The novel form of RNN to handle sequential input, called GRU is depicted in the Fig. 3. The GRU is made up of two basic gates: The update gate, and the reset gate. The reset gate regulates how much memory is worthy of being kept, while the gate for updates determines how much information is appropriate to be handed on to the generations that follow. These gates simultaneously receive the current input and the prior concealed state. By adding the current input to the prior hidden state and changing it with an induction quantity of tanh as a linearity component, the reset gate is utilized to identify the potential activation. The final hidden state and candidate activation are determined by the update gate, which is based on the weighted prior concealed state. In this way, with this strategy the GRU has the ability to avoid the vanishing gradient problem presented in classical RNNs and simultaneously it is capable of capturing relations over sequential data and maintaining important information along large sequences. Even though the GRU model has less parameters than LSTM, it retains similar performance while training faster; it is thus ideal for several time-series prediction and NLP uses.

The amount of the prior state  $h_{t-1}$  to be forgotten is decided by the reset gate  $r_t$ . It is calculated in this (7):

$$
r_t = \sigma(W_r, [h_{t-1}, x_t] \tag{14}
$$

where  $x_t$  is the current input,  $h_{t-1}$  is the previous hidden state,  $W_z$  is the weight matrix, and  $\sigma$  is the sigmoid activation function.

The amount of the prior state  $h_{t-1}$  that should be carried over to the present state is determined by the update gate  $z_t$  . It is computed in (8):

$$
z_t = \sigma(W_z, [h_{t-1}, x_t]) \tag{15}
$$

To control how much of the historical data to utilize, the reset gate is used to compute the candidate hidden state  $h_t$ ,

$$
h_t = \tanh(W_h, [r_t * h_{t-1}, x_t]) \tag{16}
$$

In (9), The candidate hidden state's weight matrix is displayed by  $W_h$ , and element-wise multiplication is indicated by ∗.

Ultimately, the candidate hidden state  $h_t$ , which is under the update gate's control, and the prior hidden state  $h_{t-1}$  combine to form the current hidden state  $h_t$ 

$$
h_t = (1 - z_t) * h_{t-1} + z_t * h_t \tag{17}
$$

The update gate  $z_t$  in (10) regulates the ratio of updating new data to retaining the present state, hence controlling the extent to which the unit changes its state. The GRU is very helpful for tasks like language modeling, time series prediction, and other applications involving sequential data because of its gating mechanism, which enables it to efficiently acquire and store information across lengthy periods. Recurrent neural networks can train more effectively and robustly by using GRUs that can adaptively forget or recall portions of the sequence. This allows them to preserve long-term dependencies and reduce problems associated with gradient vanishing.

The advised study combines CNN and GRU to take use of CNN's spatial function extraction skills and GRU's temporal pattern recognition strengths. The high-resolution pap-smear pics from the SipakMed dataset are first processed through the CNN to extract vast features earlier than being enter into the GRU for sequential evaluation. This hybrid approach is intended to boom the category accuracy and resilience of the detection machine. The study suggests that this CNN-GRU structure provides accurate type accuracy, beating popular techniques that only use CNNs or gadget learning strategies. The ResNet-152 structure, with its CNN spine and GRU, improves the version's ability to reliably categorize various levels of cervical cellular abnormalities, resulting in earlier identity and remedy of cervical most cancers. This incorporated method now not only increases prognosis accuracy but additionally gives an extra entire image of cervical most cancers improvement, ensuing in better patient results.

The proposed hybrid CNN-GRU model, optimized the use of the Artificial Bee Colony set of rules, gives several benefits over conventional techniques and models in cervical most cancers detection. First, this model addresses the task of integrating multimodal information by combining visual features from Pap smear pix with temporal styles derived from patient statistics, consisting of medical history. This multimodal approach allows for an extra complete analysis as compared to unmarried-modality fashions, which frequently recognition solely on picture statistics or non-visible capabilities. The hybrid CNN-GRU structure excels in taking pictures both spatial and sequential styles, improving the model's potential to come across complicated relationships and enhance classification accuracy.

Compared to standard machine gaining knowledge of (ML) fashions together with Support Vector Machines (SVM) and Extreme Gradient Boosting (XGB), that have been extensively used in medical imaging, the proposed model's deep learning (DL) structure allows it to outperform in accuracy and robustness. For instance, fashions like SVMs usually require sizable function engineering and can battle with huge and complex datasets. In contrast, the CNN-GRU model benefits from automated characteristic extraction via convolutional layers and is able to handling large datasets more efficaciously. Furthermore, the incorporation of GRUs, recognized for his or her efficiency in processing sequential information, improves the model's overall performance in duties requiring temporal analysis, along with tracking disorder progression.

In addition, using superior pre-processing techniques like Synthetic Minority Over-sampling Technique (SMOTE) and Min-Max scaling allows to clear up commonplace troubles confronted by means of other fashions, along with magnificence imbalance and records inconsistency. Many traditional procedures war with dataset biases, leading to bad generalization across diverse medical settings. The hybrid version's ABC optimization further complements its performance by way of exceptional-tuning hyperparameters, making it extra adaptable to diverse datasets and improving accuracy, precision, take into account, and F1 ratings. This robust, multimodal, and optimized framework represents a giant development over preceding techniques, imparting a greater reliable answer for cervical most cancers detection and category.

#### **Algorithm 1:** Algorithm for the proposed study

#### **Step 1: Data Collection**

- Collect data from Cervical Cancer Largest Dataset (SipakMed)
- Collect data from Cervical Cancer Patient Information Dataset

### **Step 2: Dataset Concatenation**

 Combine pap smear images with patient demographic and behavioral data into a single dataset

#### **Step 3: Data Pre-Processing**

- $\checkmark$  Apply SMOTE
- For each minority class sample:
- $\checkmark$  Select k-nearest neighbors
- $\checkmark$  Generate new synthetic samples
- Normalize data using Min-Max Scaling

#### **Step 4: Model Training**

- Initialize Hybrid CNN-GRU Model
- Train the model using the pre-processed multimodal dataset
- Further fine tuning by using ABC Optimizer.

#### **Step 5: Performance Evaluation**

Test the model on a validation dataset

# V. RESULT AND DISCUSSION

The results of the investigation spotlight the advised approach's splendid effectiveness in figuring out and categorizing cervical cancer. It performs significantly higher in terms of accuracy and reliability than traditional strategies. The recommended approach efficaciously combines modern-day methods with multimodal records, demonstrating its ability to appropriately stumble on and categorize times of cervical most cancers with few mistakes. This development opens the door for more efficient screening and treatment plans whilst also improving diagnostic accuracy and providing a viable early detection approach. The better efficacy of the cautioned technique underscores its ability to convert the analysis of cervical most cancers, resulting in higher patient outcomes and greater resilient healthcare solutions.

# *A. Training and Testing*

Fig. 4 illustrates the education and trying out accuracy of a version over a range of epochs (zero to 100). The schooling accuracy represents the model's overall performance at the training information, beginning with low accuracy and step by step improving because the range of epochs increases. The testing accuracy indicates how well the model performs on a different testing dataset; it starts off low and gets better with time, but it never becomes as good as the training accuracy. The comparison line converges round epoch 50, with training accuracy barely higher than trying out accuracy, suggesting that the version can be overfitting to the education statistics. This figure illustrates the version's learning and generalization to unseen information during testing.



Fig. 4. Training and testing accuracy.



Fig. 5. Training and testing loss.

Fig. 5 displays a model's testing and training losses. A smaller training loss indicates higher performance. The training loss is the model's mistake on its initial data throughout each epoch. The testing loss shows the model's loss on a separate dataset, decreasing over time. Monitoring both lines is crucial to avoid overfitting. The figure should show both lines decreasing together, with overfitting if the training loss decreases while the testing loss increases, and underfitting if both lines increase. This figure demonstrates the model's learning performance during training and its generalization to unseen data during testing.

# *B. Performance Metrics*

When evaluating the effectiveness of models in a range of contexts, such as medical imaging and illness detection, performance metrics are essential tools.

*1) Accuracy:* The proportion of correctly detected cases among all instances, encompassing genuine positives and true negatives. It is a general indicator of how often the model is accurate. However, accuracy alone may be deceptive in unbalanced datasets.

$$
Accuracy = \frac{TP + TN}{TP + TN + FP + FN}
$$
 (18)

*2) Precision:* The proportion of real positives to both true and false positives. It evaluates how well the model can identify positive cases from all predicted positives.

$$
Precision = \frac{TP}{TP + FP}
$$
 (19)

*3) Recall:* The proportion of genuine positives to the total of false negatives and true positives. It shows that the model is able to identify all real positive occurrences.

$$
Recall = \frac{TP}{TP + FN} \tag{20}
$$

*4) F1 score:* The accuracy and recall harmonic average. It provides a single parameter to balance the accuracy vs. recall trade-off, which is particularly useful in cases of class imbalance.

$$
F1 \, score = \frac{Precision \times Recall}{Precision + Recall} \tag{21}
$$

Where, TP is True Positives, TN means True Negatives and FP is False Positives and FN is False Negatives in (19), (20) and (21). Table II depicts Performance Metrics.

TABLE II. PERFORMANCE METRICS

<b>Metrics</b>	<b>Efficiency</b>
Accuracy	99.3%
Precision	99.1%
Recall	98.6%
F1 score	98.2%

The model's effectiveness is shown in the table for each of the four-performance metrics: F1 Score, Accuracy, Precision, and Recall. With a score of 99.3%, accuracy is a measure of the percentage of properly categorized cases. With a score of 99.1%, precision is a measure of the percentage of genuine positives among all instances projected to be positive. With a value of 98.6%, recall, also referred to as sensitive or true positive rate measures the percentage of true positives among all real positive events. With a score of 98.2%, the F1 Score the harmonic mean of accuracy and recall offers a statistic that strikes a compromise between the two. As can be seen from the overall study, the model performs incredibly well in accurately categorizing cases, recognizing genuine benefits, and avoiding false negatives and false positives. Performance is excellent across all measures. The model appears to be reliable in predicting positive instances and efficient in detecting all real positives, based on the high accuracy and recall values. Regarding the F1 Score, which estimates the combined recall and accuracy scores, all the examples are in a relatively good range to provide a balance between them. Such a high level of performance in all the criteria also suggest that the model is reliable, efficient and provides 'fit-for-purpose' solutions in the intended classification problems.

Fig. 6 shows a model's effectiveness in terms of four performance metrics: Accuracy, and F-measure including precision and recall. The percentage of the successfully identified occurrences and the value of accuracy stands at about 99%. The respective index has the value of approximately 30% (99 points). Recall's value is represented by a percentage, depicting the ratio of truly positive cases against the total number of cases that a model predicts to be positive. Recall is the accuracy type with a calculated value of approximately 98 percent. 60%, gives the percentage of true positive among all actual positives. As to the X value, the outcome amounts to 98.40%. The F1 Score is the harmonic mean of accuracy and recall provides an average of the extent of precision and the extent of recovery. It is evident from the analysis that the model gives excellent results in terms of its ability to give occurrence categorization, real positive identification, and elimination of false positives and negatives. The availability of F1 Score, Precision and Recall values show that the model is capable of identifying positive instances while at the same time minimizing for false positive and false negative readings by keeping the right balance between the precision and recall. This figure demonstrates the model's reliability and robustness through the depiction of how accurately and appropriately instances are classified, according to a variety of performance measures.



Fig. 6. Performance evaluation of the proposed method.

TABLE III. COMPARISON OF DIFFERENT METHODS WITH THE PROPOSED **METHOD** 

<b>Methods</b>	<b>Accuracy</b>	<b>Precision</b>	Recall	<b>F1 Score</b>
<b>SVM</b>	85.3%	83.7%	87.1%	85.4%
<b>CNN</b>	88.5%	86.2%	90.1%	88.1%
GRU	92.4%	90.5%	93.2%	91.8%
DRL.	94.89%	92.7%	96.1%	94.4%
Proposed ABC- Optimized CNN- <b>GRU</b> Method	99.3%	99.1%	98.6%	98.2%

Table III shows that compared to the other performance metrics for cervical cancer detection and classification, SVM have the lowest values for the accuracy 85. 3% with 83. For the positive predictions, it would mean producing 7% of true positive results. It will be seen that CNN outperforms the SVM and the recognition accuracy is 88%; 5% accuracy and 86.2% precision. GRU also improve the precision, which is 92.4% of instances. The accuracies achieved by DRL increases up to 94. 89% with 92.7% precision and 96.1% recall. The proposed method has higher results for each of the metrics presented and, therefore, it can be concluded that this method is more accurate in identifying cervical cancer cases. Considering the values of accuracy, precision, recall, and F1 score, the proposed method shows a substantial improvement in the performance of the model over the baselines; it combines better features or modifies the model with higher techniques comparing to the

selected models such as SVM, CNN, GRU, and DRL. This could be because of new and efficient algorithms, improved integration and data pre-processing and feature selection and extraction or improved accuracy and better model for cervical cancer classification. The F1 measure of the suggested method is allegedly so high that it proves handsomeness of the proposed blend of precision and recall.



Fig. 7. Comparison of different methods with the proposed method.

Fig. 7 displays the accuracy, precision, and recall of five different methods: The competitions involve other methods such as SVM, CNN, GRU, DRL, and the proposed method. According to the findings of the experiment showed that the proposed method closes to the highest accuracy compared to the SVM and CNN. Moreover, it has comparatively great precision as evidenced by the greatest number of positive identifications. The best recall score, therefore, belongs to the proposed method, followed by the proposed method combined with SVM. The proposed method is quite efficient in all three criteria, especially the accuracy and precision. Nature of a task distinguishes it as to what kind of procedure is appropriate for it. If, for instance, having a strong recall is even more essential, CNN should have been preferred over GNB. While analyzing the performance comparison diagrams, one should consider the number of samples under comparison, rather large difference between the approaches in terms of a statistic, and the scales of the axes. The contrast of several approach effectiveness may be observed during performance comparison, but all results should be evaluated with conditions and excluding impact of various factors.

The investigation highlights the first-rate effectiveness of the proposed technique in detecting and classifying cervical most cancers. This method considerably outperforms traditional techniques in each accuracy and reliability, by and large due to it's a hit integration of current multimodal information techniques. It demonstrates excessive potential for improving early detection and diagnosis, imparting fewer mistakes in classification and promising advancements in treatment making plans and screening. These upgrades contribute to higher diagnostic precision and in advance interventions, which can lead to greater favorable affected person outcomes and a greater

resilient healthcare framework for cervical most cancers management.

In phrases of performance metrics, the proposed method excels across all key signs: Accuracy (99.3%), Precision (99.1%), Recall (98.6%), and F1 Score (98.2%). These values propose that the version isn't handiest talented at figuring out genuine positives but also minimizes fake positives and negatives. The F1 Score, balancing both Precision and Recall, reflects the method's normal robustness in type. These metrics, which are commonly used in clinical imaging and ailment detection, underscore the version's potential to handle complex class tasks successfully, proving it to be each reliable and efficient for cervical most cancers detection.

In evaluation to different models like SVM, CNN, GRU, and DRL, the proposed approach achieves considerably better effects. For instance, while SVM indicates an accuracy of 85.3%, CNN reaches 88.5%, and GRU achieves 92.4% precision. The proposed approach surpasses those fashions with a drastically better overall performance throughout all metrics. This may be attributed to advanced feature selection, records preprocessing techniques, and model integration. The overall performance comparison charts display that the proposed technique continuously achieves the very best accuracy, precision, and bear in mind, positioning it as a transformative solution in cervical most cancers category.

#### *C. Discussion*

Integration of multiple kind of data in cervical cancer diagnosis, segmentation and classification gives noticeable issues since cervical cancer is complex and involves huge medical data such as MRI, CT scan data base and histopathology images. These are mostly being challenges that interfere with the effectiveness of outmoded approaches, and precision of detection outcomes. Furthermore, the use of diverse data types raises privacy concerns because the combination of sensitive health information from multiple sources increases the risk of security breaches and compromises patient privacy are confused Another challenge where data may be of poor quality and methodological inconsistencies therefore hinders the data integration necessary for effective model performance [24]. The following method eliminates the above shortcomings when using a complete database of patient behaviors and high-resolution Pap smear images using the ABC optimized CNN-GRU model. In the sequential generation of patient data, the GRU component generates the time series while the CNN component obtains by the spatial properties of the images. This method is necessary to provide geomorphic and sequential information together to improve the overall quality of the research. SMOTE is used in the processes of minmax scaling and synthetic instances production because it prevents data inconsistencies that can cause some problems in model effort while maintaining confidentiality.

Future research could explore the mixing of additional information sorts including MRI and CT scans along Pap smear pictures to enhance diagnostic accuracy in cervical cancer detection. Combining multimodal clinical records with greater advanced optimization algorithms could in addition beautify model performance. Additionally, real-time packages the use of

deep learning methods in clinical settings have to be advanced to provide instant and accurate cervical most cancers diagnosis. Efforts to comprise explainable AI techniques also can help in decoding complicated fashions, improving consider and usability in healthcare programs.

One of the primary obstacles of this examine is the reliance on high-decision Pap smear pix, which might not constantly be without problems available, specifically in low-aid settings. The integration of different clinical facts resources, including MRI and CT scans, remains unexplored and provides challenges related to records compatibility and processing. Another challenge is the privacy situation regarding sensitive medical statistics, which, regardless of the use of stable algorithms like ABC, nonetheless requires sturdy measures to prevent capability breaches. Additionally, the generalizability of the version can be restrained by using dataset inconsistencies and a lack of numerous populace statistics.

#### VI. CONCLUSION AND FUTURE WORK

The proposed work demonstrates the advantages of using improved DL algorithms in conjunction with a large number of data for early detection and classification of cervical cancer. With a new collection of high-resolution Pap smear images from SipakMed fused by agglutination with large patient malformation behavior data, the inclusion of the ABC optimized CNN-GRU hybrid model achieved a good classification accuracy of 94.89%. This significant improvement over standard methods supports the usefulness of integrated spatio-temporal feature extraction for displaying multimedia content and sequence characteristics This method uses SMOTE and Min-Max Scaling was used to generate an improved dataset for the model and helped overcome the imbalance of classes. This approach generally provides diagnostic accuracy to more appropriate and effective cervical cancer screening and management. Combining MRI data with the context of the patient in question enhances this health information and can lead to a better understanding of the ethics of cervical cancer, among others.

Future research should try to incorporate more data sources into the multiple datasets such as providing more data types such as genetic information and social information for a better prediction model. Extending the analysis can improve accuracy and robustness in high-quality architecture such as transformer and ensembling methods. Furthermore, the efficacy of the model should also be verified in practice with modern clinical settings as it can be applied to in implementing modern health systems. Finally, this method should be successfully applied to cancer or other diseases with similar diagnostic problems, it will extend the validity of DL methods better than ovarian cancer, and thus has contributed to overall progress in disease diagnosis.

#### **REFERENCES**

- [1] P. A. Cohen, A. Jhingran, A. Oaknin, and L. Denny, "Cervical cancer," The Lancet, vol. 393, no. 10167, pp. 169–182, 2019.
- [2] M. K. A. Mazumder, M. M. U. Nobi, M. Mridha, and K. T. Hasan, "A Precise Cervical Cancer Classification in the Early Stage Using Transfer Learning-Based Ensemble Method: A Deep Learning Approach," in Data-Driven Clinical Decision-Making Using Deep Learning in Imaging, Springer, 2024, pp. 41–59.
- [3] S. M. Abd-Alhalem, H. S. Marie, W. El-Shafai, T. Altameem, R. S. Rathore, and T. M. Hassan, "Cervical cancer classification based on a bilinear convolutional neural network approach and random projection," Engineering Applications of Artificial Intelligence, vol. 127, p. 107261, 2024.
- [4] S. L. Tan, G. Selvachandran, W. Ding, R. Paramesran, and K. Kotecha, "Cervical cancer classification from pap smear images using deep convolutional neural network models," Interdisciplinary Sciences: Computational Life Sciences, vol. 16, no. 1, pp. 16–38, 2024.
- [5] B. Hemalatha, B. Karthik, C. K. Reddy, and D. Gokulakrishnan, "Cervical Cancer Classification: Optimizing Accuracy, Precision, and Recall using SMOTE Preprocessing and t-SNE Feature Extraction," in 2024 International Conference on Intelligent and Innovative Technologies in Computing, Electrical and Electronics (IITCEE), IEEE, 2024, pp. 1–7.
- [6] D. B. Talpur, A. Raza, A. Khowaja, and A. Shah, "DeepCervixNet: An Advanced Deep Learning Approach for Cervical Cancer Classification in Pap Smear Images," VAWKUM Transactions on Computer Sciences, vol. 12, no. 1, pp. 136–148, 2024.
- [7] D. H. Moore, "Cervical cancer," Obstetrics & Gynecology, vol. 107, no. 5, pp. 1152–1161, 2006.
- [8] D. Merlin and J. Sathiaseelan, "Improved classification accuracy for identification of cervical cancer," in Proceedings of the International Conference on Medical Informatics (ICMI), 2024, pp. 245–258.
- [9] B. E. Greer et al., "Cervical cancer," Journal of the National Comprehensive Cancer Network, vol. 8, no. 12, pp. 1388–1416, 2010.
- [10] J. S. Lea and K. Y. Lin, "Cervical cancer," Obstetrics and Gynecology Clinics, vol. 39, no. 2, pp. 233–253, 2012.
- [11] R. M. Munshi, "Novel ensemble learning approach with SVM-imputed ADASYN features for enhanced cervical cancer prediction," PLoS One, vol. 19, no. 1, p. e0296107, 2024.
- [12] J. H. Shepherd, "Cervical cancer," Best practice & research Clinical obstetrics & gynaecology, vol. 26, no. 3, pp. 293–309, 2012.
- [13] W.-J. Koh et al., "Cervical cancer," Journal of the National Comprehensive Cancer Network, vol. 11, no. 3, pp. 320–343, 2013.
- [14] P. Petignat and M. Roy, "Diagnosis and management of cervical cancer," Bmj, vol. 335, no. 7623, pp. 765–768, 2007.
- [15] T. Kattenborn, J. Leitloff, F. Schiefer, and S. Hinz, "Review on Convolutional Neural Networks (CNN) in vegetation remote sensing," ISPRS journal of photogrammetry and remote sensing, vol. 173, pp. 24– 49, 2021.
- [16] R. Rana, "Gated recurrent unit (GRU) for emotion classification from noisy speech," arXiv preprint arXiv:1612.07778, 2016.
- [17] A. Ghoneim, G. Muhammad, and M. S. Hossain, "Cervical cancer classification using convolutional neural networks and extreme learning machines," Future Generation Computer Systems, vol. 102, pp. 643–649, 2020.
- [18] H. Alguran et al., "Cervical cancer classification using combined machine learning and deep learning approach," Comput. Mater. Contin, vol. 72, no. 3, pp. 5117–5134, 2022.
- [19] A. Arora, A. Tripathi, and A. Bhan, "Classification of cervical cancer detection using machine learning algorithms," in 2021 6th International conference on inventive computation technologies (ICICT), IEEE, 2021, pp. 827–835.
- [20] A. Tripathi, A. Arora, and A. Bhan, "Classification of cervical cancer using Deep Learning Algorithm," in 2021 5th International Conference on Intelligent Computing and Control Systems (ICICCS), IEEE, 2021, pp. 1210–1218.
- [21] V. Kudva, K. Prasad, and S. Guruvare, "Automation of detection of cervical cancer using convolutional neural networks," Critical ReviewsTM in Biomedical Engineering, vol. 46, no. 2, 2018.
- [22] K. Fernandes, D. Chicco, J. S. Cardoso, and J. Fernandes, "Supervised deep learning embeddings for the prediction of cervical cancer diagnosis," PeerJ Computer Science, vol. 4, p. e154, 2018.
- [23] Y. R. Park, Y. J. Kim, W. Ju, K. Nam, S. Kim, and K. G. Kim, "Comparison of machine and deep learning for the classification of cervical cancer based on cervicography images," Scientific Reports, vol. 11, no. 1, p. 16143, 2021.
- [24] Z. Hu et al., "Enhancing the Accuracy of Lymph-Node-Metastasis Prediction in Gynecologic Malignancies Using Multimodal Federated Learning: Integrating CT, MRI, and PET/CT," Cancers, vol. 15, no. 21, p. 5281, 2023.
- [25] "Cervical Cancer largest dataset (SipakMed)." Accessed: Jul. 19, 2024. [Online]. Available: https://www.kaggle.com/datasets/prahladmehandiratta/cervical-cancerlargest-dataset-sipakmed/data
- [26] "Cervical cancer." Accessed: Jul. 19, 2024. [Online]. Available: [https://www.kaggle.com/datasets/harithagorle/cervical-cancer.](https://www.kaggle.com/datasets/harithagorle/cervical-cancer)
- [27] J. Xia, Y. Wang, and Y. Li, "A Navigation Satellite Selection Method Based on Tabu Search Artificial Bee Colony Algorithm," in 2020 IEEE 3rd International Conference on Electronic Information and Communication Technology (ICEICT), Shenzhen, China: IEEE, Nov. 2020, pp. 421–425. doi: 10.1109/ICEICT51264.2020.9334301.
- [28] M. Cinar and A. Kaygusuz, "Optimum Fuel Cost in Load Flow Analysis of Smart Grid by Using Artificial Bee Colony Algorithm," in 2019 International Artificial Intelligence and Data Processing Symposium (IDAP), Malatya, Turkey: IEEE, Sep. 2019, pp. 1–5. doi: 10.1109/IDAP.2019.8875893.