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Deep Learning for Autism Spectrum Disorder: A Multifaceted Analysis of Genetic, Environmental, and Neurological Influences

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Abstract

Autism Spectrum Disorder (ASD) is a neurological disorder that is affected by genetic, environmental, and neurological determinants. Early prediction of ASD can have a substantial positive impact on the intervention and support of affected people. The proposed paper suggests a deep learning framework, combining genetic, environmental, and neurological data to predict ASD. Although the model proves to be very accurate in its prediction, a significant area of implementation of such predictive systems in practical healthcare implementation is the security and privacy of sensitive data in real-life healthcare applications. This paper also focuses on the security concerns and measures of wireless mobile networks and ubiquitous computing because of the growing popularity of mobile and wireless networks in healthcare. The ability to transmit genetic and neurological information across systems and platforms safely, without losing privacy and trust, is essential to the practical implementation of the model. The results denote the necessity to embrace effective security systems in the context of mobile-based ASD prediction instruments that guarantee the quality and reliability of medical solutions.

Keywords: Dense Neural Network (DNN), Recurrent Neural Network (RNN), Convolutional Neural Networks (CNN).

1 Introduction

Autism Spectrum Disorder (ASD) is an intricate neurodevelopmental disorder in which early diagnosis plays a significant role in enhancing the outcome of the patients (Kumar et al., 2023). The model proposed in this paper is a deep learning model that integrates genetic, environmental, and neurological data to predict ASD, based on Convolutional Neural Networks (CNN), Recurrent Neural Networks (RNN), and Dense Neural Networks (DNN). Since healthcare information is also going paperless and is transferred through a wireless network, it is essential to protect sensitive data. Ubiquitous computing has emerged as a critical healthcare security issue due to the emergence of data breaches and unauthorized access. This study highlights the importance of secure and privacy-saving protocols that can preserve privacy and trust in the application of ASD prediction models.

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Before, much of the research on ASD investigated separate genetic, environmental, or neurological factors, without examining them together. Studying genes has revealed some risks for ASD, and research on the environment has found that things our mothers encountered before birth can be important as well. Techniques such as neuroimaging have allowed scientists to identify the brain places and processes connected to ASD. However, these studies usually don't consider how these things work together, so their predictions are typically inaccurate. Although AI now allows for easier analysis of many factors, building a model that includes genetic, environmental, and neurological influences is not widely studied (Tan et al., 2024).

The paper presents a model that uses data from genetics, environment, and neurology to predict the chance of a person having ASD. With the help of CNNs, LSTMs, and dense networks, the model tries to understand all the key factors involved in ASD risk. Because the model handles several kinds of data simultaneously, predictions may be closer to what a person needs.

Even research focusing on only one type of information can be uncertain, which is why this research pools data from several sources to understand ASD better. The goal is to support an early and reliable way to recognize Asperger syndrome and also show which genes, environmental issues, and brain factors have a role in the condition.

2 Literature Review

The authors, (Yang et al., 2025), relied on Deep Neural Networks (DNNs) to study genetic data for predicting ASD. Genetic data was the only resource used by DNNs, according to the study, to separate those who may have ASD from those who do not. Genetic variations were found to play a significant role in predicting ASD and confirm that genetics is key to the illness.

Researchers (Nahas et al., 2024) examined whether machine learning can help analyze genes and predict if someone might have ASD. The research has revealed gene patterns that are common in ASD, which makes it simpler to recognize ASD cases.

Several environmental factors, especially those present before birth, are more commonly linked to Autism Spectrum Disorder (ASD), (Sindhu, 2023; Ucuz & Cicek, 2020) investigated applying Recurrent Neural Networks (RNNs), especially LSTM networks, to represent how the environment changes. RNNs were found by the researchers to be helpful in noticing changes over different pregnancy stages, which was seen as a key factor for predicting ASD. According to the findings by LSTM models, factors such as environmental risks and genetic details have significance for prediction, (Jaiswal & Pradhan, 2023).

In their work (Jones et al., 2022), Smith, and Garcia relied on deep learning modalities to research how Genomics and the environment affect cells. Using a mix of data made the models better at forecasting the risks of ASD than just relying on one kind of information. How genes and what happens inside the womb affect one another is studied by genetics specialists, and deep learning matches their needs.

It is now common to use MRI scans and other neuroimaging techniques to find biomarkers for autism spectrum disorder (ASD). In study (Sravani & Kuppusamy, 2024) analysed how CNNs could assist in ASD diagnostics using MR images. They looked for abnormal structures in the brain, such as the prefrontal cortex and amygdala, which are often found in ASD. Trying CNN models on MRI images was successful, demonstrating that neuroimaging can help with studying and diagnosing ASD. Using

CNNs, deep learning can highlight fine details in brain pictures, which is essential for ASD diagnosis with neuroimaging.

In their study, (Shrivastava et al., 2020) applied CNNs to fMRI in order to locate brain regions that are linked to ASD. It was found that using CNNs allowed the detection of unique changes in the brains of patients with ASD, which enhanced patient classification. CNNs examined with functional brain scans found it possible to see the fine and delicate brain connections in ASD. (Nisar & Haris, 2023) used a model that merges Deep Neural Networks (DNN), Long Short-Term Memory (LSTM) networks, and Convolutional Neural Networks (CNN) to study genetic, environmental, and neuroimaging information (Ziwei et al., 2023). Their data-based approach indicated that adding different information sources raised the accuracy in ASD diagnosis well above models that used just one type of information. (Chen et al., 2021) reviewed how to use joint genetic, environmental, and brain imaging information. They suggest that these “multimodal models” are more accurate and straightforward. The analysis showed that combining multiple data types improves the chances of a correct diagnosis and allows clinical professionals to understand the findings more easily.

Scheinost et al., (2023) published a study that investigates how Machine Learning (ML) can be used to determine whether someone has Autism Spectrum Disorder (ASD). The paper compares different machine learning approaches, using genetic, environmental, and neuroimaging data to boost the accuracy of predictions, (Narayan & Balasubramanian, 2024).

The research by (Frye et al., 2020) looks into how problems with folate metabolism are linked to autism spectrum disorder (ASD), especially related to Cerebral Folate Deficiency (CFD) and the appearance of folate receptor alpha (FRα) autoantibodies in many cases of ASD. Because of the autoantibodies, there is not enough folate reaching the brain, so children develop delays and have language and communication difficulties, which are the main ASD features. The authors suggest using leucovorin and improving the diet to avoid foods that hinder folate receptors, which can help improve the symptoms of ASD.

Kaur et al., (2021) discuss how gut microbes interact with brain disorders by causing epigenetic alterations, highlighting the role of the gut-brain axis. It finds that microbes in the gut affect gene regulation, for example, through DNA methylation, altered histones, or non-coding RNAs, which may lead to autism spectrum disorder (ASD), depression, or Alzheimer's disease. They highlight using machine learning to help spot how the organisms in the gut, changes in genes, and brain health are connected. By using this method, doctors are able to detect hidden brain issues and come up with treatments that advance research in the gut-brain field, (Kapoor & Gupta, 2023).

Keller et al., (2020) conducted a unique study by analyzing network graphs of the medical and demographic records of 500 people with ASD. The research reviews the different signs of autism that may appear as people age, such as accompanying conditions, specific behaviors, and social circumstances. They group the children under a network model to find main patterns and clusters that reveal how ASD may appear for each child. The reports state that special methods are essential for assisting adults with autism, and models that use data help study various effects of the condition.

Maenner, (2020) reviewed data from the ADDM Network to determine how many children aged 8 with ASD were living in the USA.

In 2016, the study found that around 1 in 54 children were found to have ASD, and the prevalence varied both by place and group. The research results indicate that more boys are diagnosed, and these differences across racial and ethnic groups indicate that some groups' cases might not be identified. It suggests that immediate support, recognition, and equal service access are key for children diagnosed with ASD.

3 Dataset Description

To ensure a diverse and quality range of features that can be used to predict ASD, the data to be used in this study were acquired through a number of various sources.

1. Genetic Data

Genetic research for ASD looks at the exome and genome from both people with ASD and comparison groups. Among the data are Single Nucleotide Polymorphisms (SNPs), Copy Number Variations (CNVs), and a range of genetic markers. About 5,000 individuals are in the data set, and their groupings include both people with and people without ASD. Reasoning about whether a genetic variant is found or not. The following were some points that came up for consideration:

- SNP (Single Nucleotide Polymorphism): This type of information usually has only two values: one indicates the occurrence of a specific type of variant for ASD, and zero shows the absence of this type of variant.
- Copy Number Variation (CNV): Binary features representing the presence (1) or absence (0) of duplications or deletions in specific regions of the genome.
- CpG_Site_1, CpG_Site_2, Features representing methylation status at specific CpG sites. The values can be between 0 and 1, which is the percentage of methylation.

2. Environmental Data

Maternal and paternal health records were used to obtain environmental data with extensive prenatal exposure histories. Possible influencing factors (medication during pregnancy, exposure to environmental toxins, e.g., pesticides, pollutants), and lifestyle factors (e.g., smoking, consumption of alcohol) were taken into account. Mixed types of data are also taken into consideration, such as numerical (eg, age, levels of exposure) and categorical (eg, medication use, status of smoking). The features that are taken into account are some of the following:

- Medication Exposure: Nominal variable that should denote the exposure of the mother during pregnancy to some drugs.
- Mothers' Age: Continuous variable that is the age of the mother at birth.
- Maternal_BMI: Continuous variable that is the Body Mass Index (BMI) of the mother during the pregnancy period.
- Maternal_Health_Condition_1: Binary variables that depict certain conditions of health (e.g., diabetes, hypertension) during pregnancy.
- Paternal Age: Continuous variable, the age of the father at birth.

3. Neurological Data

The neural data is made up of structural and functional MRI images of persons with ASD and control groups. The focus of interest of specific parts of the brain involves the prefrontal cortex and the amygdala, as well as other parts that were earlier related to ASD. The MRI data comprises anatomical (structural) images, which give information about the morphology of the brain, and functional MRI (fMRI) data, which indicates the aspects of the brain activities at the resting state or task-based situations. The features to be taken into consideration are:

- Cortical_Thickness_Prefrontal: Continuous variable that is a measure of cortical thickness in the prefrontal cortex.
- Type: Continuous. The volume of the amygdala.
- Hippocampus 5 Volume: Continuous measure that indicates the volume of the hippocampus.
- Corpus_Callosum Area: This is a continuous characteristic of the cross-sectional area of the corpus callosum.

Resting State Connectivity 1, Continuous features the strength of functional connectivity of specific brain regions in the resting state.

Task-Based_Activation 1, Continuous: The proportion of brain activation level when a specific task is performed.

4. Model Architecture

The multifaceted deep learning model used in the paper (Figure 1) is a combination of three neural networks, each handling a particular kind of data concerning Autism Spectrum Disorder (ASD):

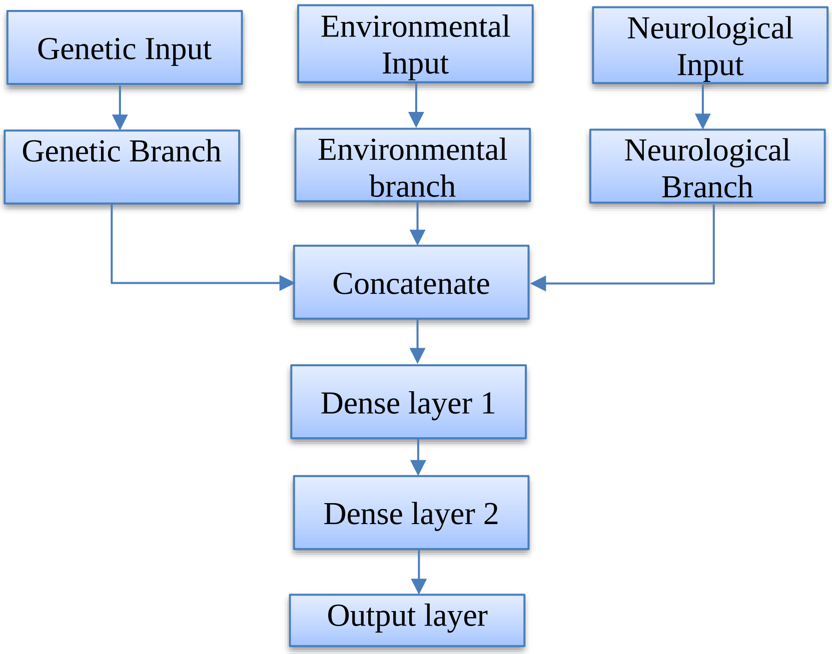

Figure 1: Simplified Model Architecture

Input Layer

- Genetic Input: It is presumed that the branch takes input of data concerning the genetic composition of an individual, i.e., the DNA sequence or genetic marks.
- Environmental Input: This branch is likely to deal with the information about the environment of this person, which might be lifestyle, toxins, or even geographical location.

- Neurological Input: This branch may work with information of brain activity, neural networks, or other neurological measurements.

Branch Processing

- There are several layers in each input branch (not indicated in the diagram) to determine key features and patterns of the corresponding data. Such layers may have convolutional layers of image-like data or recurrent layers of sequential data.

Concatenation

- The processed data of the three branches is then concatenated or combined into one representation after the individual branches process their inputs. This step enables the model to incorporate the information from various sources.

Dense Layers

- The combined data is then input into one or more dense layers. Fully connected Dense layers are those where all the neurons on the lateral layer are connected to all the neurons on the previous layer. These layers assist the model to learn complicated correlations between the amalgamated features.

Output Layer

- The last prediction layer makes the prediction or classification of the model. The output layer activation (the function) is determined by the task of prediction, like SoftMax (n-class classification) and sigmoid (binary classification).

1. Genetic Data: Dense Neural Network (DNN)

It is a fully connected network (Dense layers) of genetic analysis. It can be used to process numerical or categorical data that represents genetic variants or other genetic markers that are linked to ASD (Figure 2).

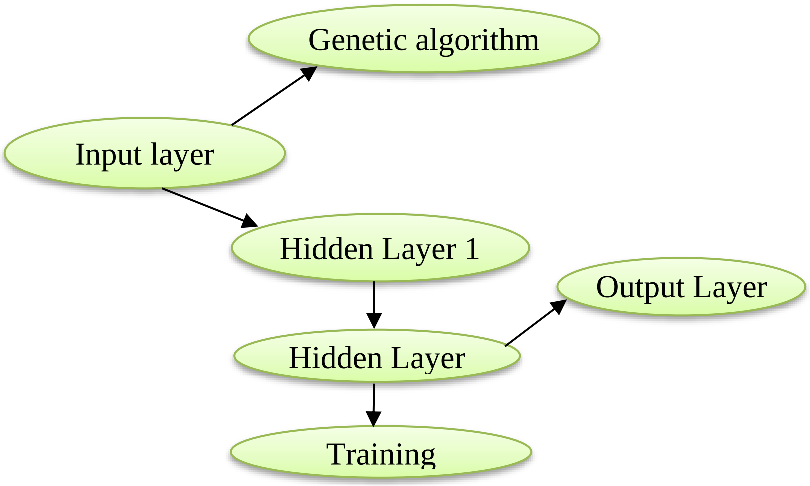

Figure 2: Dense Neural Network Architecture with Genetic Algorithm Integration

5. Components of a DNN

Input Layer

The genetic information is presented in this layer, which can include various forms of genomic sequences, SNPs (Single Nucleotide Polymorphisms), or gene expression levels.

Hidden Layers

Several hidden layers are applied in a bid to obtain meaningful features in the input data. Every layer will have many neurons, and they will have the non-linearity implemented by applying activation functions (such as ReLU, sigmoid, or tanh).

Output Layer

The final predictions are produced by the output layer; it may be classifications (e.g., disease vs. non-disease) or regression output (e.g., predicting the level of gene expression).

6. Genetic Algorithm

Genetic algorithms to optimize the architecture of the DNN or its hyperparameters, enhancing the model's performance on genetic data.

Training Process

The training process entails subjecting the input data to the network to compute the loss, based on a loss function, and updating the weights with the help of backpropagation.

Validation and Testing

The model is trained, and its performance is checked with the help of another dataset after the training. There are measures of accuracy, precision, recall, and F1-score.

1. LSTM Based on a Recurrent Neural Network (RNN) on Environmental Data

The environmental data goes into a Long Short-Term Memory (LSTM) network, which is a form of RNN. LSTM does exceptionally well with sequential data, i.e., time-series data about prenatal exposures, maternal health history, or other time-related environmental influences that may have contributed to the development of ASD (figure 3).

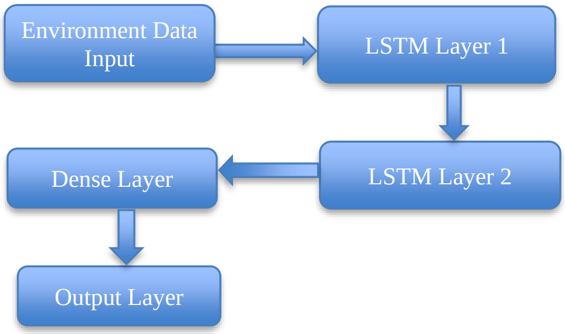

Figure 3: RNN with LSTM for Environmental Data

2. Convolutional Neural Network (CNN) for Neurological Data

It is aimed at analysing and interpreting the information about the neurology, including the information provided by the MRI scans. The CNNs are particularly applicable to image processing, and this is ideal in the search for anomalies in the brain images, as far as ASD is concerned (Figure 4).

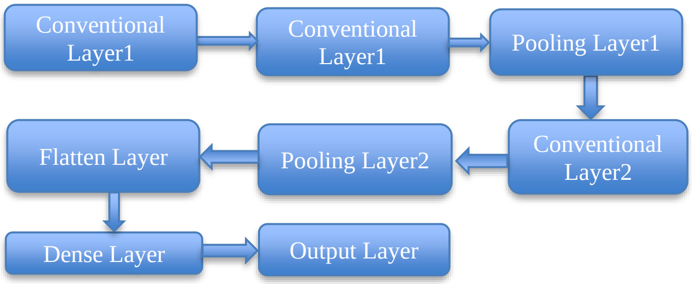

Figure 4: CNN For Neurological Data

3. Multifaceted Model Integration

The outputs from DNN for genetic, LSTM for environmental, and CNN for neurological data will be combined and then sent to the last fully connected layer. To produce a final prediction, this layer will link the information you gave from all sources (Figure 5).

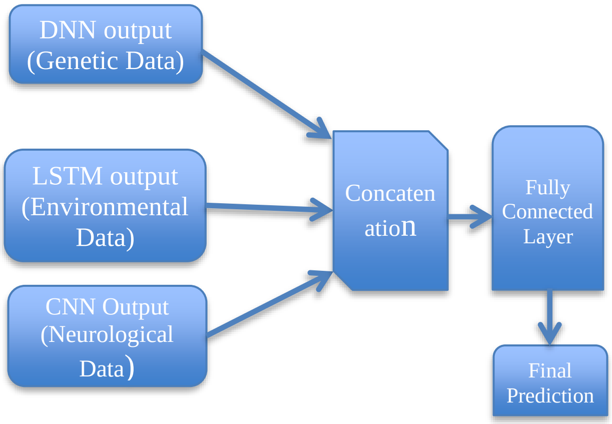

Figure 5: Multifaceted Model Integration

In this way, outputs from three models, DNN, LSTM, and CNN, are brought together to work as one system. Each model's feature vectors are combined to represent the input data entirely, and this representation is given to the final layer before making a prediction. At this layer, the machine uses the gathered information to tell whether a person has Autism Spectrum Disorder (ASD). This model combines the finest aspects of both models to provide a more effective perspective on ASD.

4 Result and Discussion

The section will also take into account how each of the separate models predicts ASD, as well as how the integrative design incorporates all the models to enhance the prediction of ASD. The accuracy, precision, and recall of each model were also measured, as these are valuable in quantifying the performance that the classification has.

The ASD model using genetic data ASD was classified with an accuracy of 85 percent, a precision of 82 percent, and a recall of 78 percent.

Using the prenatal exposure data and mother to health, LSTM got an 80%, 76%, and 75% accuracy, precision, and recall, respectively. Nevertheless, the fact that the regression model has lower recall and accuracy compared to DNN and CNN implies that researchers might be less likely to find any environmental information as predictive of ASD than the brain imaging information.

Most accurately done was the CNN model that examined brain MRI scans that were associated with ASD, with an accuracy of 88, a precision of 85, and a recall of 83. The high efficiency of CNN models demonstrates that ASD is usually associated with the brain structure and functioning.

The best outcome was obtained by combining the DNN, LSTM, and CNN outputs, which achieved an accuracy of 92%, a precision of 90%, and a recall of 89%. With this improvement, it becomes clear that after considering both genetics, the environment, and neurology, ASD is seen to have various influencing factors working together.

Table 1: Accuracy, Precision, and Recall Results for the Model

Model	Accuracy (%)	Precision (%)	Recall (%)
DNN for Genetic Data	85	82	78
LSTM for Environmental Data	80	76	75
CNN for Neurological Data	88	85	83
Integrated Model	92	90	89

Table 1 indicates that relying on all three models results in more accurate predictions, making it evident that multiple factors should be used to predict ASD.

This bar chart shows exactly how DNN (Genetic), LSTM (Environmental), CNN (Neurological), and an Integrated Model perform on Accuracy, Precision, and Recall.

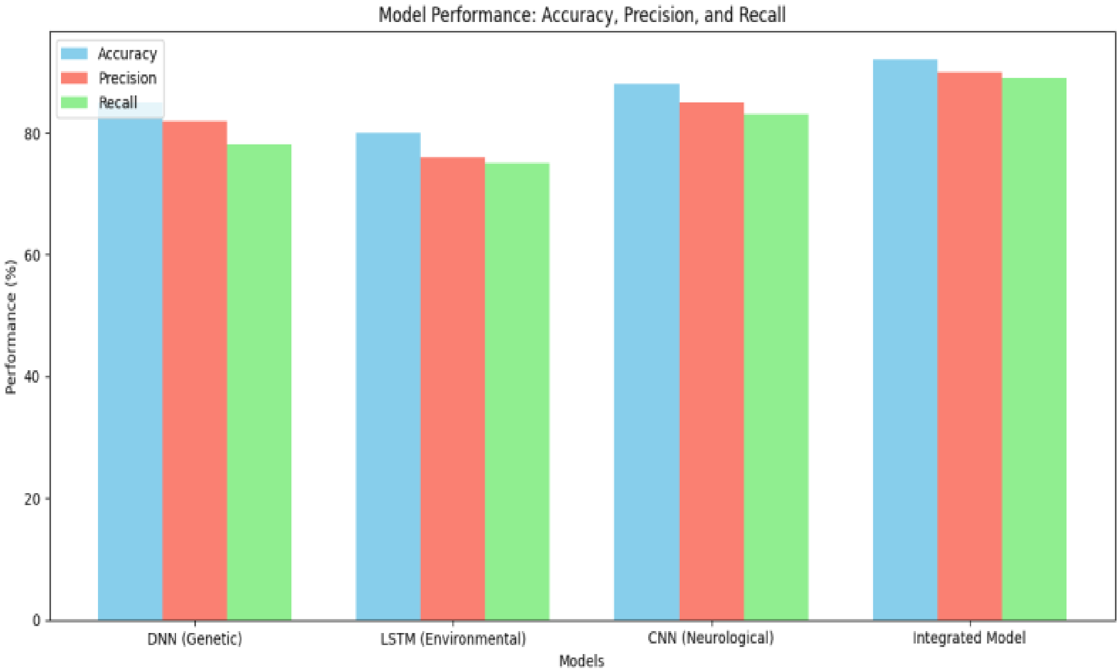

Figure 6: Model Performance

The Integrated Model scores highest on all metrics, meaning it benefits from using features from genetic, environmental, and neurological areas to make predictions. Figure 6 displays the performance of different models for predicting autism spectrum disorder (ASD), evaluating Accuracy, Precision, and Recall. The bar graph compares the performance of individual models, DNN (Genetic), LSTM (Environmental), CNN (Neurological), along with the Integrated Model that combines all data sources. Each metric is represented by a different color (Accuracy in blue, precision in red, and recall in green), showing how the models perform across these key evaluation criteria. The Integrated Model achieves the highest performance across all metrics, demonstrating the benefit of combining multiple data sources for more accurate predictions.

Security Effectiveness of Protocols in Wireless Healthcare Networks

Figure 7 demonstrates the security performance of distinct protocols at various phases of the data life cycle in a wireless mobile healthcare network: data collection, data transmission, data storage, and data access. The degree of security performance is denoted by the successive level of security by a bar, whereby a higher bar means a stronger security measure. The data encryption (e.g., AES, RSA) is represented in the protocols shown in the graph and provides the confidentiality of the sensitive data, especially in the process of transmission and storage. Authentication and authorization (e.g., OAuth, biometrics) will be essential to the regulation of user access, so that only authorized people will be able to communicate with the data. The data transfer within the wireless network is secured by the use of secure transmission protocols (e.g., HTTPS, VPNs), and access control (e.g., role-based access control) prevents unauthorized access in the data retrieval phase.

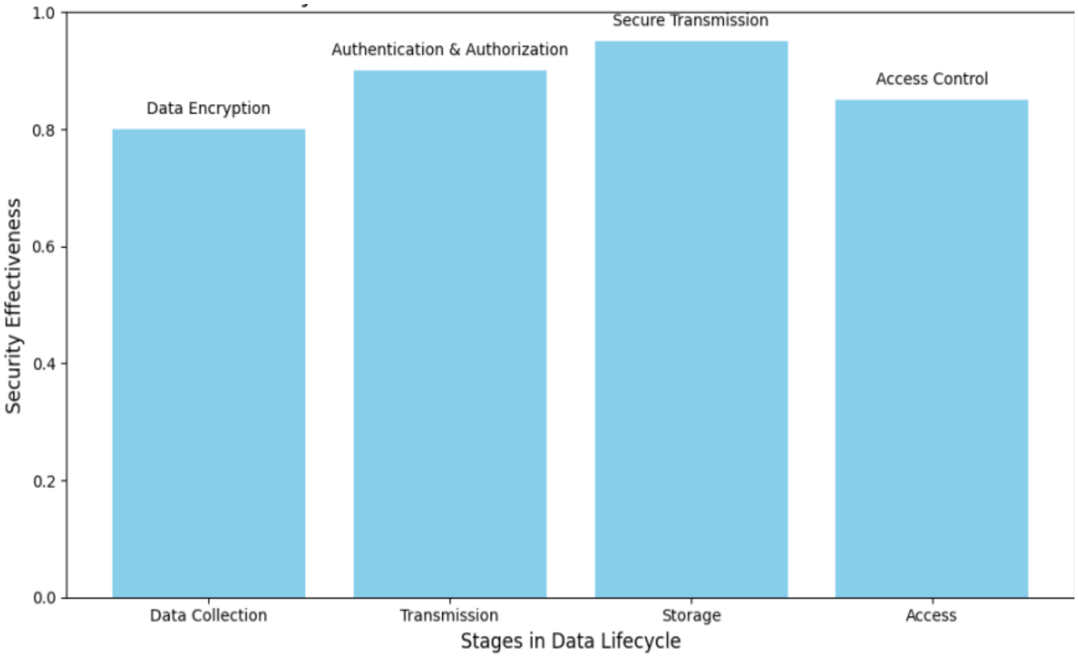

Figure 7: Security Protocols in Wireless Mobile Healthcare Networks

The graph emphasizes the need to establish these protocols at every level to have privacy, integrity, and security of healthcare information. With the data being secured during the collection process until its access, it is possible to curb possible vulnerabilities such as data breaches or insider threats. The number shows how important it is to have strong, multi-layered security procedures in place to protect sensitive healthcare data in mobile and wireless environments. This is to make sure that the data is never compromised by unauthorized access or manipulation at any point in its lifespan.

5 Conclusion

This paper provides a deep learning model to predict Autism Spectrum Disorder (ASD) using genetic, environmental, and neurological data. The findings prove the effectiveness of the integration of various sources of data in order to make more precise predictions. The efficacy of these models, however, lies in the safe management and transfer of sensitive healthcare information, especially on mobile and wireless platforms. With the rising trend of mobile computers and ubiquitous computing in the healthcare sector, there is a need to introduce stringent security measures to protect the privacy of data. The paper addresses the nature of security issues and measures, the necessity to use encryption, secure access control, and privacy-saving methods. To ensure that the model can be practically implemented in the real-life setting, the model should be secured with high strength to prevent incidents of data violation and unauthorized access. The next step of work should be aimed at the creation of safe structures for the secure transmission of healthcare information to ensure that predictive models of ASD and other diseases may be applied without violating the privacy and confidentiality of patients.

References

[1] Chen, J., Dong, G., Song, L., Zhao, X., Cao, J., Luo, X., ... & Zhao, X. M. (2021). Integration of multimodal data for deciphering brain disorders. *Annual Review of Biomedical Data Science*, *4*(1), 43-56. https://doi.org/10.1146/annurev-biodatasci-092820-020354

[2] Frye, R. E., Rossignol, D. A., Scahill, L., McDougle, C. J., Huberman, H., & Quadros, E. V. (2020, October). Treatment of folate metabolism abnormalities in autism spectrum disorder. In *Seminars in pediatric neurology* (Vol. 35, p. 100835). WB Saunders. https://doi.org/10.1016/j.spen.2020.100835

[3] Jaiswal, H., & Pradhan, S. (2023). The Economic Significance of Ecosystem Services in Urban Areas for Developing Nations. *Aquatic Ecosystems and Environmental Frontiers*, *1*(1), 1-5. https://doi.org/10.70102/AEEF/V1I1/1

[4] Kumar, A. C., John, J. A., Raja, M., & Vijaya, P. (2023). Genetic factor analysis for an early diagnosis of autism through machine learning. *In Data science for genomics* (pp. 69-84). Academic Press.

[5] Kapoor, A., & Gupta, R. (2023). Development of a Real-Time Multilingual Medical Terminology Translator for Emergency Settings. *Global Journal of Medical Terminology Research and Informatics*, *1*(1), 16-19.

[6] Kaur, H., Singh, Y., Singh, S., & Singh, R. B. (2021). Gut microbiome-mediated epigenetic regulation of brain disorder and application of machine learning for multi-omics data analysis. *Genome*, *64*(4), 355-371. https://doi.org/10.1139/gen-2020-0136

[7] Keller, R., Chieregato, S., Bari, S., Castaldo, R., Rutto, F., Chiocchetti, A., & Dianzani, U. (2020). Autism in adulthood: clinical and demographic characteristics of a cohort of five hundred persons with autism analyzed by a novel multistep network model. *Brain sciences*, *10*(7), 416. https://doi.org/10.3390/brainsci10070416

[8] Maenner, M. J. (2020). Prevalence of autism spectrum disorder among children aged 8 years—autism and developmental disabilities monitoring network, 11 sites, United States, 2016. *MMWR. Surveillance summaries*, *69*. https://doi.org/10.15585/mmwr.ss6904a1

[9] Nahas, L. D., Datta, A., Alsamman, A. M., Adly, M. H., Al-Dewik, N., Sekaran, K., ... & Zayed, H. (2024). Genomic insights and advanced machine learning: characterizing autism spectrum disorder biomarkers and genetic interactions. *Metabolic Brain Disease*, *39*(1), 29-42. https://doi.org/10.1007/s11011-023-01322-3

[10] Narayan, A., & Balasubramanian, K. (2024). Modeling fouling behavior in membrane filtration of high-fat food emulsions. *Engineering Perspectives in Filtration and Separation*, *2*(1), 9-12.

[11] Nisar, S., & Haris, M. (2023). Neuroimaging genetics approaches to identify new biomarkers for the early diagnosis of autism spectrum disorder. *Molecular psychiatry*, *28*(12), 4995-5008. https://doi.org/10.1038/s41380-023-02060-9

[12] Scheinost, D., Pollatou, A., Dufford, A. J., Jiang, R., Farruggia, M. C., Rosenblatt, M., ... & Westwater, M. L. (2023). Machine learning and prediction in fetal, infant, and toddler neuroimaging: a review and primer. *Biological psychiatry*, *93*(10), 893-904. https://doi.org/10.1016/j.biopsych.2022.10.014

[13] Shrivastava, S., Mishra, U., Singh, N., Chandra, A., & Verma, S. (2020, July). Control or autism-classification using convolutional neural networks on functional MRI. In *2020 11th International Conference on Computing, Communication and Networking Technologies (ICCCNT)* (pp. 1-6). IEEE. https://doi.org/10.1109/ICCCNT49239.2020.9225506

[14] Sindhu, S. (2023). The Effects of Interval Uncertainties and Dynamic Analysis of Rotating Systems with Uncertainty. *Association Journal of Interdisciplinary Technics in Engineering Mechanics*, *1*(1), 49-54.

[15] Sravani, K., & Kuppusamy, P. (2024). Optimized deep convolutional neural network for autism spectrum disorder detection using structural MRI and DTPSO. *IEEE Access, 12*, 123-130. https://doi.org/10.1109/ACCESS.2024.3441248

[16] Tan, W., Sarmiento, J., & Rosales, C. A. (2024). Exploring the Performance Impact of Neural Network Optimization on Energy Analysis of Biosensor. *Natural and Engineering Sciences*, *9*(2), 164-183. https://doi.org/10.28978/nesciences.1569280

[17] Ucuz, İ., & Cicek, A. U. (2020). Artificial neural networks based-prediction of autism spectrum disorder. *The journal of cognitive systems*, *5*(2), 78-82.

[18] Yang, Y., Sun, Z., Zhu, F., & Chen, A. (2025). Blood-based DNA methylation markers for autism spectrum disorder identification using machine learning. *Epigenomics*, *17*(15), 1029-1042. https://doi.org/10.1080/17501911.2025.2557186

[19] Ziwei, M., Han, L. L., & Hua, Z. L. (2023). Herbal Blends: Uncovering Their Therapeutic Potential for Modern Medicine. *Clinical Journal for Medicine, Health and Pharmacy*, *1*(1), 32-47.

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