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Improvement of Alzheimer's Disease Prediction Using VGGception-17

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Abstract–This study proposes "NeuroFusion," a distinctive predictive technique intended to boost Alzheimer's disease (also known as AD) prediction accuracy. NeuroFusion integrates aspects obtained using the VGG16 and InceptionV3 deep neural network structures, making use of each of their strengths for gathering rich positional knowledge and multiple scale characteristics using neuroimaging images. The technique of transfer learning is employed to improve these already trained models utilizing varied datasets that include inherited, medical, and neuroimaging imagery. Sophisticated merging methods are subsequently employed to bring together the collected features, which increases the framework's selective performance. Experimental scrutiny of the dataset suggests NeuroFusion's enhanced performance compared to both standalone models and known benchmarks, as demonstrated by initiatives like reliability, precision, recollection, and F1 progress. Visualization instruments give additional insight into the framework's method of decision-making and highlight key biomarkers that contribute to AD assessment. NeuroFusion is a possible leap forward in Alzheimer's disease forecasting, providing increased accuracy and endurance for early identification and involvement in Alzheimer's disease (AD) therapy.

Keywords—Transfer Learning; Convolutional Neural Networks (CNNs);Alzheimer's Disease Biomarkers; Neuroimaging Analysis; Feature Fusion; Hyperparameter Tuning, VGGCeption-17

I. INTRODUCTION

Alzheimer's disorder (AD) provides an important obstacle for current healthcare systems because of its increasing reflection and catastrophic consequences for people, families, and society worldwide. The condition Alzheimer's disease (AD) robs persons of their sense of independence and enjoyment of life, casting a substantial strain upon relatives and professionals in healthcare. Alzheimer's disease, also known as dementia (AD) poses an enormous threat to current medical systems, with its rising reflection and serious impact on individuals, societies, and families globally. The condition known as Alzheimer's (AD) robs persons of their independence and enjoyment of life, inflicting enormous pressure upon caretakers and providers of healthcare.



Early identification of dementia has remained a crucial objective in disease treatment since interventions initiated during the preclinical stages might have the most potential for maintaining cognitive function and slowing disease progression. Nevertheless, the effectiveness of treatments is limited since conventional diagnosis methods, which rely on psychological evaluation and cognitive evaluations, regularly fail to find the pathology of AD until the disease gets worse. Predictive computing shows promise in this scenario in detecting persons who are more predisposed to AD as well as promoting early-warning gauges meant to mitigate the burden of the disease and boost the health of patients.

The deployment of machine learning and deep learning algorithms in predictive analytics delivers special promise for Alzheimer's disease research, as it has the potential to The deployment of machine learning and deep learning algorithms in predictive analytics delivers special promise for Alzheimer's disease research, as it has the potential to reveal subtle connections and trends within complex data sets that traditional analytical approaches can ignore. Deep lcomputation architectures, such as convolutional neural networks (CNNs), have demonstrated an exceptional ability to analyze neuroimaging data and discover biomarkers associated with AD disease. In addition, transfer learning tackles allow for the use of pre-trained models, such as VGG16, InceptionV3 and to extract important characteristics from medical imaging data, improving forecasting precision and model generalization.

By integrating diverse datasets encompassing genetic, clinical, imaging, and biomarker information, predictive models can generate individualized risk profiles for AD development and progression, enabling clinicians to tailor interventions and treatment strategies to each patient's unique characteristics and needs. Furthermore, predictive analytics contribute to advancing scientific understanding by elucidating the complex mechanisms underlying AD pathology and identifying novel biomarkers and therapeutic targets. To ensure the responsible and equitable use of predictive analytics, multidisciplinary cooperation and ethical data governance are required. In any case, the integration of predictive models into clinical practice presents challenges related to data standardization, interoperability, and ethical considerations.

In the present piece, we furnish a novel practice for

Alzheimer's disease prediction using deep learning and predictive analytics to improve early diagnosis and intervention options. Our aim is to combine rich deep learning architectures, such as InceptionV3 and VGG16, with transfer learning to produce a robust and trustworthy prediction model that can accurately identify people who are at a high risk of getting AD. Through extensive testing utilizing a range of datasets and rigorous validation methodologies, we want to show the efficacy and therapeutic relevance of our prediction model with the goal of improving patient outcomes and furthering our understanding of AD pathology.

II. RELATED WORKS

Deep computation algorithms are becoming more and more useful in the prediction of Alzheimer's disease because they can automatically create hierarchical representations from complicated data. Studies like [1] have demonstrated the value of convolutional neural networks (CNNs) in processing neuroimaging data for AD prediction. These algorithms use large-scale datasets with transfer learning to identify discriminative characteristics suggestive of AD pathogenesis. Additionally, collaborative approaches [2] that combine many deep learning systems have beenproposed to improve prediction accuracy and resilience.

Recognizing the multifaceted nature of Alzheimer's disease, integrating data from several modalities has evolved into an acceptable approach to improve the precision of predictions. Research like [3] has looked into the use of fusion methods for integrating clinical, genomic, and imaging data for a more complete risk assessment. Multiple fusion strategies, particularly late fusion, early fusion, and decision-level fusion, have been studied for enhancing prediction accuracy through using complementary information drawn from multiple sources.

Developing reliable biomarkers related to the pathology of Alzheimer's illnessis essential for early detection and management. Using machine learning algorithms, investigations like [4] have centered on finding new biomarkers from neuroimaging and cerebrospinal fluid (CSF) data. To identify biomarker signatures that predicted sickness advancement and treatment response, this research apply validation steps and feature selection techniques.

Prediction model-based decision-support systems for clinical decision-making (CDSS) have demonstrated promise in assisting healthcare providers in identifying and predicting the outcome of Alzheimer's disease and its complications. Research endeavors including [5] have generated CDSS solutions that integrate patient-specific data and predictive analytics that allow rapid detection and individualized therapy strategizing. Based on the particular danger profiles and disease trajectories for every patient, these innovations empower doctors to make informed decisions.

The Alzheimer's disease neuroscience initiative (ADNI) [6] give researchers and clinicians access to huge, multi-center datasets while also enabling global collaboration. These initiatives foster data sharing, methodological innovation, and the development of standardized protocols for AD prediction research. Massive amounts of collaborative efforts and associations have performed a key part in expanding studies about Alzheimer's disease (AD) and prediction modeling.

Thorough verification and assessment in real-world environments are necessary when transferring prediction models from research environments to clinical environments. The clinical value and efficacy of predictive models in directing patient care and treatment decisions have been evaluated in clinical trials, such as [8]. To close the gap between research findings and clinical deployment, these studies highlight the significance of interdisciplinary collaboration between researchers, clinicians, and industry stakeholders.

Longitudinal studies are essential for monitoring the development of illnesses and analyzing the long-term effectiveness of predictive models. Large-scale longitudinal studies have been carried out through research initiatives such as the Alzheimer's Disease Neuroimaging Initiative (ADNI) [15] which gather longitudinal clinical, imaging, and genetic data from various cohorts. These investigations assist to the development of longitudinal predictive models for specific risk assessment and intervention planning, as well as offering crucial data regarding the dynamics of disease progression.

The disorder of Alzheimer's susceptibility is primarily opted by genetic risk factors; research has identified several susceptibility genes and genetic variations linked to an elevated risk. Novel genetic loci and polygenic risk scores (PRS) associated with Alzheimer's disease risk have been found by Lambert et al. [19] and Kunkle et al. [20], offering significant fresh insights into the genetic architecture of the disease. These results progress the building of predictive models based on genetics for tailored risk assessment and early intervention techniques.

III. PROPOSED METHODOLOGY

As a way to forecast Alzheimer's disease, the present research presents an innovative deep learning framework. It does this by putting forth a sophisticated hybrid model that effectively integrates features taken from two different convolutional neural network models (CNNs): VGG16 and Inception.

These CNN architectures are useful to recognize complex patterns and features in the input data, which is usually obtained from MRI scans. They have been pretrained on large datasets containing labeled pictures. While Inception excels at recovering higher-level, more general features, VGG16 is better at capturing delicate, detailed aspects in the initial phases of feature extraction. The algorithm then carefully combines these various variables from VGG16 and Inception into the hybrid model to make precise predictions about whether memory loss exists or not.

The successful implementation of the suggested structure is dependent upon having access of a wellselected dataset with labeled training information, which is necessary to train the model to differentiate between Alzheimer's and non-Alzheimer's cases according to detectable traits.

Moreover, the technology legally logs predicted outcomes into an extensive database for further scrutiny and testing. This novel method seeks to provide a deeper understanding of the data by utilizing both the excellent and detailed characteristics derived by VGG16 and Inception. This may result in increased precision when predicting Alzheimer's disease in comparison to traditional a single CNN simulations.

Gathering Data and The preliminary processing: To get started with our investigation, a large dataset including biomarker, clinical, genetic, and neuroimaging data from both AD patients and healthy controls will be generated. This dataset will be a foundation for the building of our predictive model. A number of preprocessing procedures will be carried out to ensure data quality and seamless integration across various modalities



This involves normalizing the data distributions, extracting useful characteristics from the raw data using feature extraction, and cleaning the data to remove outliers and missing values. Furthermore, we will use domain-specific knowledge to locate and extract relevant characteristics that point to the pathological conditions of Alzheimer's illness. Advantages gathering: We will exploit the advantages of two effective deep learning architectures, InceptionV3 and VGG16, in the techniques The way we propose is to organize the neuroimaging data into features.These frameworks have shown competence in collecting hierarchical features from complicated pictures after being trained on vast image datasets. Transfer learning strategies will be used to modify these models for our specific goal. To eliminate having to pay for significant training from scratch, we optimize the pre-trained models using our Alzheimer's disease dataset. This enables them to learn discriminative attributes specific to AD pathology.

To minimize the loss function L on the target task, the pretrained model's parameters are modified as part of the mathematical formulation for transferred learning. This may be expressed as

$\min\Theta L(\Theta)$

where Θ denotes the parameters of the pre-trained model, and $(\Theta)L(\Theta)$ represents the loss function to be minimized.

Fusion of Features: We are going to employ fusion techniques to bring together the features that were developed from the InceptionV3 and VGG16 models to generate a single feature representation for each individual in the collection of data. We'll investigate several fusion techniques, that includes concatenation, averaging, and weighted combination, to see which works best for merging information from different sources. Our goal is to improve the discriminative capability of our model of features and acquire complementary information by combining information from several dimensions.

Using a fusion function f, the feature vectors XInc and VGGXVGG from the InceptionV3 and VGG16 models, respectively, are merged in the mathematical formulation for feature fusion. The representation of this is

$$\mathbf{X} fusion = f(\mathbf{X} Inc, \mathbf{X} VGG)$$

Design of the Prediction Model: Using the fused qualities as a basis, we will create a prediction model that will allow us to determine the probability of developing AD. We will use Learning by machine mechanisms like logistic regression, and random forest classifiers is employed for this. These algorithms offer adaptability when it comes of interpretability and model complexity, which makes them excellent for jobs including binary classification. We will employ regularization approaches like L1 or L2 regularization to minimize overfitting while improving generalization performance.

Modeling the probability P(y=1|x) of an individual belonging to the AD class given the input qualities x is the theoretical framework for logistic regression. This could be written in the form:

P(y=1|x)=1+e-wTx-b1

where \mathbf{w} denotes the weight vector, and b represents the bias term.

Model Training and Evaluation: After the predictive model is constructed, we will use a systematic experimental development method to train and evaluate its performance. Using stratified sampling, we will split the dataset into training, validation, and testing sets to make sure that each subset has an equal representation of AD and non-AD cases. Following training on the training set, cross-validation methods like k-fold, and cross-validation will be used to optimize the model. Implementation on the validation set will be evaluated using metrics such as accuracy, recall, lucidity, F1-score, and area under the receiver operating characteristic curve (AUC-ROC). Lastly, a second testing set will be used to assess the trained model's broad generalization abilities to make sure it is consistent and robust.

After building the predictive model, we will train then assess its performance using a well-organized experimental development process. Using stratified sampling, we will split the dataset into training, validation, and testing sets to ensure that each subset has a balanced representation of AD and non-AD instances. After training on the training set, the model will be optimized using cross-validation techniques such as k-fold cross-validation. Metrics including as preciseness, remembering, clarity, AUC-ROC will be utilized for assessing performance on the validation set. Finally, to ensure the trained model's robustness and consistency, its generalization skills will be tested on an additional testing set.

Accuracy(ACC): =<u>Number of Correct Predictions</u> Total Number of predictions

Interpretation and Visualization: The final step of our methodology involves interpreting the learned model parameters to gain insights into the underlying mechanisms driving AD prediction. We will visualize decision range, class probabilities, and feature importance scores to aid in clinical interpretation and offer an understanding of the model's decision-making procedure.

IV. RESULT AND DISCUSSIONS

This section contains a research study of the proposed design and its impact, as well asmore details on the dataset that was used to train and validate the model.An opensource dataset gathered by Kaggle was used to test the proposed model. The dataset originated from several places, and the process of hand labeling was aided by a radiologist. where MRI stands for resonance imaging, and the images can be found in this collection. One of the four categories listed below is applied to every image in the collection: Relatively mild dementia, moderate dementia, mild dementia, or no dementia These photos are categorized, and the classifications are utilized for training analysis. The data used for training appears in one main folder, while the data used for testing is contained in the other. 1,023 of the 4,098 images in the training folder ended up being used in the validation operation. There were 1,279 pictures in the "test" folder. A 75% to 25% ratio of the entire data set was used for both the training and test cases, respectively.

Following the successful completion of our model, we present the statistical outcomes of the training and testing phases in alignment with NeuroFusion: Enhancing Alzheimer's Disease Prediction with VGGception. Upon comparison with the VGG16 architecture, our findings indicate that the Inception algorithm exhibits superior accuracy across both training and testing phases.



Consequently, we have determined that continued processing utilizing the Inception model is the most effective approach. Visual representation of these results, including model loss and AUC values, is provided in Figure. Additionally, Figure showcases the training outcomes specifically for the Inception model, depicted through model loss and model AUC graphs. Notably, as illustrated in Figure, Inception consistently outperforms its counterparts throughout both training and validation stages. Following the successful training of our proposed model with the training dataset, evaluation was conducted in the testing stage, comprising four sequential test cases.



The graph gives significant details about our model's performance throughout the training and testing phases. Its depiction of the model's performance at every stage of evaluation, with the X-AXIS labeled "Train Test" and the Y-AXIS labeled "Performance," presents a clear visual representation of our model's capabilities. The graph shows that the model always performs better on training data than on test data. This indicates that our model is effectively learning from the training data but may encounter challenges in generalizing its learnings to unseen data during the testing phase. While this discrepancy suggests the presence of potential overfitting, further investigation and refinement of the model are required to optimize its performance on unseen data. Overall, the graph serves as a valuable tool for understanding the performance dynamics of our model and guiding future efforts towards enhancing its predictive capabilities for Alzheimer's disease detection.

With the x-axis labeled "Train Test" and the y-axis labeled "Performance," it shows the model's performance over multiple evaluation stages offering a clear visual of our model's capabilities. The graph reveals a noteworthy tendency whereby the model continuously performs better on training data when compared to test data. This suggests that while our model is successfully learning from the training set, it might have difficulty applying what it learned from previously unseen data when it comes time for testing. Although this disparity points to the possibility of overfitting, more research and improvement to the model are necessary for improving the model's performance on data that was not observed. All things taken into account, the graph is an asset to analyze the dynamics of our model's performance and focusing subsequent study efforts aimed at enhancing its prognosis capacity for Alzheimer's disease detection.



An extensive overview of each algorithm's performance in forecasting Alzheimer's disease may be observed in the bar graph that shows its accuracy. With algorithms on the X-AXIS and reliability (%) on the Y-AXIS, the graph offers an easy overview of the efficiency of each algorithm Out of all the possibilities, the VGG16-17 algorithm is the most precise with a phenomenal accuracy rate of 100%. The DEEP-CNN algorithm is not far behind, showing significant effectiveness with a detection rate of 80%. The accuracy rates of other algorithms, such CNN, 3D-CNN, and SVM, which have more modest correctness rates, are likewise displayed on the graph.



V. CONCLUSION

As a consequence, the study we conducted demonstrates the potential of NeuroFusion: Optimizing Alzheimer's Disease Prediction with VGGception-17 to completely change the prediction precision of AD diagnosis. Based on exploiting the positive characteristics of VGGception-17A, our efforts provide an innovative method for enhancing AD prediction. Our model shows positive developments through comprehensive examination and validation, demonstrating its effectiveness in precisely identifying and categorizing AD cases.The incorporation of advanced deep learning techniques, including VGGception-17A, has enormous

promise to improve the exactness of identification and provide early intervention methods to benefit people with AD. To strengthen the NeuroFusion model's efficacy and acceptability for application in clinical settings, our research attempts to further develop and validate it by examining auxiliary datasets and measurement measurements. The objective of our organization is to boost patient outcomes as well as treatment through improving the capabilities of AD prediction with NeuroFusion while contributing to the current attempts to combat this awful neurodegeneration problems.

REFERENCES

[1] Nandhini I, Tejaswini Katale, Pundru ChandraShaker Reddy, S Baskar, Mudarakola Lakshmi Prasad, Nipun Sharma (2023). "An Accurate Prediction and Diagnosis Of Alzheimer's Disease Using Deep Learning. " IEEE North KarnatakaSubsection Flagship International Conference(NKCon) 59507.2023.10396132

[2] Johnson, K. A. et al. (2012). "The Alzheimer's Disease Neuroimaging Initiative: A review of papers published since its inception." Alzheimer's & Dementia, 8(1), S1-S68.

[3] Jack Jr, C. R. et al. (2010). "The Alzheimer's Disease Neuroimaging Initiative (ADNI): MRI methods." Journal of Magnetic Resonance Imaging, 27(4), 685-691.

[4] Hansson, O. et al. (2006). "Association between CSF biomarkers and incipient Alzheimer's disease in patients with mild cognitive impairment: A follow-up study." The Lancet Neurology, 5(3), 228-234.

[5] Shaw, L. M. et al. (2009). "Cerebrospinal fluid biomarker signature in Alzheimer's disease neuroimaging initiative subjects." Annals of Neurology, 65(4), 403-413.

[6] Maroco, J. et al. (2011). "Data mining methods in the prediction of Dementia: A real-data comparison of the accuracy, sensitivity and specificity of linear discriminant analysis, logistic regression, neural networks, support vector machines, classification trees and random forests." BMC Research Notes, 4(1), 1-12.

[7] Liu, S. et al. (2018). "Deep learning in medical image analysis." Advances in Experimental Medicine and Biology, 1090, 323-337.

[8] Hosseini-Asl, E. et al. (2016). "Alzheimer's disease diagnostics by a deeply supervised adaptable 3D convolutional network." arXiv preprint arXiv:1607.00556.

[9] Lambert, J. C. et al. (2013). "Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci

for Alzheimer's disease." Nature Genetics, 45(12), 1452-1458.

[10] Kunkle, B. W. et al. (2019). "Genetic metaanalysis of diagnosed Alzheimer's disease identifies new risk loci and implicates $A\beta$, tau, immunity and lipid processing." Nature Genetics, 51(3), 414-430.

[11] Ritchie, C. W. et al. (2019). "Multimodal markers of brain structure and function in the diagnosis of Alzheimer's disease." Alzheimer's Research & Therapy, 11(1), 1-13.

[12] Seyfried, N. T. et al. (2014). "A multi-network approach identifies protein-specific co-expression in asymptomatic and symptomatic Alzheimer's disease." Cell Systems, 4(1), 60-72.

[13] Ramanan, V. K. et al. (2012). "Genome-wide association study of Alzheimer's disease." Neurobiology of Aging, 33(8), 1845-e15.

[14] Tan, M. et al. (2020). "EfficientNet: Rethinking model scaling for convolutional neural networks." International Conference on Machine Learning, 97, 6105-6114.

[15] Alzheimer's Association. (2020). "2020 Alzheimer's disease facts and figures." Alzheimer's & Dementia, 16(3), 391-460.

[16] Alzheimer's Disease International. (2019). "World Alzheimer Report 2019: Attitudes to dementia." London: Alzheimer's Disease International.

[17] World Health Organization. (2019). "Risk reduction of cognitive decline and dementia: WHO guidelines."

[18] American Psychiatric Association. (2013). "Diagnostic and statistical manual of mental disorders (DSM-5®)." American Psychiatric Pub.

[19] Dubois, B. et al. (2014). "Advancing research diagnostic criteria for Alzheimer's disease: The IWG-2 criteria." The Lancet Neurology, 13(6), 614-629.

[20] McKhann, G. M. et al. (2011). "The diagnosis of dementia due to Alzheimer's disease: Recommendations from the National Institute on

Aging-Alzheimer's Association workgroups on diagnostic guidelines for Alzheimer's disease." Alzheimer's & Dementia, 7(3), 263-269.

[21] Seyfried, N. T., et al. (2014). "A multinetwork approach identifies protein-specific coexpression in asymptomatic and symptomatic Alzheimer's disease."*Cell Systems*, 4(1), 60-72.

[22] Ramanan, V. K., et al. (2012). "Genome-wide association study of Alzheimer's disease." *Neurobiology of Aging*, 33(8), 1845-e15.

[23] Tan, M., et al. (2020). "EfficientNet: Rethinking model scaling for convolutional neural networks." *International Conference on Machine Learning*, 97, 6105-6114.

[24] Alzheimer's Association. (2020). "2020 Alzheimer's disease facts and figures."*Alzheimer's & Dementia*, 16(3), 391-460.

[25] Alzheimer's Disease International. (2019)."World Alzheimer Report 2019: Attitudes to dementia."London: Alzheimer's Disease International.